Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6663	**SOX10**	**transcription factor SOX-10**	37	548	30	**2.1**	**2E-16**	**0.6**	**2E-16**	**2.1**	**2E-16**	**0.7**	**3E-06**	1.4	**2E-16**	Transcription factor activity	Nucleus	Transcription factor
476	**ATP1A1**	**sodium/potassium-transporting ATPase subunit alpha-1 isoform a**	38	247	38	**1.6**	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	0.9	**2E-16**	1.1	**4E-11**	ATPase activity	Plasma membrane	ATPase
1308	**COL17A1**	**collagen alpha-1(XVII) chain**	32	236	32	**1.7**	**2E-16**	1.0	3E-01	0.8	**1E-05**	**0.5**	**2E-10**	1.0	**2E-03**	Structural molecule activity	Plasma membrane	Anchor protein
3009	**HIST1H1B**	**histone H1.5**	14	197	11	**1.8**	**2E-16**	1.1	**2E-16**	**1.7**	**7E-07**	1.0	**5E-12**	1.0	2E-01	DNA binding	Nucleus	DNA binding protein
8349	**HIST2H2BE**	**histone H2B type 2-E**	12	409	4	**1.5**	**2E-16**	1.0	**2E-16**	1.4	7E-01	1.3	**9E-15**	1.0	**1E-07**	DNA binding	Nucleus	DNA binding protein
9221	**NOLC1**	**nucleolar and coiled-body phosphoprotein 1 isoform 1**	21	144	21	**1.6**	**2E-16**	1.0	**2E-16**	**1.7**	**1E-07**	0.9	**4E-10**	1.0	8E-01	Transcription factor activity	Nucleolus	Transcription factor
6273	**S100A2**	**protein S100-A2**	6	548	6	**1.5**	**2E-16**	0.9	**2E-16**	**1.5**	**6E-03**	0.8	**3E-06**	1.0	**1E-04**	Calcium ion binding	Nucleus	Calcium binding protein
1956	**EGFR**	**epidermal growth factor receptor isoform a**	30	168	29	**1.7**	**1E-15**	0.9	**2E-16**	1.0	1E-01	**0.5**	**2E-10**	1.0	**5E-04**	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane;Nucleus;Cytoplasm	Receptor tyrosine kinase
3688	**ITGB1**	**integrin beta-1 isoform 1A**	24	177	24	**2.0**	**1E-14**	0.7	**9E-15**	1.3	**2E-07**	**0.7**	**8E-05**	1.1	**9E-09**	Receptor activity	Plasma membrane	Cell surface receptor
5757	**PTMA**	**prothymosin alpha isoform 1**	4	128	4	**1.5**	**2E-14**	0.9	**2E-15**	1.3	1E+00	**0.6**	**2E-07**	1.0	6E-02	Molecular function unknown	Nucleus	Unclassified
2512	**FTL**	**ferritin light chain**	8	99	8	**1.9**	**4E-14**	**0.5**	**2E-14**	**2.3**	**1E-10**	1.3	**1E-14**	1.1	**2E-03**	Storage protein	Cytoplasm	Storage protein
3007	**HIST1H1D**	**histone H1.3**	13	162	5	**2.9**	**4E-14**	1.2	**3E-14**	**2.2**	**2E-06**	1.0	**2E-09**	1.1	**1E-03**	DNA binding	Nucleus	DNA binding protein
6520	**SLC3A2**	**4F2 cell-surface antigen heavy chain isoform b**	20	241	20	**1.9**	**5E-14**	0.9	**4E-13**	1.3	4E-01	**0.6**	**3E-05**	1.0	6E-01	Auxiliary transport protein activity	Plasma membrane;Nucleus;Cytoplasm	Membrane transport protein
10949	**HNRNPA0**	**heterogeneous nuclear ribonucleoprotein A0**	8	127	6	**1.6**	**2E-12**	1.0	**2E-09**	1.4	**1E-02**	0.7	4E-01	0.9	7E-02	RNA binding	Nucleus	Ribonucleoprotein
9188	**DDX21**	**nucleolar RNA helicase 2 isoform 1**	20	106	18	**1.5**	**4E-12**	0.7	**1E-10**	1.1	**8E-11**	**0.6**	**2E-09**	1.0	1E+00	ATPase activity	Nucleolus	ATPase
5106	**PCK2**	**phosphoenolpyruvate carboxykinase [GTP], mitochondrial isoform 1**	19	133	19	**1.6**	**4E-12**	1.1	**1E-12**	1.3	**4E-06**	1.3	**4E-14**	1.0	9E-02	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
309	**ANXA6**	**annexin A6 isoform 1**	24	121	24	**1.7**	**8E-12**	1.2	**2E-12**	**1.8**	**1E-09**	1.3	**1E-12**	1.3	**1E-07**	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein
6513	**SLC2A1**	**solute carrier family 2, facilitated glucose transporter member 1**	8	93	8	**1.5**	**1E-11**	1.0	**2E-12**	1.2	**9E-03**	0.9	**2E-06**	1.1	**4E-02**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
5654	**HTRA1**	**serine protease HTRA1**	15	113	15	**2.3**	**2E-11**	**2.0**	**1E-12**	**2.2**	**3E-10**	**2.3**	**1E-11**	**1.5**	**6E-11**	Serine-type peptidase activity	Extracellular	Serine protease
3875	**KRT18**	**keratin, type I cytoskeletal 18**	26	784	24	**1.6**	**4E-11**	1.2	**2E-16**	1.4	**7E-08**	**1.9**	**2E-16**	1.4	**1E-07**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
3675	**ITGA3**	**integrin alpha-3 isoform a**	15	109	15	**2.0**	**7E-11**	0.8	**6E-12**	1.3	**3E-08**	**0.4**	**6E-09**	1.1	**3E-03**	Receptor activity	Plasma membrane	Cell surface receptor
26156	**RSL1D1**	**ribosomal L1 domain-containing protein 1**	15	106	15	**1.9**	**9E-11**	0.8	**8E-11**	1.2	**2E-03**	**0.6**	**5E-07**	1.1	**3E-03**	Molecular function unknown	Nucleolus	Unclassified
29968	**PSAT1**	**phosphoserine aminotransferase isoform 1**	13	94	13	**1.6**	**2E-10**	**0.6**	**2E-10**	1.1	**3E-09**	**0.7**	**2E-03**	0.9	**3E-05**	Transaminase activity	Cytosol	Enzyme: Aminotransferase
440	**ASNS**	**asparagine synthetase [glutamine-hydrolyzing] isoform a*gi|168229250|ref|NP_001664.3|asparagine synthetase [glutamine-hydrolyzing] isoform a*gi|168229252|ref|NP_899199.2|asparagine synthetase [glutamine-hydrolyzing] isoform a**	16	108	16	**1.7**	**2E-10**	**0.4**	**2E-09**	0.8	**2E-10**	**0.2**	**5E-09**	0.8	**1E-08**	Ligase activity	Cytoplasm	Enzyme: Synthase
3159	**HMGA1**	**high mobility group protein HMG-I/HMG-Y isoform a**	7	62	7	**1.6**	**7E-10**	1.0	**2E-10**	**2.0**	**3E-03**	**1.7**	**3E-09**	1.1	**1E-03**	DNA binding	Nucleus	DNA binding protein
55660;	**PRPF40A**	**pre-mRNA-processing factor 40 homolog A**	14	31	2	**2.0**	**7E-10**	**1.5**	**2E-08**	**2.3**	**7E-05**	**1.8**	**2E-08**	1.1	5E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
483	**ATP1B3**	**sodium/potassium-transporting ATPase subunit beta-3**	9	71	9	**1.5**	**1E-09**	1.2	**2E-10**	1.1	**2E-08**	0.8	**1E-03**	1.0	3E-01	ATPase activity	Plasma membrane	ATPase
2495	**FTH1**	**ferritin heavy chain**	10	109	10	**2.7**	**2E-09**	**0.7**	**4E-10**	**2.7**	**3E-10**	1.4	**2E-10**	1.1	**1E-03**	Storage protein	Cytoplasm	Storage protein
162394	**SLFN5**	**schlafen family member 5**	14	48	13	**1.7**	**2E-09**	0.7	**5E-09**	1.0	**4E-06**	**0.5**	**1E-06**	0.9	**9E-04**	Molecular function unknown	-	Unclassified
6510	**SLC1A5**	**neutral amino acid transporter B(0) isoform 1**	12	104	12	**1.9**	**3E-09**	0.7	**9E-10**	1.3	**3E-07**	**0.5**	**5E-07**	1.1	**9E-06**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
4323	**MMP14**	**matrix metalloproteinase-14 preproprotein**	11	57	11	**1.5**	**4E-09**	**0.7**	**1E-08**	1.3	**2E-04**	0.7	8E-01	1.3	**1E-08**	Metallopeptidase activity	Extracellular	Metallo protease
27250	**PDCD4**	**programmed cell death protein 4 isoform 1**	13	68	13	**1.6**	**1E-08**	1.1	**4E-10**	1.3	**2E-06**	0.9	**1E-06**	1.0	9E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
11328	**FKBP9**	**peptidyl-prolyl cis-trans isomerase FKBP9 isoform 1**	13	76	13	**1.6**	**1E-08**	0.9	**3E-10**	1.1	6E-01	0.8	2E-01	0.9	2E-01	Chaperone activity	Endoplasmic reticulum	Chaperone
4678	**NASP**	**nuclear autoantigenic sperm protein isoform 2**	18	80	18	**1.5**	**1E-08**	0.8	**4E-08**	1.3	**6E-03**	**0.5**	**5E-06**	1.0	4E-01	Histone binding	Nucleus;Cytoplasm	Cell cycle control protein
8140	**SLC7A5**	**large neutral amino acids transporter small subunit 1**	7	57	7	**2.1**	**3E-08**	0.9	**2E-08**	1.3	6E-01	**0.5**	**1E-04**	1.0	4E-01	Transporter activity	Plasma membrane	Transport/cargo protein
6386	**SDCBP**	**syntenin-1 isoform 1**	6	26	6	**1.6**	**4E-08**	**0.4**	**1E-07**	1.0	**4E-06**	**0.7**	**8E-03**	1.0	2E-01	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
5519	PPP2R1B	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform b	10	73	3	**1.6**	**7E-08**	0.9	**1E-09**	1.2	4E-01	0.9	**1E-06**	0.9	8E-02	Protein serine/threonine phosphatase activity;Enzyme regulator activity	Cytoplasm	Regulatory/other subunit;Serine/threonine phosphatase
4175	MCM6	DNA replication licensing factor MCM6	10	45	10	**2.2**	**1E-07**	0.8	**5E-08**	**1.5**	**1E-03**	**0.5**	**9E-05**	1.0	3E-01	Protein binding	Nucleus	Cell cycle control protein
1829	DSG2	desmoglein-2 preproprotein	11	44	11	**1.5**	**1E-07**	0.7	**4E-07**	1.0	**5E-05**	**0.6**	**1E-03**	1.0	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
7345	UCHL1	ubiquitin carboxyl-terminal hydrolase isozyme L1	8	46	8	**1.6**	**2E-07**	0.8	**2E-07**	**1.5**	**5E-04**	1.3	**2E-08**	1.1	**2E-05**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
290	ANPEP	PREDICTED: aminopeptidase N isoform X1	16	62	16	**2.8**	**2E-07**	0.8	**2E-07**	**1.9**	**5E-03**	1.2	**4E-08**	**1.7**	**2E-07**	Metallopeptidase activity	Plasma membrane	Metallo protease
10885	WDR3	WD repeat-containing protein 3	12	56	12	**1.5**	**2E-07**	0.8	**1E-07**	1.2	**4E-02**	**0.6**	**2E-04**	1.0	**5E-02**	Molecular function unknown	Nucleus	Unclassified
5754	PTK7	inactive tyrosine-protein kinase 7 isoform e	11	43	11	**1.6**	**3E-07**	1.0	**7E-06**	1.0	2E-01	**0.5**	**4E-05**	1.0	6E-01	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase
3925	STMN1	stathmin isoform b	9	68	9	**1.6**	**3E-07**	0.7	**2E-07**	**1.6**	**4E-05**	**0.7**	**2E-03**	1.1	**4E-03**	Structural molecule activity;Signal transducer activity	Cytoplasm	Structural protein
134430	WDR36	WD repeat-containing protein 36	12	49	12	**1.5**	**7E-07**	0.9	**2E-08**	1.3	2E-01	0.7	1E+00	1.1	**4E-02**	Molecular function unknown	Nucleolus	Unclassified
1294	COL7A1	PREDICTED: collagen alpha-1(VII) chain isoform X1	9	37	9	**1.5**	**7E-07**	1.0	**3E-07**	1.2	**3E-02**	0.8	**2E-02**	1.0	1E-01	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
56945	MRPS22	28S ribosomal protein S22, mitochondrial	13	69	13	**1.5**	**1E-06**	1.1	**2E-07**	1.4	**2E-06**	0.9	**2E-08**	0.9	9E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
4719	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 5	16	69	16	**1.6**	**1E-06**	0.8	**2E-08**	1.1	**4E-02**	0.8	5E-02	1.0	9E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
1329	COX5B	cytochrome c oxidase subunit 5B, mitochondrial	5	30	5	**1.8**	**1E-06**	1.0	**3E-07**	1.4	**5E-05**	1.0	**1E-05**	1.1	**2E-03**	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
6917	TCEA1	transcription elongation factor A protein 1 isoform 1	9	43	9	**1.6**	**2E-06**	0.8	**7E-07**	1.4	**2E-03**	0.8	7E-01	0.9	2E-01	Transcription regulator activity	Nucleus;Cytoplasm	Transcription factor
3008	HIST1H1E	histone H1.4	13	178	4	**1.9**	**2E-06**	1.2	**3E-06**	**1.6**	**7E-05**	0.9	**1E-02**	0.9	**2E-03**	DNA binding	Nucleus	DNA binding protein
3146	HMGB1	PREDICTED: high mobility group protein B1 isoform X1	10	86	7	**1.5**	**5E-06**	1.0	**1E-06**	1.6	2E-01	0.9	**2E-02**	1.0	7E-01	DNA binding	Nucleus	DNA binding protein
3936	LCP1	plastin-2	19	185	11	**1.5**	**5E-06**	**1.5**	**1E-08**	1.3	1E-01	1.3	**3E-13**	1.1	2E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
3673	ITGA2	integrin alpha-2	22	56	22	**1.6**	**6E-06**	**0.7**	**3E-06**	**1.6**	**8E-05**	1.0	**6E-08**	1.1	**1E-03**	Receptor activity	Plasma membrane	Cell surface receptor
55131	RBM28	RNA-binding protein 28 isoform 1	8	36	8	**1.5**	**6E-06**	0.8	**6E-06**	1.3	**2E-02**	**0.6**	**4E-04**	1.0	5E-01	RNA binding	Nucleolus	RNA binding protein
123	PLIN2	perilipin-2	6	28	6	**1.9**	**7E-06**	0.9	**3E-06**	2.2	6E-01	**2.2**	**3E-06**	0.8	**9E-03**	Lipid transporter activity	Endoplasmic reticulum	Storage protein
79050	NOC4L	nucleolar complex protein 4 homolog	7	25	7	**1.6**	**1E-05**	0.9	**4E-05**	1.2	7E-01	**0.6**	**4E-02**	1.1	**4E-02**	Molecular function unknown	-	Unclassified
3930	LBR	lamin-B receptor	6	21	6	**1.6**	**1E-05**	0.9	**3E-06**	1.5	3E-01	1.1	**7E-06**	1.1	3E-01	Chromatin binding	Nuclear membrane	Integral membrane protein
9497	SLC4A7	sodium bicarbonate cotransporter 3 isoform b	10	47	10	**1.5**	**1E-05**	1.0	**3E-06**	1.3	**4E-03**	0.9	**4E-04**	1.0	9E-01	Transporter activity	Plasma membrane	Transport/cargo protein
1340	COX6B1	cytochrome c oxidase subunit 6B1	5	28	5	**1.5**	**1E-05**	0.9	**6E-06**	1.5	5E-01	0.9	**5E-03**	1.0	4E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
23646	PLD3	PREDICTED: phospholipase D3 isoform X1	5	24	5	**1.6**	**2E-05**	0.9	**6E-06**	1.1	1E+00	0.8	**5E-02**	1.0	7E-01	Phospholipase activity	Endoplasmic reticulum;Golgi apparatus	Enzyme: Phospholipase
4085	MAD2L1	mitotic spindle assembly checkpoint protein MAD2A	4	22	4	**1.5**	**2E-05**	**0.7**	**1E-06**	1.2	**4E-03**	**0.4**	**6E-03**	0.9	8E-02	Protein binding	Nucleus	Cell cycle control protein
28987	NOB1	RNA-binding protein NOB1	4	18	4	**1.8**	**3E-05**	0.7	**2E-05**	1.3	**1E-02**	**0.6**	**3E-02**	1.0	7E-01	Ribonuclease activity	-	Ribonuclease
5111	PCNA	proliferating cell nuclear antigen	12	61	12	**1.7**	**3E-05**	**0.6**	**2E-06**	1.0	**1E-04**	**0.5**	**8E-04**	0.8	**1E-03**	DNA binding	Nucleus	Cell cycle control protein
4173	MCM4	DNA replication licensing factor MCM4*gi|33469919|ref|NP_005905.2| DNA replication licensing factor MCM4	6	21	6	**2.2**	**4E-05**	0.9	**6E-05**	1.6	3E-01	0.7	3E-01	1.0	1E+00	DNA binding	Nucleus	DNA binding protein
9790	BMS1	ribosome biogenesis protein BMS1 homolog	8	21	8	**1.6**	**5E-05**	0.9	**8E-04**	1.2	7E-01	0.8	3E-01	1.0	6E-01	Molecular function unknown	Nucleolus	Unclassified
4513	COX2	cytochrome c oxidase subunit II (mitochondrion)	3	11	3	**1.8**	**6E-05**	1.0	**5E-05**	1.4	**5E-03**	1.2	**8E-06**	1.1	**3E-03**	#N/A	#N/A	#N/A
94239	H2AFV	histone H2A.V isoform 1	4	71	2	**1.6**	**7E-05**	1.1	**5E-06**	1.9	1E-01	**1.6**	**1E-04**	1.0	4E-01	DNA binding	Nucleus	DNA binding protein
6319	SCD	acyl-CoA desaturase	5	22	4	**2.0**	**8E-05**	1.1	**3E-05**	**2.2**	**2E-02**	0.7	7E-01	1.0	7E-01	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase
1327	COX4I1	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	6	42	6	**1.6**	**1E-04**	1.0	**6E-05**	**1.5**	**8E-04**	1.1	**3E-05**	1.0	5E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
79081; 102288414	C11orf48; LBHD1; LOC102288414; C11orf98	uncharacterized protein LOC102288414	4	24	4	**1.6**	**1E-04**	0.8	**3E-05**	1.4	7E-02	**0.6**	**3E-04**	0.9	6E-02	#N/A	#N/A	#N/A
8626	TP63	tumor protein 63 isoform 1	5	21	5	**1.7**	**1E-04**	0.8	**1E-05**	1.4	**2E-02**	0.6	5E-02	0.8	**2E-02**	Transcription factor activity	Nucleus	Transcription factor
3014	H2AFX	histone H2AX	7	143	2	**1.6**	**1E-04**	1.2	**7E-05**	1.7	6E-01	**2.0**	**1E-04**	1.1	**4E-03**	DNA binding	Nucleus	DNA binding protein
23246	BOP1	ribosome biogenesis protein BOP1	7	29	7	**1.6**	**1E-04**	0.8	**2E-03**	1.3	1E-01	0.7	6E-01	1.1	1E-01	Molecular function unknown	Nucleolus	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
51491	**NOP16**	**nucleolar protein 16 isoform 3**	6	24	6	**1.5**	**1E-04**	0.9	**3E-05**	1.3	2E-01	**0.6**	**4E-04**	0.9	8E-01	Molecular function unknown	Nucleolus	Unclassified
1522	**CTSZ**	**cathepsin Z preproprotein**	3	14	3	**1.6**	**2E-04**	1.0	**2E-04**	1.8	8E-02	1.0	**2E-04**	1.1	3E-01	Cysteine-type peptidase activity	Lysosome	Cysteine protease
4495	**MT1G**	**metallothionein-1G isoform 2**	3	39	3	**1.5**	**2E-04**	1.2	**2E-04**	1.4	**6E-04**	0.7	1E-01	1.2	**7E-03**	Molecular function unknown	-	Unclassified
3148	**HMGB2**	**high mobility group protein B2**	8	38	6	**1.8**	**2E-04**	1.0	**2E-04**	1.8	2E-01	0.8	8E-01	1.0	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
8340	**HIST1H2BL**	**histone H2B type 1-L**	11	422	2	**1.6**	**2E-04**	1.0	**2E-05**	**1.5**	**4E-02**	1.3	**1E-04**	1.0	4E-01	DNA binding	Nucleus	DNA binding protein
9168	**TMSB10**	**thymosin beta-10**	5	82	3	**1.5**	**2E-04**	**0.3**	**2E-04**	**1.6**	**6E-05**	0.7	7E-02	0.9	1E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
26574	**AATF**	**protein AATF**	6	19	6	**1.6**	**2E-04**	1.2	**2E-04**	**1.5**	**1E-03**	0.9	3E-01	1.2	**5E-04**	Transcription factor activity	Nucleus	Transcription factor
4171	**MCM2**	**DNA replication licensing factor MCM2**	10	32	10	**2.1**	**3E-04**	0.9	**3E-04**	1.5	4E-01	**0.5**	**5E-03**	1.0	8E-01	DNA binding	Nucleus	DNA binding protein
3006	**HIST1H1C**	**histone H1.2**	11	168	3	**2.4**	**3E-04**	1.3	**3E-04**	**2.0**	**1E-02**	**1.6**	**1E-03**	1.0	1E+00	DNA binding	Nucleus	DNA binding protein
56902	**PNO1**	**RNA-binding protein PNO1**	6	29	6	**1.8**	**3E-04**	0.9	**2E-03**	1.1	8E-01	0.9	5E-01	1.1	**1E-02**	Molecular function unknown	-	Unclassified
92906	**HNRNPLL; HNRPLL**	**heterogeneous nuclear ribonucleoprotein L-like isoform 1**	4	33	3	**1.5**	**3E-04**	0.9	**5E-06**	1.4	9E-02	1.1	**2E-04**	1.0	3E-01	#N/A	#N/A	#N/A
4724	**NDUFS4**	**NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial**	1	12	1	**1.7**	**4E-04**	0.9	**3E-04**	1.2	8E-01	0.7	7E-01	1.2	**7E-03**	Catalytic activity	Mitochondrion	Enzyme: Reductase
949	**SCARB1**	**scavenger receptor class B member 1 isoform 1**	7	30	7	**1.6**	**5E-04**	**0.6**	**5E-05**	1.1	**5E-03**	**0.6**	**3E-02**	1.2	**5E-02**	Receptor activity	Plasma membrane	Cell surface receptor
7528	**YY1**	**transcriptional repressor protein YY1**	2	10	2	**1.5**	**6E-04**	0.9	**3E-03**	1.4	7E-01	0.8	2E-01	1.1	3E-01	Transcription factor activity	Nucleus	Transcription factor
5985	**RFC5**	**PREDICTED: replication factor C subunit 5 isoform X1**	2	10	2	**1.5**	**7E-04**	0.9	**2E-03**	1.3	6E-01	0.6	3E-01	1.0	6E-01	DNA binding	Nucleus	DNA binding protein
84128	**WDR75**	**WD repeat-containing protein 75 isoform 1**	7	23	7	**1.6**	**7E-04**	1.0	**4E-04**	1.3	2E-01	0.8	2E-01	1.0	6E-01	Molecular function unknown	-	Unclassified
7169	**TPM2**	**tropomyosin beta chain isoform Tpm2.1sm/cy**	19	257	6	**2.0**	**9E-04**	1.0	**2E-06**	1.3	3E-01	0.5	8E-01	1.5	9E-01	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
51752	**ERAP1**	**endoplasmic reticulum aminopeptidase 1 isoform b**	2	12	2	**1.6**	**1E-03**	0.7	**2E-02**	1.0	1E+00	**0.5**	**7E-03**	1.0	8E-01	Aminopeptidase activity	Endoplasmic reticulum	Aminopeptidase
54407	**SLC38A2**	**sodium-coupled neutral amino acid transporter 2**	3	16	3	**2.0**	**1E-03**	**0.7**	**1E-03**	0.9	**2E-02**	1.0	**9E-03**	1.3	**6E-04**	Transporter activity	Plasma membrane	Transport/cargo protein
10988	**METAP2**	**methionine aminopeptidase 2**	11	36	11	**1.5**	**1E-03**	1.1	**8E-04**	1.4	1E-01	0.9	4E-01	0.9	2E-01	Translation regulator activity	-	Translation regulatory protein
83666	**PARP9**	**PREDICTED: poly [ADP-ribose] polymerase 9 isoform X1**	7	19	7	**1.6**	**1E-03**	0.9	2E-01	0.8	7E-01	0.5	2E-01	1.0	9E-01	Molecular function unknown	Nucleus	Unclassified
1374	**CPT1A**	**carnitine O-palmitoyltransferase 1, liver isoform isoform 1**	7	22	7	**1.8**	**1E-03**	1.0	**1E-03**	**2.1**	**2E-02**	**2.8**	**5E-03**	1.1	**5E-02**	Palmitoyltransferase activity	Mitochondrial membrane	Enzyme: Palmitoyltransferase
22822	**PHLDA1**	**pleckstrin homology-like domain family A member 1**	3	20	3	**1.6**	**1E-03**	0.8	**5E-04**	1.1	6E-02	0.7	1E-01	1.1	9E-02	Transcription factor activity	Cytoplasm	Transcription factor
1347	**COX7A2**	**PREDICTED: cytochrome c oxidase subunit 7A2, mitochondrial isoform X1**	2	12	2	**1.7**	**1E-03**	1.1	**4E-03**	1.4	**5E-03**	1.2	**2E-03**	1.3	5E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
10410	**IFITM3**	**interferon-induced transmembrane protein 3**	2	10	2	**1.7**	**1E-03**	0.5	1E-01	**0.6**	**1E-02**	**0.3**	**3E-04**	1.0	7E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
23028	**KDM1A**	**lysine-specific histone demethylase 1A isoform a**	6	26	6	**1.6**	**1E-03**	1.2	**1E-03**	**1.6**	**1E-02**	1.1	**2E-04**	0.9	7E-02	Transcription regulator activity;Deacetylase activity	Nucleus;Cytoplasm	Enzyme: Deacetylase;Transcription regulatory protein
9532	**BAG2**	**BAG family molecular chaperone regulator 2**	4	14	4	**1.6**	**2E-03**	**0.7**	**2E-03**	1.2	**2E-02**	0.6	2E-01	0.9	8E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
27340	**UTP20**	**small subunit processome component 20 homolog**	4	7	4	**1.6**	**2E-03**	0.9	**2E-02**	1.3	8E-01	0.9	7E-01	1.1	4E-01	Molecular function unknown	Nucleolus	Unclassified
84295	**PHF6**	**PHD finger protein 6 isoform 1**	4	16	4	**1.6**	**2E-03**	0.9	**7E-04**	1.3	8E-01	0.7	7E-01	1.0	4E-01	Transcription regulator activity	Nucleolus;Nucleus;Cytoplasm	Transcription regulatory protein
771	**CA12**	**carbonic anhydrase 12 isoform 1**	5	18	5	**1.6**	**2E-03**	1.0	**3E-04**	1.2	**1E-02**	**0.4**	**2E-02**	0.9	1E-01	Catalytic activity	Plasma membrane	Enzyme: Carbonic anhydrase
29796	**UQCR10**	**cytochrome b-c1 complex subunit 9 isoform a**	3	15	3	**1.7**	**2E-03**	**1.6**	**6E-04**	**2.0**	**2E-03**	**1.9**	**8E-04**	**1.5**	**3E-03**	Oxidoreductase activity	Mitochondrial membrane	Enzyme: Oxidoreductase
983	**CDK1**	**PREDICTED: cyclin-dependent kinase 1 isoform X1**	5	32	4	**2.4**	**2E-03**	**0.6**	**6E-04**	1.4	**4E-02**	0.4	6E-02	0.8	1E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
29889	**GNL2**	**nucleolar GTP-binding protein 2**	2	10	2	**1.6**	**2E-03**	**0.7**	**6E-03**	1.2	**3E-03**	**0.5**	**1E-03**	0.9	3E-01	GTPase activity	Nucleolus	GTPase
23175	**LPIN1**	**phosphatidate phosphatase LPIN1 isoform 3**	10	31	10	**1.6**	**2E-03**	0.8	**9E-04**	1.2	8E-02	0.9	**9E-04**	1.1	2E-01	Molecular function unknown	Nucleus	Unclassified
5935	**RBM3**	**RNA-binding protein 3**	1	6	1	**2.4**	**3E-03**	0.8	**6E-03**	1.5	8E-01	0.5	2E-01	0.8	7E-02	RNA binding	Nucleolus	RNA binding protein
705;	**BYSL**	**bystin**	5	9	5	**1.7**	**3E-03**	0.9	**2E-03**	1.2	7E-01	**0.6**	**4E-02**	1.1	**4E-02**	Cell adhesion molecule activity	Cytoplasm	Adhesion molecule
11168	**PSIP1**	**PC4 and SFRS1-interacting protein isoform 2**	5	22	4	**2.1**	**3E-03**	0.8	**1E-03**	1.9	7E-01	0.8	4E-01	0.9	4E-01	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
81611	ANP32E	acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 1	4	23	4	**1.6**	**3E-03**	1.0	**2E-03**	1.5	1E-01	1.0	**1E-03**	1.0	3E-01	Molecular function unknown	Nucleus	Unclassified
1350	COX7C	cytochrome c oxidase subunit 7C, mitochondrial	1	10	1	**1.8**	**4E-03**	0.9	**1E-03**	1.4	2E-01	0.8	**5E-02**	1.0	**5E-02**	Molecular function unknown	Mitochondrion	Regulatory/other subunit
10813	UTP14A	U3 small nucleolar RNA-associated protein 14 homolog A isoform 1	6	22	6	**1.7**	**4E-03**	0.9	**2E-02**	1.3	9E-01	0.7	3E-01	1.0	5E-01	Molecular function unknown	Ribosome	Unclassified
4172	MCM3	DNA replication licensing factor MCM3 isoform 1	6	21	6	**2.1**	**4E-03**	0.8	**1E-03**	1.4	1E-01	**0.4**	**3E-02**	1.0	9E-01	DNA binding	Nucleus	DNA binding protein
9123	SLC16A3	monocarboxylate transporter 4	7	30	7	**1.6**	**4E-03**	0.7	**1E-03**	1.4	2E-01	0.8	5E-01	1.3	**8E-05**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
4131	MAP1B	microtubule-associated protein 1B	8	25	8	**1.5**	**4E-03**	0.8	**6E-03**	1.2	9E-02	0.8	4E-01	1.2	5E-02	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
1345	COX6C	cytochrome c oxidase subunit 6C proprotein	3	13	3	**1.8**	**4E-03**	1.1	**7E-03**	1.4	**1E-02**	1.1	**6E-03**	1.2	**1E-03**	Oxidoreductase activity	Mitochondrion	Regulatory/other subunit
3705	ITPK1	inositol-tetrakisphosphate 1-kinase isoform a	5	22	5	**1.5**	**5E-03**	0.8	**2E-03**	1.7	2E-01	1.0	**6E-04**	1.0	2E-01	Catalytic activity	-	Enzyme: Phosphotransferase
54534	MRPL50	39S ribosomal protein L50, mitochondrial	3	20	3	**1.6**	**5E-03**	1.1	**2E-03**	1.3	7E-02	1.0	**7E-04**	1.0	8E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
90121	TSR2	pre-rRNA-processing protein TSR2 homolog	2	9	2	**1.6**	**6E-03**	0.8	**1E-02**	1.3	3E-01	0.7	5E-01	0.9	1E-01	Molecular function unknown	-	Unclassified
26037	SIPA1L1	PREDICTED: signal-induced proliferation-associated 1-like protein 1 isoform X2	3	10	3	**1.5**	**6E-03**	1.0	**5E-03**	1.5	6E-01	**1.5**	**1E-02**	1.6	1E-01	GTPase activator activity	Nucleus	GTPase activating protein
1643	DDB2	DNA damage-binding protein 2	7	20	7	**1.7**	**6E-03**	1.3	**4E-03**	**1.6**	**2E-02**	0.9	**4E-02**	1.0	8E-01	DNA binding	Nucleus;Cytoplasm	DNA binding protein
4697	NDUFA4	cytochrome c oxidase subunit NDUFA4	2	12	2	**2.4**	**6E-03**	0.8	**8E-03**	2.0	1E-01	1.0	**5E-02**	0.9	9E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
92856	IMP4	U3 small nucleolar ribonucleoprotein protein IMP4	2	8	2	**1.6**	**6E-03**	0.9	**8E-03**	1.3	2E-01	**0.6**	**1E-02**	1.0	3E-01	Ribonucleoprotein	Nucleolus	RNA binding protein
7508	XPC	DNA repair protein complementing XP-C cells	5	11	5	**1.6**	**6E-03**	0.8	**1E-02**	1.3	5E-01	0.8	5E-01	1.0	9E-01	DNA repair protein	Nucleus	DNA binding protein
4729	NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	4	18	4	**1.7**	**6E-03**	0.9	8E-02	1.0	6E-01	0.8	9E-01	1.0	2E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
51013	EXOSC1	exosome complex component CSL4	2	10	2	**1.7**	**7E-03**	1.1	**1E-03**	1.9	2E-01	1.0	**4E-02**	1.3	5E-01	Ribonuclease activity	Nucleus	Ribonuclease
57129	MRPL47	39S ribosomal protein L47, mitochondrial isoform a	3	9	3	**1.5**	**7E-03**	1.2	**3E-03**	**1.5**	**3E-02**	1.2	**5E-03**	1.2	8E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
51373	MRPS17	28S ribosomal protein S17, mitochondrial	2	12	2	**1.6**	**7E-03**	1.1	**1E-02**	**1.6**	**9E-03**	1.0	**1E-02**	0.9	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
90480	GADD45GIP1	growth arrest and DNA damage-inducible proteins-interacting protein 1	3	9	3	**1.6**	**7E-03**	1.3	**1E-02**	1.4	**2E-02**	1.0	**3E-02**	1.1	7E-01	Protein binding	Nucleus	Cell cycle control protein
9918	NCAPD2	condensin complex subunit 1	11	36	11	**1.7**	**8E-03**	0.8	**1E-03**	1.3	1E-01	0.6	3E-01	1.1	6E-02	DNA binding	Cytoplasm	DNA binding protein
4701	NDUFA7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	1	6	1	**2.0**	**9E-03**	0.9	**4E-03**	1.1	7E-01	0.6	3E-01	1.2	1E-01	Molecular function unknown	Mitochondrion	Unclassified
28958	COA3	cytochrome c oxidase assembly factor 3 homolog, mitochondrial	3	16	3	**1.8**	**1E-02**	0.9	**1E-02**	1.3	8E-01	1.0	**4E-03**	1.0	3E-01	#N/A	#N/A	#N/A
4726	NDUFS6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	1	6	1	**1.6**	**1E-02**	0.8	**2E-02**	1.1	2E-01	**0.6**	**4E-02**	1.0	3E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
51406	NOL7	nucleolar protein 7	4	14	4	**1.5**	**1E-02**	1.0	**4E-03**	1.3	4E-01	0.6	6E-01	1.1	2E-01	Molecular function unknown	Nucleolus	Unclassified
114823	LENG8	PREDICTED: leukocyte receptor cluster member 8 isoform X5	2	8	2	**1.7**	**1E-02**	1.1	**4E-03**	1.5	2E-01	1.3	**2E-02**	1.3	2E-01	Molecular function unknown	-	Unclassified
93436	ARMC6	armadillo repeat-containing protein 6 isoform 1	5	18	5	**1.5**	**1E-02**	0.9	**7E-03**	1.2	6E-01	0.7	8E-01	1.0	1E-01	Molecular function unknown	-	Unclassified
84271	POLDIP3	polymerase delta-interacting protein 3 isoform 3	4	10	4	**1.7**	**1E-02**	0.9	**7E-03**	1.3	8E-01	1.0	5E-01	1.1	2E-01	RNA binding	Nucleolus	RNA binding protein
81539	SLC38A1	sodium-coupled neutral amino acid transporter 1 isoform 2	3	16	3	**1.5**	**1E-02**	0.7	**1E-02**	1.0	**4E-02**	0.8	5E-01	1.2	5E-02	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
64151	NCAPG	condensin complex subunit 3	6	19	6	**1.7**	**1E-02**	**0.7**	**9E-03**	1.4	1E-01	0.4	8E-02	1.1	**3E-02**	DNA binding	Nucleus	DNA binding protein
10653	SPINT2	kunitz-type protease inhibitor 2 isoform a	3	22	3	**1.5**	**1E-02**	**0.7**	**9E-03**	0.9	**2E-02**	0.7	4E-01	1.1	**3E-02**	Protease inhibitor activity	Plasma membrane	Protease inhibitor
4695	NDUFA2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 isoform 1	1	6	1	**1.7**	**1E-02**	0.8	8E-02	1.1	4E-01	0.7	3E-01	1.1	8E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
5822	PWP2	periodic tryptophan protein 2 homolog	8	26	8	**1.5**	**1E-02**	0.9	**9E-03**	1.3	4E-01	0.6	1E-01	1.0	6E-02	Signal transducer activity	Nucleolus	Cell cycle control protein
7443	VRK1	serine/threonine-protein kinase VRK1	8	28	8	**1.8**	**1E-02**	1.0	**4E-03**	1.5	2E-01	0.8	1E+00	1.1	7E-02	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8733	GPAA1	glycosylphosphatidylinositol anchor attachment 1 protein	3	14	3	**1.6**	**1E-02**	1.3	**7E-03**	1.2	**5E-03**	1.2	**9E-04**	1.3	1E-01	Cytoskeletal anchoring activity	Endoplasmic reticulum	Anchor protein
4904	YBX1	nuclease-sensitive element-binding protein 1	11	71	7	**1.5**	**1E-02**	0.9	**2E-02**	1.3	2E-01	0.9	**3E-02**	1.0	5E-01	Transcription factor activity	Nucleus	Transcription factor
1854	DUT	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 1	2	14	2	**1.7**	**2E-02**	0.8	**6E-03**	**1.5**	**5E-02**	0.8	6E-01	1.0	7E-01	Hydrolase activity	Cytoplasm;Nucleus;Mitochondrion	Enzyme: Hydrolase
4176	MCM7	DNA replication licensing factor MCM7 isoform 1	8	24	8	**2.3**	**2E-02**	1.0	**1E-02**	1.5	1E+00	**0.5**	**5E-03**	0.9	8E-01	Helicase activity	Nucleus	Unclassified;DNA helicase
8697	CDC23	cell division cycle protein 23 homolog	7	24	7	**1.7**	**2E-02**	1.1	**2E-02**	1.4	7E-02	0.8	4E-01	0.9	8E-01	Binding	Nucleus	Ubiquitin proteasome system protein;Cell cycle control protein
23468	CBX5	chromobox protein homolog 5*gi|188035910|ref|NP_001120794.1| chromobox protein homolog 5*gi|6912292|ref|NP_036249.1| chromobox protein homolog 5	5	14	5	**1.8**	**2E-02**	0.9	**8E-03**	1.6	6E-01	0.7	1E-01	0.9	5E-01	DNA binding	Nucleus	DNA binding protein
10360	NPM3	nucleoplasmin-3	2	10	2	**1.7**	**2E-02**	0.8	**2E-02**	1.5	2E-01	**0.5**	**3E-02**	0.8	3E-01	Chaperone activity	Nucleus	Chaperone
1633	DCK	deoxycytidine kinase	1	8	1	**1.7**	**2E-02**	**0.6**	**3E-02**	1.3	1E-01	0.7	2E-01	1.1	3E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
6240	RRM1	ribonucleoside-diphosphate reductase large subunit	7	25	7	**1.7**	**2E-02**	0.9	**1E-02**	1.2	4E-01	**0.4**	**3E-02**	0.7	**2E-02**	Oxidoreductase activity	Cytoplasm	Cell cycle control protein
6001	RGS10	regulator of G-protein signaling 10 isoform a	2	6	2	**1.6**	**2E-02**	0.8	**1E-02**	1.2	**2E-02**	0.9	3E-01	1.2	**1E-02**	GTPase activator activity	Plasma membrane	GTPase activating protein
4713	NDUFB7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	2	12	2	**1.6**	**2E-02**	0.8	**5E-02**	1.1	4E-01	0.8	1E-01	1.0	4E-01	Cell adhesion molecule activity	Mitochondrion	Adhesion molecule
8968; 8352; 8351; 8355; 8357; 8358; 8350; 8353; 8354; 8356	HIST1H3F; HIST1H3C; HIST1H3D; HIST1H3G; HIST1H3H; HIST1H3B; HIST1H3A; HIST1H3E; HIST1H3I; HIST1H3J	histone H3.1	7	285	2	**2.6**	**3E-02**	0.9	**2E-02**	2.0	8E-01	1.0	**2E-02**	1.1	1E-01	#N/A	#N/A	#N/A
6015	RING1	E3 ubiquitin-protein ligase RING1	4	12	4	**1.6**	**3E-02**	1.0	**2E-02**	1.5	4E-01	1.1	**1E-02**	1.0	7E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
23515	MORC3	MORC family CW-type zinc finger protein 3	3	8	3	**1.6**	**3E-02**	1.1	6E-02	1.6	2E-01	1.2	**9E-03**	1.3	**4E-02**	RNA binding	Nucleus	RNA binding protein
5792	PTPRF	receptor-type tyrosine-protein phosphatase F isoform 1	12	41	12	**1.6**	**3E-02**	1.1	**7E-04**	0.9	**5E-05**	0.8	9E-01	1.1	1E-01	Receptor signaling protein tyrosine phosphatase activity	Plasma membrane	Receptor tyrosine phosphatase
113444	C1orf212; SMIM12	PREDICTED: small integral membrane protein 12 isoform X1	3	6	3	**2.0**	**3E-02**	0.7	**2E-02**	2.1	1E-01	1.3	1E-01	0.9	4E-01	#N/A	#N/A	#N/A
4174	MCM5	DNA replication licensing factor MCM5	5	19	5	**2.1**	**3E-02**	0.9	**3E-02**	1.5	7E-01	0.6	1E-01	1.1	2E-01	DNA binding	Nucleus	DNA binding protein
26521	TIMM8B	mitochondrial import inner membrane translocase subunit Tim8 B	2	10	2	**1.8**	**3E-02**	0.7	**2E-02**	1.6	3E-01	1.2	**7E-03**	0.9	3E-01	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
2697	GJA1	gap junction alpha-1 protein	2	8	2	**1.7**	**3E-02**	1.2	1E+00	0.8	**3E-02**	0.4	6E-02	0.8	8E-02	Auxiliary transport protein activity	Cell surface	Membrane transport protein
2752	GLUL	glutamine synthetase	1	6	1	**2.2**	**3E-02**	1.0	8E-02	0.9	4E-01	0.6	7E-01	1.3	**9E-03**	Transaminase activity	Cytosol	Enzyme: Aminotransferase
10628	TXNIP; LOC101060503	thioredoxin-interacting protein	1	6	1	**1.8**	**3E-02**	1.1	**4E-02**	**1.5**	**2E-02**	0.8	1E-01	1.1	5E-01	#N/A	#N/A	#N/A
4059	BCAM	basal cell adhesion molecule isoform 1	4	14	4	**2.2**	**3E-02**	1.1	5E-01	0.8	1E-01	0.4	6E-02	0.9	1E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
1153	CIRBP	PREDICTED: cold-inducible RNA-binding protein isoform X1	1	6	1	**2.3**	**4E-02**	1.4	1E-01	1.1	6E-01	0.5	3E-01	0.7	3E-01	RNA binding	Nucleus	RNA binding protein
723790; 8337	HIST2H2AA4; HIST2H2AA3	histone H2A type 2-A	7	151	2	**1.6**	**4E-02**	1.1	**1E-02**	**1.8**	**3E-02**	**1.5**	**2E-02**	1.1	**6E-03**	#N/A	#N/A	#N/A
6509	SLC1A4	neutral amino acid transporter A isoform 1	2	10	2	**1.8**	**4E-02**	0.7	1E-01	1.3	**4E-02**	**0.4**	**6E-04**	0.8	**3E-02**	Transporter activity	Plasma membrane	Transport/cargo protein
55272;	IMP3	U3 small nucleolar ribonucleoprotein protein IMP3	3	6	3	**1.5**	**4E-02**	0.9	**1E-02**	1.4	5E-01	0.7	2E-01	1.1	5E-02	Ribonucleoprotein	Nucleolus	RNA binding protein
80781	COL18A1	collagen alpha-1(XVIII) chain isoform 3 preproprotein	3	9	3	**1.8**	**5E-02**	0.9	**4E-02**	1.3	8E-01	0.9	**3E-02**	1.2	7E-02	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
94274	PPP1R14A	protein phosphatase 1 regulatory subunit 14A isoform 1	1	6	1	**1.6**	**5E-02**	0.8	**2E-02**	1.5	8E-02	1.0	**4E-02**	1.2	6E-02	Enzyme regulator activity	-	Regulatory/other subunit

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
51021	**MRPS16**	**28S ribosomal protein S16, mitochondrial**	2	7	2	**1.5**	**5E-02**	0.9	**3E-02**	1.3	3E-01	1.0	**3E-02**	1.3	**1E-02**	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
144568	**A2ML1**	**alpha-2-macroglobulin-like protein 1 isoform 1**	34	257	34	**0.4**	**2E-16**	0.9	**1E-09**	**0.6**	**6E-07**	0.9	**2E-16**	0.9	**1E-03**	Protease inhibitor activity	Cytoplasmic vesicle	Protease inhibitor
1828	**DSG1**	**desmoglein-1 preproprotein**	21	147	21	**0.3**	**2E-16**	1.1	**2E-16**	**0.2**	**5E-10**	**0.3**	**2E-16**	0.8	**2E-07**	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
2125	**EVPL**	**envoplakin**	79	473	78	**0.5**	**2E-16**	1.3	**5E-13**	**0.6**	**2E-16**	1.0	**2E-16**	0.9	**1E-10**	Structural molecule activity	Plasma membrane	Structural protein
2171	**FABP5**	**fatty acid-binding protein, epidermal**	11	325	11	**0.4**	**2E-16**	1.4	**1E-10**	**0.6**	**2E-16**	**0.5**	**2E-16**	0.8	**2E-16**	Transporter activity	Cytoplasm	Transport/cargo protein
3713	**IVL**	**PREDICTED: involucrin isoform X1**	35	544	35	**0.2**	**2E-16**	1.2	**2E-16**	**0.3**	**2E-16**	**0.6**	**2E-16**	0.9	**2E-16**	Structural molecule activity	Cytoplasm	Structural protein
144501	**KRT80**	**keratin, type II cytoskeletal 80 isoform K80**	29	229	1	**0.2**	**2E-16**	1.4	**4E-13**	**0.5**	**2E-16**	**3.6**	**2E-16**	1.2	**2E-16**	Structural constituent of cytoskeleton	-	Cytoskeletal protein
5493	**PPL**	**periplakin**	107	726	106	**0.4**	**2E-16**	1.3	**4E-07**	**0.7**	**2E-16**	**1.8**	**2E-16**	1.0	**7E-12**	Structural constituent of cytoskeleton	Plasma membrane	Cytoskeletal protein
374897	**SBSN**	**suprabasin isoform 1**	25	375	15	**0.1**	**2E-16**	**1.5**	**2E-16**	**0.3**	**2E-16**	1.2	**2E-16**	**1.5**	**2E-16**	Molecular function unknown	-	Unclassified
374897	**SBSN**	**suprabasin isoform 2**	11	271	1	**0.1**	**2E-16**	1.3	**2E-16**	**0.2**	**2E-16**	1.0	**2E-16**	**1.7**	**2E-16**	Molecular function unknown	-	Unclassified
7051	**TGM1**	**protein-glutamine gamma-glutamyltransferase K**	29	191	29	**0.4**	**2E-16**	**1.5**	**5E-06**	**0.7**	**2E-16**	**1.8**	**2E-16**	1.2	**2E-16**	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase
6280	**S100A9**	**protein S100-A9**	7	211	7	**0.3**	**3E-16**	1.4	**2E-16**	1.1	**2E-16**	1.2	**2E-16**	0.9	**4E-05**	Calcium ion binding	Cytoplasm	Calcium binding protein
6699	**SPRR1B**	**cornifin-B**	6	184	2	**0.3**	**7E-16**	**1.6**	**6E-13**	**0.6**	**2E-16**	1.0	**3E-08**	1.2	9E-01	Structural molecule activity	Cytoplasm	Structural protein
9119	**KRT75**	**keratin, type II cytoskeletal 75**	44	6786	18	**0.4**	**3E-13**	0.7	**3E-12**	**0.3**	**2E-16**	**0.6**	**7E-15**	1.2	**2E-16**	Structural molecule activity	-	Structural protein
2312	**FLG**	**filaggrin**	65	309	65	**0.1**	**2E-12**	**1.5**	**4E-12**	**0.2**	**2E-13**	**1.5**	**4E-14**	1.3	**2E-11**	Calcium ion binding	Nucleus	Calcium binding protein
1410	**CRYAB**	**alpha-crystallin B chain*gi|577019571|ref|NP_001276736.1 | alpha-crystallin B chain*gi|577019573|ref|NP_001276737.1 | alpha-crystallin B chain**	8	101	8	**0.2**	**3E-12**	0.9	**9E-12**	**0.2**	**4E-02**	0.8	1E-01	1.0	**5E-05**	Heat shock protein activity	Nucleus	Heat shock protein
5055	**SERPINB2**	**plasminogen activator inhibitor 2**	21	337	21	**0.7**	**4E-12**	**0.5**	**2E-16**	1.1	**2E-16**	**1.6**	**2E-16**	1.1	**4E-07**	Protease inhibitor activity	Cytoplasm	Protease inhibitor
8796	**SCEL**	**sciellin isoform 1**	24	124	3	**0.3**	**4E-11**	1.0	**6E-10**	**0.5**	**2E-09**	1.1	**8E-13**	1.0	2E-01	Structural molecule activity	Cytoplasm	Structural protein
4070	**TACSTD2**	**tumor-associated calcium signal transducer 2**	10	89	10	**0.6**	**6E-11**	0.9	**2E-11**	**0.5**	**1E-02**	**0.7**	**2E-03**	1.0	3E-01	Receptor activity	Plasma membrane	Cell surface receptor
79983	**POF1B**	**protein POF1B**	22	192	22	**0.3**	**5E-10**	1.4	**9E-09**	**0.4**	**5E-11**	**1.9**	**2E-11**	1.1	**2E-05**	Molecular function unknown	-	Unclassified
6249	**CLIP1**	**CAP-Gly domain-containing linker protein 1 isoform b**	61	328	55	**0.6**	**2E-09**	1.1	2E-01	0.7	**2E-16**	1.3	**2E-16**	1.0	1E-01	Structural molecule activity	Microtubule;Cytoplasm	Structural protein
6279	**S100A8**	**protein S100-A8**	10	118	10	**0.3**	**3E-09**	1.4	**3E-08**	1.2	**8E-09**	1.2	**1E-08**	0.9	**5E-03**	Calcium ion binding	Cytoplasm	Calcium binding protein
4008	**LMO7**	**PREDICTED: LIM domain only protein 7 isoform X2**	31	71	31	**0.4**	**4E-09**	1.1	**1E-06**	**0.5**	**2E-08**	**1.9**	**6E-12**	1.4	**1E-10**	Transcription regulator activity	Nucleus	Transcription regulatory protein
9022	**CLIC3**	**chloride intracellular channel protein 3**	9	54	9	**0.2**	**6E-09**	0.8	**2E-07**	**0.5**	**1E-03**	**1.6**	**1E-09**	0.9	**9E-05**	Intracellular ligand-gated ion channel activity	Nucleus	Intracellular ligand gated channel
3858	**KRT10**	**PREDICTED: keratin, type I cytoskeletal 10 isoform X1**	36	1338	4	**0.2**	**8E-09**	**2.7**	**3E-08**	**0.1**	**8E-13**	**0.2**	**5E-07**	0.9	**2E-03**	Structural molecule activity	Cytoplasm	Structural protein
5275	**SERPINB13**	**serpin B13**	13	70	13	**0.5**	**9E-09**	1.3	**3E-07**	0.9	**8E-13**	1.2	**3E-11**	0.9	1E-01	Protease inhibitor activity	Cytoplasm	Protease inhibitor
8710	**SERPINB7**	**serpin B7 isoform 1**	14	78	14	**0.4**	**1E-08**	1.1	**3E-06**	0.8	**5E-09**	**1.9**	**5E-09**	1.2	**9E-08**	Protease inhibitor activity	Cytoplasm	Protease inhibitor
1476	**CSTB**	**cystatin-B**	5	86	5	**0.6**	**1E-08**	1.0	**7E-07**	0.8	5E-02	1.2	**6E-13**	0.9	**2E-02**	Protease inhibitor activity	Nucleus	Protease inhibitor
93099	**DMKN**	**dermokine isoform 3**	12	63	12	**0.2**	**5E-08**	1.4	**2E-04**	**0.6**	**6E-06**	0.9	**2E-02**	1.1	**4E-02**	Cytokine activity	Extracellular	Cytokine
7739	**ZNF185**	**zinc finger protein 185 isoform 3**	33	237	33	**0.7**	**1E-07**	1.3	**2E-16**	1.0	**2E-16**	**1.8**	**2E-16**	0.9	**2E-08**	Transcription regulator activity	Nucleus	Transcription regulatory protein
6703	**SPRR2D**	**small proline-rich protein 2D**	4	40	4	**0.1**	**3E-07**	**0.7**	**3E-07**	**0.2**	**1E-02**	1.0	**1E-07**	1.3	**1E-07**	#N/A	#N/A	#N/A
25984	**KRT23**	**keratin, type I cytoskeletal 23 isoform 1**	28	541	25	**0.2**	**3E-07**	**1.9**	**5E-05**	**0.5**	**1E-07**	**5.3**	**8E-09**	**2.0**	**3E-07**	Molecular function unknown	Cytoplasm	Unclassified
4134	**MAP4**	**PREDICTED: microtubule-associated protein 4 isoform X5**	52	213	8	**0.6**	**3E-07**	**0.6**	**1E-06**	0.7	7E-02	1.0	**2E-10**	0.8	**5E-07**	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein
3606	**IL18**	**interleukin-18 isoform 1 proprotein**	8	76	8	**0.6**	**5E-07**	0.8	**2E-03**	**0.6**	**7E-05**	1.1	**1E-07**	1.0	5E-01	Cytokine activity	Extracellular	Cytokine
54869	**EPS8L1**	**PREDICTED: epidermal growth factor receptor kinase substrate 8-like protein 1 isoform X1**	20	48	20	**0.4**	**2E-06**	1.1	**6E-04**	**0.6**	**1E-09**	**1.5**	**4E-11**	1.1	**4E-04**	Molecular function unknown	-	Unclassified
195814	**SDR16C5**	**epidermal retinol dehydrogenase 2**	10	57	10	**0.4**	**2E-06**	1.3	**5E-03**	**0.6**	**4E-07**	**1.7**	**3E-08**	1.2	**5E-08**	Catalytic activity	-	Enzyme: Dehydrogenase
284110	**GSDMA**	**gasdermin-A**	12	79	12	**0.4**	**3E-06**	1.2	1E-01	0.7	**5E-06**	**6.7**	**6E-07**	1.2	**4E-05**	Molecular function unknown	Cytoplasm	Unclassified
6590	**SLPI**	**antileukoproteinase**	6	38	6	**0.1**	**3E-06**	0.9	**3E-06**	0.3	7E-01	1.0	**9E-06**	1.0	4E-01	Protease inhibitor activity	Extracellular	Protease inhibitor
4133	**MAP2**	**microtubule-associated protein 2 isoform 5**	16	76	3	**0.6**	**3E-06**	0.7	**2E-05**	0.5	6E-02	0.6	2E-01	0.8	5E-02	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein
6820	**SULT2B1**	**sulfotransferase family cytosolic 2B member 1 isoform b**	9	89	9	**0.4**	**3E-06**	1.1	7E-02	0.7	2E-01	**2.1**	**8E-08**	1.0	3E-01	Sulfotransferase activity	Cytoplasm;Cytosol	Enzyme: Sulphotransferase
196374	**KRT78**	**keratin, type II cytoskeletal 78 isoform 1**	25	1602	18	**0.3**	**5E-06**	**1.6**	**4E-04**	**0.5**	**2E-06**	**1.9**	**8E-08**	1.2	**3E-05**	Structural molecule activity	-	Structural protein
1475	**CSTA**	**cystatin-A**	8	99	8	**0.6**	**1E-05**	1.1	**3E-03**	0.8	**4E-02**	0.9	**1E-05**	0.9	9E-01	Protease inhibitor activity	Cytoplasm	Protease inhibitor
1528;	**CYB5A**	**cytochrome b5 isoform 2**	6	18	4	**0.5**	**2E-05**	1.4	**9E-06**	0.9	**8E-06**	0.9	**4E-06**	0.9	**3E-02**	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10552	**ARPC1A**	**actin-related protein 2/3 complex subunit 1A isoform 1**	14	80	14	**0.6**	**2E-05**	1.1	**5E-02**	0.7	**8E-08**	1.0	**3E-06**	0.9	**1E-02**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
51228	**GLTP**	**glycolipid transfer protein**	9	66	9	**0.4**	**3E-05**	1.5	8E-01	0.7	**2E-07**	1.2	**6E-09**	0.9	1E-01	Transporter activity	Cytoplasm	Transport/cargo protein
8824	**CES2**	**cocaine esterase isoform 1**	15	117	15	**0.6**	**3E-05**	**1.6**	**1E-06**	1.0	**3E-06**	**1.6**	**1E-06**	0.9	9E-02	Hydrolase activity	Microsome	Enzyme: Esterase
151516	**ASPRV1**	**retroviral-like aspartic protease 1**	7	77	7	**0.1**	**3E-05**	**1.8**	**7E-04**	**0.5**	**2E-05**	**5.3**	**6E-06**	**1.6**	**8E-06**	Peptidase activity	-	Aspartic protease
80223	**RAB11FIP1**	**rab11 family-interacting protein 1 isoform 3**	16	90	16	**0.6**	**4E-05**	1.3	**1E-02**	0.8	**4E-08**	**2.0**	**1E-12**	1.2	**8E-08**	GTPase activator activity	Endosome;Nucleus;Cytoplasm	GTPase activating protein
286887	**KRT6C**	**keratin, type II cytoskeletal 6C**	67	15141	2	**0.2**	**4E-05**	1.3	**1E-04**	**0.2**	**9E-05**	**0.4**	**6E-04**	0.9	**2E-03**	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
23581	**CASP14**	**caspase-14**	10	62	10	**0.4**	**6E-05**	1.2	**2E-04**	**0.4**	**6E-04**	1.1	**1E-04**	0.9	**2E-02**	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
5650	**KLK7**	**kallikrein-7 isoform 1 preproprotein**	5	31	5	**0.1**	**6E-05**	0.9	**7E-05**	0.3	9E-02	0.9	**9E-04**	1.0	7E-02	Serine-type peptidase activity	Apical membrane	Serine protease
1041	**CDSN**	**corneodesmosin**	4	54	4	**0.1**	**6E-05**	1.1	**6E-04**	**0.4**	**1E-03**	0.8	6E-01	1.2	**6E-06**	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
51479;	**ANKFY1**	**rabankyrin-5 isoform 3**	10	15	3	**0.0**	**6E-05**	0.8	**4E-05**	0.0	4E-01	**2.3**	**6E-05**	0.9	8E-01	Transporter activity	Cytoplasm	Transport/cargo protein
7277	**TUBA4A**	**tubulin alpha-4A chain isoform 1**	23	858	6	**0.7**	**1E-04**	0.9	9E-01	0.7	9E-01	1.0	**8E-11**	0.9	**2E-11**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
57111	**RAB25**	**ras-related protein Rab-25**	8	50	7	**0.4**	**1E-04**	1.3	**5E-04**	**0.6**	**1E-04**	0.8	**8E-05**	1.0	5E-01	GTPase activity	Golgi apparatus	GTPase
23475	**QPRT**	**nicotinate-nucleotide pyrophosphorylase [carboxylating]**	6	36	6	**0.5**	**1E-04**	0.7	8E-01	0.7	**5E-03**	1.4	**3E-05**	1.1	2E-01	Catalytic activity	-	Enzyme: Ribosyltransferase
3885	**KRT34**	**keratin, type I cuticular Ha4**	18	142	10	**0.5**	**2E-04**	**0.5**	**5E-04**	**0.5**	**3E-05**	**1.8**	**3E-05**	1.2	**2E-02**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
6275	**S100A4**	**protein S100-A4**	4	22	4	**0.3**	**2E-04**	1.2	1E-01	0.7	**8E-04**	**1.5**	**4E-04**	1.0	1E+00	Calcium ion binding	Cytoplasm	Calcium binding protein
26353	**HSPB8**	**heat shock protein beta-8**	4	26	4	**0.2**	**2E-04**	1.1	**4E-04**	**0.2**	**2E-02**	1.2	**4E-04**	1.2	9E-02	Heat shock protein activity	Cytoplasm	Heat shock protein
57447	**NDRG2**	**protein NDRG2 isoform a**	2	15	2	**0.6**	**3E-04**	1.4	2E-01	0.8	**1E-03**	1.4	**2E-04**	1.0	6E-01	Hydrolase activity	Perinuclear region	Enzyme: Hydrolase
3162	**HMOX1**	**heme oxygenase 1**	6	34	6	**0.4**	**3E-04**	1.3	**2E-04**	**0.5**	**9E-04**	**3.8**	**3E-04**	1.4	**1E-04**	Catalytic activity	Endoplasmic reticulum;Microsome	Enzyme: Oxygenase
1364	**CLDN4**	**claudin-4**	3	25	3	**0.4**	**4E-04**	2.0	4E-01	**0.7**	**7E-03**	**1.8**	**3E-03**	**1.7**	**1E-04**	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
121214	**SDR9C7**	**short-chain dehydrogenase/reductase family 9C member 7**	11	60	11	**0.3**	**4E-04**	1.4	8E-01	0.7	**3E-05**	**3.7**	**1E-05**	1.0	1E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
84659	**RNASE7**	**ribonuclease 7**	4	29	4	**0.5**	**4E-04**	1.2	**3E-02**	**0.6**	**3E-05**	**7.2**	**7E-06**	1.1	**2E-02**	Ribonuclease activity	Extracellular	Ribonuclease
3851	**KRT4**	**keratin, type II cytoskeletal 4**	14	1743	3	**0.3**	**5E-04**	1.3	**3E-04**	**0.2**	**8E-08**	**0.4**	**4E-05**	1.0	2E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
4013	**VWA5A**	**von Willebrand factor A domain-containing protein 5A isoform 1**	16	93	16	**0.6**	**5E-04**	0.8	7E-02	**0.7**	**3E-07**	0.8	**3E-03**	0.9	**5E-04**	Molecular function unknown	Cytoplasm	Unclassified
124790;	**HEXIM2**	**protein HEXIM2 isoform 2**	3	9	3	**0.6**	**5E-04**	1.0	**8E-04**	**0.5**	**5E-02**	0.8	9E-01	0.9	1E-01	Kinase regulator activity;RNA binding;Transcription regulator activity	Nucleus	Transcription regulatory protein
338322	**NLRP10**	**PREDICTED: NACHT, LRR and PYD domains-containing protein 10 isoform X1**	17	74	17	**0.6**	**6E-04**	0.9	8E-01	0.8	1E-01	**1.9**	**8E-12**	1.1	**5E-03**	Molecular function unknown	-	Unclassified
4210	**MEFV**	**pyrin isoform 1**	2	15	1	**0.5**	**6E-04**	1.2	**1E-02**	**0.5**	**2E-02**	0.9	**3E-02**	0.9	**5E-02**	Transcription factor activity	Cytoplasm	Transcription factor
79153	**GDPD3**	**glycerophosphodiester phosphodiesterase domain-containing protein 3**	5	27	5	**0.4**	**6E-04**	1.3	**2E-06**	1.4	**1E-03**	**7.7**	**5E-06**	1.1	7E-02	Molecular function unknown	-	Unclassified
1.01E+08	**OCLN**	**occludin isoform a*gi|4505487|ref|NP_002529.1| occludin isoform a**	6	28	6	**0.6**	**6E-04**	0.9	**1E-03**	0.6	9E-01	1.1	**7E-05**	1.2	**1E-04**	Cell adhesion molecule activity	Plasma membrane	Integral membrane protein
388533	**KRTDAP**	**keratinocyte differentiation-associated protein isoform 1**	3	29	3	**0.3**	**7E-04**	1.7	2E-01	**0.6**	**1E-04**	0.8	2E-01	0.8	**4E-03**	Molecular function unknown	-	Unclassified
1893	**ECM1**	**extracellular matrix protein 1 isoform 3**	11	46	5	**0.6**	**1E-03**	0.8	7E-01	0.8	**2E-02**	**2.1**	**8E-04**	1.2	**3E-04**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
1893	**ECM1**	**extracellular matrix protein 1 isoform 2**	7	32	1	**0.5**	**1E-03**	1.4	7E-01	**0.6**	**2E-02**	**14.0**	**8E-04**	1.3	**3E-04**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
2689	**GH2**	**growth hormone variant isoform 2**	1	16	1	**0.6**	**1E-03**	1.2	3E-01	0.7	**1E-04**	**1.5**	**7E-06**	1.2	**1E-03**	Cytokine activity	Extracellular	Cytokine
10626	**TRIM16**	**tripartite motif-containing protein 16**	15	57	15	**0.6**	**1E-03**	0.8	**6E-04**	1.1	9E-02	1.4	**1E-04**	0.8	**5E-03**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
10982	**MAPRE2**	**microtubule-associated protein RP/EB family member 2 isoform 1**	5	28	4	**0.5**	**1E-03**	0.9	**4E-03**	0.5	2E-01	**1.5**	**9E-06**	1.0	8E-02	Cytoskeletal protein binding	Centrosome;Cytoplasm	Cytoskeletal associated protein
10205	**MPZL2**	**myelin protein zero-like protein 2**	3	16	3	**0.7**	**2E-03**	1.0	**9E-03**	0.6	1E-01	**0.5**	**1E-04**	0.9	**7E-03**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
57662	**CAMSAP3**	**calmodulin-regulated spectrin-associated protein 3 isoform 1**	8	32	8	**0.6**	**2E-03**	1.1	7E-01	0.7	**2E-03**	**1.6**	**5E-05**	1.0	2E-01	#N/A	#N/A	#N/A
55076	**TMEM45A**	**transmembrane protein 45A**	3	18	3	**0.2**	**2E-03**	**2.1**	**5E-03**	**0.4**	**1E-03**	0.9	**1E-02**	1.2	**4E-02**	Molecular function unknown	-	Unclassified
3934	**LCN2**	**neutrophil gelatinase-associated lipocalin**	6	29	6	**0.3**	**2E-03**	0.9	**1E-06**	1.0	2E-01	**3.2**	**4E-05**	0.9	3E-01	Transporter activity	Extracellular	Transport/cargo protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
1382	**CRABP2**	**cellular retinoic acid-binding protein 2*gi|4503029|ref|NP_001869.1| cellular retinoic acid-binding protein 2**	4	28	4	**0.4**	**2E-03**	1.2	1E-01	**0.7**	**5E-04**	**0.4**	**6E-04**	0.8	**9E-03**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
80352	**RNF39**	**RING finger protein 39 isoform 1**	7	38	7	**0.6**	**3E-03**	1.9	2E-01	0.7	**3E-05**	**3.0**	**1E-05**	**2.2**	**2E-05**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
6286	**S100P**	**protein S100-P**	3	18	3	**0.2**	**3E-03**	1.2	**3E-02**	**0.6**	**8E-04**	**10.2**	**6E-04**	1.1	**2E-02**	Calcium ion binding	Cytoplasm	Calcium binding protein
126410	**CYP4F22**	**cytochrome P450 4F22**	5	15	5	**0.3**	**3E-03**	1.8	7E-01	**0.6**	**2E-02**	1.2	1E-01	1.1	2E-01	Catalytic activity	-	Enzyme: Hydroxylase;Integral membrane protein
388698	**FLG2**	**filaggrin-2**	7	38	7	**0.5**	**3E-03**	1.6	5E-02	**0.5**	**5E-05**	**1.7**	**1E-05**	1.4	**3E-05**	Calcium ion binding	Extracellular	Calcium binding protein
128308	**MRPL55**	**39S ribosomal protein L55, mitochondrial isoform b**	1	6	1	**0.6**	**3E-03**	1.3	1E-01	**0.7**	**3E-02**	0.8	1E-01	0.8	1E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
388555	**IGFL3**	**insulin growth factor-like family member 3**	2	16	2	**0.6**	**4E-03**	**2.2**	**9E-03**	1.0	**5E-03**	**1.7**	**3E-03**	1.1	**1E-02**	Molecular function unknown	-	Unclassified
27111	**SDCBP2**	**syntenin-2 isoform a**	9	50	9	**0.5**	**4E-03**	0.9	2E-01	0.7	4E-01	1.4	**9E-05**	0.9	**2E-02**	Protein binding	Cytoplasm	Adapter molecule
448834	**KPRP**	**keratinocyte proline-rich protein**	4	21	4	**0.2**	**4E-03**	**2.2**	**2E-03**	**0.2**	**5E-03**	**7.9**	**2E-03**	**1.8**	**1E-02**	Molecular function unknown	-	Unclassified
374918	**IGFL1**	**insulin growth factor-like family member 1**	2	8	2	**0.1**	**4E-03**	1.1	**4E-03**	**0.1**	**3E-02**	**0.2**	**4E-03**	0.8	**7E-03**	Molecular function unknown	-	Integral membrane protein
6698	**SPRR1A**	**cornifin-A*gi|45827734|ref|NP_005978.2| cornifin-A**	6	148	2	**0.1**	**5E-03**	**1.5**	**9E-03**	**0.4**	**9E-03**	1.1	**3E-03**	1.2	**2E-02**	Structural molecule activity	Cytoplasm	Structural protein
9289	**GPR56; ADGRG1**	**PREDICTED: G-protein coupled receptor 56 isoform X1**	4	22	4	**0.6**	**6E-03**	1.2	**2E-02**	0.8	**3E-04**	1.0	**4E-04**	1.1	**3E-02**	#N/A	#N/A	#N/A
10666;	**CD226**	**CD226 antigen isoform a*gi|746816106|ref|NP_001290547.1| CD226 antigen isoform a**	1	3	1	**0.5**	**7E-03**	0.9	**4E-03**	0.6	9E-01	0.9	**4E-02**	1.2	**4E-02**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
10553	**HTATIP2**	**oxidoreductase HTATIP2 isoform a**	12	58	12	**0.7**	**7E-03**	1.0	1E-01	**0.7**	**2E-04**	0.9	**3E-06**	0.9	**1E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
5266	**PI3**	**elafin preproprotein**	4	16	4	**0.2**	**9E-03**	0.7	2E-01	0.7	**9E-03**	**0.4**	**7E-03**	0.7	**5E-03**	Protease inhibitor activity	Extracellular	Protease inhibitor
147645	**VSIG10L**	**V-set and immunoglobulin domain-containing protein 10-like**	4	8	4	**0.2**	**9E-03**	1.5	2E-01	**0.6**	**2E-03**	1.3	**1E-03**	1.1	**1E-02**	#N/A	#N/A	#N/A
7077	**TIMP2**	**metalloproteinase inhibitor 2**	1	6	1	**0.4**	**9E-03**	0.9	**2E-03**	0.5	6E-01	1.4	**3E-02**	1.3	1E-01	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
6317	**SERPINB3**	**serpin B3**	13	73	7	**0.6**	**9E-03**	**2.5**	**2E-03**	**2.1**	**2E-03**	**2.8**	**1E-03**	0.9	**1E-02**	Protease inhibitor activity	Cytoplasm	Protease inhibitor
353091	**RAET1G**	**retinoic acid early transcript 1G protein preproprotein**	5	24	5	**0.6**	**9E-03**	0.9	5E-01	0.8	4E-01	0.7	8E-01	0.8	6E-02	Receptor binding	Plasma membrane	Ligand
5097	**PCDH1**	**protocadherin-1 isoform 2**	6	15	6	**0.5**	**1E-02**	1.0	7E-01	0.7	3E-01	1.2	**7E-05**	1.0	9E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
9076	**CLDN1**	**claudin-1**	2	12	2	**0.5**	**1E-02**	1.1	**2E-02**	**0.4**	**6E-04**	**0.5**	**9E-03**	1.0	8E-01	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
9322	**TRIP10**	**cdc42-interacting protein 4 isoform 1**	18	83	1	**0.6**	**1E-02**	1.2	**6E-08**	0.7	**2E-04**	**1.8**	**6E-09**	1.4	2E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
56998	**CTNNBIP1**	**beta-catenin-interacting protein 1*gi|9910390|ref|NP_064633.1| beta-catenin-interacting protein 1**	3	22	3	**0.4**	**1E-02**	1.3	**1E-02**	**0.5**	**2E-04**	0.8	9E-01	1.1	7E-01	Transcription regulator activity;Protein binding	Cytoplasm	Transcription regulatory protein
59082	**CARD18**	**caspase recruitment domain-containing protein 18**	1	6	1	**0.3**	**1E-02**	0.9	**4E-02**	0.4	4E-01	1.3	**1E-02**	0.8	**2E-03**	Molecular function unknown	-	Unclassified
51806	**CALML5**	**calmodulin-like protein 5**	7	75	7	**0.3**	**1E-02**	**2.5**	**5E-02**	**0.4**	**4E-03**	1.1	**5E-06**	0.9	3E-01	Calcium ion binding	Extracellular	Calcium binding protein
3860	**KRT13**	**keratin, type I cytoskeletal 13 isoform a**	23	1736	5	**0.4**	**1E-02**	**0.7**	**5E-02**	**0.3**	**2E-02**	0.7	**6E-04**	1.4	**4E-03**	Structural molecule activity	Cytoplasm;Nucleus	Structural protein
29094	**LGALSL**	**galectin-related protein**	6	32	6	**0.5**	**2E-02**	1.2	**2E-02**	**0.5**	**1E-02**	**0.6**	**3E-02**	1.0	9E-01	#N/A	#N/A	#N/A
7062	**TCHH**	**trichohyalin**	18	71	18	**0.4**	**2E-02**	**0.7**	**5E-02**	0.4	5E-02	0.9	4E-01	1.1	**2E-02**	Calcium ion binding	-	Calcium binding protein
342897	**NCCRP1**	**F-box only protein 50**	6	34	6	**0.3**	**2E-02**	1.4	5E-01	**0.7**	**6E-03**	**3.5**	**2E-03**	1.1	3E-01	Molecular function unknown	-	Unclassified
810	**CALML3**	**calmodulin-like protein 3**	11	102	9	**0.6**	**2E-02**	1.4	**7E-03**	**0.4**	**2E-09**	0.3	1E-01	0.7	**2E-05**	Calcium ion binding	Cytoplasm	Calcium binding protein
22839	**DLGAP4**	**disks large-associated protein 4 isoform b**	8	32	8	**0.6**	**3E-02**	0.9	3E-01	0.7	4E-01	1.3	**1E-02**	1.0	6E-01	Molecular function unknown	Cytosol	Adapter molecule;Unclassified
7280	**TUBB2A**	**tubulin beta-2A chain**	20	994	3	**0.5**	**3E-02**	1.1	**4E-06**	**0.6**	**6E-03**	0.9	**1E-13**	0.9	7E-01	#N/A	#N/A	#N/A
118932	**ANKRD22**	**ankyrin repeat domain-containing protein 22**	6	38	6	**0.4**	**3E-02**	1.1	4E-01	0.7	**6E-03**	**1.9**	**1E-02**	1.0	4E-01	Molecular function unknown	-	Unclassified
374454	**KRT77**	**keratin, type II cytoskeletal 1b**	16	1699	10	**0.5**	**3E-02**	**1.7**	**3E-05**	**0.7**	**9E-07**	0.9	**7E-07**	**1.7**	**3E-11**	Structural molecule activity	-	Structural protein
6785	**ELOVL4**	**elongation of very long chain fatty acids protein 4**	2	7	2	**0.6**	**4E-02**	1.3	**1E-04**	1.1	**5E-02**	**3.4**	**1E-02**	1.3	8E-02	Molecular function unknown	Plasma membrane	Unclassified
11005	**SPINK5**	**serine protease inhibitor Kazal-type 5 isoform a**	3	12	3	**0.3**	**4E-02**	1.3	**3E-02**	**0.4**	**2E-02**	**0.5**	**5E-02**	1.0	7E-01	Protease inhibitor activity	Extracellular	Protease inhibitor
57118	**CAMK1D**	**calcium/calmodulin-dependent protein kinase type 1D isoform 2**	2	10	2	**0.6**	**4E-02**	1.0	1E-01	**0.6**	**2E-02**	1.2	**9E-03**	0.9	4E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
10043	**TOM1**	**target of Myb protein 1 isoform 2**	5	23	5	**0.6**	**4E-02**	1.2	**2E-02**	0.8	**7E-03**	**1.6**	**8E-03**	0.9	7E-02	Transporter activity	Cytoplasm	Transport/cargo protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
644054; 643161; 100132929; 100133093	FAM25C; FAM25A; FAM25B; FAM25BP; FAM25G	protein FAM25G	6	20	6	**0.5**	**4E-02**	0.7	5E-01	0.7	3E-01	0.7	8E-01	0.7	5E-02	#N/A	#N/A	#N/A
25818	KLK5	kallikrein-5 preproprotein	2	8	2	**0.3**	**4E-02**	0.9	**5E-02**	0.5	1E-01	0.9	6E-02	1.1	**5E-02**	Serine-type peptidase activity	Extracellular	Serine protease
667	DST	dystonin isoform 1eA	60	320	3	**1.5**	**2E-16**	1.1	**9E-07**	1.0	**2E-16**	0.7	**2E-16**	1.1	**2E-16**	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
3848	KRT1	keratin, type II cytoskeletal 1	45	1237	38	**0.3**	**2E-16**	**2.9**	**2E-15**	**0.2**	**2E-16**	**0.4**	**7E-08**	1.3	**3E-13**	Structural molecule activity	Plasma membrane	Structural protein
3868	KRT16	keratin, type I cytoskeletal 16	56	7951	33	**0.5**	**2E-16**	**1.5**	**2E-16**	**0.5**	**2E-16**	0.9	**2E-16**	1.2	**2E-16**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
3854	KRT6B	keratin, type II cytoskeletal 6B	65	14092	2	**0.5**	**2E-16**	1.4	**2E-16**	**0.5**	**2E-16**	1.1	**2E-16**	1.2	**2E-16**	Structural molecule activity	Cytoplasm	Structural protein
83481	EPPK1	epiplakin	122	1404	115	**0.5**	**2E-16**	1.3	**2E-16**	**0.4**	**2E-16**	**0.5**	**2E-16**	0.9	**2E-16**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
3315	HSPB1	heat shock protein beta-1	17	860	17	**0.6**	**2E-16**	1.2	**2E-16**	**0.6**	**2E-16**	0.9	**2E-16**	0.9	**2E-07**	Chaperone activity	Cytoplasm	Chaperone
1832	DSP	desmoplakin isoform I	197	2899	196	**0.6**	**2E-16**	1.2	**2E-16**	**0.6**	**2E-16**	0.7	7E-02	0.9	**2E-16**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
3963; 653499	LGALS7; LGALS7B	galectin-7	10	985	10	**0.6**	**2E-16**	1.2	**1E-11**	**0.7**	**2E-16**	**0.6**	**2E-16**	0.9	**2E-16**	#N/A	#N/A	#N/A
3880	KRT19	keratin, type I cytoskeletal 19	29	4347	14	**0.5**	**3E-07**	**0.7**	**2E-02**	**0.6**	**2E-16**	**3.0**	**2E-16**	1.3	**2E-16**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
6747	SSR3	translocon-associated protein subunit gamma	3	8	3	1.6	6E-02	1.3	5E-02	1.4	5E-01	1.2	9E-02	1.2	1E-01	Auxiliary transport protein activity	Microsome	Membrane transport protein
9415	FADS2	fatty acid desaturase 2 isoform 1	1	6	1	1.8	6E-02	0.7	6E-02	2.5	2E-01	0.6	2E-01	1.2	1E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxidase
29090	TIMM21	mitochondrial import inner membrane translocase subunit Tim21	3	14	3	1.5	6E-02	1.0	1E-01	1.6	8E-02	1.2	**1E-02**	1.2	3E-01	#N/A	#N/A	#N/A
4494	MT1F	metallothionein-1F isoform 1	2	10	2	1.5	7E-02	1.3	**1E-02**	1.2	**1E-02**	0.9	4E-01	1.1	6E-01	Transporter activity	Cytoplasm	Transport/cargo protein
23169	SLC35D1	UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter	2	8	2	1.5	7E-02	1.7	7E-02	1.5	8E-02	1.5	7E-02	1.1	4E-01	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein
1385	CREB1	PREDICTED: cyclic AMP-responsive element-binding protein 1 isoform X1	2	6	2	1.6	8E-02	0.9	**3E-02**	1.5	7E-01	0.9	2E-01	0.9	3E-01	Transcription factor activity	Nucleus	Transcription factor
875	CBS	PREDICTED: cystathionine beta-synthase isoform X1	2	4	2	1.7	8E-02	**0.5**	**3E-02**	1.2	**2E-02**	0.7	4E-01	1.0	9E-01	Hydro-lyase activity	Cytoplasm	Enzyme: Synthase
5743	PTGS2	prostaglandin G/H synthase 2	2	12	2	1.8	8E-02	0.6	9E-02	1.1	1E-01	0.9	5E-02	1.6	1E-01	Peroxidase activity	Cytoplasm	Enzyme: Synthase
1272	CNTN1	PREDICTED: contactin-1 isoform X1	6	21	6	1.5	8E-02	0.8	6E-02	1.2	1E-01	0.6	2E-01	1.1	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
23657	SLC7A11	cystine/glutamate transporter	1	6	1	2.4	9E-02	0.9	9E-02	1.5	2E-01	0.6	4E-01	1.2	1E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
3459	IFNGR1	interferon gamma receptor 1	2	10	2	1.7	1E-01	0.7	6E-02	1.3	1E-01	0.7	2E-01	1.1	**4E-02**	Transmembrane receptor activity	Plasma membrane	Cytokine receptor
27292	DIMT1	probable dimethyladenosine transferase	3	14	3	1.7	1E-01	0.6	9E-02	1.4	1E-01	0.4	2E-01	1.0	8E-01	#N/A	#N/A	#N/A
10544	PROCR	endothelial protein C receptor	2	10	2	1.5	1E-01	1.0	1E-01	1.6	3E-01	0.7	5E-02	1.1	2E-01	Antigen binding	Plasma membrane	Immunoglobulin
728340; 730394	GTF2H2C; GTF2H2D; GTF2H2C_2	general transcription factor IIH subunit 2-like protein	1	6	1	1.5	1E-01	0.9	9E-02	1.4	1E+00	0.9	8E-02	1.2	6E-02	#N/A	#N/A	#N/A
284273	ZADH2	zinc-binding alcohol dehydrogenase domain-containing protein 2	1	6	1	1.8	1E-01	1.6	9E-02	1.4	9E-02	1.2	1E-01	1.2	4E-01	Catalytic activity	-	Enzyme: Dehydrogenase
9949	AMMECR1	AMME syndrome candidate gene 1 protein isoform 1	3	7	3	1.6	2E-01	1.1	1E-01	1.3	3E-01	0.8	5E-01	0.5	5E-01	Molecular function unknown	-	Unclassified
6599	SMARCC1	SWI/SNF complex subunit SMARCC1	11	29	6	1.6	2E-01	1.0	1E-01	1.3	7E-01	0.7	7E-01	1.0	5E-01	Transcription factor activity	Nucleus	Transcription factor
54583	EGLN1	egl nine homolog 1	2	7	2	1.6	2E-01	1.0	6E-02	1.2	1E+00	0.7	2E-01	1.0	4E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
57205	ATP10D	probable phospholipid-transporting ATPase VD	2	6	2	1.7	2E-01	0.8	2E-01	1.3	9E-01	1.0	1E-01	1.1	6E-01	ATPase activity	Plasma membrane	ATPase
9324	HMGN3	high mobility group nucleosome-binding domain-containing protein 3 isoform HMGN3d	2	5	2	1.6	5E-01	1.7	1E-01	1.5	2E-01	1.1	2E-01	1.0	5E-01	DNA binding	Nucleus	DNA binding protein
3024	HIST1H1A	histone H1.1	5	83	1	3.0	#N/A	0.9	#N/A	2.2	#N/A	0.6	#N/A	1.4	#N/A	DNA binding	Nucleus	DNA binding protein
3106	HLA-B	PREDICTED: major histocompatibility complex, class I, B isoform X3	4	14	1	1.8	#N/A	0.9	#N/A	0.7	#N/A	0.3	#N/A	1.0	#N/A	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein
151636	DTX3L	E3 ubiquitin-protein ligase DTX3L	6	7	6	1.6	#N/A	1.0	#N/A	0.7	#N/A	0.5	#N/A	1.3	#N/A	#N/A	#N/A	#N/A

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3856	**KRT8**	**keratin, type II cytoskeletal 8 isoform 1**	35	2957	20	**1.5**	**2E-16**	1.1	**3E-03**	0.8	**1E-12**	1.0	**1E-11**	1.4	**5E-12**	Structural molecule activity	Cytoplasm	Structural protein
3956	**LGALS1**	**galectin-1**	8	228	8	**1.5**	**2E-16**	0.8	**2E-16**	1.4	**3E-09**	0.9	**2E-16**	1.1	**5E-05**	Receptor binding	Extracellular	Ligand
6418	**SET**	**protein SET isoform 2**	10	102	2	**1.5**	**2E-12**	0.9	**5E-14**	1.4	1E-01	1.1	**3E-12**	1.0	6E-01	MHC class I receptor activity;MHC class II receptor activity	Nucleus	MHC complex protein
8886	**DDX18**	**ATP-dependent RNA helicase DDX18**	16	83	16	**1.5**	**2E-11**	0.9	**2E-10**	1.3	7E-01	**0.7**	**5E-04**	1.0	8E-01	Transporter activity	Nucleus	Transport/cargo protein
22984	**PDCD11**	**protein RRP5 homolog**	21	91	21	**1.5**	**2E-10**	0.9	**2E-11**	1.3	1E+00	**0.6**	**1E-05**	1.0	4E-01	Transcription factor binding	Nucleus	Transcription regulatory protein
3371	**TNC**	**tenascin**	29	109	29	**1.5**	**2E-09**	0.5	3E-01	0.8	**6E-08**	0.7	**5E-03**	1.1	**3E-03**	Cell adhesion molecule activity	Extracellular	Adhesion molecule
51081;	**MRPS7**	**28S ribosomal protein S7, mitochondrial**	7	17	7	**1.5**	**2E-06**	1.1	**7E-06**	1.3	**8E-04**	1.0	**2E-04**	1.1	5E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
23517	**SKIV2L2**	**superkiller viralicidic activity 2-like 2**	9	36	9	**1.5**	**1E-05**	0.9	**5E-06**	1.3	3E-01	0.9	**2E-02**	1.0	9E-01	Helicase activity	Nucleus	RNA helicase
8086	**AAAS**	**aladin isoform 1**	4	24	4	**1.5**	**2E-05**	1.0	**8E-06**	1.2	8E-02	1.2	**7E-06**	1.1	**4E-04**	Molecular function unknown	Peroxisome	Unclassified
6672	**SP100**	**nuclear autoantigen Sp-100 isoform 2**	10	60	8	**1.5**	**2E-05**	0.9	**2E-03**	0.8	6E-01	0.4	9E-02	0.9	**1E-03**	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein
3838	**KPNA2**	**importin subunit alpha-1**	7	34	7	**1.5**	**4E-05**	**0.6**	**7E-04**	1.0	**7E-05**	0.7	2E-01	0.8	**7E-05**	Transporter activity	Cytoplasm	Transport/cargo protein
11335; 90416	**CBX3; C15orf57**	**chromobox protein homolog 3**	7	39	6	**1.5**	**1E-04**	0.9	**2E-04**	1.3	2E-01	0.8	5E-02	1.0	4E-01	#N/A	#N/A	#N/A
10199	**MPHOSPH10**	**U3 small nucleolar ribonucleoprotein protein MPP10**	7	22	7	**1.5**	**1E-04**	0.9	**8E-05**	1.3	9E-01	0.8	7E-01	0.9	6E-01	Ribonucleoprotein	Nucleolus	RNA binding protein
23029	**RBM34**	**RNA-binding protein 34 isoform 1**	4	16	4	**1.5**	**1E-04**	1.0	**1E-06**	1.4	2E-01	0.8	4E-01	1.1	4E-01	RNA binding	Nucleolus	RNA binding protein
65005	**MRPL9**	**39S ribosomal protein L9, mitochondrial isoform 1**	5	21	5	**1.5**	**2E-04**	1.0	**3E-04**	1.3	**6E-03**	1.0	**2E-03**	1.0	9E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
59342	**SCPEP1**	**retinoid-inducible serine carboxypeptidase**	6	26	6	**1.5**	**2E-04**	1.1	**2E-04**	**1.5**	**1E-03**	1.0	**2E-03**	1.0	8E-01	Carboxypeptidase activity	Cytoplasm	Carboxypeptidase
30833	**NT5C**	**5'(3')-deoxyribonucleotidase, cytosolic type isoform 1**	4	18	4	**1.5**	**3E-04**	1.2	**1E-04**	**1.7**	**3E-03**	**1.5**	**2E-04**	1.1	4E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
29087	**THYN1**	**thymocyte nuclear protein 1 isoform 1**	9	47	9	**1.5**	**4E-04**	1.0	**3E-04**	1.5	1E-01	0.8	**1E-02**	1.0	5E-01	Molecular function unknown	Nucleus	Unclassified
64968	**MRPS6**	**28S ribosomal protein S6, mitochondrial**	3	16	3	**1.5**	**6E-04**	1.3	**2E-04**	1.3	**8E-03**	1.1	**8E-04**	1.1	6E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
79077	**DCTPP1**	**dCTP pyrophosphatase 1**	5	41	5	**1.5**	**8E-04**	0.7	**5E-04**	1.4	**4E-04**	**0.6**	**3E-03**	1.0	4E-01	Molecular function unknown	-	Unclassified
9377	**COX5A**	**cytochrome c oxidase subunit 5A, mitochondrial**	3	31	3	**1.5**	**9E-04**	1.0	**1E-03**	1.5	9E-02	1.0	**8E-05**	1.0	6E-01	Oxidoreductase activity	Mitochondrion	Regulatory/other subunit
8974	**P4HA2**	**PREDICTED: prolyl 4-hydroxylase subunit alpha-2 isoform X2**	6	23	6	**1.5**	**1E-03**	0.7	**1E-02**	0.8	**1E-02**	**0.7**	**2E-02**	0.8	**3E-04**	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase
54148	**MRPL39**	**39S ribosomal protein L39, mitochondrial isoform a**	5	22	5	**1.5**	**1E-03**	1.2	**7E-04**	1.4	**1E-03**	1.0	**2E-03**	1.0	7E-01	Structural constituent of ribosome;RNA binding	Mitochondrion	Ribosomal subunit
23234	**DNAJC9**	**dnaJ homolog subfamily C member 9**	8	29	8	**1.5**	**1E-03**	0.8	**1E-03**	1.5	8E-02	0.8	**2E-02**	1.0	1E-01	Chaperone activity	-	Chaperone
10557	**RPP38**	**PREDICTED: ribonuclease P protein subunit p38 isoform X1**	4	10	4	**1.5**	**1E-03**	1.0	**2E-02**	1.1	4E-01	0.8	9E-01	1.0	1E+00	Ribonuclease activity	Nucleolus	Ribonucleoprotein
54517	**PUS7**	**pseudouridylate synthase 7 homolog**	5	20	5	**1.5**	**2E-03**	1.0	**8E-03**	1.5	4E-01	0.9	1E-01	1.0	5E-01	Lyase activity	-	Enzyme: Lyase
83443	**SF3B5**	**splicing factor 3B subunit 5**	2	10	2	**1.5**	**2E-03**	1.1	**6E-03**	1.3	**4E-02**	1.1	**1E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
5437	**POLR2H**	**PREDICTED: DNA-directed RNA polymerases I, II, and III subunit RPABC3 isoform X2**	5	22	5	**1.5**	**3E-03**	1.0	**4E-03**	1.5	5E-01	1.1	**2E-04**	1.0	5E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
10491	**CRTAP**	**cartilage-associated protein**	6	29	6	**1.5**	**3E-03**	0.8	**3E-03**	1.1	**4E-03**	0.8	9E-02	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
4236	**MFAP1**	**microfibrillar-associated protein 1**	5	24	4	**1.5**	**4E-03**	1.0	**2E-03**	1.7	3E-01	1.1	**5E-03**	1.0	9E-02	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
51611	**DPH5**	**diphthine synthase isoform a**	4	16	4	**1.5**	**5E-03**	1.0	**3E-03**	1.5	5E-01	0.9	**4E-02**	1.0	4E-01	Molecular function unknown	-	Unclassified
25983	**NGDN**	**neuroguidin isoform 1**	4	18	4	**1.5**	**5E-03**	0.9	**1E-02**	1.5	7E-01	0.8	2E-01	1.1	8E-02	Molecular function unknown	Nucleolus;Nucleus	Unclassified
5925	**RB1**	**retinoblastoma-associated protein**	2	13	2	**1.5**	**6E-03**	0.9	**2E-03**	1.4	9E-01	0.8	5E-01	1.1	7E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
26097	**CHTOP**	**chromatin target of PRMT1 protein isoform 2**	5	17	5	**1.5**	**7E-03**	0.9	**1E-02**	1.5	7E-01	0.8	3E-01	0.9	2E-01	#N/A	#N/A	#N/A
3991	**LIPE**	**hormone-sensitive lipase**	4	21	4	**1.5**	**8E-03**	0.9	**7E-04**	1.4	8E-01	1.1	**2E-02**	1.1	1E-01	Lipase activity	Cytoplasm	Enzyme: Lipase
5698	**PSMB9**	**proteasome subunit beta type-9 proprotein**	2	11	2	**1.5**	**9E-03**	1.0	**2E-02**	1.2	6E-02	1.0	**5E-03**	1.1	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
2962	**GTF2F1**	**general transcription factor IIF subunit 1**	10	24	10	**1.5**	**9E-03**	1.0	**1E-02**	1.2	3E-01	0.9	3E-01	1.1	9E-01	Transcription factor activity	Nucleus	Transcription factor
4696	**NDUFA3**	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3**	2	10	2	**1.5**	**1E-02**	0.8	**2E-02**	1.1	4E-01	0.7	8E-01	1.0	9E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
11270	**NRM**	**nurim isoform 2**	5	14	5	**1.5**	**1E-02**	1.3	**3E-02**	**1.5**	**3E-02**	1.3	**3E-02**	1.2	5E-02	Molecular function unknown	Nucleus	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
2071	**ERCC3**	**TFIIH basal transcription factor complex helicase XPB subunit isoform a**	3	10	3	**1.5**	**1E-02**	1.1	**1E-03**	1.4	9E-02	1.2	**7E-03**	1.1	9E-02	DNA repair protein	Nucleus	DNA repair protein
51264	**MRPL27**	**39S ribosomal protein L27, mitochondrial**	3	16	3	**1.5**	**1E-02**	1.0	**1E-02**	1.3	2E-01	1.0	**6E-03**	1.0	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
55667	**DENND4C**	**DENN domain-containing protein 4C**	7	25	7	**1.5**	**2E-02**	**2.1**	**1E-02**	1.7	8E-02	**1.7**	**8E-03**	1.1	5E-01	Molecular function unknown	Nucleus	Unclassified
11091	**WDR5**	**WD repeat-containing protein 5*gi|16554629|ref|NP_438172.1| WD repeat-containing protein 5**	3	10	3	**1.5**	**2E-02**	1.0	**2E-02**	1.5	3E-01	0.9	1E-01	1.0	1E+00	Histone binding	Cytoplasm	Cell cycle control protein
8602	**NOP14**	**nucleolar protein 14 isoform 1*gi|634743243|ref|NP_001278907.1| nucleolar protein 14 isoform 1**	6	20	6	**1.5**	**2E-02**	0.8	**7E-03**	1.2	5E-01	0.8	9E-01	1.1	7E-02	Molecular function unknown	Nucleus	Unclassified
6942	**TCF20**	**transcription factor 20 isoform 2**	2	7	2	**1.5**	**3E-02**	0.9	**4E-03**	1.4	6E-01	1.0	1E-01	1.0	4E-01	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor
51150	**SDF4**	**45 kDa calcium-binding protein isoform 2**	3	16	3	**1.5**	**3E-02**	1.0	**2E-02**	1.1	9E-02	0.9	6E-02	1.2	2E-01	Calcium ion binding	Golgi lumen	Calcium binding protein
23397	**NCAPH**	**condensin complex subunit 2 isoform 1**	5	17	5	**1.5**	**3E-02**	0.7	**5E-02**	1.2	7E-02	**0.5**	**2E-02**	1.0	7E-01	Molecular function unknown	Nucleolus	Cell cycle control protein
10025	**MED16**	**mediator of RNA polymerase II transcription subunit 16**	3	9	3	**1.5**	**3E-02**	1.1	**3E-02**	1.5	2E-01	1.3	**9E-03**	1.0	7E-01	Transcription factor activity	Nucleus	Transcription factor
4715	**NDUFB9**	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 isoform 1**	2	8	2	**1.5**	**3E-02**	0.8	5E-02	0.9	7E-02	0.7	**4E-02**	0.9	6E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
6422	**SFRP1**	**secreted frizzled-related protein 1**	4	14	4	**1.5**	**3E-02**	1.2	**4E-02**	1.2	**4E-02**	0.8	1E+00	1.4	7E-02	Molecular function unknown	Extracellular	Secreted polypeptide
10200	**MPHOSPH6**	**M-phase phosphoprotein 6**	5	13	5	**1.5**	**4E-02**	1.2	8E-02	1.6	1E-01	1.1	2E-01	1.0	5E-01	Protein binding	Nucleus	Cell cycle control protein
4155	**MBP**	**Golli-MBP isoform 1**	1	6	1	**1.5**	**4E-02**	0.9	**3E-02**	1.2	5E-01	1.0	5E-02	1.3	**6E-03**	Structural constituent of myelin sheath	Plasma membrane;Cytoplasm	Structural protein
64207	**IRF2BPL**	**interferon regulatory factor 2-binding protein-like**	4	13	2	1.5	5E-02	0.9	**4E-02**	1.3	8E-01	0.9	1E-01	0.9	3E-01	#N/A	#N/A	#N/A
219927	**MRPL21**	**39S ribosomal protein L21, mitochondrial isoform d**	2	7	2	1.5	6E-02	1.2	6E-02	1.3	8E-02	1.0	**5E-02**	1.0	4E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
4288	**MKI67**	**antigen KI-67 isoform 1**	2	8	2	1.5	8E-02	0.7	**3E-02**	1.0	8E-02	0.6	1E-01	1.0	7E-01	Protein binding	Nucleolus	Cell cycle control protein
2113	**ETS1**	**protein C-ets-1 isoform 2**	1	6	1	1.5	9E-02	0.9	1E-01	1.4	7E-01	0.9	2E-01	1.0	6E-01	Transcription factor activity	Nucleus	Transcription factor
10084	**PQBP1**	**polyglutamine-binding protein 1 isoform 1**	1	6	1	1.5	1E-01	0.9	1E-01	1.4	4E-01	0.8	5E-01	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
51642	**MRPL48**	**39S ribosomal protein L48, mitochondrial**	1	6	1	1.5	1E-01	1.1	1E-01	1.3	2E-01	1.2	**4E-02**	0.8	6E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
10762	**NUP50**	**nuclear pore complex protein Nup50 isoform b**	4	10	4	1.5	2E-01	0.8	3E-01	1.2	4E-01	1.1	**4E-02**	1.2	3E-01	Transporter activity	Nucleoplasm	Transport/cargo protein
25793	**FBXO7**	**F-box only protein 7 isoform 1**	2	7	2	1.5	2E-01	1.0	9E-02	1.5	2E-01	1.2	2E-01	1.1	1E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
79020	**C7orf25**	**UPF0415 protein C7orf25 isoform a**	1	3	1	1.5	2E-01	1.2	**2E-02**	1.8	6E-01	**4.2**	**2E-02**	**1.9**	**1E-02**	Molecular function unknown	Nucleus	Unclassified
78988	**MRP63; MRPL57**	**ribosomal protein 63, mitochondrial**	2	6	2	1.5	3E-01	1.1	3E-01	1.2	1E-01	0.8	3E-01	1.1	4E-01	#N/A	#N/A	#N/A
84310	**C7orf50**	**uncharacterized protein C7orf50**	3	5	3	1.5	7E-01	1.4	5E-01	1.4	3E-01	1.0	4E-01	1.3	3E-01	Molecular function unknown	Nucleus	Unclassified
1.01E+08	**PTGES3L-AARSD1**	**PTGES3L-AARSD1 protein isoform 1**	3	12	3	1.5	#N/A	0.9	#N/A	1.2	#N/A	0.7	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
79154	**DHRS11**	**dehydrogenase/reductase SDR family member 11**	2	10	2	0.6	5E-02	0.9	9E-01	0.7	7E-01	1.1	**3E-02**	0.9	1E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
10809	**STARD10**	**PCTP-like protein**	2	8	2	0.5	5E-02	1.0	**1E-02**	0.6	3E-01	1.0	2E-01	0.9	2E-01	Molecular function unknown	-	Unclassified
1515	**CTSL2; CTSV**	**cathepsin L2 preproprotein**	4	27	4	0.6	6E-02	0.9	8E-01	0.7	2E-01	**2.1**	**7E-04**	1.2	**8E-04**	#N/A	#N/A	#N/A
132864	**CPEB2**	**cytoplasmic polyadenylation element-binding protein 2 isoform D**	3	8	3	0.6	6E-02	1.2	5E-01	0.7	8E-02	0.7	7E-01	1.0	7E-01	RNA binding	Cytoplasm	RNA binding protein
284348	**LYPD5**	**ly6/PLAUR domain-containing protein 5 isoform A**	2	16	2	0.3	7E-02	1.5	9E-01	0.7	7E-02	**3.8**	**4E-02**	1.3	**3E-02**	Molecular function unknown	-	Unclassified
4014	**LOR**	**loricrin**	1	6	1	0.4	8E-02	**7.4**	**4E-02**	**0.4**	**4E-02**	**2.0**	**3E-02**	**1.7**	**2E-02**	Structural molecule activity	Plasma membrane	Structural protein
64065	**PERP**	**p53 apoptosis effector related to PMP-22**	2	10	2	0.6	8E-02	0.8	6E-02	0.4	7E-01	0.6	1E+00	1.0	6E-01	Molecular function unknown	Plasma membrane	Unclassified
2878	**GPX3**	**glutathione peroxidase 3**	1	8	1	0.6	1E-01	**2.1**	**3E-02**	1.0	**5E-02**	**1.8**	**2E-02**	0.9	1E+00	Peroxidase activity	Extracellular	Enzyme: Peroxidase
388697	**HRNR**	**hornerin**	3	11	3	0.4	1E-01	0.9	4E-01	0.5	4E-01	1.4	**5E-03**	**1.7**	**7E-03**	Molecular function unknown	Plasma membrane	Unclassified
11345	**GABARAPL2**	**gamma-aminobutyric acid receptor-associated protein-like 2**	5	41	4	0.6	1E-01	0.9	2E-01	0.6	7E-01	1.2	**5E-07**	1.1	**2E-02**	Transporter activity	Golgi apparatus	Transport/cargo protein
245973	**ATP6V1C2**	**V-type proton ATPase subunit C 2 isoform a**	3	14	2	0.6	1E-01	1.7	6E-01	0.9	1E-01	1.3	**4E-02**	**1.6**	**1E-02**	ATPase activity	-	ATPase
5630	**PRPH**	**peripherin**	7	45	3	0.4	1E-01	1.2	3E-01	0.5	1E-01	1.1	**3E-02**	1.1	5E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
2335	**FN1**	**fibronectin isoform 1 preproprotein**	5	20	5	0.5	1E-01	0.4	5E-01	**0.6**	**4E-02**	0.8	3E-01	**1.6**	**2E-02**	Extracellular matrix structural constituent	Extracellular;Nucleus	Extracellular matrix protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7053	**TGM3**	**protein-glutamine gamma-glutamyltransferase E**	3	10	3	0.5	1E-01	1.4	9E-02	1.1	8E-02	2.0	7E-02	1.0	2E-01	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase
114569	**MAL2**	**protein MAL2**	1	6	1	0.6	1E-01	1.1	1E-01	0.5	1E-01	0.8	2E-01	1.1	2E-01	Transporter activity	Endosome	Transport/cargo protein
5292	**PIM1**	**serine/threonine-protein kinase pim-1 isoform 1**	3	9	3	0.5	1E-01	1.1	4E-01	0.6	3E-01	1.1	5E-02	1.0	3E-01	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase
51218	**GLRX5**	**glutaredoxin-related protein 5, mitochondrial**	2	11	2	0.7	1E-01	1.0	1E-01	1.5	2E-01	2.6	2E-01	0.9	6E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
5412	**UBL3**	**ubiquitin-like protein 3**	1	6	1	0.7	1E-01	0.9	2E-01	0.7	9E-01	**2.8**	**6E-03**	1.2	8E-02	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
3801	**KIFC3**	**kinesin-like protein KIFC3 isoform 1**	3	15	2	0.6	2E-01	1.1	4E-01	0.8	9E-02	1.3	**2E-02**	1.0	6E-01	Motor activity	Cytoplasm	Motor protein
84283	**TMEM79**	**transmembrane protein 79**	3	10	3	0.4	2E-01	0.8	2E-01	0.5	1E-01	1.0	5E-02	0.8	1E-01	Molecular function unknown	Integral to membrane	Unclassified
84290	**CAPNS2**	**calpain small subunit 2**	10	68	8	0.6	2E-01	1.0	5E-01	0.6	8E-02	0.9	**3E-07**	0.9	**2E-03**	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
25819	**CCRN4L; NOCT**	**nocturnin**	2	8	2	0.6	2E-01	0.7	4E-01	0.6	3E-01	0.9	3E-01	0.9	6E-01	#N/A	#N/A	#N/A
11219	**TREX2**	**three prime repair exonuclease 2**	5	22	5	0.4	2E-01	1.4	4E-01	0.9	**1E-02**	**9.3**	**2E-02**	1.2	2E-01	Deoxyribonuclease activity	Nucleus	DNA exonuclease;Deoxyribonuclease
563	**AZGP1**	**zinc-alpha-2-glycoprotein**	2	10	2	0.5	2E-01	1.8	3E-01	0.6	1E-01	3.4	5E-02	2.0	7E-02	Cell adhesion molecule activity	Extracellular	Adhesion molecule
3034	**HAL**	**histidine ammonia-lyase isoform 1**	3	8	3	0.5	3E-01	1.6	2E-01	0.5	2E-01	1.6	3E-01	0.8	6E-01	Lyase activity	Cytoplasm	Enzyme: Lyase
144110	**TMEM86A**	**lysoplasmalogenase-like protein TMEM86A**	1	3	1	0.3	3E-01	0.9	4E-01	0.7	3E-01	3.3	8E-02	1.2	2E-01	Molecular function unknown	-	Integral membrane protein
84525	**HOPX**	**homeodomain-only protein isoform a**	1	6	1	0.1	3E-01	1.6	3E-01	0.4	3E-01	1.2	3E-01	1.5	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
262	**AMD1**	**S-adenosylmethionine decarboxylase proenzyme isoform 1**	4	8	4	0.6	3E-01	0.9	5E-01	0.9	1E+00	0.9	3E-01	0.9	9E-02	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase
11076	**TPPP**	**tubulin polymerization-promoting protein**	1	6	1	0.6	3E-01	0.8	1E-01	1.0	4E-01	**1.5**	**4E-02**	0.9	4E-01	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
55432	**YOD1**	**PREDICTED: ubiquitin thioesterase OTU1 isoform X1**	2	9	2	0.6	4E-01	1.5	2E-01	0.8	**2E-03**	**2.6**	**5E-03**	**1.5**	**5E-03**	DNA binding	-	DNA binding protein
11254	**SLC6A14**	**sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)**	2	7	2	0.6	4E-01	1.2	7E-01	0.7	6E-02	**1.6**	**3E-02**	1.2	6E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
145226	**RDH12**	**retinol dehydrogenase 12**	7	39	5	0.4	4E-01	1.0	**4E-02**	**0.6**	**1E-05**	0.8	**1E-04**	0.9	3E-01	Catalytic activity	Plasma membrane	Enzyme: Dehydrogenase
10254	**STAM2**	**signal transducing adapter molecule 2**	6	25	6	0.6	5E-01	1.3	5E-01	0.7	1E-01	0.7	1E+00	1.0	1E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
4938	**OAS1**	**2'-5'-oligoadenylate synthase 1 isoform 3**	2	7	1	0.6	5E-01	0.9	1E-01	0.4	1E+00	0.3	9E-02	0.7	**6E-03**	Ligase activity	Cytoplasm	Enzyme: Ligase
10170	**DHRS9**	**dehydrogenase/reductase SDR family member 9 isoform 2**	3	12	3	0.6	5E-01	1.1	7E-02	1.7	4E-01	9.8	8E-02	1.0	2E-01	Catalytic activity	Integral to membrane	Enzyme: Dehydrogenase
1768	**DNAH6**	**PREDICTED: dynein heavy chain 6, axonemal isoform X1**	2	4	2	0.6	5E-01	0.9	3E-01	0.8	7E-01	1.2	**2E-02**	1.0	4E-01	Nucleotide binding	-	Unclassified
5653	**KLK6**	**kallikrein-6 isoform A preproprotein**	2	7	2	0.2	7E-01	1.0	1E-01	0.9	2E-01	**3.1**	**4E-02**	1.8	1E-01	Serine-type peptidase activity	Cytoplasm	Serine protease
10642	**IGF2BP1**	**insulin-like growth factor 2 mRNA-binding protein 1 isoform 1**	3	14	2	0.2	7E-01	1.5	3E-01	0.5	2E-01	0.9	**3E-02**	1.6	9E-02	RNA binding	Cytoplasm	RNA binding protein
6623	**SNCG**	**gamma-synuclein**	5	15	5	0.6	8E-01	0.8	1E-01	1.0	6E-01	2.4	1E-01	1.0	9E-01	Chaperone activity	Cytoplasm	Chaperone
8689	**KRT36**	**keratin, type I cuticular Ha6**	4	536	1	0.6	9E-01	1.0	7E-01	0.5	2E-01	0.9	**6E-03**	1.1	**2E-02**	Structural molecule activity	-	Structural protein
723961	**INS-IGF2**	**insulin, isoform 2**	1	12	1	0.5	#N/A	0.7	#N/A	0.7	#N/A	1.4	#N/A	1.1	#N/A	#N/A	#N/A	#N/A
27076	**LYPD3**	**ly6/PLAUR domain-containing protein 3**	7	62	7	**0.7**	**9E-04**	1.3	7E-01	0.7	**2E-08**	**0.5**	**3E-08**	0.7	**8E-10**	Molecular function unknown	-	Unclassified
10999	**SLC27A4**	**long-chain fatty acid transport protein 4**	15	61	14	0.7	8E-02	1.0	**3E-04**	0.9	**4E-04**	1.4	**2E-03**	1.0	**8E-03**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
389337	**ARHGEF37**	**PREDICTED: rho guanine nucleotide exchange factor 37 isoform X2**	5	7	5	0.7	#N/A	1.0	#N/A	0.8	#N/A	1.0	#N/A	0.8	#N/A	#N/A	#N/A	#N/A
4688	**NCF2**	**PREDICTED: neutrophil cytosol factor 2 isoform X1**	8	35	8	**0.7**	**3E-03**	1.0	**2E-05**	1.3	7E-02	**1.5**	**2E-05**	1.0	7E-01	Catalytic activity	Cytoplasm	Enzyme: Oxidase
10103	**TSPAN1**	**tetraspanin-1**	1	6	1	**0.7**	**6E-03**	**0.3**	**4E-02**	**0.4**	**2E-02**	0.8	8E-01	1.2	**4E-02**	-	Plasma membrane;Cell surface	-
126917	**IFFO2**	**intermediate filament family orphan 2**	8	32	8	**0.7**	**5E-03**	1.2	**4E-03**	**0.6**	**1E-03**	**0.6**	**6E-04**	0.8	**2E-04**	Molecular function unknown	-	Unclassified
3047	**HBG1**	**hemoglobin subunit gamma-1**	3	31	3	**0.7**	**1E-02**	1.2	**3E-04**	1.3	**3E-03**	**2.8**	**6E-04**	1.2	**1E-04**	Transporter activity	-	Transport/cargo protein
51200	**CPA4**	**carboxypeptidase A4 preproprotein**	5	20	5	**0.7**	**1E-02**	0.7	7E-01	0.7	**8E-03**	**2.7**	**5E-03**	1.0	4E-01	Metallopeptidase activity	-	Metallo protease
837;	**CASP4**	**caspase-4 isoform alpha**	14	30	14	0.7	6E-02	0.8	7E-01	0.8	9E-01	0.9	3E-01	0.9	6E-02	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
6990	**DYNLT3**	**dynein light chain Tctex-type 3**	1	6	1	0.7	8E-02	1.2	8E-01	0.8	**9E-03**	1.2	**1E-03**	0.9	3E-01	Molecular function unknown	-	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
204219	**CERS3**	**PREDICTED: ceramide synthase 3 isoform X1**	6	43	6	**0.7**	**4E-05**	**1.6**	**5E-08**	1.0	**3E-07**	**1.7**	**2E-07**	1.1	**1E-03**	#N/A	#N/A	#N/A
2281	**FKBP1B**	**peptidyl-prolyl cis-trans isomerase FKBP1B isoform a**	2	11	2	0.7	2E-01	1.0	5E-01	0.8	2E-01	0.6	5E-01	0.9	6E-01	Isomerase activity	Cytoplasm	Enzyme: Isomerase
6278	**S100A7**	**protein S100-A7**	3	12	3	0.7	1E-01	0.9	9E-01	0.7	1E-01	**2.4**	**3E-04**	0.7	**2E-02**	Calcium ion binding	Cytoplasm	Calcium binding protein
26154	**ABCA12**	**ATP-binding cassette sub-family A member 12 isoform a**	14	47	14	0.7	1E-01	1.2	2E-01	0.8	**3E-04**	1.2	**5E-06**	1.1	**3E-03**	Transporter activity	Plasma membrane	Transport/cargo protein
85456	**TNKS1BP1**	**PREDICTED: 182 kDa tankyrase-1-binding protein isoform X3**	35	105	1	0.7	7E-01	**1.5**	**1E-11**	1.0	**2E-16**	**1.9**	**2E-02**	1.1	**4E-12**	Molecular function unknown	Nucleus	Unclassified
3859	**KRT12**	**keratin, type I cytoskeletal 12**	8	883	2	**0.7**	**3E-02**	1.1	6E-02	0.6	1E-01	1.1	**6E-03**	1.2	**3E-02**	Structural molecule activity	Nucleus	Structural protein
79861	**TUBAL3**	**tubulin alpha chain-like 3 isoform 1**	5	324	1	**0.7**	**4E-06**	0.9	**2E-16**	0.8	4E-01	0.9	**2E-16**	0.9	6E-01	Structural molecule activity	-	Structural protein
81607	**PVRL4; NECTIN4**	**nectin-4**	12	45	12	**0.7**	**1E-02**	1.1	2E-01	0.8	**1E-03**	0.8	5E-01	1.0	4E-01	#N/A	#N/A	#N/A
5317	**PKP1**	**plakophilin-1 isoform 1a**	34	324	34	**0.7**	**2E-16**	1.0	**2E-16**	**0.5**	**2E-05**	**0.4**	**2E-16**	0.7	**2E-16**	Cell adhesion molecule activity	Nucleus	Cell junction protein
29984	**RHOD**	**rho-related GTP-binding protein RhoD isoform 1**	7	28	7	**0.7**	**2E-04**	1.0	**1E-03**	**0.7**	**8E-05**	1.1	**6E-05**	0.9	**7E-04**	GTPase activity	Plasma membrane	GTPase
56169	**GSDMC**	**gasdermin-C**	10	42	10	**0.7**	**3E-03**	1.0	**3E-04**	0.9	**9E-04**	1.2	**7E-06**	0.9	9E-02	Transcription factor activity	Nucleus	Transcription factor
29108	**PYCARD**	**apoptosis-associated speck-like protein containing a CARD isoform a**	8	64	7	**0.7**	**3E-04**	1.1	**1E-04**	0.8	**5E-06**	**0.6**	**2E-05**	0.8	**6E-07**	Caspase activator activity	Cytoplasm	Adapter molecule
5478	**PPIA**	**peptidyl-prolyl cis-trans isomerase A isoform 2**	11	315	2	**0.7**	**2E-16**	1.1	**2E-16**	0.7	1E-01	0.8	**2E-16**	0.9	7E-01	Isomerase activity	Cytoplasm	Enzyme: Isomerase
79017	**GGCT**	**gamma-glutamylcyclotransferase isoform 1**	7	40	7	**0.7**	**4E-04**	1.0	**1E-03**	0.8	**3E-03**	0.9	**1E-07**	1.0	9E-01	Molecular function unknown	-	Unclassified
9540	**TP53I3**	**quinone oxidoreductase PIG3 isoform 1*gi|22538446|ref|NP_671713.1| quinone oxidoreductase PIG3 isoform 1**	6	25	6	0.7	6E-02	**0.7**	**2E-04**	0.9	**2E-02**	1.1	**1E-03**	1.0	6E-01	Oxidoreductase activity	Cytoplasm	Cell cycle control protein
54809	**SAMD9**	**sterile alpha motif domain-containing protein 9**	12	31	12	**0.7**	**3E-03**	0.7	**6E-03**	**0.5**	**4E-02**	0.7	1E-01	0.8	**2E-03**	Molecular function unknown	-	Unclassified
5824	**PEX19**	**peroxisomal biogenesis factor 19 isoform a**	7	30	7	0.7	5E-01	0.7	9E-01	0.8	3E-01	0.9	8E-01	0.8	**3E-02**	Protein binding	Cytoplasm	Integral membrane protein
81706	**PPP1R14C**	**protein phosphatase 1 regulatory subunit 14C**	4	15	4	0.7	5E-01	1.0	2E-01	0.7	5E-02	0.6	1E-01	0.9	**4E-02**	Molecular function unknown	Integral to membrane	Regulatory/other subunit
84961	**FBXL20**	**F-box/LRR-repeat protein 20 isoform 1**	2	8	2	0.7	7E-01	1.2	2E-01	0.8	**1E-02**	1.4	**5E-02**	1.0	4E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
9531	**BAG3**	**BAG family molecular chaperone regulator 3**	16	131	16	**0.7**	**3E-05**	1.0	5E-01	0.7	**6E-05**	1.1	**5E-11**	1.0	1E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
10066	**SCAMP2**	**PREDICTED: secretory carrier-associated membrane protein 2 isoform X1**	4	5	4	0.7	7E-02	1.0	7E-01	**0.7**	**4E-02**	1.1	**4E-02**	0.9	5E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
9367	**RAB9A**	**ras-related protein Rab-9A**	9	41	9	**0.7**	**1E-02**	1.0	**5E-05**	0.9	**1E-04**	1.2	**6E-07**	1.0	1E-01	Molecular function unknown	Endosome	Unclassified
120224	**TMEM45B**	**transmembrane protein 45B**	3	18	3	0.7	3E-01	1.4	**7E-04**	1.1	**8E-03**	**2.1**	**6E-03**	1.1	9E-02	Molecular function unknown	Integral to membrane	Integral membrane protein
754	**PTTG1IP**	**pituitary tumor-transforming gene 1 protein-interacting protein isoform 1**	2	10	2	0.7	2E-01	1.0	5E-01	0.7	7E-02	1.4	**3E-02**	1.0	8E-01	Transporter activity	Nucleus	Transport/cargo protein
8416	**ANXA9**	**annexin A9**	1	4	1	0.7	9E-01	1.5	5E-01	0.9	**2E-03**	1.3	7E-02	0.9	1E+00	Calcium ion binding	Cytoplasm	Calcium binding protein
1718	**DHCR24**	**delta(24)-sterol reductase**	7	58	7	0.7	**3E-03**	1.2	**7E-05**	1.2	**3E-06**	1.4	**2E-05**	1.0	7E-01	Catalytic activity	Plasma membrane	Enzyme: Reductase
6662	**SOX9**	**transcription factor SOX-9**	4	14	4	0.7	**3E-02**	1.2	5E-01	0.8	1E-01	0.8	6E-01	0.9	5E-01	Transcription factor activity	Nucleus	Transcription factor
79784	**MYH14**	**myosin-14 isoform 3**	19	226	7	0.7	**3E-08**	0.9	**2E-10**	0.6	1E-01	0.9	**9E-13**	1.1	2E-01	Structural molecule activity	-	Structural protein
216	**ALDH1A1**	**retinal dehydrogenase 1**	8	36	6	0.7	3E-01	0.9	7E-01	0.7	1E-01	1.2	**5E-04**	1.1	9E-01	Aldehyde dehydrogenase activity	-	Enzyme: Dehydrogenase
81790	**RNF170**	**E3 ubiquitin-protein ligase RNF170 isoform a**	4	14	4	0.7	7E-01	1.0	5E-01	0.7	4E-01	0.7	6E-01	0.9	5E-01	Molecular function unknown	-	Unclassified
5595	**MAPK3**	**mitogen-activated protein kinase 3 isoform 1**	13	114	8	0.7	**1E-03**	1.1	**7E-07**	1.1	**5E-04**	**1.7**	**5E-06**	1.0	3E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
79086	**SMIM7**	**small integral membrane protein 7 isoform 1**	1	6	1	0.7	1E+00	1.1	8E-01	0.7	**4E-02**	1.1	8E-02	1.2	2E-01	#N/A	#N/A	#N/A
545	**ATR**	**serine/threonine-protein kinase ATR**	1	5	1	0.7	**1E-03**	0.8	**3E-03**	0.7	6E-01	0.7	2E-01	0.9	7E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
6713	**SQLE**	**squalene monooxygenase**	13	63	13	0.7	1E-01	1.0	8E-02	0.8	2E-01	0.8	6E-01	0.9	4E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase
9231	**DLG5**	**disks large homolog 5**	3	6	3	0.7	7E-01	1.1	5E-01	0.8	4E-01	1.0	3E-01	1.0	3E-01	Cell adhesion molecule activity	Plasma membrane;Nucleus	Cell junction protein
84557	**MAP1LC3A**	**microtubule-associated proteins 1A/1B light chain 3A isoform b**	2	8	1	0.7	1E+00	1.0	6E-01	0.7	7E-01	1.2	**4E-03**	0.9	8E-01	Cytoskeletal protein binding	Unknown membrane	Cytoskeletal associated protein
6712	**SPTBN2**	**spectrin beta chain, non-erythrocytic 2**	56	246	44	0.7	1E+00	1.3	**1E-09**	0.8	**2E-16**	1.1	**1E-10**	1.0	6E-01	Cytoskeletal protein binding	Golgi apparatus	Cytoskeletal associated protein
5268	**SERPINB5**	**serpin B5**	22	974	22	0.7	**2E-10**	1.0	**2E-16**	1.0	**2E-14**	1.0	**2E-16**	0.9	**7E-06**	Protease inhibitor activity	Cytoplasm	Protease inhibitor

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3728	JUP	junction plakoglobin	36	598	29	0.7	**3E-15**	1.0	**2E-10**	0.7	**2E-16**	**0.6**	**2E-16**	0.9	**3E-05**	Cell adhesion molecule activity	Cytoplasm	Adhesion molecule
79671	NLRX1	NLR family member X1*gi|531034767|ref|NP_001269072.1|NLR family member X1*gi|531034770|ref|NP_001269073.1|NLR family member X1*gi|537544581|ref|NP_001269287.1|NLR family member X1	6	31	6	0.7	**1E-02**	1.2	**1E-02**	0.8	**3E-04**	1.3	**7E-06**	1.0	7E-01	Molecular function unknown	-	Unclassified
301	ANXA1	annexin A1	20	476	20	0.7	**8E-12**	0.7	**2E-16**	0.9	**2E-16**	1.3	**2E-16**	1.0	**6E-04**	Calcium ion binding	Plasma membrane	Calcium binding protein
2770	GNAI1	guanine nucleotide-binding protein G(i) subunit alpha-1 isoform 1	9	98	3	0.7	**4E-02**	1.2	**3E-04**	0.9	**7E-04**	**0.7**	**1E-02**	0.9	2E-01	GTPase activity	Plasma membrane	G protein
9052	GPRC5A	retinoic acid-induced protein 3	1	6	1	0.7	4E-01	0.8	6E-01	0.8	7E-01	1.8	1E-01	1.1	7E-01	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor
760	CA2	carbonic anhydrase 2 isoform 1	11	130	11	0.7	**2E-04**	1.4	**1E-04**	0.8	**3E-09**	0.8	**1E-03**	0.9	**7E-05**	Catalytic activity	Cytoplasm	Enzyme: Carbonic anhydrase
11214	AKAP13	A-kinase anchor protein 13 isoform 1	10	27	10	0.7	3E-01	0.9	8E-01	0.8	4E-01	1.1	**2E-02**	0.9	2E-01	Guanyl-nucleotide exchange factor activity	Plasma membrane	Guanine nucleotide exchange factor
10890	RAB10	ras-related protein Rab-10	15	252	12	0.7	**3E-02**	1.1	**2E-16**	0.9	**3E-15**	1.3	**2E-16**	1.0	**2E-04**	GTPase activity	Nucleus;Golgi vesicle	GTPase
5329	PLAUR	urokinase plasminogen activator surface receptor isoform 1	3	7	3	0.7	1E-01	1.1	3E-01	0.9	2E-01	1.0	2E-01	1.4	1E-01	Receptor activity	Plasma membrane	Cell surface receptor
79746	ECHDC3	enoyl-CoA hydratase domain-containing protein 3, mitochondrial	1	5	1	0.7	4E-01	1.2	2E-01	1.0	6E-02	1.2	2E-01	0.9	5E-01	Molecular function unknown	-	Unclassified
146691	TOM1L2	TOM1-like protein 2 isoform 3	10	42	10	0.7	**4E-02**	1.1	**3E-02**	0.8	**9E-05**	1.1	**1E-06**	0.9	3E-01	Transporter activity	-	Transport/cargo protein
23473	CAPN7	calpain-7	3	7	3	0.7	7E-01	0.8	2E-01	1.0	3E-01	0.6	5E-01	1.0	9E-01	Cysteine-type peptidase activity	Nucleus	Cysteine protease
5333	PLCD1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 isoform 1	17	90	17	0.7	**2E-02**	1.1	**2E-06**	0.9	**2E-06**	1.3	**2E-12**	0.9	1E-01	Phospholipase activity	Plasma membrane	Enzyme: Phospholipase
997	CDC34	ubiquitin-conjugating enzyme E2 R1	3	10	2	0.7	7E-01	0.9	2E-01	0.8	8E-01	3.5	2E-01	1.1	2E-01	Ligase activity	Nucleus	Enzyme: Ligase
79603	CERS4	PREDICTED: ceramide synthase 4 isoform X1	1	6	1	0.7	8E-01	1.3	5E-01	0.9	**1E-02**	0.6	5E-01	1.0	8E-01	#N/A	#N/A	#N/A
242	ALOX12B	arachidonate 12-lipoxygenase, 12R-type	6	16	6	0.7	**3E-02**	1.1	3E-01	1.0	2E-01	1.2	**3E-03**	1.1	7E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
8266	UBL4A	ubiquitin-like protein 4A	7	36	7	0.7	6E-01	0.7	2E-01	0.9	1E-01	0.7	6E-01	0.7	8E-02	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
23582	CCNDBP1	cyclin-D1-binding protein 1	3	10	3	0.7	1E-01	0.7	3E-01	0.8	9E-02	1.1	**1E-02**	0.7	**3E-02**	Molecular function unknown	Extracellular	Unclassified
55222	LRRC20	leucine-rich repeat-containing protein 20 isoform 1	2	7	2	0.7	2E-01	0.8	2E-01	0.6	4E-01	**1.5**	**2E-02**	1.1	2E-01	Molecular function unknown	-	Unclassified
2745	GLRX	glutaredoxin-1	2	8	2	0.7	2E-01	1.0	**2E-02**	1.1	6E-02	**2.2**	**3E-02**	1.0	6E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
9520	NPEPPS	puromycin-sensitive aminopeptidase	37	273	37	0.7	**3E-10**	0.9	7E-02	0.7	**2E-04**	1.1	**2E-16**	0.9	**3E-07**	Aminopeptidase activity	Cytoplasm	Aminopeptidase
54843	SYTL2	PREDICTED: synaptotagmin-like protein 2 isoform X3	2	3	2	0.7	5E-01	1.0	8E-01	0.7	5E-01	0.8	8E-01	0.8	**4E-03**	Molecular function unknown	Endosome	Unclassified
7873	MANF	mesencephalic astrocyte-derived neurotrophic factor	10	74	10	0.7	1E-01	1.1	**2E-04**	0.9	**4E-03**	0.9	**7E-05**	1.1	**4E-02**	Molecular function unknown	Cytoplasm	Unclassified
2065	ERBB3	receptor tyrosine-protein kinase erbB-3 isoform 1	3	6	3	0.7	4E-01	1.4	2E-01	1.0	**3E-02**	1.3	9E-02	1.2	8E-02	Transmembrane receptor protein tyrosine kinase activity	Extracellular	Receptor tyrosine kinase
221079	ARL5B	ADP-ribosylation factor-like protein 5B	2	9	2	0.7	1E+00	1.2	3E-01	0.7	4E-01	1.0	**2E-02**	0.8	6E-01	GTPase activity	-	GTPase
11187	PKP3	plakophilin-3 isoform PKP3b	35	258	35	0.7	**1E-02**	1.1	**1E-03**	0.8	**1E-13**	0.9	**5E-05**	0.9	**2E-02**	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
818	CAMK2G	calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 1	8	30	5	0.7	5E-01	1.2	2E-01	0.9	2E-01	1.2	8E-02	1.0	2E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
83442	SH3BGRL3	SH3 domain-binding glutamic acid-rich-like protein 3	6	80	6	0.7	7E-01	0.8	**6E-05**	0.9	**2E-04**	0.8	2E-01	0.9	**2E-03**	Molecular function unknown	Cytoplasm	Unclassified
55577	NAGK	N-acetyl-D-glucosamine kinase	12	61	12	0.7	**3E-02**	1.0	**1E-04**	0.9	**1E-05**	1.0	**6E-08**	0.9	6E-01	Catalytic activity	-	Enzyme: Phosphotransferase
57530	CGN	cingulin	12	33	12	0.7	5E-01	1.1	6E-01	0.9	**2E-02**	**1.9**	**5E-04**	1.3	**3E-02**	Cell adhesion molecule activity	Nucleus	Cell junction protein
150696	PROM2	prominin-2	1	6	1	0.7	**3E-02**	1.1	4E-01	0.8	2E-01	0.9	1E-01	1.0	8E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
10247	HRSP12; RIDA	ribonuclease UK114	4	24	4	0.7	5E-01	0.6	6E-01	0.8	2E-01	0.8	7E-01	**0.6**	**5E-02**	#N/A	#N/A	#N/A
8407	TAGLN2	transgelin-2 isoform a	16	340	15	0.7	**3E-02**	0.9	1E-01	0.7	6E-01	**0.7**	**3E-04**	1.1	5E-02	Molecular function unknown	-	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
79689	**STEAP4**	**metalloreductase STEAP4 isoform 1*gi|328887949|ref|NP_001192244.1| metalloreductase STEAP4 isoform 1**	4	12	4	0.7	4E-01	0.8	8E-01	0.8	6E-01	0.9	8E-02	0.9	7E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
23002	**DAAM1**	**disheveled-associated activator of morphogenesis 1 isoform 1**	5	10	5	0.7	8E-01	1.1	**1E-02**	1.0	8E-01	1.1	1E-01	1.2	3E-01	Molecular function unknown	Cytoplasm;Nucleus	Unclassified
10381	**TUBB3**	**tubulin beta-3 chain isoform 1**	18	688	4	0.7	**5E-06**	**0.6**	**2E-07**	**0.6**	**1E-08**	0.9	**2E-06**	0.9	**4E-07**	Structural molecule activity	Cytoplasm	Structural protein
23052	**ENDOD1**	**endonuclease domain-containing 1 protein**	7	30	7	0.7	9E-02	1.2	**8E-03**	0.8	**3E-05**	1.1	**6E-06**	1.0	9E-01	Molecular function unknown	-	Unclassified
817	**CAMK2D**	**calcium/calmodulin-dependent protein kinase type II subunit delta isoform 3**	12	70	9	0.7	**3E-03**	1.1	**1E-05**	0.9	**6E-04**	**1.7**	**8E-06**	1.1	6E-02	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
29982	**NRBF2**	**nuclear receptor-binding factor 2 isoform 1**	3	16	3	0.7	**2E-02**	0.8	**3E-02**	0.9	**3E-02**	1.2	**5E-04**	0.9	**2E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
57016	**AKR1B10**	**aldo-keto reductase family 1 member B10**	10	50	10	0.7	3E-01	**2.6**	**2E-03**	0.9	**2E-04**	1.0	**5E-05**	1.1	5E-01	Catalytic activity	-	Enzyme: Reductase
8638	**OASL**	**2'-5'-oligoadenylate synthase-like protein isoform a**	7	23	7	0.7	3E-01	1.0	3E-01	0.8	**2E-03**	**1.5**	**7E-04**	**1.5**	**3E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
10457	**GPNMB**	**transmembrane glycoprotein NMB isoform a**	2	31	2	0.7	2E-01	1.2	8E-01	0.7	**7E-05**	**0.6**	**2E-02**	0.9	**2E-02**	Molecular function unknown	Plasma membrane	Integral membrane protein;Unclassified
388	**RHOB**	**rho-related GTP-binding protein RhoB**	3	16	1	0.7	6E-01	1.1	3E-01	0.9	1E-01	1.3	**2E-03**	1.1	2E-01	GTPase activity	Plasma membrane	GTPase
6236	**RRAD**	**GTP-binding protein RAD**	4	13	4	0.7	2E-01	1.3	9E-02	1.4	7E-02	3.1	8E-02	1.4	8E-02	GTPase activity	Cytoplasm	GTPase
2885	**GRB2**	**growth factor receptor-bound protein 2 isoform 1**	6	32	6	0.7	3E-01	0.9	4E-01	0.8	1E+00	0.8	5E-01	1.0	5E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
205; 100507855	**AK4; LOC100507855**	**adenylate kinase 4, mitochondrial**	9	70	9	0.7	**8E-03**	0.9	5E-01	0.7	9E-01	0.8	8E-01	0.9	**4E-02**	#N/A	#N/A	#N/A
537	**ATP6AP1**	**V-type proton ATPase subunit S1**	9	50	9	0.7	**2E-02**	1.1	**2E-02**	0.8	**5E-03**	1.2	**2E-06**	1.1	**4E-03**	Transporter activity	-	Transport/cargo protein
8655	**DYNLL1**	**dynein light chain 1, cytoplasmic**	4	43	2	0.7	2E-01	1.2	1E+00	0.7	**1E-02**	0.9	**6E-03**	0.8	**1E-02**	Motor activity	Cytoplasm	Motor protein
6050	**RNH1**	**PREDICTED: ribonuclease inhibitor isoform X1**	22	294	22	0.8	**2E-10**	0.9	**2E-16**	0.9	**2E-02**	0.9	**2E-16**	0.8	**2E-16**	Translation regulator activity	Cytoplasm	Translation regulatory protein
2934	**GSN**	**gelsolin isoform b**	26	182	26	0.8	**4E-03**	1.1	**6E-05**	0.9	**2E-13**	1.2	**6E-09**	1.0	6E-01	Structural constituent of cytoskeleton	Extracellular	Cytoskeletal protein
55057	**AIM1L**	**PREDICTED: absent in melanoma 1-like protein isoform X1**	14	55	14	0.8	**7E-03**	1.0	**8E-05**	1.2	**2E-04**	**1.7**	**4E-06**	0.8	**1E-03**	Molecular function unknown	-	Unclassified
8139	**GAN**	**gigaxonin**	9	34	9	0.8	2E-01	1.1	6E-01	0.9	8E-01	1.3	3E-01	1.0	4E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
957	**ENTPD5**	**ectonucleoside triphosphate diphosphohydrolase 5**	1	6	1	0.8	6E-01	1.3	**4E-02**	1.0	1E-01	1.1	1E-01	0.9	9E-01	Hydrolase activity	Extracellular	Enzyme: Hydrolase
7430	**EZR**	**ezrin**	38	629	23	0.8	**1E-03**	1.0	**6E-13**	0.8	**1E-09**	0.9	**2E-16**	0.9	**4E-08**	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein
85379	**KIAA1671**	**uncharacterized protein KIAA1671**	16	53	16	0.8	1E+00	1.1	**3E-02**	0.9	**4E-02**	0.7	7E-01	1.0	5E-01	Molecular function unknown	-	Unclassified
8775	**NAPA**	**alpha-soluble NSF attachment protein**	16	87	16	0.8	**3E-02**	1.0	**2E-02**	0.8	**3E-05**	0.9	**7E-06**	0.9	**1E-05**	Receptor signaling complex scaffold activity	Golgi apparatus	Adapter molecule
523	**ATP6V1A**	**V-type proton ATPase catalytic subunit A**	20	146	20	0.8	**4E-02**	1.1	**6E-09**	0.9	**8E-09**	1.4	**8E-12**	1.0	6E-01	Transporter activity	Endosome	Transport/cargo protein
51;	**ACOX1**	**peroxisomal acyl-coenzyme A oxidase 1 isoform a**	14	36	9	0.8	3E-01	1.2	**2E-06**	1.0	**2E-04**	**1.5**	**6E-06**	1.0	**5E-02**	Catalytic activity	Peroxisome;Nucleus	Enzyme: Oxidase
51382	**ATP6V1D**	**V-type proton ATPase subunit D**	10	63	10	0.8	2E-01	1.1	**7E-05**	0.8	**3E-06**	1.2	**2E-06**	0.9	**5E-02**	ATPase activity	Integral to membrane	ATPase
2584	**GALK1**	**galactokinase**	6	28	6	0.8	3E-01	1.2	**8E-06**	1.1	**1E-04**	**1.7**	**6E-06**	0.9	**5E-02**	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
3872	**KRT17**	**keratin, type I cytoskeletal 17**	53	9925	29	0.8	**7E-08**	1.1	**2E-13**	**0.7**	**2E-16**	1.0	**2E-16**	1.1	**2E-16**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
218	**ALDH3A1**	**aldehyde dehydrogenase, dimeric NADP-preferring**	3	9	2	0.8	#N/A	2.7	#N/A	2.8	#N/A	2.7	#N/A	1.0	#N/A	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
51763	**INPP5K**	**inositol polyphosphate 5-phosphatase K isoform 1**	3	8	3	0.8	8E-01	1.0	**6E-03**	0.9	**3E-02**	1.1	**4E-02**	0.9	1E+00	Lipid phosphatase activity	Golgi apparatus;Endoplasmic reticulum	Lipid phosphatase
140609	**NEK7**	**serine/threonine-protein kinase Nek7**	7	24	7	0.8	1E-01	0.9	**4E-02**	0.8	4E-01	0.9	**6E-04**	0.9	5E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
23384	**SPECC1L**	**cytospin-A isoform 1**	10	26	9	0.8	3E-01	1.2	2E-01	0.7	8E-02	0.9	**3E-02**	0.9	7E-01	#N/A	#N/A	#N/A
25989	**ULK3**	**serine/threonine-protein kinase ULK3 isoform a**	1	5	1	0.8	6E-01	1.3	6E-01	0.8	3E-01	0.9	1E-01	1.1	4E-01	Protein serine/threonine kinase activity	-	Serine/threonine kinase
3898	**LAD1**	**ladinin-1**	31	250	31	0.8	**3E-03**	1.0	**6E-15**	0.9	**5E-12**	1.0	**2E-16**	1.0	5E-01	Cytoskeletal anchoring activity	Plasma membrane	Anchor protein
9026	**HIP1R**	**huntingtin-interacting protein 1-related protein isoform 1**	17	64	16	0.8	5E-01	1.1	**4E-05**	0.9	**5E-04**	**1.6**	**6E-12**	1.0	1E-01	Cytoskeletal protein binding	Cytoplasmic vesicle	Cytoskeletal associated protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
5603	**MAPK13**	**mitogen-activated protein kinase 13**	10	58	9	0.8	5E-01	1.2	**2E-05**	0.9	**1E-07**	1.0	**5E-06**	0.9	**8E-04**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
51465	**UBE2J1**	**ubiquitin-conjugating enzyme E2 J1**	3	17	3	0.8	6E-01	1.0	**1E-02**	1.0	1E-01	**1.5**	**5E-03**	1.0	6E-01	Ubiquitin-specific protease activity	Endoplasmic reticulum	Ubiquitin proteasome system protein
201562	**PTPLB; HACD2**	**very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2**	3	16	3	0.8	1E+00	1.3	7E-01	0.8	**2E-02**	1.2	**5E-02**	1.1	2E-01	#N/A	#N/A	#N/A
5644	**PRSS1**	**trypsin-1 preproprotein**	3	42	2	0.8	2E-01	1.6	4E-01	0.7	**5E-04**	1.1	**2E-03**	**1.7**	**4E-03**	Serine-type peptidase activity	Extracellular	Serine protease
50807	**ASAP1**	**arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 isoform 1**	4	19	3	0.8	1E-01	0.9	**3E-02**	0.7	1E-01	1.1	**5E-03**	0.9	8E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
6342	**SCP2**	**non-specific lipid-transfer protein isoform 1 proprotein**	11	70	11	0.8	4E-01	1.2	**2E-04**	1.0	**5E-07**	1.1	**8E-09**	0.9	**3E-03**	Auxiliary transport protein activity;Sterol transporter activity	Cytoplasm	Membrane transport protein
6415	**SEPW1**	**selenoprotein W**	3	8	3	0.8	6E-01	0.9	3E-01	0.9	5E-01	0.6	6E-01	1.0	7E-01	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase
9414	**TJP2**	**tight junction protein ZO-2 isoform 3**	44	274	43	0.8	**3E-02**	0.9	**7E-12**	0.9	2E-01	1.2	**2E-16**	1.0	**2E-06**	Cell adhesion molecule activity	Cytoplasm	Cell junction protein
144108	**SPTY2D1**	**protein SPT2 homolog**	3	9	3	0.8	7E-01	0.8	8E-02	0.8	9E-01	0.7	2E-01	0.8	4E-01	Molecular function unknown	-	Unclassified
2664	**GDI1**	**rab GDP dissociation inhibitor alpha**	16	177	9	0.8	**6E-07**	1.0	**1E-15**	1.1	**6E-03**	1.4	**4E-14**	0.9	4E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
1890	**TYMP**	**thymidine phosphorylase isoform 2 proprotein**	14	69	14	0.8	1E-01	0.9	**3E-04**	0.6	4E-01	**0.6**	**2E-04**	0.9	**1E-04**	Growth factor activity	Extracellular	Growth factor
91942	**NDUFAF2**	**mimitin, mitochondrial**	11	64	11	0.8	7E-01	0.9	**5E-07**	1.2	7E-01	1.2	**8E-06**	0.6	2E-01	Molecular function unknown	Mitochondrion	Unclassified
2886	**GRB7**	**growth factor receptor-bound protein 7 isoform b**	6	17	6	0.8	5E-01	1.0	**2E-02**	1.0	**4E-02**	1.2	6E-02	0.9	3E-01	Binding	Plasma membrane	Adapter molecule
146050;	**ZSCAN29**	**zinc finger and SCAN domain-containing protein 29**	3	6	2	0.8	9E-01	0.8	1E-01	1.0	6E-01	3.0	1E-01	2.3	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
645	**BLVRB**	**flavin reductase (NADPH)**	6	54	6	0.8	4E-01	1.1	1E-01	1.0	9E-01	1.4	**5E-02**	0.9	**1E-02**	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
388115	**C15orf52**	**uncharacterized protein C15orf52**	3	13	3	0.8	2E-01	1.2	8E-02	1.7	2E-01	**3.0**	**6E-03**	**1.5**	**2E-02**	Molecular function unknown	-	Unclassified
83786	**FRMD8**	**FERM domain-containing protein 8 isoform 1**	4	13	4	0.8	6E-01	1.1	**4E-02**	1.0	4E-01	0.8	6E-01	0.8	2E-01	Cytoskeletal protein binding	-	Cytoskeletal associated protein
5052	**PRDX1**	**peroxiredoxin-1**	14	362	11	0.8	8E-01	0.9	**8E-16**	1.0	**2E-02**	1.1	**2E-16**	1.0	3E-01	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase
56006;	**SMG9**	**protein SMG9**	31	76	31	0.8	5E-01	1.0	**2E-10**	0.9	**6E-07**	**0.6**	**1E-02**	0.9	**4E-05**	#N/A	#N/A	#N/A
78991	**PCYOX1L**	**prenylcysteine oxidase-like isoform 1**	4	15	4	0.8	6E-01	1.4	**2E-02**	1.0	**9E-03**	0.9	**1E-03**	0.9	**5E-02**	Molecular function unknown	-	Unclassified
1824	**DSC2**	**desmocollin-2 isoform Dsc2a preproprotein**	13	75	13	0.8	6E-01	0.8	7E-02	0.8	**5E-05**	0.8	**7E-04**	0.7	**2E-08**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
3241	**HPCAL1**	**PREDICTED: hippocalcin-like protein 1 isoform X1**	9	43	9	0.8	5E-01	1.0	**8E-03**	0.9	4E-01	1.0	**4E-05**	1.0	3E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
79670	**ZCCHC6**	**terminal uridylyltransferase 7 isoform 1*gi|58331272|ref|NP_078893.2| terminal uridylyltransferase 7 isoform 1**	16	52	16	0.8	6E-01	1.2	**3E-06**	0.9	**2E-04**	1.0	**6E-08**	1.1	**3E-03**	DNA binding	Nucleus	DNA binding protein
3306	**HSPA2**	**heat shock-related 70 kDa protein 2**	28	537	15	0.8	**2E-16**	1.2	**2E-16**	0.9	**5E-07**	1.1	**6E-14**	0.9	**4E-16**	Heat shock protein activity	Nucleus	Heat shock protein
25831	**HECTD1**	**E3 ubiquitin-protein ligase HECTD1**	30	59	30	0.8	3E-01	0.9	**2E-02**	0.8	5E-02	1.3	**6E-07**	1.0	3E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
5297	**PI4KA**	**phosphatidylinositol 4-kinase alpha**	3	6	3	0.8	3E-01	1.2	2E-01	0.9	2E-01	1.2	1E-01	1.0	9E-01	Lipid kinase activity	Golgi apparatus	Lipid Kinase
2055	**CLN8**	**PREDICTED: protein CLN8 isoform X1**	2	8	2	0.8	6E-01	1.4	3E-01	0.9	1E-01	2.3	2E-01	**1.5**	**2E-02**	Molecular function unknown	Plasma membrane	Integral membrane protein
2026	**ENO2**	**gamma-enolase**	5	72	2	0.8	2E-01	0.9	**1E-02**	1.0	9E-01	0.9	**3E-02**	0.8	2E-01	Catalytic activity	Cytoplasm	Enzyme: Hydratase
8675	**STX16**	**syntaxin-16 isoform a**	3	14	3	0.8	4E-01	0.9	5E-01	0.9	5E-01	0.9	8E-01	0.9	2E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
51361	**HOOK1**	**protein Hook homolog 1**	17	75	17	0.8	5E-01	1.1	**1E-02**	0.8	**1E-04**	1.1	**2E-10**	1.0	5E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
1974	**EIF4A2**	**eukaryotic initiation factor 4A-II**	19	274	8	0.8	9E-01	1.0	**2E-03**	1.0	**6E-03**	1.1	**2E-05**	1.0	8E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
3664	**IRF6**	**interferon regulatory factor 6 isoform 1**	12	101	12	0.8	5E-01	0.7	**2E-13**	1.0	**1E-07**	**0.7**	**2E-03**	0.9	**2E-05**	Transcription factor activity	Nucleus	Transcription factor
3557	**IL1RN**	**interleukin-1 receptor antagonist protein isoform 2**	6	83	6	0.8	5E-01	0.8	**8E-05**	1.1	**6E-03**	1.2	**3E-09**	0.8	**2E-05**	Cytokine activity	Extracellular	Cytokine
10226	**PLIN3**	**perilipin-3 isoform 1**	20	141	2	0.8	**2E-05**	0.8	**1E-12**	1.1	**4E-03**	1.1	**2E-16**	1.0	4E-01	Transporter activity	Cytoplasm	Transport/cargo protein
2588	**GALNS**	**N-acetylgalactosamine-6-sulfatase**	4	18	3	0.8	1E-01	0.9	**2E-02**	1.0	7E-02	1.2	**9E-03**	0.9	4E-01	Catalytic activity	Lysosome	Enzyme: Sulphatase
831	**CAST**	**PREDICTED: calpastatin isoform X2**	36	144	36	0.8	4E-01	1.1	**9E-13**	0.9	**1E-14**	1.3	**2E-16**	1.0	4E-01	Protease inhibitor activity	Nucleus;Cytoplasm;Perinuclear region	Protease inhibitor
254102	**EHBP1L1**	**EH domain-binding protein 1-like protein 1**	8	20	6	0.8	3E-01	1.2	**1E-03**	1.0	**3E-04**	0.8	6E-02	0.9	9E-01	Molecular function unknown	-	Unclassified
57614	**KIAA1468**	**PREDICTED: lisH domain and HEAT repeat-containing protein KIAA1468 isoform X3**	12	21	12	0.8	8E-01	1.1	**3E-03**	0.9	**3E-02**	**1.9**	**5E-03**	1.2	**4E-02**	Molecular function unknown	Cytoplasm	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9547	CXCL14	C-X-C motif chemokine 14	2	6	2	0.8	#N/A	2.7	#N/A	0.3	#N/A	0.4	#N/A	1.0	#N/A	Chemokine activity	-	Chemokine
54502	RBM47	PREDICTED: RNA-binding protein 47 isoform X2	4	16	4	0.8	5E-01	0.9	**1E-03**	1.0	6E-01	1.3	**1E-03**	0.9	3E-01	RNA binding	-	RNA binding protein
10654	PMVK	phosphomevalonate kinase	9	42	9	0.8	6E-01	1.3	**1E-05**	0.9	**1E-06**	0.9	**8E-07**	0.9	**1E-02**	Lipid kinase activity	Peroxisome	Lipid Kinase
283635	FAM177A1	protein FAM177A1 isoform 1	4	10	4	0.8	7E-01	0.8	1E-01	1.0	8E-01	1.1	1E-01	1.0	9E-01	Molecular function unknown	-	Unclassified
10749	KIF1C	kinesin-like protein KIF1C	16	67	11	0.8	1E+00	0.9	**4E-04**	0.9	8E-01	0.9	**3E-02**	0.8	8E-02	Motor activity	Golgi apparatus	Motor protein
5328	PLAU	urokinase-type plasminogen activator isoform 1 preproprotein	6	28	6	0.8	4E-01	0.9	**2E-02**	0.9	1E+00	1.0	**3E-04**	1.1	**5E-02**	Serine-type peptidase activity	Plasma membrane	Serine protease
203	AK1	PREDICTED: adenylate kinase isoenzyme 1 isoform X1	12	70	12	0.8	7E-01	1.3	**2E-09**	1.1	**3E-07**	1.4	**1E-09**	1.0	1E+00	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
84270	C9orf89; CARD19	bcl10-interacting CARD protein	3	10	3	0.8	3E-01	0.8	**2E-02**	1.0	2E-01	1.1	**2E-02**	0.9	5E-01	#N/A	#N/A	#N/A
10554	AGPAT1	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	2	7	2	0.8	4E-01	1.2	**2E-02**	1.3	2E-01	1.4	7E-02	1.3	**5E-02**	Acyltransferase activity	Endoplasmic reticulum membrane	Enzyme: Acyltransferase
64855	FAM129B	niban-like protein 1 isoform 1	24	227	24	0.8	6E-01	0.9	**2E-16**	1.0	8E-02	1.2	**2E-16**	0.9	**1E-07**	Molecular function unknown	Nucleus	Unclassified
192666	KRT24	keratin, type I cytoskeletal 24	12	645	8	0.8	**3E-06**	1.4	**1E-09**	**0.6**	**4E-08**	1.3	9E-01	**1.7**	**5E-03**	Structural molecule activity	-	Structural protein
64834	ELOVL1	elongation of very long chain fatty acids protein 1 isoform 1	2	10	2	0.8	6E-01	1.1	**4E-02**	1.2	1E-01	1.7	6E-02	1.2	**2E-02**	Molecular function unknown	-	Unclassified
54472	TOLLIP	toll-interacting protein	7	30	7	0.8	8E-01	1.1	**3E-03**	0.9	**1E-05**	1.1	**3E-06**	0.9	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
7286	TUFT1	tuftelin isoform 3	11	45	11	0.8	9E-01	1.0	1E+00	0.7	6E-02	1.0	**1E-02**	0.9	**2E-02**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
5868	RAB5A	ras-related protein Rab-5A isoform 1	6	41	3	0.8	**7E-03**	1.1	**6E-04**	1.0	**4E-02**	**1.5**	**1E-06**	1.0	8E-02	GTPase activity	Plasma membrane	GTPase
23673	STX12	syntaxin-12	6	37	6	0.8	4E-01	1.0	**7E-05**	0.9	**1E-02**	1.2	**8E-06**	0.9	8E-01	Auxiliary transport protein activity	Endosome	Membrane transport protein
1466	CSRP2	cysteine and glycine-rich protein 2	9	53	9	0.8	5E-01	0.7	2E-01	0.8	**1E-03**	**0.6**	**1E-02**	0.9	8E-02	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
7108	TM7SF2	delta(14)-sterol reductase isoform 1	3	9	3	0.8	8E-01	1.3	5E-01	0.7	**4E-02**	1.1	**5E-02**	1.0	4E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase
307	ANXA4	PREDICTED: annexin A4 isoform X1	18	193	17	0.8	9E-01	1.0	**4E-04**	0.8	**3E-10**	0.8	**5E-05**	0.9	**2E-02**	Calcium ion binding	Nucleus	Calcium binding protein
28962	OSTM1	osteopetrosis-associated transmembrane protein 1	2	9	2	0.8	1E+00	1.0	**6E-03**	1.0	6E-01	1.0	**4E-02**	0.9	**3E-02**	Molecular function unknown	Plasma membrane	Unclassified
55276	PGM2	phosphoglucomutase-2	22	116	21	0.8	5E-01	1.2	**1E-11**	0.9	**4E-09**	1.0	**3E-08**	1.0	2E-01	Catalytic activity	-	Enzyme: Phosphotransferase
221496	LEMD2	LEM domain-containing protein 2 isoform 1	12	59	12	0.8	8E-01	1.1	**1E-03**	1.0	**1E-05**	1.4	**9E-05**	1.0	1E+00	Molecular function unknown	Integral to membrane	Integral membrane protein
54623	PAF1	RNA polymerase II-associated factor 1 homolog isoform 1	4	11	4	0.8	4E-01	1.0	7E-02	0.8	4E-01	1.0	7E-02	1.0	1E+00	Molecular function unknown	Nucleus	Unclassified
1725	DHPS	deoxyhypusine synthase isoform a	4	15	4	0.8	5E-01	0.9	**2E-03**	1.1	2E-01	1.1	**2E-03**	0.9	**4E-02**	Transferase activity	-	Enzyme: Synthase
23218	NBEAL2	neurobeachin-like protein 2	18	62	18	0.8	5E-01	1.2	**2E-06**	1.0	**1E-03**	1.1	**1E-07**	1.0	4E-01	Molecular function unknown	-	Unclassified
51606	ATP6V1H	V-type proton ATPase subunit H isoform 1	14	81	14	0.8	5E-01	1.1	**1E-06**	0.9	**4E-06**	1.3	**2E-06**	1.0	7E-01	ATPase activity	-	ATPase
23012	STK38L	serine/threonine-protein kinase 38-like	9	33	7	0.8	1E-01	1.3	**8E-07**	1.1	**7E-03**	1.3	**1E-04**	1.1	8E-02	Protein serine/threonine kinase activity	-	Serine/threonine kinase
51706	CYB5R1	NADH-cytochrome b5 reductase 1	12	131	12	0.8	4E-01	1.3	2E-01	0.8	**1E-07**	1.1	**3E-06**	1.0	1E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase
128876	FAM83C	protein FAM83C	5	18	5	0.8	9E-01	1.2	**1E-02**	0.9	**9E-04**	0.8	7E-01	0.9	1E-01	Molecular function unknown	-	Unclassified
3983	ABLIM1	actin-binding LIM protein 1 isoform a	13	48	11	0.8	4E-01	1.3	**8E-03**	0.8	**1E-04**	0.9	**1E-03**	0.9	**1E-02**	Cytoskeletal protein binding	Actin cytoskeleton;Nucleus	Cytoskeletal associated protein
29085	PHPT1	14 kDa phosphohistidine phosphatase isoform 3	6	36	6	0.8	6E-01	1.2	5E-02	0.8	**4E-05**	0.9	**2E-03**	0.9	**3E-02**	Phosphoprotein phosphatase activity	Cytoplasm	Enzyme: Phosphatase
5002	SLC22A18	PREDICTED: solute carrier family 22 member 18 isoform X8	3	18	3	0.8	7E-01	1.2	6E-02	1.1	**3E-03**	1.1	7E-02	0.9	3E-01	Auxiliary transport protein activity;Ion transporter activity	Plasma membrane	Membrane transport protein
8821	INPP4B	type II inositol 3,4-bisphosphate 4-phosphatase	5	16	5	0.8	9E-01	0.7	**2E-03**	1.0	5E-02	**1.7**	**1E-02**	1.0	5E-02	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
1E+08	TSTD1	thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1 isoform 1	5	38	5	0.8	6E-01	1.0	**1E-05**	0.9	**2E-02**	0.9	**2E-02**	0.8	**6E-04**	Molecular function unknown	-	Unclassified
22924	MAPRE3	microtubule-associated protein RP/EB family member 3*gi|733216453|ref|NP_001289979.1| microtubule-associated protein RP/EB family member 3	8	38	5	0.8	3E-01	1.0	6E-01	0.8	6E-01	1.0	8E-02	1.0	3E-01	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein
55655	NLRP2	NACHT, LRR and PYD domains-containing protein 2 isoform 1*gi|8923473|ref|NP_060322.1| NACHT, LRR and PYD domains-containing protein 2 isoform 1	21	88	21	0.8	8E-01	0.8	**9E-03**	0.8	6E-02	0.7	**2E-02**	0.8	**1E-05**	Molecular function unknown	Cytoplasm	Unclassified

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
22824	HSPA4L	heat shock 70 kDa protein 4L	30	93	3	0.8	2E-01	1.0	7E-01	0.7	**3E-06**	**0.7**	**2E-05**	0.8	**2E-09**	Heat shock protein activity	Cytoplasm	Heat shock protein
56904	SH3GLB2	endophilin-B2 isoform b*gi|9910352|ref|NP_064530.1| endophilin-B2 isoform b	10	57	9	0.8	6E-01	1.2	**6E-06**	1.0	**2E-05**	1.3	**7E-07**	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
54953	C1orf27	protein odr-4 homolog isoform 1	6	18	6	0.8	5E-01	1.1	8E-02	0.8	**9E-03**	1.2	**2E-02**	1.1	4E-01	Molecular function unknown	Integral to membrane	Unclassified
79174	CRELD2	cysteine-rich with EGF-like domain protein 2 isoform a	4	12	4	0.8	6E-01	0.9	6E-01	0.8	1E-01	0.9	6E-02	0.8	5E-01	Calcium ion binding	Extracellular	Calcium binding protein
91624	NEXN	nexilin isoform 1	2	6	2	0.8	7E-01	1.0	2E-01	0.6	5E-01	0.8	4E-01	1.1	4E-01	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
50618	ITSN2	intersectin-2 isoform 1	11	28	10	0.8	1E+00	1.1	**4E-05**	0.9	**3E-04**	**1.5**	**1E-04**	1.2	**4E-03**	Protein domain specific binding	Endosome;Cytoplasm	Adapter molecule
9453	GGPS1	geranylgeranyl pyrophosphate synthase	8	32	8	0.8	6E-01	1.0	**1E-04**	1.0	1E-01	1.4	**1E-04**	1.0	8E-01	Transferase activity	Cytoplasm	Enzyme: Prenyltransferase
81932	HDHD3	haloacid dehalogenase-like hydrolase domain-containing protein 3	2	12	2	0.8	6E-01	1.2	**2E-04**	1.0	**8E-03**	1.3	**4E-04**	1.0	6E-01	Hydrolase activity	-	Enzyme: Hydrolase
7172	TPMT	thiopurine S-methyltransferase	8	38	8	0.8	6E-01	0.8	**2E-04**	0.8	**9E-03**	0.9	**3E-04**	0.9	**8E-03**	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase
127829	ARL8A	ADP-ribosylation factor-like protein 8A isoform 1	9	65	2	0.8	2E-01	1.1	**6E-07**	1.1	**2E-07**	1.4	**2E-09**	1.1	2E-01	GTPase activity	-	GTPase
85456	TNKS1BP1	182 kDa tankyrase-1-binding protein	55	338	21	0.8	7E-01	1.0	**1E-11**	0.8	**2E-16**	0.8	**2E-02**	0.9	**4E-12**	Molecular function unknown	Nucleus	Unclassified
9961	MVP	major vault protein isoform 1	30	241	30	0.8	8E-01	0.9	**2E-13**	0.8	**3E-02**	1.1	**2E-16**	1.0	1E-01	Nucleocytoplasmic transporter activity	Cytoplasm	Transport/cargo protein
57458	TMCC3	transmembrane and coiled-coil domains protein 3 isoform 1	3	12	3	0.8	8E-01	0.7	**4E-02**	0.9	6E-02	1.2	**2E-02**	1.0	4E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
10424	PGRMC2	membrane-associated progesterone receptor component 2	7	60	6	0.8	6E-01	1.1	**5E-05**	0.9	**2E-06**	1.4	**1E-08**	1.0	**5E-02**	Steroid hormone receptor activity	Plasma membrane	Integral membrane protein
1152	CKB	creatine kinase B-type	6	21	6	0.8	2E-01	1.0	**3E-02**	**0.5**	**1E-02**	1.0	**3E-04**	0.9	9E-02	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
27071	DAPP1	dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	5	18	5	0.8	4E-01	1.0	**3E-02**	0.9	2E-01	1.2	**1E-02**	1.3	**4E-03**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
65083	NOL6	nucleolar protein 6 alpha isoform	5	12	5	0.8	5E-01	1.0	9E-01	0.6	3E-01	0.6	5E-02	1.0	4E-01	RNA binding	Nucleolus	RNA binding protein
3304; 3303	HSPA1B; HSPA1A	heat shock 70 kDa protein 1A/1B*gi|167466173|ref|NP_005337.2| heat shock 70 kDa protein 1A/1B	36	747	30	0.8	9E-01	0.8	**2E-16**	0.9	**6E-14**	1.1	**2E-16**	0.9	**9E-08**	#N/A	#N/A	#N/A
8682	PEA15	astrocytic phosphoprotein PEA-15 isoform a	8	84	8	0.8	3E-01	1.0	**2E-05**	0.8	**4E-02**	0.8	7E-01	0.9	**4E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
978	CDA	cytidine deaminase	3	14	3	0.8	9E-01	1.0	**2E-03**	1.1	5E-01	**1.7**	**1E-02**	0.9	2E-01	Deaminase activity	Nucleus	Enzyme: Deaminase
89848	FCHSD1	FCH and double SH3 domains protein 1	2	12	2	0.8	9E-01	1.0	2E-01	0.9	1E-01	**3.9**	**1E-02**	1.2	6E-02	Receptor signaling complex scaffold activity	-	Adapter molecule
3939	LDHA	L-lactate dehydrogenase A chain isoform 3	20	810	19	0.8	4E-01	0.9	**3E-02**	0.7	**9E-08**	0.7	**5E-04**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
9114	ATP6V0D1	V-type proton ATPase subunit d 1	8	72	8	0.8	8E-01	1.0	**5E-07**	0.9	**7E-06**	1.1	**3E-07**	1.0	6E-01	ATPase activity	-	ATPase
11313	LYPLA2	acyl-protein thioesterase 2	8	57	8	0.8	7E-02	1.0	**2E-05**	0.9	**1E-03**	1.1	**9E-07**	1.0	7E-01	Phospholipase activity	-	Enzyme: Phospholipase
2760	GM2A	ganglioside GM2 activator isoform 1	6	60	6	0.8	3E-01	**1.8**	**2E-06**	1.3	**3E-07**	**1.9**	**5E-07**	0.9	**2E-02**	Transporter activity	Lysosome	Transport/cargo protein
493	ATP2B4	plasma membrane calcium-transporting ATPase 4 isoform 4b	29	149	19	0.8	5E-01	1.2	**2E-10**	1.2	**1E-07**	1.4	**1E-10**	1.1	1E-01	ATPase activity	Plasma membrane	ATPase
9526	MPDU1	mannose-P-dolichol utilization defect 1 protein	1	16	1	0.8	1E-01	1.0	**7E-03**	1.0	**2E-04**	1.1	**1E-03**	1.0	7E-02	Molecular function unknown	Integral to membrane	Integral membrane protein
80271	ITPKC	inositol-trisphosphate 3-kinase C	10	51	10	0.8	8E-01	1.0	**5E-05**	0.9	**3E-04**	**1.6**	**3E-08**	1.0	1E-01	Lipid kinase activity	Cytoplasm	Lipid Kinase
55738	ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1 isoform a	5	22	5	0.8	2E-01	0.9	**4E-03**	0.9	3E-01	0.9	**9E-03**	0.9	4E-01	GTPase activator activity	Golgi apparatus	GTPase activating protein
81	ACTN4	PREDICTED: alpha-actinin-4 isoform X1	57	644	6	0.8	**1E-03**	1.0	**4E-09**	0.8	5E-02	1.2	**2E-16**	1.0	6E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
3853	KRT6A	keratin, type II cytoskeletal 6A	66	15257	4	0.8	4E-01	1.4	2E-01	0.7	**2E-16**	0.9	**2E-16**	1.3	**2E-16**	Structural molecule activity	Cytoplasm	Structural protein
669	BPGM	bisphosphoglycerate mutase	4	15	4	0.8	6E-02	**0.7**	**1E-02**	0.9	1E-01	0.9	**2E-02**	0.8	**1E-02**	Catalytic activity	-	Enzyme: Mutase
1429	CRYZ	quinone oxidoreductase isoform a	13	102	13	0.8	5E-01	1.0	**7E-11**	0.9	**1E-08**	0.9	**8E-08**	1.0	4E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
51727	CMPK1	UMP-CMP kinase isoform a	5	50	5	0.8	5E-01	1.0	**4E-03**	0.9	**2E-03**	1.0	**2E-07**	1.0	7E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
23423	TMED3	transmembrane emp24 domain-containing protein 3 isoform a	5	33	5	0.8	3E-01	1.2	**9E-03**	0.8	**1E-03**	0.8	8E-01	0.9	3E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
23682	RAB38	ras-related protein Rab-38	8	51	6	0.8	5E-01	0.9	**4E-03**	0.8	6E-01	**0.6**	**6E-04**	0.9	**2E-03**	GTPase activity	Cytoplasm	GTPase
427	ASAH1	acid ceramidase isoform b	10	51	10	0.8	7E-01	0.9	**2E-04**	0.9	9E-01	1.0	**1E-02**	0.9	**2E-02**	Hydrolase activity	Lysosome	Enzyme: Hydrolase
348938	NIPAL4	magnesium transporter NIPA4 isoform 1	3	8	3	0.8	4E-01	1.1	4E-01	0.8	2E-01	0.9	5E-01	1.0	2E-01	Transmembrane receptor activity	Plasma membrane	Transport/cargo protein
65991	FUNDC2	FUN14 domain-containing protein 2	2	10	2	0.8	8E-01	1.1	**2E-03**	0.9	**5E-02**	1.0	**6E-03**	1.0	**3E-02**	Molecular function unknown	Nucleus	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
526	ATP6V1B2	V-type proton ATPase subunit B, brain isoform	22	185	22	0.8	3E-01	1.1	**2E-16**	1.0	**6E-14**	1.3	**2E-16**	0.9	**1E-02**	Transporter activity	Endosome	Transport/cargo protein
10314	LANCL1	lanC-like protein 1	7	37	7	0.8	3E-01	1.0	**7E-03**	0.8	**1E-02**	0.8	6E-02	0.9	**3E-04**	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor
5358	PLS3	plastin-3 isoform 1*gi|7549809|ref|NP_005023.2| plastin-3 isoform 1	35	537	25	0.8	3E-01	0.9	**3E-07**	0.8	**4E-03**	0.9	**2E-16**	1.0	1E-01	Structural molecule activity	Cytoplasm	Structural protein
8773	SNAP23	PREDICTED: synaptosomal-associated protein 23 isoform X1	7	31	7	0.8	7E-01	0.7	9E-01	0.8	1E-01	0.8	8E-01	0.7	2E-01	Transporter activity	Plasma membrane	Transport/cargo protein
221035	REEP3	receptor expression-enhancing protein 3	4	18	4	0.8	3E-01	1.0	9E-02	0.8	2E-01	0.9	1E-01	1.0	9E-01	Molecular function unknown	-	Unclassified
5230	PGK1	phosphoglycerate kinase 1	29	577	24	0.8	**2E-02**	0.9	**8E-10**	0.8	**2E-08**	0.8	**7E-03**	0.9	**5E-13**	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
6809	STX3	PREDICTED: syntaxin-3 isoform X1	3	12	3	0.8	8E-01	1.0	**5E-02**	0.9	4E-01	0.9	2E-01	1.0	6E-01	Transporter activity	Plasma membrane	Transport/cargo protein
113146	AHNAK2	protein AHNAK2	158	1172	156	0.8	**7E-04**	1.0	**4E-02**	0.7	**2E-16**	**0.6**	**2E-16**	0.9	**1E-10**	Molecular function unknown	Nucleus	Unclassified
2810	SFN	14-3-3 protein sigma	24	1522	20	0.8	1E-01	1.1	**2E-16**	1.0	**2E-16**	1.0	**2E-16**	1.0	7E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
23650	TRIM29	tripartite motif-containing protein 29	34	443	34	0.8	3E-01	1.3	2E-01	0.8	**2E-16**	**0.6**	**2E-07**	0.8	**2E-13**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
9411	ARHGAP29	PREDICTED: rho GTPase-activating protein 29 isoform X1	1	6	1	0.8	4E-01	0.7	**3E-02**	1.0	2E-01	1.3	5E-02	1.2	2E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
10965	ACOT2	acyl-coenzyme A thioesterase 2, mitochondrial	4	45	4	0.8	2E-01	1.1	**5E-08**	1.0	**3E-07**	1.1	**6E-09**	1.0	7E-02	Hydrolase activity	Peroxisome	Enzyme: Hydrolase
55740	ENAH	protein enabled homolog isoform a	15	76	15	0.8	5E-01	0.9	**3E-02**	0.8	2E-01	0.7	**2E-02**	0.8	**2E-05**	Structural constituent of cytoskeleton	Cytoplasm;Nucleus	Cytoskeletal protein
55207	ARL8B	ADP-ribosylation factor-like protein 8B	11	96	4	0.8	**3E-02**	1.2	**1E-05**	1.1	**2E-03**	**1.5**	**7E-04**	1.0	5E-01	GTPase activity	Cytoskeleton	GTPase
26229	B3GAT3	galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 isoform 1	4	15	4	0.8	4E-01	1.1	7E-02	0.8	2E-01	1.1	**5E-03**	1.0	1E+00	Transferase activity	Golgi apparatus	Integral membrane protein
9476	NAPSA	PREDICTED: napsin-A isoform X1	1	6	1	0.8	7E-01	1.1	7E-01	0.7	7E-02	0.7	1E-01	0.9	3E-01	Aspartic-type signal peptidase activity	Cytoplasm	Aspartic protease
9525	VPS4B	vacuolar protein sorting-associated protein 4B	17	128	11	0.8	**3E-05**	0.9	**7E-09**	0.9	3E-01	1.1	**2E-11**	0.9	**3E-06**	Transporter activity	Perinuclear region	Transport/cargo protein
2950	GSTP1	glutathione S-transferase P	14	725	14	0.8	**9E-03**	1.1	**2E-16**	0.9	**2E-16**	0.9	**2E-16**	0.9	**9E-07**	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase
57406	ABHD6	monoacylglycerol lipase ABHD6	4	15	4	0.8	4E-01	1.0	5E-01	0.7	6E-02	0.8	4E-01	1.0	2E-01	Molecular function unknown	-	Unclassified
830	CAPZA2	F-actin-capping protein subunit alpha-2	9	135	7	0.8	**1E-06**	1.0	**6E-15**	0.9	1E-01	1.0	**2E-13**	0.9	9E-02	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
6801	STRN	striatin	12	63	11	0.8	7E-02	1.1	**5E-07**	0.9	**5E-08**	1.3	**1E-08**	1.0	8E-01	Molecular function unknown	Cytoplasm	Unclassified
9550	ATP6V1G1	V-type proton ATPase subunit G 1	4	24	4	0.8	2E-01	1.3	**3E-03**	1.0	**2E-02**	1.4	**2E-03**	1.0	7E-01	Transporter activity	Lysosome	Transport/cargo protein
10938	EHD1	EH domain-containing protein 1 isoform 2	26	190	22	0.8	**1E-02**	0.7	**2E-11**	0.9	**4E-09**	1.2	**2E-16**	1.0	8E-02	Calcium ion binding	Plasma membrane	Calcium binding protein
10423	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase isoform 1	3	14	3	0.8	2E-01	1.2	**5E-02**	0.8	**8E-04**	1.2	**4E-03**	1.3	9E-02	Transferase activity	Integral to membrane	Enzyme: Transferase
26355	FAM162A	protein FAM162A	6	47	6	0.8	8E-01	1.4	**4E-05**	1.1	**4E-04**	1.2	**2E-04**	1.0	2E-01	Molecular function unknown	-	Unclassified
3916	LAMP1	lysosome-associated membrane glycoprotein 1	6	63	6	0.8	1E-01	1.0	**7E-05**	0.9	**6E-04**	0.8	**3E-02**	1.0	8E-01	Molecular function unknown	Lysosome	Integral membrane protein
84293	FAM213A	PREDICTED: redox-regulatory protein FAM213A isoform X1	10	91	10	0.8	1E-01	1.2	**1E-06**	1.0	**2E-07**	1.1	**5E-09**	1.0	5E-01	#N/A	#N/A	#N/A
55191	NADSYN1	glutamine-dependent NAD(+) synthetase	2	8	2	0.8	2E-01	1.1	6E-02	1.0	**4E-02**	1.4	**5E-02**	0.9	4E-01	Ligase activity	-	Enzyme: Ligase;Enzyme: Synthase
4240	MFGE8	lactadherin isoform a preproprotein	10	51	10	0.8	4E-01	1.0	5E-01	0.8	**4E-03**	0.8	8E-02	1.0	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
10974	ADIRF; C10orf116	adipogenesis regulatory factor	4	40	4	0.8	1E-01	**0.6**	**3E-05**	1.0	**2E-04**	1.4	**4E-05**	1.0	6E-01	#N/A	#N/A	#N/A
83874	TBC1D10A	TBC1 domain family member 10A isoform 1	6	20	6	0.8	2E-01	1.1	**4E-03**	1.0	**1E-02**	1.4	**5E-03**	1.0	3E-01	GTPase activator activity	-	GTPase activating protein
127262	TPRG1L	tumor protein p63-regulated gene 1-like protein	5	12	5	0.8	3E-01	1.2	**2E-02**	1.2	1E-01	**1.5**	**8E-03**	1.4	1E-01	Molecular function unknown	-	Unclassified
7360	UGP2	UTP--glucose-1-phosphate uridylyltransferase isoform a	23	251	23	0.8	**5E-04**	0.8	**1E-02**	0.8	**1E-05**	0.8	**5E-03**	0.9	**2E-10**	Nucleotidyltransferase activity	-	Enzyme: Nucleotidyltransferase
50488	MINK1	misshapen-like kinase 1 isoform 3	15	59	9	0.8	5E-02	1.0	**1E-02**	0.9	**2E-02**	0.8	**1E-02**	0.9	5E-01	Protein serine/threonine kinase activity	Golgi apparatus;Nucleus;Cytoplasm	Serine/threonine kinase
7163	TPD52	tumor protein D52 isoform 2	8	51	8	0.8	**5E-02**	1.0	**5E-06**	0.9	**5E-06**	0.9	**7E-06**	1.0	1E-01	Molecular function unknown	-	Unclassified
342574	KRT27	keratin, type I cytoskeletal 27	6	629	2	0.8	2E-01	0.7	4E-01	0.8	3E-01	1.0	2E-01	1.2	**8E-04**	Structural molecule activity	-	Structural protein
767558; 136319	LUZP6; MTPN	myotrophin	5	48	5	0.8	4E-01	0.9	**7E-04**	0.9	8E-01	0.9	**9E-03**	0.9	7E-01	#N/A	#N/A	#N/A
84928	TMEM209	transmembrane protein 209 isoform 1	3	10	3	0.8	8E-01	1.1	9E-02	0.9	**2E-02**	1.2	**4E-02**	0.9	9E-01	Molecular function unknown	-	Integral membrane protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
5606	MAP2K3	dual specificity mitogen-activated protein kinase kinase 3 isoform B	10	46	10	0.8	3E-01	1.0	**3E-03**	0.9	3E-01	1.4	**1E-07**	1.0	2E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
30011	SH3KBP1	SH3 domain-containing kinase-binding protein 1 isoform a	9	26	9	0.8	7E-01	1.0	**1E-04**	1.0	4E-01	**1.6**	**2E-04**	1.1	**3E-02**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
3920	LAMP2	lysosome-associated membrane glycoprotein 2 isoform C	5	88	5	0.8	**4E-02**	1.0	**2E-08**	0.9	**2E-04**	1.2	**2E-09**	1.0	3E-01	Cell adhesion molecule activity	Lysosome	Adhesion molecule
64601	VPS16	vacuolar protein sorting-associated protein 16 homolog isoform 1	5	24	5	0.8	2E-01	1.0	6E-02	0.9	7E-02	0.9	1E-01	1.0	1E+00	Transporter activity	Late endosome	Transport/cargo protein
5805	PTS	6-pyruvoyl tetrahydrobiopterin synthase	3	20	3	0.8	7E-02	1.0	**5E-03**	1.1	**2E-02**	1.1	**1E-02**	0.9	5E-01	Lyase activity	Cytoplasm	Enzyme: Synthase
57146	TMEM159	promethin isoform 2*gi|685156920|ref|NP_001288698.1| promethin isoform 2*gi|685156922|ref|NP_001288700.1| promethin isoform 2	3	9	3	0.8	3E-01	1.2	2E-01	0.9	5E-02	0.8	2E-01	0.9	**5E-02**	Molecular function unknown	Cytoplasm	Unclassified
129642	MBOAT2	lysophospholipid acyltransferase 2	5	33	5	0.8	6E-01	1.2	**3E-04**	1.6	**4E-04**	**2.1**	**2E-04**	1.0	7E-01	Molecular function unknown	Plasma membrane	Unclassified
1212	CLTB	clathrin light chain B isoform a	11	108	11	0.8	7E-02	1.0	**9E-09**	0.8	**9E-06**	1.0	**3E-12**	1.0	7E-01	Structural molecule activity	Cytoplasm	Structural protein
56926	NCLN	nicalin	11	73	11	0.8	**8E-04**	1.4	**5E-04**	0.8	2E-01	0.9	**1E-03**	1.0	8E-01	Peptidase activity	Plasma membrane	Protease
3337	DNAJB1	dnaJ homolog subfamily B member 1 isoform 1	20	142	19	0.8	**2E-02**	1.0	**9E-12**	1.0	**2E-04**	1.1	**4E-12**	0.9	**4E-05**	Heat shock protein activity	Cytoplasm	Heat shock protein
54936	ADPRHL2	poly(ADP-ribose) glycohydrolase ARH3	9	42	9	0.8	2E-01	1.0	**1E-05**	1.0	**1E-03**	1.1	**9E-06**	0.9	**2E-02**	Hydrolase activity	-	Enzyme: Hydrolase
319101	KRT73	keratin, type II cytoskeletal 73	13	2199	3	0.8	9E-02	2.0	5E-01	0.9	**2E-16**	1.0	**2E-16**	1.4	**7E-09**	Structural molecule activity	-	Structural protein
7057	THBS1	thrombospondin-1	41	269	41	0.8	**6E-06**	**0.6**	**2E-16**	1.0	**4E-14**	1.2	**2E-16**	1.4	**2E-16**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
147700	KLC3	kinesin light chain 3	23	146	19	0.8	8E-02	1.1	**1E-13**	1.0	**1E-09**	1.4	**4E-16**	1.0	9E-02	Motor activity	-	Motor protein
10105	PPIF	peptidyl-prolyl cis-trans isomerase F, mitochondrial	9	60	7	0.8	3E-01	1.1	**7E-05**	0.9	**4E-05**	**1.7**	**3E-07**	1.2	**4E-06**	Isomerase activity	Mitochondrion	Enzyme: Isomerase
84336	TMEM101	PREDICTED: transmembrane protein 101 isoform X2	1	6	1	0.8	4E-01	0.9	8E-02	1.0	4E-01	1.1	1E-01	0.9	3E-01	Molecular function unknown	-	Unclassified
10159	ATP6AP2	renin receptor	7	29	7	0.8	7E-01	0.9	**4E-03**	0.9	4E-01	0.9	**2E-03**	1.0	3E-01	Receptor activity	Plasma membrane	Cell surface receptor
729830	FAM160A1	PREDICTED: protein FAM160A1 isoform X1	7	25	7	0.8	2E-01	1.3	**1E-06**	0.9	**2E-02**	1.4	**5E-04**	1.1	**4E-02**	#N/A	#N/A	#N/A
3155	HMGCL	hydroxymethylglutaryl-CoA lyase, mitochondrial isoform 1	9	46	9	0.8	2E-01	1.3	**1E-05**	1.1	**2E-06**	**1.6**	**2E-06**	1.0	3E-01	Lyase activity	Mitochondrion	Enzyme: Lyase
6431	SRSF6	serine/arginine-rich splicing factor 6	9	60	4	0.8	**7E-04**	0.8	**1E-02**	0.7	8E-01	0.7	**9E-03**	1.3	3E-01	#N/A	#N/A	#N/A
23313	KIAA0930	uncharacterized protein KIAA0930 isoform a	3	20	3	0.8	**5E-02**	1.0	**8E-04**	0.8	**4E-02**	0.7	6E-01	1.0	1E+00	#N/A	#N/A	#N/A
829	CAPZA1	F-actin-capping protein subunit alpha-1	12	183	10	0.8	5E-02	1.0	**1E-07**	0.9	**7E-04**	1.0	**1E-10**	1.0	5E-01	Structural molecule activity	Cytoplasm	Structural protein
23764	MAFF	transcription factor MafF isoform a	3	12	3	0.8	8E-01	1.6	5E-02	1.1	**5E-02**	**1.7**	**2E-02**	1.1	8E-02	Transcription factor activity;Transcription factor binding	Nucleus	Transcription factor
10409	BASP1	brain acid soluble protein 1	14	130	14	0.8	**1E-04**	0.9	**3E-09**	0.8	**7E-03**	0.8	**3E-06**	1.0	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
1830	DSG3	desmoglein-3 preproprotein	25	173	25	0.8	**8E-04**	0.8	**1E-04**	0.8	**5E-04**	0.9	**3E-12**	0.9	**2E-08**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
2629	GBA	glucosylceramidase isoform 1	10	56	10	0.8	8E-02	1.1	**7E-05**	1.0	**1E-04**	**1.7**	**3E-05**	1.1	**1E-05**	Glucosidase activity	Lysosome	Enzyme: Glucosidase
80856	KIAA1715	protein lunapark isoform 1	6	38	6	0.8	1E-01	1.1	**6E-06**	0.9	**2E-03**	1.1	**9E-05**	1.0	6E-01	Protein binding	Integral to membrane	Integral membrane protein
975	CD81	CD81 antigen isoform 1	4	17	4	0.8	1E-01	0.9	**3E-02**	0.7	7E-02	**0.7**	**4E-03**	1.0	6E-01	Catalytic activity	Plasma membrane	Enzyme: Oxidase
23380	SRGAP2	PREDICTED: SLIT-ROBO Rho GTPase-activating protein 2 isoform X1	5	15	5	0.8	**3E-02**	0.9	**1E-02**	0.9	3E-01	0.8	**2E-03**	1.0	9E-01	GTPase activator activity	Nucleus;Cytoplasm	GTPase activating protein
4860	PNP	purine nucleoside phosphorylase	13	155	13	0.8	**4E-03**	0.8	**2E-16**	1.0	**4E-03**	1.2	**2E-16**	1.0	8E-01	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase
26232	FBXO2	F-box only protein 2	7	42	7	0.8	**5E-03**	0.9	**2E-04**	0.9	9E-02	1.1	**4E-04**	0.9	**1E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
1312	COMT	catechol O-methyltransferase isoform MB-COMT*gi|205830453|ref|NP_001128634.1| catechol O-methyltransferase isoform MB-COMT*gi|4502969|ref|NP_000745.1| catechol O-methyltransferase isoform MB-COMT	10	87	10	0.8	**1E-02**	1.0	**1E-07**	0.9	**2E-02**	1.1	**7E-12**	0.9	**2E-03**	Acyltransferase activity	Endoplasmic reticulum;Cytoplasm	Enzyme: Acyltransferase
9482	STX8	syntaxin-8	5	23	5	0.8	2E-01	1.1	6E-01	0.7	**5E-03**	0.9	3E-01	1.0	6E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6648	**SOD2**	**superoxide dismutase [Mn], mitochondrial isoform A*gi|67782307|ref|NP_001019636.1| superoxide dismutase [Mn], mitochondrial isoform A**	6	38	6	0.8	2E-01	1.1	**8E-10**	1.0	**4E-03**	1.3	**2E-04**	1.1	**1E-02**	Superoxide dismutase activity	Mitochondrion	Enzyme: Superoxide dismutase
63894	**VIPAS39**	**spermatogenesis-defective protein 39 homolog isoform 1**	4	17	4	0.8	7E-01	1.1	2E-01	0.9	**2E-02**	1.0	**7E-03**	1.0	2E-01	#N/A	#N/A	#N/A
23541	**SEC14L2**	**SEC14-like protein 2 isoform 1**	10	64	8	0.8	**2E-02**	1.3	**3E-08**	1.6	**5E-06**	**2.1**	**7E-08**	0.9	**1E-02**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
2992	**GYG1**	**glycogenin-1 isoform 1**	6	28	6	0.8	**4E-02**	1.0	**5E-05**	1.0	**2E-03**	1.2	**8E-05**	0.9	1E-01	Molecular function unknown	-	Unclassified
10397	**NDRG1**	**protein NDRG1 isoform 1**	10	184	10	0.8	**4E-03**	0.8	**2E-07**	1.0	**5E-09**	0.8	1E-01	0.9	4E-01	Molecular function unknown	Cytoplasm	Unclassified
55823	**VPS11**	**vacuolar protein sorting-associated protein 11 homolog isoform 1**	9	27	9	0.8	7E-02	1.0	**5E-03**	0.9	1E-01	1.0	**6E-04**	0.9	3E-01	Transporter activity	Endosome	Transport/cargo protein
6388	**SDF2**	**stromal cell-derived factor 2**	3	14	3	0.8	2E-01	0.9	7E-02	0.9	4E-01	1.1	7E-02	0.9	1E-01	Molecular function unknown	Extracellular	Secreted polypeptide
10916	**MAGED2**	**melanoma-associated antigen D2**	12	76	12	0.8	3E-01	0.8	**5E-12**	1.4	**6E-06**	0.9	**6E-08**	1.1	**6E-04**	Molecular function unknown	Nucleus	Unclassified
27291	**R3HCC1L**	**coiled-coil domain-containing protein R3HCC1L isoform 1**	1	3	1	0.8	7E-01	0.9	**5E-03**	0.8	1E-01	1.0	**4E-02**	1.0	1E-01	#N/A	#N/A	#N/A
302	**ANXA2**	**annexin A2 isoform 1**	30	2087	30	0.8	**8E-04**	0.8	**2E-16**	1.0	**6E-08**	1.0	**2E-16**	1.1	**2E-16**	Calcium ion binding	Nucleus	Calcium binding protein
25946	**ZNF385A**	**zinc finger protein 385A isoform a**	2	9	2	0.9	3E-01	1.0	1E-01	1.0	5E-01	0.7	8E-01	1.0	8E-01	Transcription factor activity	Nucleolus	Transcription factor
6455	**SH3GL1**	**endophilin-A2 isoform 1**	15	114	15	0.9	4E-01	1.0	**3E-04**	1.0	**2E-03**	**1.5**	**1E-09**	1.0	7E-01	Molecular function unknown	Cytoplasm	Unclassified
529	**ATP6V1E1**	**V-type proton ATPase subunit E 1 isoform a**	14	105	14	0.9	**2E-03**	1.1	**2E-11**	1.0	**6E-09**	1.3	**2E-11**	1.0	8E-01	ATPase activity	Lysosome	ATPase
139322	**APOOL**	**MICOS complex subunit MIC27**	4	13	4	0.9	6E-02	1.0	**3E-03**	1.0	**3E-02**	**1.5**	**5E-03**	1.0	9E-01	Molecular function unknown	Nucleus	Unclassified
51700	**CYB5R2**	**NADH-cytochrome b5 reductase 2 isoform 1**	7	36	7	0.9	1E-01	1.2	**3E-04**	1.4	**4E-04**	**1.9**	**2E-04**	1.0	6E-01	Catalytic activity	Cytosol	Enzyme: Reductase
65108	**MARCKSL1**	**MARCKS-related protein**	3	19	2	0.9	**4E-02**	0.8	**9E-04**	1.2	7E-02	1.8	1E-01	1.1	**4E-02**	Receptor signaling complex scaffold activity	-	Adapter molecule
3163	**HMOX2**	**PREDICTED: heme oxygenase 2 isoform X1**	13	96	13	0.9	2E-01	0.8	**8E-07**	0.9	**3E-02**	1.4	**2E-09**	1.0	6E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase
220	**ALDH1A3**	**aldehyde dehydrogenase family 1 member A3 isoform 1**	19	175	18	0.9	**5E-05**	0.8	**4E-13**	1.6	**5E-03**	**2.8**	**2E-12**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
1845	**DUSP3**	**dual specificity protein phosphatase 3**	6	26	6	0.9	5E-02	0.9	**8E-05**	0.9	2E-01	0.9	**1E-05**	1.0	4E-01	Protein tyrosine/serine/threonine phosphatase activity	Nucleus	Dual specificity phosphatase
3029	**HAGH**	**hydroxyacylglutathione hydrolase, mitochondrial isoform 1**	4	22	4	0.9	1E-01	1.2	**6E-03**	0.9	**1E-03**	1.0	**2E-02**	0.9	7E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
26578	**OSTF1**	**osteoclast-stimulating factor 1**	5	40	5	0.9	2E-01	0.9	**6E-05**	1.0	4E-01	0.9	**3E-04**	1.0	5E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
10134	**BCAP31**	**B-cell receptor-associated protein 31 isoform a**	19	167	19	0.9	**5E-05**	1.1	**2E-15**	1.1	**1E-08**	1.4	**8E-14**	1.1	**2E-07**	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
202333	**CMYA5**	**cardiomyopathy-associated protein 5**	1	10	1	0.9	3E-01	1.1	1E-01	0.8	6E-02	0.9	**4E-02**	1.0	5E-01	Molecular function unknown	Microsome	Unclassified
6786	**STIM1**	**stromal interaction molecule 1 isoform 1**	17	96	17	0.9	**3E-04**	1.0	**3E-05**	0.8	**2E-07**	**0.7**	**1E-04**	0.9	**3E-02**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
2110	**ETFDH**	**electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial isoform 1**	8	33	8	0.9	**9E-03**	1.2	**7E-06**	0.9	**2E-05**	1.3	**2E-07**	1.1	7E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
79095	**C9orf16**	**UPF0184 protein C9orf16**	1	4	1	0.9	1E-01	0.8	2E-01	0.8	1E-01	0.7	2E-01	0.9	1E-01	Molecular function unknown	-	Unclassified
3552	**IL1A**	**interleukin-1 alpha proprotein**	2	8	2	0.9	2E-01	0.9	**9E-04**	1.9	9E-01	**1.8**	**2E-03**	1.0	6E-01	Cytokine activity	Cytoplasm	Cytokine
391059	**FRRS1**	**ferric-chelate reductase 1**	1	6	1	0.9	2E-01	1.1	2E-01	0.8	8E-02	0.7	6E-01	0.8	3E-01	Catalytic activity	Integral to membrane	Enzyme: Oxygenase
11180	**WDR6**	**WD repeat-containing protein 6**	2	6	2	0.9	4E-01	1.1	2E-01	1.2	6E-01	1.1	**4E-02**	1.6	3E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
64114	**TMBIM1**	**PREDICTED: protein lifeguard 3 isoform X1**	2	16	2	0.9	6E-01	0.9	**2E-02**	1.0	9E-01	1.1	9E-02	1.0	8E-01	Molecular function unknown	-	Unclassified
3799	**KIF5B**	**kinesin-1 heavy chain**	51	326	42	0.9	**5E-04**	1.0	**2E-16**	1.0	**2E-04**	1.2	**2E-16**	0.9	**2E-09**	Motor activity	Mitochondrion	Motor protein
23603	**CORO1C**	**coronin-1C isoform a**	23	181	23	0.9	**7E-04**	0.9	**2E-06**	0.9	7E-01	1.0	**3E-15**	1.0	8E-02	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
378	**ARF4**	**ADP-ribosylation factor 4**	10	163	5	0.9	**5E-03**	0.8	**3E-06**	0.9	**3E-02**	1.1	**8E-16**	1.1	**4E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
3993	**LLGL2**	**lethal(2) giant larvae protein homolog 2 isoform c**	8	30	8	0.9	7E-01	1.1	2E-01	0.8	**2E-02**	1.3	**2E-03**	1.1	2E-01	Molecular function unknown	Perinuclear region	Cell cycle control protein
6692	**SPINT1**	**kunitz-type protease inhibitor 1 isoform 1**	10	32	10	0.9	**3E-02**	1.0	**2E-02**	0.8	**2E-03**	1.0	**1E-05**	1.2	**2E-02**	Protease inhibitor activity	Membrane fraction	Protease inhibitor
3281	**HSBP1**	**heat shock factor-binding protein 1**	3	12	3	0.9	**4E-02**	0.9	**2E-02**	0.9	4E-01	0.9	2E-01	0.8	**1E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
35	**ACADS**	**short-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 1**	2	6	2	0.9	2E-01	1.1	1E-01	1.1	2E-01	1.4	**3E-02**	1.0	9E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
7319	**UBE2A**	**ubiquitin-conjugating enzyme E2 A isoform 1**	1	6	1	0.9	9E-01	1.2	2E-01	1.3	3E-01	0.8	3E-01	0.9	9E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
9053	**MAP7**	**ensconsin isoform 3**	15	73	14	0.9	**1E-03**	0.9	**2E-05**	0.9	7E-02	0.9	**4E-04**	0.9	1E+00	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
81502	HM13	minor histocompatibility antigen H13 isoform 3	6	56	6	0.9	**2E-02**	1.0	**4E-04**	1.1	**9E-03**	**1.6**	**3E-04**	1.1	**1E-03**	Peptidase activity	Integral to membrane	Protease
966	CD59	CD59 glycoprotein preproprotein	2	36	2	0.9	**4E-02**	0.7	**3E-03**	0.8	**1E-05**	0.9	**5E-04**	1.2	**2E-03**	Receptor activity	Plasma membrane	Cell surface receptor
80004	ESRP2	epithelial splicing regulatory protein 2	4	12	4	0.9	1E-01	0.7	**1E-02**	1.1	9E-02	1.0	**2E-02**	0.9	**4E-02**	RNA binding	Nucleus	RNA binding protein
23189	KANK1	KN motif and ankyrin repeat domain-containing protein 1 isoform a	5	18	5	0.9	4E-01	1.0	6E-02	0.8	6E-02	0.9	4E-01	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
647024	C6orf132	uncharacterized protein C6orf132	17	57	17	0.9	7E-01	1.1	**7E-03**	0.9	**4E-02**	**1.5**	**2E-06**	1.0	6E-01	#N/A	#N/A	#N/A
9885	OSBPL2	oxysterol-binding protein-related protein 2 isoform 2	9	42	9	0.9	2E-01	1.1	**4E-04**	1.1	**3E-03**	1.2	**3E-06**	0.9	1E-01	Lipid binding	Golgi apparatus	Transport/cargo protein
80153	EDC3	PREDICTED: enhancer of mRNA-decapping protein 3 isoform X1	4	8	4	0.9	**3E-02**	0.8	6E-02	0.9	6E-01	0.7	4E-01	0.8	8E-01	RNA binding	Cytoplasm	RNA binding protein
26284	ERAL1	GTPase Era, mitochondrial	4	9	4	0.9	3E-01	1.0	**4E-02**	0.9	2E-01	0.9	2E-01	1.0	4E-01	GTPase activity	Endoplasmic reticulum	GTPase
9877	ZC3H11A	PREDICTED: zinc finger CCCH domain-containing protein 11A isoform X1	7	23	7	0.9	8E-01	0.8	9E-01	0.7	5E-01	0.9	2E-01	0.9	6E-01	DNA binding	Nucleus	DNA binding protein
2049	EPHB3	ephrin type-B receptor 3	10	38	7	0.9	**5E-02**	1.0	**9E-03**	0.9	2E-01	0.9	**1E-02**	0.9	6E-01	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase
1785	DNM2	dynamin-2 isoform 1	28	184	20	0.9	8E-02	1.0	**2E-12**	1.0	**1E-06**	1.4	**7E-14**	1.0	1E+00	GTPase activity	Cytoskeleton	GTPase
10587	TXNRD2	thioredoxin reductase 2, mitochondrial isoform 1	7	21	6	0.9	1E-01	1.1	**3E-02**	1.0	**3E-02**	1.3	**3E-02**	1.0	5E-01	Catalytic activity	Mitochondrion	Enzyme: Reductase
80131	LRRC8E	PREDICTED: volume-regulated anion channel subunit LRRC8E isoform X1	5	22	4	0.9	2E-01	0.8	2E-01	**0.7**	**4E-03**	0.7	1E-01	0.9	1E-01	Molecular function unknown	-	Integral membrane protein
1130	LYST	lysosomal-trafficking regulator*gi|672424497|ref|NP_001288294.1| lysosomal-trafficking regulator	1	6	1	0.9	3E-01	1.0	6E-02	1.0	6E-01	0.9	7E-02	0.9	2E-01	Receptor signaling complex scaffold activity	Lysosome	Adapter molecule
55680	RUFY2	RUN and FYVE domain-containing protein 2 isoform a	6	32	4	0.9	3E-01	1.1	1E-01	1.1	**7E-03**	1.2	6E-02	0.9	5E-01	Molecular function unknown	-	Unclassified
64787	EPS8L2	epidermal growth factor receptor kinase substrate 8-like protein 2	18	85	18	0.9	**2E-05**	1.1	**5E-05**	0.9	**2E-07**	0.8	3E-01	0.9	**2E-05**	Receptor signaling complex scaffold activity	-	Adapter molecule
7447	VSNL1	visinin-like protein 1	10	61	10	0.9	**2E-05**	1.0	**2E-03**	**0.6**	**1E-05**	**0.4**	**3E-06**	0.8	**4E-04**	Calcium ion binding	Plasma membrane	Calcium binding protein
2538;	G6PC	glucose-6-phosphatase isoform 1	3	9	3	0.9	2E-01	1.1	**2E-03**	1.4	**2E-03**	1.4	**2E-03**	0.9	4E-01	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase
55103	RALGPS2	PREDICTED: ras-specific guanine nucleotide-releasing factor RalGPS2 isoform X1	3	7	3	0.9	2E-01	1.0	6E-02	0.9	3E-01	1.2	9E-02	0.8	3E-01	Guanyl-nucleotide exchange factor activity	Nucleus	Guanine nucleotide exchange factor
23176	SEPT8	septin-8 isoform a	7	49	6	0.9	8E-01	1.1	1E-01	0.8	**2E-03**	1.0	**2E-02**	0.9	1E-01	#N/A	#N/A	#N/A
5306	PITPNA	phosphatidylinositol transfer protein alpha isoform	14	101	10	0.9	**1E-06**	1.0	**2E-12**	0.9	**2E-05**	0.7	5E-01	0.9	**7E-05**	Transporter activity	Cytoplasm	Transport/cargo protein
7317	UBA1	ubiquitin-like modifier-activating enzyme 1	35	458	35	0.9	**3E-05**	1.0	**2E-16**	1.0	**5E-12**	1.0	**2E-16**	0.9	**6E-03**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
23478	SEC11A	signal peptidase complex catalytic subunit SEC11A isoform 3	6	59	6	0.9	**7E-03**	1.1	**5E-07**	0.9	**5E-05**	1.2	**5E-05**	1.2	**4E-03**	Aminopeptidase activity	-	Aminopeptidase
23593	HEBP2	heme-binding protein 2	8	56	8	0.9	**4E-02**	0.9	**4E-08**	0.9	1E-01	1.1	**3E-08**	0.9	**3E-04**	Molecular function unknown	Cytoplasm	Unclassified
57609	DIP2B	disco-interacting protein 2 homolog B	21	88	21	0.9	7E-02	1.1	**7E-07**	0.9	**2E-07**	1.1	**5E-11**	0.9	**3E-02**	Molecular function unknown	-	Unclassified
23204	ARL6IP1	ADP-ribosylation factor-like protein 6-interacting protein 1	1	6	1	0.9	2E-01	1.0	1E-01	0.9	3E-01	1.4	**2E-02**	0.9	2E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
60673	C12orf44; ATG101	autophagy-related protein 101	2	10	2	0.9	3E-01	0.9	8E-02	0.9	9E-02	1.0	**1E-02**	0.9	3E-01	#N/A	#N/A	#N/A
6515	SLC2A3	solute carrier family 2, facilitated glucose transporter member 3	3	13	3	0.9	8E-01	0.7	**2E-02**	1.9	7E-01	1.4	**7E-03**	1.1	3E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
823	CAPN1	calpain-1 catalytic subunit	32	292	32	0.9	**2E-07**	1.0	**2E-16**	1.0	**2E-10**	1.1	**2E-16**	0.9	**2E-04**	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
4646	MYO6	unconventional myosin-VI isoform 2	37	203	37	0.9	**7E-04**	1.1	**2E-15**	1.0	**1E-13**	**1.6**	**2E-16**	1.0	2E-01	Motor activity	Golgi apparatus	Motor protein
51635	DHRS7	dehydrogenase/reductase SDR family member 7	10	79	10	0.9	**4E-03**	1.0	**2E-07**	1.0	**1E-05**	1.4	**3E-11**	1.0	8E-01	Catalytic activity	-	Enzyme: Dehydrogenase
26088	GGA1	ADP-ribosylation factor-binding protein GGA1 isoform 1	6	34	5	0.9	**1E-02**	1.0	**6E-04**	1.1	**6E-03**	1.0	**4E-04**	0.9	2E-01	Molecular function unknown;Transporter activity	Golgi membrane	Transport/cargo protein;Unclassified
5524	PPP2R4; PTPA	serine/threonine-protein phosphatase 2A activator isoform b*gi|30065643|ref|NP_821067.1| serine/threonine-protein phosphatase 2A activator isoform b	8	31	8	0.9	2E-01	1.1	**3E-02**	0.9	**7E-03**	1.0	**7E-04**	0.9	6E-02	#N/A	#N/A	#N/A
54978	C2orf18; SLC35F6	solute carrier family 35 member F6	4	22	4	0.9	7E-01	1.1	8E-01	0.8	**2E-02**	0.9	**1E-02**	0.9	3E-01	#N/A	#N/A	#N/A

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
59338	**PLEKHA1**	PREDICTED: pleckstrin homology domain-containing family A member 1 isoform X1	3	16	3	0.9	9E-01	1.0	**2E-03**	0.9	2E-01	1.0	**1E-02**	1.0	5E-01	Receptor signaling complex scaffold activity;Signal transducer activity	Cytoplasm	Adapter molecule
3831	**KLC1**	kinesin light chain 1 isoform 3	21	120	12	0.9	**2E-03**	0.9	**3E-11**	1.0	2E-01	1.0	**3E-14**	0.9	**6E-03**	Motor activity	Cytoplasm	Motor protein
51726	**DNAJB11**	dnaJ homolog subfamily B member 11	8	53	8	0.9	5E-02	0.9	**4E-06**	0.9	1E+00	1.2	**6E-06**	1.0	3E-01	Chaperone activity	Endoplasmic reticulum	Chaperone
391	**RHOG**	rho-related GTP-binding protein RhoG	5	30	4	0.9	9E-02	0.9	**3E-03**	0.9	7E-01	1.0	**5E-04**	1.0	9E-02	GTPase activity	Nucleus	GTPase
9559	**VPS26A**	vacuolar protein sorting-associated protein 26A isoform 1	10	72	8	0.9	**1E-03**	0.9	**1E-08**	1.0	8E-01	1.0	**2E-07**	0.9	**7E-03**	Transporter activity	Cytoplasm	Transport/cargo protein
3732	**CD82**	PREDICTED: CD82 antigen isoform X2	5	19	5	0.9	6E-02	0.9	1E-01	0.9	8E-01	0.9	1E+00	0.9	3E-01	Receptor activity;Receptor regulator activity	Plasma membrane	Integral membrane protein;Cell surface receptor
89845	**ABCC10**	PREDICTED: multidrug resistance-associated protein 7 isoform X1	1	8	1	0.9	3E-01	1.1	5E-02	0.9	**3E-02**	1.1	**4E-02**	1.2	9E-02	Transporter activity	Plasma membrane	Transport/cargo protein
84064	**HDHD2**	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2 isoform X1	4	22	4	0.9	7E-01	1.3	1E-01	1.0	**1E-04**	0.9	6E-02	1.0	5E-01	Hydrolase activity	-	Enzyme: Hydrolase
811	**CALR**	calreticulin	24	343	24	0.9	**9E-05**	0.9	**2E-16**	1.0	8E-01	1.0	**2E-16**	1.1	**2E-06**	Chaperone activity	Endoplasmic reticulum	Chaperone
81876	**RAB1B**	ras-related protein Rab-1B	14	203	5	0.9	**8E-03**	1.0	**3E-03**	0.9	**3E-05**	1.1	**5E-04**	0.9	8E-02	GTPase activity	Golgi apparatus	GTPase
6102	**RP2**	protein XRP2	9	54	9	0.9	**9E-03**	0.9	**4E-08**	1.0	2E-01	1.0	**3E-06**	1.0	2E-01	Structural molecule activity	Plasma membrane	Structural protein
8644	**AKR1C3**	aldo-keto reductase family 1 member C3 isoform 1	13	155	3	0.9	**2E-02**	1.4	**4E-04**	2.8	**1E-04**	**2.5**	**2E-04**	**0.6**	**8E-04**	Catalytic activity	Cytoplasm	Enzyme: Reductase
84284	**NTPCR**	cancer-related nucleoside-triphosphatase	3	16	3	0.9	3E-01	1.0	9E-02	0.9	**3E-02**	0.7	7E-01	0.9	6E-01	#N/A	#N/A	#N/A
9524	**TECR**	very-long-chain enoyl-CoA reductase	12	101	12	0.9	**6E-04**	1.2	**4E-11**	1.0	**6E-10**	1.0	**1E-12**	0.9	**1E-02**	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase
7779	**SLC30A1**	zinc transporter 1	8	31	8	0.9	1E-01	1.2	2E-01	0.8	**2E-04**	1.1	**3E-04**	1.1	**2E-02**	Auxiliary transport protein activity	Integral to membrane	Membrane transport protein
57020	**C16orf62**	UPF0505 protein C16orf62 isoform 1	8	32	8	0.9	6E-01	1.1	**9E-03**	1.0	**3E-02**	1.1	**1E-03**	1.1	2E-01	Molecular function unknown	Nucleus	Unclassified
7417	**VDAC2**	voltage-dependent anion-selective channel protein 2 isoform 1	13	188	13	0.9	**7E-04**	1.1	**1E-15**	1.0	**2E-08**	**1.5**	**2E-16**	1.0	5E-02	Voltage-gated ion channel activity	Mitochondrion	Voltage gated channel
3678	**ITGA5**	integrin alpha-5	6	24	6	0.9	3E-01	0.6	6E-02	0.9	**1E-02**	0.6	8E-02	0.8	7E-01	Receptor activity	Plasma membrane	Cell surface receptor
91782	**CHMP7**	charged multivesicular body protein 7	3	10	3	0.9	4E-01	1.0	**5E-03**	1.0	1E+00	1.0	**8E-03**	0.8	4E-01	Molecular function unknown	-	Unclassified
7534	**YWHAZ**	14-3-3 protein zeta/delta	16	1124	11	0.9	**7E-04**	0.9	**2E-16**	0.9	6E-02	0.9	**5E-14**	0.9	6E-02	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
5525	**PPP2R5A**	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform isoform 1	5	18	4	0.9	2E-01	1.0	**3E-02**	1.1	1E-01	1.1	**3E-02**	1.0	9E-01	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
4967	**OGDH**	2-oxoglutarate dehydrogenase, mitochondrial isoform 1	28	205	28	0.9	**3E-05**	1.2	**2E-16**	1.0	**2E-16**	1.3	**2E-16**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
65082	**VPS33A**	vacuolar protein sorting-associated protein 33A	4	25	4	0.9	**3E-02**	0.9	**6E-04**	1.0	4E-01	1.0	**5E-04**	0.9	8E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
10380	**BPNT1**	PREDICTED: 3'(2'),5'-bisphosphate nucleotidase 1 isoform X1	9	48	9	0.9	**3E-02**	0.9	**1E-04**	1.0	**9E-03**	1.0	**1E-06**	0.9	7E-02	Hydrolase activity	-	Enzyme: Esterase
55346	**TCP11L1**	T-complex protein 11-like protein 1	4	16	4	0.9	**3E-02**	1.0	**5E-02**	0.8	1E-01	1.0	**6E-03**	0.9	2E-01	Molecular function unknown	-	Unclassified
83548	**COG3**	conserved oligomeric Golgi complex subunit 3	5	14	5	0.9	1E-01	1.0	**2E-02**	1.0	4E-01	1.3	**4E-02**	1.0	1E+00	Transporter activity	Golgi apparatus	Transport/cargo protein
79634;	**SCRN3**	secernin-3 isoform 1	8	20	8	0.9	2E-01	1.2	**2E-05**	1.2	**3E-03**	1.3	**1E-04**	0.9	7E-01	Peptidase activity	-	Protease
65983	**GRAMD3**	GRAM domain-containing protein 3 isoform 1	4	17	4	0.9	5E-01	1.1	**3E-02**	1.0	**7E-03**	**1.8**	**5E-04**	1.1	6E-02	Molecular function unknown	Nucleus;Cytoplasm	Integral membrane protein
2180	**ACSL1**	long-chain-fatty-acid--CoA ligase 1 isoform a	26	138	26	0.9	**2E-05**	1.3	**1E-13**	1.3	**2E-14**	**1.9**	**2E-13**	0.9	**2E-02**	Ligase activity	Endoplasmic reticulum	Enzyme: Ligase
7905	**REEP5**	receptor expression-enhancing protein 5	6	60	6	0.9	**9E-04**	1.0	**1E-07**	1.0	**9E-05**	1.2	**2E-08**	1.0	6E-01	Molecular function unknown	-	Integral membrane protein
80230	**RUFY1**	RUN and FYVE domain-containing protein 1 isoform a	18	68	16	0.9	**1E-02**	1.0	**9E-04**	1.0	**3E-04**	1.0	**8E-05**	0.9	**1E-02**	Ubiquitin-specific protease activity	Endosome	Ubiquitin proteasome system protein
192669	**AGO3; EIF2C3**	protein argonaute-3 isoform a	4	16	1	0.9	4E-01	1.4	1E-01	0.9	6E-02	1.4	**5E-02**	1.2	1E-01	#N/A	#N/A	#N/A
22931	**RAB18**	ras-related protein Rab-18 isoform 1	8	56	8	0.9	**5E-04**	1.0	**4E-04**	0.8	**6E-07**	0.8	**2E-02**	1.0	5E-01	GTPase activity	Plasma membrane	GTPase
115817	**DHRS1**	dehydrogenase/reductase SDR family member 1	7	42	7	0.9	**6E-03**	1.0	**2E-05**	1.4	**3E-02**	**1.6**	**3E-05**	**0.7**	**8E-05**	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
51124	**IER3IP1**	immediate early response 3-interacting protein 1	1	12	1	0.9	5E-02	0.8	2E-01	0.8	5E-01	0.8	8E-01	0.9	4E-01	Molecular function unknown	Endoplasmic reticulum	Unclassified

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
55611	OTUB1	ubiquitin thioesterase OTUB1	7	114	7	0.9	5E-02	1.0	**6E-06**	1.0	**4E-05**	1.0	**6E-06**	0.9	**3E-04**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
51026	GOLT1B	vesicle transport protein GOT1B	1	12	1	0.9	8E-02	1.0	**6E-03**	1.4	**2E-02**	1.3	**8E-03**	1.2	**1E-02**	Molecular function unknown	-	Unclassified
6744	SSFA2	sperm-specific antigen 2 isoform 1	10	45	10	0.9	**1E-02**	0.9	**4E-02**	0.8	1E-01	1.0	**4E-05**	1.0	3E-01	Molecular function unknown	Plasma membrane	Unclassified
92597	MOB1B	PREDICTED: MOB kinase activator 1B isoform X1	6	34	6	0.9	2E-01	0.8	**5E-02**	0.9	7E-02	**0.6**	**1E-02**	1.0	9E-01	#N/A	#N/A	#N/A
3836;	KPNA1	importin subunit alpha-5	15	52	8	0.9	**5E-08**	0.9	**3E-10**	0.8	5E-01	0.8	**3E-09**	0.9	**5E-04**	Transporter activity	Cytoplasm	Transport/cargo protein
22872	SEC31A	protein transport protein Sec31A isoform 1	32	212	32	0.9	**2E-04**	1.0	**2E-16**	1.0	**3E-03**	1.0	**2E-16**	1.0	8E-01	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
51451	LCMT1	leucine carboxyl methyltransferase 1 isoform a	7	38	7	0.9	**1E-02**	1.2	**8E-06**	1.1	**2E-04**	**1.5**	**1E-05**	1.0	5E-01	Methyltransferase activity	-	Enzyme: Methyltransferase
7165	TPD52L2	tumor protein D54 isoform a	10	76	10	0.9	**1E-02**	0.9	**1E-06**	1.0	2E-01	0.9	**8E-07**	1.0	7E-01	Molecular function unknown	Cytoplasm;Nucleus	Unclassified
57551	TAOK1	serine/threonine-protein kinase TAO1 isoform 1	7	18	3	0.9	9E-02	1.3	**4E-03**	1.1	9E-01	1.2	**2E-02**	0.9	2E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
285941;	C7orf71	putative uncharacterized protein C7orf71 isoform b	4	10	4	0.9	9E-02	1.3	8E-02	0.8	**6E-03**	1.0	**3E-03**	1.0	**1E-02**	#N/A	#N/A	#N/A
1192	CLIC1	chloride intracellular channel protein 1	14	155	14	0.9	**5E-08**	0.8	**1E-10**	1.0	**4E-05**	1.0	**4E-08**	0.9	**3E-02**	Intracellular ligand-gated ion channel activity	Nucleus	Intracellular ligand gated channel
226	ALDOA	fructose-bisphosphate aldolase A isoform 1*gi|34577110|ref|NP_908930.1| fructose-bisphosphate aldolase A isoform 1*gi|34577112|ref|NP_908932.1| fructose-bisphosphate aldolase A isoform 1*gi|4557305|ref|NP_000025.1| fructose-bisphosphate aldolase A isoform 1	26	662	19	0.9	**9E-03**	0.9	**2E-16**	1.0	**8E-06**	1.0	**2E-16**	0.9	**2E-04**	Lyase activity	Cytoplasm	Enzyme: Lyase;Enzyme: Aldolase
834	CASP1	caspase-1 isoform alpha*gi|380254457|ref|NP_001244047.1 | caspase-1 isoform alpha	11	43	10	0.9	**1E-02**	0.9	**8E-04**	0.9	3E-01	0.9	**6E-04**	0.9	**4E-02**	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
3295	HSD17B4	peroxisomal multifunctional enzyme type 2 isoform 2	25	191	25	0.9	**3E-10**	1.1	**2E-16**	1.0	**2E-16**	1.1	**2E-16**	1.0	7E-01	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase
55845	BRK1	protein BRICK1	6	46	6	0.9	**3E-04**	0.9	**3E-06**	1.0	**1E-02**	1.0	**7E-06**	0.9	**4E-03**	#N/A	#N/A	#N/A
81873	ARPC5L	PREDICTED: actin-related protein 2/3 complex subunit 5-like protein isoform X1	7	66	6	0.9	**1E-02**	1.0	**3E-03**	0.8	**4E-04**	1.0	**9E-07**	0.9	3E-01	Molecular function unknown	-	Unclassified
10579	TACC2	transforming acidic coiled-coil-containing protein 2 isoform a	14	47	11	0.9	4E-01	1.1	6E-01	0.8	**7E-04**	0.9	**3E-02**	1.0	9E-01	Molecular function unknown	Centrosome	Cell cycle control protein
84335	AKT1S1	proline-rich AKT1 substrate 1 isoform a	2	8	2	0.9	9E-01	0.8	1E-01	0.8	5E-01	0.6	4E-01	1.0	5E-01	Molecular function unknown	Cytoplasm	Unclassified
10097	ACTR2	actin-related protein 2 isoform b	11	121	11	0.9	**3E-05**	0.9	**6E-09**	0.9	3E-01	1.0	**3E-11**	0.9	9E-02	Structural constituent of cytoskeleton	Actin cytoskeleton	Cytoskeletal protein
57153	SLC44A2	choline transporter-like protein 2 isoform 1	9	55	9	0.9	**4E-02**	1.0	**2E-05**	1.1	5E-01	**1.5**	**7E-06**	1.1	**9E-03**	Signal transducer activity	Integral to membrane	Integral membrane protein
8797	TNFRSF10A	tumor necrosis factor receptor superfamily member 10A	2	6	2	0.9	3E-01	0.8	1E-01	1.1	1E-01	0.8	8E-02	1.0	3E-01	Receptor activity	Integral to membrane	Cell surface receptor
64236	PDLIM2	PDZ and LIM domain protein 2 isoform 2	8	41	8	0.9	**3E-03**	0.9	**8E-04**	0.8	1E-01	1.1	**2E-04**	1.0	9E-01	Cell adhesion molecule activity	Cytoskeleton;Nucleus	Adapter molecule
57175	CORO1B	coronin-1B	13	116	13	0.9	**2E-02**	0.9	**1E-09**	1.0	**1E-02**	1.2	**1E-13**	1.0	2E-01	Molecular function unknown	-	Unclassified
1605	DAG1	dystroglycan preproprotein	3	10	3	0.9	1E-01	0.8	6E-02	1.0	2E-01	0.7	6E-01	0.8	6E-02	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
79143	MBOAT7	PREDICTED: lysophospholipid acyltransferase 7 isoform X1	3	20	3	0.9	1E-01	1.0	**4E-04**	0.9	**2E-02**	0.9	**6E-03**	1.0	6E-01	Receptor activity	Plasma membrane	Integral membrane protein
392	ARHGAP1	PREDICTED: rho GTPase-activating protein 1 isoform X1	15	106	15	0.9	**8E-05**	1.0	**5E-10**	1.0	**4E-03**	1.1	**7E-15**	1.0	2E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
9761	MLEC	malectin isoform1	8	59	8	0.9	**2E-04**	1.1	**2E-06**	1.0	**1E-06**	1.1	**2E-06**	1.1	**2E-02**	Molecular function unknown	Integral to membrane	Unclassified
873; 54093	CBR1; SETD4	carbonyl reductase [NADPH] 1 isoform 1	17	231	17	0.9	**8E-04**	1.2	**1E-09**	1.0	**2E-10**	0.7	3E-01	0.9	**2E-03**	#N/A	#N/A	#N/A
6840	SVIL	supervillin isoform 2	17	74	17	0.9	**3E-03**	1.1	**2E-10**	1.0	**7E-07**	1.2	**1E-10**	1.0	8E-02	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
813	CALU	calumenin isoform d	12	100	3	0.9	**1E-09**	1.0	**2E-11**	0.9	**5E-03**	0.9	**5E-10**	1.4	**2E-04**	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein
23233	EXOC6B	exocyst complex component 6B	15	70	15	0.9	**7E-03**	1.0	**1E-06**	0.9	**7E-04**	1.1	**3E-08**	1.0	4E-01	Molecular function unknown	-	Unclassified
10005	ACOT8	acyl-coenzyme A thioesterase 8	3	13	3	0.9	6E-02	1.0	**3E-02**	1.1	2E-01	1.4	8E-02	1.0	7E-01	Hydrolase activity	Peroxisomal matrix	Enzyme: Thioesterase
84836	ABHD14B	alpha/beta hydrolase domain-containing protein 14B isoform 1*gi|226443152|ref|NP_001139786.1| alpha/beta hydrolase domain-containing protein 14B isoform 1	6	32	6	0.9	7E-02	1.1	**2E-03**	1.1	**5E-05**	1.2	**1E-05**	0.9	9E-02	Molecular function unknown	-	Unclassified
55238	SLC38A7	putative sodium-coupled neutral amino acid transporter 7	2	8	2	0.9	1E-01	1.1	**2E-02**	1.0	**4E-03**	1.2	**2E-02**	1.1	3E-01	Transporter activity	-	Transport/cargo protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8079	**MLF2**	**myeloid leukemia factor 2**	4	22	4	0.9	9E-01	1.1	2E-01	0.8	1E-01	1.0	**7E-04**	0.9	7E-01	Molecular function unknown	Nucleus	Unclassified
10015	**PDCD6IP**	**programmed cell death 6-interacting protein isoform 1**	47	392	47	0.9	**3E-08**	1.0	**2E-16**	1.0	**1E-12**	1.2	**2E-16**	0.9	**2E-12**	Molecular function unknown	Cytoplasm	Unclassified
30	**ACAA1**	**3-ketoacyl-CoA thiolase, peroxisomal isoform a**	8	52	8	0.9	**2E-04**	0.9	**1E-04**	1.0	1E-01	1.2	**4E-04**	0.9	8E-02	Acyltransferase activity	Peroxisome	Enzyme: Acyltransferase
5095	**PCCA**	**propionyl-CoA carboxylase alpha chain, mitochondrial isoform a**	5	13	5	0.9	5E-01	1.4	**4E-05**	1.0	**3E-02**	1.1	**2E-02**	1.1	1E-01	Ligase activity	Mitochondrion	Enzyme: Carboxylase
4643	**MYO1E**	**unconventional myosin-Ie**	27	147	27	0.9	**1E-10**	0.9	**6E-14**	0.9	2E-01	1.1	**2E-16**	1.0	2E-01	Motor activity	Cytoplasm	Motor protein
286410	**ATP11C**	**phospholipid-transporting ATPase IG isoform a**	2	8	2	0.9	5E-02	1.1	7E-02	0.8	1E-01	0.9	1E-01	1.1	4E-01	ATPase activity	-	ATPase
54874	**FNBP1L**	**formin-binding protein 1-like isoform 3**	4	14	4	0.9	7E-02	0.8	1E-01	0.8	1E-01	0.8	9E-01	0.8	1E-01	Cytoskeletal protein binding	Microtubule	Cytoskeletal protein
9776	**ATG13**	**PREDICTED: autophagy-related protein 13 isoform X3**	2	8	2	0.9	7E-02	1.0	**3E-02**	0.9	2E-01	1.0	**2E-03**	1.3	**2E-02**	#N/A	#N/A	#N/A
54578	**UGT1A6**	**UDP-glucuronosyltransferase 1-6 isoform 1**	4	13	4	0.9	2E-01	1.2	**1E-02**	1.2	**4E-02**	1.4	**1E-02**	1.1	3E-01	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase
51024	**FIS1**	**mitochondrial fission 1 protein**	2	32	2	0.9	**2E-04**	1.1	**1E-05**	1.0	**4E-05**	0.9	**3E-07**	0.9	**2E-02**	Molecular function unknown	Mitochondrion	Unclassified
8717	**TRADD**	**PREDICTED: tumor necrosis factor receptor type 1-associated DEATH domain protein isoform X1**	5	22	5	0.9	**2E-02**	0.9	**2E-03**	1.0	9E-01	1.1	**5E-04**	0.9	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
5271	**SERPINB8**	**serpin B8 isoform a**	11	80	10	0.9	**2E-04**	0.9	**4E-11**	1.0	8E-01	1.2	**3E-11**	1.0	9E-01	Protease inhibitor activity	Nucleus	Protease inhibitor
57403	**RAB22A**	**ras-related protein Rab-22A**	6	32	5	0.9	**2E-02**	1.1	**1E-04**	1.0	**4E-04**	1.2	**4E-05**	1.1	2E-01	GTPase activity	Endosome	GTPase
90102	**PHLDB2**	**pleckstrin homology-like domain family B member 2 isoform a**	7	34	7	0.9	**2E-02**	0.9	**1E-03**	1.0	5E-01	1.1	**4E-04**	1.2	**4E-03**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
60496	**AASDHPPT**	**L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase**	7	28	7	0.9	**4E-02**	1.0	**5E-03**	1.0	3E-01	0.9	2E-01	0.9	**1E-02**	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
94081	**SFXN1**	**sideroflexin-1**	10	64	8	0.9	5E-02	1.1	**7E-04**	1.0	**3E-06**	1.3	**9E-07**	1.2	**8E-03**	Transporter activity	Mitochondrion	Transport/cargo protein
23163	**GGA3**	**ADP-ribosylation factor-binding protein GGA3 isoform long**	5	15	4	0.9	8E-02	0.9	**3E-02**	1.1	6E-01	1.4	8E-02	1.2	8E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
11035	**RIPK3**	**receptor-interacting serine/threonine-protein kinase 3**	2	6	2	0.9	2E-01	0.7	1E-01	0.9	8E-02	0.5	7E-02	0.9	3E-01	Protein serine/threonine kinase activity	Mitochondrion	Serine/threonine kinase
1604	**CD55**	**complement decay-accelerating factor isoform 5**	4	20	4	0.9	3E-01	1.0	4E-01	**0.6**	**1E-02**	0.9	7E-02	1.2	**3E-02**	Complement activity	Plasma membrane	Complement protein
3418	**IDH2**	**isocitrate dehydrogenase [NADP], mitochondrial isoform 1**	19	222	18	0.9	**1E-11**	**1.8**	**2E-16**	1.1	**3E-16**	1.4	**2E-16**	1.0	**6E-04**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
5756	**TWF1**	**twinfilin-1 isoform 2**	13	101	9	0.9	**2E-05**	0.8	**2E-04**	0.9	**1E-04**	0.8	**4E-04**	0.9	**5E-02**	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase
3613	**IMPA2**	**inositol monophosphatase 2**	6	33	6	0.9	**1E-04**	1.2	**1E-06**	1.0	**4E-05**	0.9	**5E-05**	0.8	**3E-04**	Catalytic activity	-	Enzyme: Phosphotransferase
80232	**WDR26**	**WD repeat-containing protein 26 isoform a**	6	38	6	0.9	**2E-03**	1.1	**3E-04**	0.9	**1E-02**	1.3	**5E-05**	1.1	2E-01	Molecular function unknown	-	Unclassified
8659	**ALDH4A1**	**delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial isoform a**	19	105	19	0.9	**1E-02**	**1.5**	**2E-04**	0.8	**3E-13**	0.8	3E-01	1.0	4E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
6120	**RPE**	**ribulose-phosphate 3-epimerase isoform 1**	4	18	4	0.9	5E-02	0.9	**3E-02**	1.0	4E-01	0.9	**3E-02**	0.9	2E-01	Racemase and epimerase activity	Cytoplasm	Enzyme: Epimerase
175	**AGA**	**N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase isoform 1 preproprotein**	2	8	2	0.9	9E-02	1.2	**6E-03**	1.0	**2E-03**	1.2	**6E-03**	0.9	3E-01	Hydrolase activity	Lysosome	Enzyme: Hydrolase
10096	**ACTR3**	**actin-related protein 3 isoform 1**	16	142	16	0.9	**1E-06**	0.9	**2E-12**	0.9	3E-01	1.0	**2E-13**	0.9	1E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
4905	**NSF**	**vesicle-fusing ATPase**	23	129	22	0.9	**2E-04**	1.1	**2E-10**	0.9	**1E-10**	1.4	**6E-12**	1.0	7E-01	ATPase activity	Cytoplasm	ATPase
10383	**TUBB4B**	**tubulin beta-4B chain**	23	1122	1	0.9	**3E-03**	0.8	**2E-03**	0.9	**8E-03**	1.1	**4E-03**	0.9	**4E-02**	#N/A	#N/A	#N/A
10325	**RRAGB**	**ras-related GTP-binding protein B short isoform**	5	28	5	0.9	**3E-02**	0.8	**1E-02**	0.9	**4E-02**	0.8	**1E-02**	0.9	**1E-02**	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
399687	**MYO18A**	**unconventional myosin-XVIIIa isoform a**	48	244	48	0.9	**8E-11**	1.1	**2E-16**	1.1	**2E-16**	1.4	**2E-16**	1.0	4E-01	Structural molecule activity	Endoplasmic reticulum;Nucleus	Structural protein
64743	**WDR13**	**PREDICTED: WD repeat-containing protein 13 isoform X1**	4	14	4	0.9	5E-02	1.3	7E-02	1.1	**2E-02**	1.6	1E-01	1.1	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
6500	**SKP1**	**S-phase kinase-associated protein 1 isoform b**	10	75	10	0.9	**1E-05**	0.9	**6E-08**	1.0	1E-01	1.0	**2E-07**	0.9	**5E-05**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
51646	**YPEL5**	**protein yippee-like 5**	2	6	2	0.9	6E-01	1.0	4E-01	0.8	3E-01	1.2	1E-01	1.0	4E-01	Molecular function unknown	-	Unclassified
58533	**SNX6**	**sorting nexin-6 isoform b**	17	111	16	0.9	**1E-04**	1.0	**2E-07**	0.9	**2E-03**	1.0	**1E-11**	0.9	9E-02	Transporter activity	Cytoplasm	Transport/cargo protein
29086	**BABAM1**	**BRISC and BRCA1-A complex member 1 isoform 1**	5	27	5	0.9	2E-01	1.0	**8E-05**	1.0	2E-01	0.9	**5E-03**	0.8	**2E-02**	#N/A	#N/A	#N/A
291	**SLC25A4**	**ADP/ATP translocase 1**	18	225	4	0.9	5E-01	1.1	**1E-02**	1.0	**3E-02**	**1.6**	**5E-04**	1.0	5E-01	Transporter activity	Mitochondrion	Transport/cargo protein
4000	**LMNA**	**lamin isoform A**	49	1006	5	0.9	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	**1.5**	**2E-16**	1.0	**2E-03**	Structural molecule activity	Nucleus;Cytoplasm	Structural protein
57402	**S100A14**	**PREDICTED: protein S100-A14 isoform X1**	7	135	7	0.9	**1E-05**	1.2	**7E-10**	1.0	**8E-11**	1.0	**2E-12**	1.0	3E-01	Calcium ion binding	Cytoplasm	Calcium binding protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
28956	LAMTOR2	ragulator complex protein LAMTOR2 isoform 1	5	23	5	0.9	**4E-03**	1.0	**3E-04**	1.0	**1E-02**	0.9	**6E-03**	0.9	3E-01	#N/A	#N/A	#N/A
5229;	PGGT1B	geranylgeranyl transferase type-1 subunit beta	5	12	1	0.9	**8E-03**	1.1	**9E-04**	1.3	**3E-02**	**2.3**	**4E-04**	0.9	**2E-02**	Transferase activity	-	Enzyme: Prenyltransferase
2017	CTTN	src substrate cortactin isoform a	23	161	23	0.9	**7E-08**	1.0	**1E-09**	0.9	**1E-06**	0.8	2E-01	0.9	**5E-02**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
2224	FDPS	farnesyl pyrophosphate synthase isoform a	9	104	9	0.9	**2E-04**	0.7	**2E-11**	1.3	**8E-09**	1.0	**2E-09**	1.0	5E-01	Transferase activity	Peroxisome	Enzyme: Prenyltransferase
4615	MYD88	myeloid differentiation primary response protein MyD88 isoform 1	8	36	8	0.9	**2E-03**	0.8	**2E-06**	1.0	**3E-02**	1.0	**1E-06**	0.9	**4E-02**	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
11078	TRIOBP	TRIO and F-actin-binding protein isoform 6	7	25	6	0.9	9E-02	1.0	6E-02	1.0	1E-01	0.9	9E-02	1.1	2E-01	Cytoskeletal protein binding	-	Cytoskeletal associated protein
55665	URGCP	up-regulator of cell proliferation isoform 3	3	6	3	0.9	8E-01	0.8	7E-01	0.9	3E-01	0.8	7E-01	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
83985	SPNS1	protein spinster homolog 1 isoform 1	3	14	3	0.9	**3E-02**	1.1	**3E-05**	1.1	**6E-03**	1.4	**2E-05**	1.0	3E-01	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule
535	ATP6V0A1	V-type proton ATPase 116 kDa subunit a isoform 1 isoform a	10	47	8	0.9	**4E-02**	1.3	2E-01	0.8	**2E-05**	1.0	**8E-04**	1.0	1E-01	Ion channel activity	Brush border	Ion channel
57658	CALCOCO1	calcium-binding and coiled-coil domain-containing protein 1 isoform 1	6	23	6	0.9	8E-02	0.9	2E-01	0.6	4E-01	1.2	**5E-03**	1.1	**1E-02**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
10640	EXOC5	exocyst complex component 5	21	83	20	0.9	**3E-05**	1.1	**2E-09**	1.0	**2E-08**	1.0	**2E-10**	1.0	9E-01	Transporter activity	Cytoplasm	Transport/cargo protein
3421	IDH3G	isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial isoform a	7	38	7	0.9	**6E-03**	1.1	**1E-03**	1.1	**5E-04**	1.3	**2E-05**	1.0	9E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
8566	PDXK	pyridoxal kinase	11	76	11	0.9	**2E-02**	0.9	**6E-04**	1.0	1E-01	1.2	**1E-05**	0.9	**1E-02**	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
27349	MCAT	malonyl-CoA-acyl carrier protein transacylase, mitochondrial isoform a	4	18	4	0.9	**4E-02**	1.1	**1E-02**	1.1	**1E-02**	1.1	**3E-02**	1.0	7E-01	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
29952;	DPP7	dipeptidyl peptidase 2 preproprotein	4	8	4	0.9	6E-02	0.9	**4E-05**	1.0	9E-01	0.9	**2E-04**	1.0	5E-01	Serine-type peptidase activity	Lysosome	Serine protease
23303	KIF13B	kinesin-like protein KIF13B	6	23	4	0.9	4E-01	1.1	**4E-03**	1.0	**9E-03**	**1.5**	**2E-04**	1.3	4E-01	Motor activity	Cytoplasm	Motor protein
3845	KRAS	GTPase KRas isoform a	6	25	4	0.9	**1E-03**	1.2	**2E-04**	1.1	**3E-02**	1.2	**2E-04**	0.9	4E-01	GTPase activity	Plasma membrane	GTPase
8729	GBF1	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 2	20	77	19	0.9	**2E-03**	0.9	**4E-06**	0.9	7E-01	1.0	**4E-07**	1.0	3E-01	Guanyl-nucleotide exchange factor activity	Golgi apparatus	Guanine nucleotide exchange factor
1977	EIF4E	eukaryotic translation initiation factor 4E isoform 2	7	39	7	0.9	**4E-03**	0.9	**1E-05**	1.0	8E-01	1.0	**5E-07**	1.0	8E-01	Translation regulator activity	Nucleus	Translation regulatory protein
59286	UBL5	ubiquitin-like protein 5	3	18	3	0.9	**7E-03**	**0.7**	**2E-03**	0.8	**1E-02**	**0.5**	**2E-02**	0.7	**3E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
81532	MOB2	MOB kinase activator 2 isoform 1	5	21	5	0.9	**4E-02**	1.0	**1E-03**	0.9	8E-02	1.1	**2E-03**	1.0	8E-01	#N/A	#N/A	#N/A
4329	ALDH6A1	methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial isoform 1	7	34	7	0.9	5E-02	1.2	**1E-03**	1.1	**7E-05**	1.1	**3E-05**	1.0	1E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
11329	STK38	PREDICTED: serine/threonine-protein kinase 38 isoform X1	11	21	10	0.9	5E-02	1.1	**8E-03**	0.9	**2E-02**	1.0	**2E-04**	1.0	7E-02	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
25820	ARIH1	E3 ubiquitin-protein ligase ARIH1	5	19	5	0.9	2E-01	0.8	**2E-02**	1.0	1E+00	1.0	**6E-03**	0.9	3E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
201931	TMEM192	transmembrane protein 192	2	8	2	0.9	2E-01	1.1	**5E-02**	1.2	9E-02	1.2	**3E-02**	1.0	5E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
10808	HSPH1	heat shock protein 105 kDa isoform 1	39	337	36	0.9	**7E-14**	0.7	**2E-08**	0.8	**2E-16**	0.8	**2E-03**	0.9	**5E-12**	Heat shock protein activity;Chaperone activity	Cytoplasm	Heat shock protein;Chaperone
4301	MLLT4	PREDICTED: afadin isoform X5	33	81	1	0.9	**1E-11**	1.0	**2E-16**	1.1	**6E-12**	1.2	**2E-16**	0.8	**8E-04**	Cell adhesion molecule activity	Cytoplasm	Cell junction protein
2232	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial isoform 3	16	80	16	0.9	**4E-05**	1.4	**7E-06**	0.8	**3E-06**	1.1	**9E-07**	1.0	6E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
25824	PRDX5	peroxiredoxin-5, mitochondrial isoform a	9	196	9	0.9	**5E-05**	1.0	**2E-16**	1.1	**4E-08**	1.1	**2E-16**	0.9	**2E-03**	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
51155	HN1	hematological and neurological expressed 1 protein isoform 2	4	28	4	0.9	**2E-04**	0.8	**8E-05**	0.9	**1E-03**	0.9	**1E-03**	0.8	**4E-03**	Molecular function unknown	Nucleus;Cytoplasm	Cell cycle control protein
221955	DAGLB	sn1-specific diacylglycerol lipase beta isoform 1	4	17	4	0.9	8E-02	0.8	8E-02	0.9	3E-01	1.0	**3E-02**	1.0	7E-01	Lipase activity	-	Enzyme: Lipase
63892	THADA	PREDICTED: thyroid adenoma-associated protein isoform X1	3	9	3	0.9	3E-01	0.9	7E-02	1.0	4E-01	1.2	**3E-02**	0.9	1E-01	Receptor binding	-	Unclassified
578	BAK1	PREDICTED: bcl-2 homologous antagonist/killer isoform X1	2	10	2	0.9	5E-01	1.1	9E-02	1.1	7E-02	1.2	**2E-02**	1.1	1E-01	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule
4478	MSN	moesin	49	721	34	0.9	**5E-12**	0.8	**2E-16**	1.0	**2E-16**	0.9	**2E-16**	1.0	**4E-02**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
6697	SPR	sepiapterin reductase	7	37	7	0.9	**4E-03**	0.8	**3E-05**	0.9	**9E-05**	0.9	**2E-05**	0.9	**3E-02**	Catalytic activity	-	Enzyme: Reductase

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10973	ASCC3	activating signal cointegrator 1 complex subunit 3 isoform a	24	85	24	0.9	**2E-02**	0.8	3E-01	0.8	4E-01	0.7	5E-01	1.0	2E-01	Molecular function unknown	Nucleus	Unclassified
8050	PDHX	pyruvate dehydrogenase protein X component, mitochondrial isoform 1	7	38	7	0.9	**5E-02**	1.1	**3E-04**	1.1	**8E-05**	1.1	**1E-05**	0.9	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
550	AUP1	ancient ubiquitous protein 1	6	34	6	0.9	1E-01	1.1	**3E-03**	0.9	**2E-02**	1.3	**4E-03**	1.0	6E-02	Molecular function unknown	Cytoplasm	Unclassified
57504	MTA3	metastasis-associated protein MTA3 isoform b	8	34	4	0.9	2E-01	1.2	**2E-03**	1.0	**3E-02**	1.2	**8E-03**	1.0	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
81890	QTRT1	queuine tRNA-ribosyltransferase	2	10	2	0.9	3E-01	0.9	9E-02	0.9	7E-01	0.8	4E-01	**0.5**	**2E-02**	Catalytic activity	-	Enzyme: Ribosyltransferase
1500	CTNND1	catenin delta-1 isoform 1AC	35	277	35	0.9	**4E-10**	1.1	**2E-16**	1.0	**2E-16**	0.9	**8E-13**	0.9	**6E-03**	Cell adhesion molecule activity	Cytoplasm;Nucleus	Adhesion molecule
4134	MAP4	microtubule-associated protein 4 isoform 1	48	406	2	0.9	**3E-07**	0.8	**1E-06**	0.8	7E-02	**0.6**	**2E-10**	0.8	**5E-07**	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein
80221	ACSF2	acyl-CoA synthetase family member 2, mitochondrial isoform 1	9	54	9	0.9	**9E-05**	**1.6**	**1E-06**	0.9	**5E-08**	0.9	**8E-05**	1.0	6E-01	Molecular function unknown	-	Unclassified
6813	STXBP2	syntaxin-binding protein 2 isoform a	16	56	16	0.9	**1E-02**	0.9	**2E-08**	1.0	4E-01	1.0	**1E-05**	0.9	**2E-03**	Molecular function unknown	Cytoplasm	Unclassified
134492	NUDCD2	nudC domain-containing protein 2	3	16	3	0.9	**2E-02**	1.0	**2E-02**	1.0	1E-01	0.8	**2E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
129450	TYW5	tRNA wybutosine-synthesizing protein 5	2	10	2	0.9	7E-02	0.8	8E-02	1.0	2E-01	1.1	9E-02	0.9	1E-01	#N/A	#N/A	#N/A
64121	RRAGC	ras-related GTP-binding protein C isoform 1	10	52	10	0.9	1E-01	0.9	**9E-05**	1.0	8E-01	1.1	**1E-06**	1.0	4E-01	GTPase activity	Cytoplasm	G protein
6282	S100A11	protein S100-A11	6	204	6	0.9	**2E-05**	0.9	**4E-11**	1.2	**3E-02**	1.2	**9E-11**	0.9	8E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
5576	PRKAR2A	PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit isoform X1	15	87	15	0.9	**3E-04**	1.0	**7E-11**	1.1	**1E-03**	1.3	**1E-13**	1.0	9E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
51534	VTA1	vacuolar protein sorting-associated protein VTA1 homolog isoform a	7	39	7	0.9	**6E-04**	0.9	**4E-08**	1.0	2E-01	1.1	**2E-07**	0.9	**3E-04**	Molecular function unknown	-	Unclassified
9517	SPTLC2	serine palmitoyltransferase 2	4	26	4	0.9	**4E-03**	1.1	**6E-04**	1.0	**2E-02**	1.0	**6E-07**	1.0	**2E-02**	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase
11034	DSTN	PREDICTED: destrin isoform X1	9	116	8	0.9	**5E-03**	1.0	**1E-08**	1.0	**9E-03**	1.2	**3E-07**	1.1	7E-01	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein
11226	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6	5	14	4	0.9	1E-01	0.8	5E-02	0.9	4E-01	0.9	8E-02	1.0	5E-01	Transferase activity	Golgi apparatus	Enzyme: Glycosyltransferase
80157	CWH43	PGAP2-interacting protein isoform 1	4	14	4	0.9	1E-01	1.2	**3E-02**	0.8	**2E-03**	**0.6**	**6E-03**	0.9	6E-01	Molecular function unknown	-	Unclassified
999	CDH1	cadherin-1 preproprotein	15	101	14	0.9	**3E-07**	1.1	**9E-11**	1.0	**3E-07**	0.8	**4E-02**	1.0	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
3301	DNAJA1	dnaJ homolog subfamily A member 1	13	90	12	0.9	**1E-05**	0.8	**3E-05**	0.9	**1E-03**	1.0	**8E-08**	0.9	**1E-02**	Heat shock protein activity	Acrosome	Heat shock protein
9296	ATP6V1F	V-type proton ATPase subunit F isoform 2	3	13	3	0.9	6E-02	1.1	**4E-02**	1.1	5E-02	1.2	**3E-02**	1.0	3E-01	ATPase activity	Plasma membrane	ATPase
60561	RINT1	RAD50-interacting protein 1	7	30	7	0.9	2E-01	1.1	**9E-04**	0.9	**2E-04**	0.9	**3E-04**	1.0	6E-01	Protein binding	Endoplasmic reticulum	Cell cycle control protein
285237	C3orf38	uncharacterized protein C3orf38	2	4	2	0.9	3E-01	0.7	2E-01	0.9	3E-01	0.8	6E-01	0.9	5E-01	Molecular function unknown	-	Unclassified
1.01E+08	HSPE1-MOB4	HSPE1-MOB4 protein	9	127	4	0.9	#N/A	1.0	#N/A	0.9	#N/A	1.2	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
5464	PPA1	inorganic pyrophosphatase	17	181	16	0.9	**3E-14**	1.0	**2E-16**	1.0	**8E-04**	1.1	**6E-15**	1.0	**5E-03**	Catalytic activity	Cytoplasm	Enzyme: Phosphohydrolase
10971	YWHAQ	14-3-3 protein theta	19	1028	13	0.9	**2E-07**	1.0	**6E-14**	1.1	**1E-07**	1.1	**9E-14**	0.9	**1E-06**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
54960	GEMIN8	gem-associated protein 8	4	16	4	0.9	**8E-03**	0.9	**1E-02**	1.0	8E-01	1.0	**5E-02**	0.9	2E-01	Molecular function unknown	-	Unclassified
5877;	RABIF	guanine nucleotide exchange factor MSS4	5	12	4	0.9	**2E-02**	0.9	6E-01	1.0	1E-01	1.1	9E-01	0.8	**4E-03**	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
10313	RTN3	reticulon-3 isoform a	4	38	4	0.9	**2E-02**	1.2	**3E-03**	0.9	**2E-04**	**1.5**	**1E-04**	1.0	8E-02	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein
30000	TNPO2	transportin-2 isoform 2	13	65	9	0.9	**3E-02**	1.0	**4E-06**	1.0	5E-02	1.0	**1E-03**	1.0	6E-01	Transporter activity	Nucleoplasm	Transport/cargo protein
738	VPS51	vacuolar protein sorting-associated protein 51 homolog	9	31	9	0.9	**5E-02**	0.9	**4E-06**	1.0	5E-01	1.0	**2E-03**	0.9	4E-01	#N/A	#N/A	#N/A
162427	FAM134C	protein FAM134C	5	26	5	0.9	7E-02	1.1	**4E-03**	1.0	**2E-02**	1.3	**7E-04**	1.0	6E-01	Molecular function unknown	-	Integral membrane protein
391356	PTRHD1	putative peptidyl-tRNA hydrolase PTRHD1	3	11	3	0.9	1E-01	0.8	2E-01	0.8	**2E-02**	0.9	8E-01	0.9	8E-02	#N/A	#N/A	#N/A
8678	BECN1	beclin-1	2	7	2	0.9	2E-01	1.1	8E-02	0.9	4E-01	1.4	**2E-02**	1.2	**5E-02**	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
5861	RAB1A	ras-related protein Rab-1A isoform 1	15	208	6	0.9	**2E-05**	1.0	**2E-08**	1.0	**7E-09**	1.2	**7E-12**	1.0	7E-01	GTPase activity	Golgi apparatus	GTPase
1622	DBI	acyl-CoA-binding protein isoform 4	3	63	3	0.9	**2E-04**	1.0	**3E-13**	1.0	**8E-04**	0.8	2E-01	0.9	3E-01	Receptor binding	Mitochondrion	Ligand
8672	EIF4G3	eukaryotic translation initiation factor 4 gamma 3 isoform 1	17	111	9	0.9	**4E-04**	1.1	**1E-04**	0.9	2E-01	0.8	**5E-05**	1.0	**2E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
55748	CNDP2	PREDICTED: cytosolic non-specific dipeptidase isoform X1	14	91	14	0.9	**2E-03**	0.8	**1E-02**	0.8	**2E-03**	**0.7**	**4E-04**	1.0	**5E-02**	Metallopeptidase activity	Cytoplasm	Metallo protease
2987	GUK1	guanylate kinase isoform a	8	38	8	0.9	**7E-03**	0.9	**5E-05**	0.9	5E-01	0.9	**3E-03**	0.9	3E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
157506	**RDH10**	**retinol dehydrogenase 10**	2	8	2	0.9	**1E-02**	1.0	9E-02	0.9	**4E-02**	1.0	6E-02	0.9	7E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
8560	**DEGS1**	**sphingolipid delta(4)-desaturase DES1**	2	10	2	0.9	2E-01	1.1	**4E-04**	0.9	**6E-03**	0.9	5E-02	1.0	4E-01	Oxidoreductase activity	Endoplasmic reticulum membrane	Enzyme: Oxidoreductase
64374	**SIL1**	**nucleotide exchange factor SIL1**	4	12	4	0.9	3E-01	1.0	5E-02	1.0	3E-01	1.0	**1E-02**	1.1	**9E-05**	Chaperone activity	Endoplasmic reticulum	Chaperone
5093	**PCBP1**	**poly(rC)-binding protein 1**	14	152	9	0.9	**1E-04**	0.8	**3E-05**	0.9	**6E-04**	1.0	**8E-07**	0.9	**2E-02**	RNA binding	Nucleus	RNA binding protein
9554	**SEC22B**	**vesicle-trafficking protein SEC22b**	10	67	10	0.9	**2E-04**	1.0	**3E-07**	1.0	**1E-04**	1.3	**4E-07**	1.0	5E-01	Transporter activity	Endoplasmic reticulum	Integral membrane protein
3839	**KPNA3**	**importin subunit alpha-4**	9	80	5	0.9	1E-01	0.9	2E-01	0.8	5E-01	1.0	**4E-03**	1.0	5E-01	Transporter activity	Nucleus	Transport/cargo protein
6433	**SFSWAP**	**splicing factor, suppressor of white-apricot homolog isoform 1**	4	10	4	0.9	2E-01	0.7	**4E-02**	1.0	3E-01	1.1	1E-01	1.1	8E-01	#N/A	#N/A	#N/A
9140	**ATG12**	**ubiquitin-like protein ATG12 isoform 1**	3	10	3	0.9	3E-01	0.9	2E-01	1.1	5E-01	1.3	1E-01	1.1	7E-01	Molecular function unknown	Cytoplasm	Unclassified
11161	**C14orf1**	**probable ergosterol biosynthetic protein 28**	4	22	4	0.9	4E-01	1.2	**2E-02**	1.1	**2E-02**	1.2	**4E-03**	1.0	8E-01	Molecular function unknown	Plasma membrane	Unclassified
5768	**QSOX1**	**sulfhydryl oxidase 1 isoform a**	2	6	2	0.9	9E-01	1.0	2E-01	1.0	4E-01	0.9	3E-01	1.0	9E-01	Molecular function unknown	Extracellular	Cell cycle control protein
1267	**CNP**	**2',3'-cyclic-nucleotide 3'-phosphodiesterase**	12	75	11	0.9	**2E-07**	1.0	**5E-09**	1.0	**1E-03**	1.0	**3E-06**	1.0	2E-01	Phosphoric diester hydrolase activity	Cytoplasm	Enzyme: Phosphodiesterase
10652	**YKT6**	**synaptobrevin homolog YKT6**	10	68	10	0.9	**6E-07**	0.9	**2E-11**	0.9	6E-01	0.8	**7E-05**	0.9	**2E-03**	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein
5510	**PPP1R7**	**protein phosphatase 1 regulatory subunit 7 isoform 1**	16	99	16	0.9	**6E-03**	1.1	**4E-11**	1.0	**3E-06**	1.2	**4E-13**	0.9	**2E-03**	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase
1730	**DIAPH2**	**protein diaphanous homolog 2 isoform 156**	8	21	7	0.9	**1E-02**	1.0	**7E-03**	1.0	2E-01	1.0	**2E-02**	1.0	5E-01	Receptor binding	Cytoplasm	Ligand
23061	**TBC1D9B**	**TBC1 domain family member 9B isoform a**	10	41	10	0.9	**2E-02**	0.9	**9E-09**	1.1	5E-01	1.2	**1E-03**	1.0	3E-01	Molecular function unknown	-	Unclassified
8996	**NOL3**	**PREDICTED: nucleolar protein 3 isoform X1**	3	11	3	0.9	**5E-02**	1.3	**4E-02**	1.4	**2E-02**	1.0	**2E-02**	1.1	2E-01	Protease inhibitor activity	Nucleolus	Cell cycle control protein
79755	**ZNF750**	**zinc finger protein 750**	2	5	2	0.9	4E-01	1.3	2E-01	1.1	2E-01	1.0	1E-01	1.3	3E-01	Molecular function unknown	-	Unclassified
9943	**OXSR1**	**serine/threonine-protein kinase OSR1**	15	117	14	0.9	**3E-06**	0.9	**1E-13**	1.1	2E-01	**1.5**	**2E-16**	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
6643	**SNX2**	**sorting nexin-2 isoform 1**	16	109	14	0.9	**9E-05**	1.0	**5E-12**	0.9	2E-01	1.1	**4E-08**	0.9	**5E-03**	Transporter activity	Endosome	Transport/cargo protein
1652	**DDT**	**D-dopachrome decarboxylase**	4	29	4	0.9	**3E-03**	0.9	**8E-04**	1.0	3E-01	0.8	5E-02	0.9	**7E-04**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
23086	**EXPH5**	**exophilin-5**	9	24	9	0.9	**3E-03**	1.1	4E-01	0.8	**5E-03**	0.8	4E-01	1.0	**2E-02**	Molecular function unknown	Nucleus	Unclassified
26046	**LTN1**	**E3 ubiquitin-protein ligase listerin**	9	29	9	0.9	**4E-03**	1.0	**6E-04**	0.9	9E-01	1.0	**3E-02**	1.0	8E-01	#N/A	#N/A	#N/A
5480	**PPIC**	**peptidyl-prolyl cis-trans isomerase C**	3	14	2	0.9	**5E-03**	1.1	**2E-02**	1.0	**3E-02**	0.7	6E-01	0.9	7E-01	Chaperone activity	-	Chaperone
285636	**C5orf51**	**UPF0600 protein C5orf51**	4	18	4	0.9	**1E-02**	0.8	**1E-03**	1.0	3E-01	1.1	**4E-03**	0.8	**1E-02**	Molecular function unknown	-	Unclassified
255252	**LRRC57**	**leucine-rich repeat-containing protein 57**	6	26	6	0.9	7E-02	1.0	**5E-04**	1.1	**4E-02**	1.1	**3E-04**	1.1	4E-01	Molecular function unknown	-	Unclassified
54499	**TMCO1**	**transmembrane and coiled-coil domain-containing protein 1 isoform a**	5	29	5	0.9	4E-01	1.0	**3E-02**	1.2	2E-01	1.4	**3E-03**	1.1	8E-02	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein
5211	**PFKL**	**ATP-dependent 6-phosphofructokinase, liver type isoform b**	21	163	16	0.9	**5E-08**	1.0	**3E-12**	1.0	**4E-06**	1.0	**2E-15**	1.0	1E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
8030	**CCDC6**	**coiled-coil domain-containing protein 6**	18	93	17	0.9	**3E-05**	0.9	**1E-05**	0.8	9E-01	0.7	1E-01	0.9	**7E-04**	Structural constituent of cytoskeleton	Cytoplasm	Unclassified;Cell cycle control protein
5869	**RAB5B**	**ras-related protein Rab-5B isoform 1**	8	65	5	0.9	**1E-02**	1.1	**2E-04**	1.0	**4E-03**	1.3	**8E-04**	1.0	1E-01	GTPase activity	Plasma membrane	GTPase
528	**ATP6V1C1**	**V-type proton ATPase subunit C 1**	15	80	14	0.9	**4E-02**	0.9	**4E-05**	1.0	2E-01	1.2	**6E-10**	1.0	3E-01	ATPase activity	-	ATPase
1072	**CFL1**	**cofilin-1**	16	297	11	0.9	**2E-16**	0.8	**2E-16**	1.0	**1E-09**	0.9	**6E-09**	0.9	**4E-04**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
1452	**CSNK1A1**	**casein kinase I isoform alpha isoform 2**	13	130	12	0.9	**2E-09**	1.1	**4E-15**	1.0	**1E-11**	0.9	**3E-09**	0.9	**1E-05**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
7532	**YWHAG**	**14-3-3 protein gamma**	15	982	10	0.9	**8E-09**	0.9	**3E-14**	1.0	**1E-02**	1.1	**9E-13**	0.9	**5E-02**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
10493	**VAT1**	**synaptic vesicle membrane protein VAT-1 homolog**	13	107	13	0.9	**8E-08**	1.0	**3E-09**	1.1	**2E-03**	1.3	**1E-10**	0.9	**5E-03**	Transporter activity	Cytoplasmic vesicle	Transport/cargo protein
57095	**PITHD1**	**PITH domain-containing protein 1**	6	26	6	0.9	**2E-03**	1.1	**1E-06**	1.1	**9E-05**	1.0	**4E-05**	0.9	**2E-02**	#N/A	#N/A	#N/A
64342	**HS1BP3**	**HCLS1-binding protein 3**	7	33	7	0.9	**5E-02**	1.1	**1E-02**	1.0	6E-02	1.0	**4E-03**	1.0	1E+00	Molecular function unknown	-	Unclassified
57617	**VPS18**	**vacuolar protein sorting-associated protein 18 homolog**	11	41	10	0.9	2E-01	1.0	**2E-03**	0.9	2E-01	1.0	**2E-04**	1.0	8E-01	Transporter activity	Cytoplasm	Transport/cargo protein
29985	**SLC39A3**	**zinc transporter ZIP3 isoform a**	1	6	1	0.9	5E-01	0.8	2E-01	1.0	5E-01	0.8	2E-01	0.9	7E-01	Transporter activity	Plasma membrane;Cytoplasm	Membrane transport protein
1629	**DBT**	**lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial**	13	87	13	0.9	**2E-05**	1.2	**4E-11**	1.0	**5E-11**	1.1	**5E-15**	1.0	1E+00	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
5515	**PPP2CA**	**serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform**	13	92	2	0.9	**4E-02**	0.8	**8E-03**	1.0	**4E-02**	1.2	**2E-03**	0.8	**2E-02**	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
23332	**CLASP1**	**CLIP-associating protein 1 isoform 1**	17	68	13	0.9	8E-02	1.0	**4E-03**	0.9	**2E-03**	1.0	**4E-05**	0.9	4E-01	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
81889	FAHD1	acylpyruvase FAHD1, mitochondrial isoform 1	4	12	4	0.9	9E-02	1.1	**7E-03**	0.9	**2E-02**	1.2	**1E-02**	1.1	7E-02	Molecular function unknown	-	Unclassified
93974	ATPIF1	ATPase inhibitor, mitochondrial isoform 1	5	50	5	0.9	4E-01	1.2	8E-01	0.9	3E-01	0.9	6E-01	1.0	7E-01	Enzyme inhibitor activity	Mitochondrion	Enzyme regulator
2896	GRN	granulins	9	47	9	0.9	**5E-02**	1.0	9E-01	0.7	**2E-03**	0.6	6E-02	0.8	**2E-02**	Growth factor activity	Extracellular	Growth factor
7167	TPI1	triosephosphate isomerase isoform 2	18	354	18	0.9	**2E-16**	0.9	**2E-16**	1.1	2E-01	1.1	**2E-16**	0.9	**1E-09**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
55898	UNC45A	protein unc-45 homolog A isoform 2	32	189	32	0.9	**3E-12**	1.0	**2E-16**	1.0	**4E-03**	0.9	**2E-13**	0.9	**4E-05**	Molecular function unknown	Nucleus	Unclassified
6051	RNPEP	aminopeptidase B	21	129	21	0.9	**2E-09**	1.1	**2E-12**	1.0	**2E-09**	1.0	**3E-15**	0.9	**6E-03**	Aminopeptidase activity	Golgi apparatus	Aminopeptidase
5829	PXN	paxillin isoform 3	16	91	2	0.9	**3E-09**	0.8	**1E-09**	**0.7**	**3E-06**	**0.7**	**9E-04**	1.3	6E-01	Cell adhesion molecule activity	Focal adhesion	Cytoskeletal associated protein
25996	REXO2	oligoribonuclease, mitochondrial	7	27	7	0.9	**4E-06**	0.9	**9E-05**	0.8	6E-02	**0.6**	**7E-06**	0.9	**1E-03**	Ribonuclease activity	Mitochondrion	Ribonuclease
149371	EXOC8	exocyst complex component 8	14	55	14	0.9	**7E-05**	1.0	**4E-06**	0.9	**1E-03**	1.0	**4E-08**	0.9	3E-01	Transporter activity	Plasma membrane	Transport/cargo protein
8649	LAMTOR3	ragulator complex protein LAMTOR3 isoform 1	5	38	5	0.9	**1E-02**	1.0	**2E-03**	1.0	**2E-03**	1.0	**2E-04**	0.9	2E-01	#N/A	#N/A	#N/A
9341	VAMP3	vesicle-associated membrane protein 3	3	25	3	0.9	**3E-02**	1.0	**1E-03**	1.2	**4E-02**	1.2	**4E-03**	0.9	1E-01	Protein binding;Transporter activity	Plasma membrane	Integral membrane protein
581	BAX	apoptosis regulator BAX isoform 1	5	28	5	0.9	1E-01	1.0	**8E-03**	0.9	9E-02	0.8	2E-01	0.9	3E-01	Receptor signaling complex scaffold activity	Cytoplasm;Mitochondrion	Adapter molecule
23248	RPRD2	regulation of nuclear pre-mRNA domain-containing protein 2 isoform 1	3	7	3	0.9	3E-01	1.0	2E-01	0.9	6E-01	1.2	**3E-02**	0.8	3E-01	Molecular function unknown	-	Unclassified
26060	APPL1	DCC-interacting protein 13-alpha	9	34	9	0.9	**1E-03**	1.1	**1E-06**	1.0	**2E-03**	1.1	**1E-05**	0.9	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
8803	SUCLA2	succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	15	100	15	0.9	**4E-03**	1.1	**2E-08**	1.0	**8E-13**	1.1	**5E-12**	1.0	4E-01	Ligase activity	Mitochondrion	Enzyme: Synthase
28970	C11orf54	ester hydrolase C11orf54 isoform c	2	12	2	0.9	**2E-02**	1.2	**2E-02**	1.1	**8E-03**	**1.5**	**1E-02**	1.0	3E-01	Molecular function unknown	-	Unclassified
6146	RPL22	60S ribosomal protein L22 proprotein	3	61	3	0.9	**4E-02**	1.0	5E-01	0.7	**8E-03**	**0.7**	**1E-03**	1.2	**2E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
55129	ANO10	anoctamin-10 isoform 1	7	34	7	0.9	1E-01	1.3	**2E-03**	1.0	**2E-04**	1.4	**5E-05**	1.1	**2E-02**	Molecular function unknown	-	Integral membrane protein
89122	TRIM4	E3 ubiquitin-protein ligase TRIM4 isoform alpha	4	9	4	0.9	1E-01	1.0	1E-01	0.9	5E-01	1.1	2E-01	1.0	1E+00	Molecular function unknown	Cytoplasm	Water channel
26056	RAB11FIP5	PREDICTED: rab11 family-interacting protein 5 isoform X3	10	17	10	0.9	2E-01	0.9	**9E-03**	0.9	8E-01	1.1	**2E-03**	1.0	7E-01	Transporter activity	Mitochondrion	Transport/cargo protein
51575	ESF1	ESF1 homolog*gi|444909146|ref|NP_001263309.1| ESF1 homolog	3	7	3	0.9	3E-01	0.8	**4E-02**	1.0	7E-01	0.7	5E-01	1.0	4E-01	Molecular function unknown	Nucleolus	Unclassified
2744	GLS	glutaminase kidney isoform, mitochondrial isoform 1	13	72	3	0.9	**2E-05**	0.9	**4E-09**	1.0	7E-02	1.3	**8E-06**	1.0	8E-01	Deaminase activity	Mitochondrion	Enzyme: Deaminase
55114	ARHGAP17	rho GTPase-activating protein 17 isoform 2	5	24	5	0.9	**3E-03**	0.9	**7E-04**	1.1	4E-01	1.2	**7E-04**	0.9	4E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
11336	EXOC3	exocyst complex component 3	11	52	11	0.9	**4E-03**	1.0	**1E-05**	1.0	**8E-03**	1.1	**3E-05**	1.0	5E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
7095	SEC62	translocation protein SEC62	8	47	8	0.9	**5E-03**	1.1	**2E-03**	0.9	8E-02	**1.6**	**2E-02**	1.1	7E-02	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
5689	PSMB1	proteasome subunit beta type-1	8	66	8	0.9	**1E-02**	0.9	**3E-07**	1.0	2E-01	1.0	**2E-08**	0.9	**3E-02**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
23049	SMG1	serine/threonine-protein kinase SMG1	6	11	6	0.9	2E-01	0.9	1E-01	1.3	7E-01	1.1	**2E-02**	0.9	1E+00	Molecular function unknown	Nucleus	Unclassified
5478	PPIA	peptidyl-prolyl cis-trans isomerase A isoform 1	14	848	5	0.9	**2E-16**	0.9	**2E-16**	1.1	1E-01	0.9	**2E-16**	0.9	7E-01	Isomerase activity	Cytoplasm	Enzyme: Isomerase
11343	MGLL	monoglyceride lipase isoform 1	3	8	3	0.9	4E-01	0.7	**4E-02**	1.0	3E-01	**2.2**	**2E-02**	1.1	1E-01	Lipase activity	-	Enzyme: Lipase
10963	STIP1	stress-induced-phosphoprotein 1 isoform a	37	344	37	0.9	**2E-16**	0.9	**2E-16**	1.0	**1E-03**	1.1	**2E-16**	1.0	6E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
6888	TALDO1	transaldolase	20	272	20	0.9	**2E-16**	1.1	**2E-16**	1.2	**2E-16**	1.2	**2E-16**	1.0	1E+00	Transferase activity, transferring aldehyde or ketonic groups	Nucleus	Enzyme: Transaldolase
79717	PPCS	phosphopantothenate--cysteine ligase isoform a	11	58	11	0.9	**3E-04**	1.1	**4E-08**	1.2	**2E-08**	1.2	**2E-09**	1.0	8E-01	Ligase activity	-	Enzyme: Synthase
382	ARF6	ADP-ribosylation factor 6	6	66	5	0.9	**4E-03**	1.1	**4E-08**	1.1	**1E-04**	1.3	**1E-10**	1.0	5E-01	Transporter activity	Cytosol	Transport/cargo protein
637	BID	BH3-interacting domain death agonist isoform 1	2	7	2	0.9	3E-01	0.7	3E-01	0.8	1E-01	0.9	2E-01	1.1	**4E-02**	Receptor binding	Mitochondrion	Ligand
5716	PSMD10	26S proteasome non-ATPase regulatory subunit 10 isoform 1	6	49	6	0.9	**8E-05**	1.1	**5E-05**	1.1	**3E-04**	1.3	**4E-06**	1.0	7E-01	Ubiquitin-specific protease activity	Cytoplasm	Regulatory/other subunit
7984	ARHGEF5	rho guanine nucleotide exchange factor 5	12	42	12	0.9	**8E-04**	0.9	**7E-05**	1.0	1E-01	1.0	**7E-06**	1.0	9E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
514	ATP5E	ATP synthase subunit epsilon, mitochondrial	3	15	3	0.9	**2E-02**	1.1	**4E-04**	1.1	**3E-03**	1.1	**5E-03**	1.0	8E-01	ATPase activity	Mitochondrial membrane	ATPase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10390	**CEPT1**	**choline/ethanolaminephosphotransferase 1*gi|56118223|ref|NP_001007795.1| choline/ethanolaminephosphotransferase 1**	2	19	2	0.9	**4E-02**	1.1	**2E-04**	1.1	**8E-03**	1.2	**7E-04**	1.0	1E-01	Catalytic activity	Integral to membrane	Enzyme: Phosphotransferase
54785	**C17orf59; BORCS6**	**uncharacterized protein C17orf59**	4	22	4	0.9	5E-02	0.9	**3E-04**	1.1	5E-01	1.1	**4E-04**	0.9	9E-02	#N/A	#N/A	#N/A
10908	**PNPLA6**	**neuropathy target esterase isoform a**	12	44	12	0.9	**2E-03**	1.0	**3E-07**	0.9	**4E-03**	1.1	**3E-08**	1.1	**7E-03**	Hydrolase activity	Endoplasmic reticulum	Enzyme: Esterase
85363	**TRIM5**	**PREDICTED: tripartite motif-containing protein 5 isoform X1**	4	16	4	0.9	**1E-02**	0.8	**1E-02**	0.9	6E-01	0.8	1E-01	0.9	**4E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
11018	**TMED1**	**transmembrane emp24 domain-containing protein 1**	4	16	4	0.9	**2E-02**	0.9	**2E-03**	1.1	2E-01	1.4	**8E-05**	1.0	9E-01	Receptor binding	Plasma membrane	Ligand
55610	**CCDC132; VPS50**	**coiled-coil domain-containing protein 132 isoform a**	8	28	8	0.9	1E-01	1.0	**1E-03**	1.0	**1E-02**	1.1	**4E-05**	1.1	5E-01	#N/A	#N/A	#N/A
283377	**SPRYD4**	**SPRY domain-containing protein 4**	6	25	6	0.9	1E-01	1.2	**1E-03**	1.0	**3E-06**	1.2	**9E-05**	1.1	2E-01	Molecular function unknown	-	Unclassified
83605	**CCM2**	**malcavernin isoform 2**	3	10	3	0.9	3E-01	1.1	7E-02	0.9	3E-01	0.9	1E-01	1.0	8E-01	Molecular function unknown;Receptor signaling complex scaffold activity	Cytoplasm	Unclassified
9879	**DDX46**	**probable ATP-dependent RNA helicase DDX46 isoform 1**	29	132	29	0.9	9E-01	0.9	**3E-02**	1.0	5E-01	0.9	8E-01	0.8	1E-01	Helicase activity	Nucleus;Cytoplasm	RNA helicase
23191	**CYFIP1**	**cytoplasmic FMR1-interacting protein 1 isoform a**	33	223	33	0.9	**2E-10**	1.0	**2E-16**	1.1	**2E-08**	1.1	**2E-16**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
23265	**EXOC7**	**exocyst complex component 7 isoform 4**	10	57	10	0.9	**2E-04**	1.0	**2E-07**	1.0	**2E-02**	1.0	**4E-08**	1.0	5E-01	Molecular function unknown	Cytoplasm	Unclassified
5580	**PRKCD**	**PREDICTED: protein kinase C delta type isoform X1**	9	36	8	0.9	**1E-03**	1.2	**3E-06**	1.1	**9E-05**	1.2	**8E-07**	1.1	8E-02	Protein serine/threonine kinase activity	Cytosol	Serine/threonine kinase
10093	**ARPC4**	**actin-related protein 2/3 complex subunit 4 isoform c**	9	94	9	0.9	3E-01	0.9	**1E-02**	0.9	4E-01	1.0	**1E-02**	0.9	1E-01	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein
51194	**IPO11**	**importin-11 isoform 1**	10	39	10	0.9	4E-01	1.0	**2E-02**	0.9	6E-02	1.0	**3E-05**	1.0	5E-01	Transporter activity	Nucleus	Transport/cargo protein
51062	**ATL1**	**atlastin-1 isoform a**	6	14	5	0.9	5E-01	1.1	3E-01	0.8	4E-01	0.8	3E-01	1.3	1E-01	GTPase activity	Golgi apparatus	GTPase
29934	**SNX12**	**sorting nexin-12 isoform 1*gi|371874557|ref|NP_001243114.1| sorting nexin-12 isoform 1**	6	49	4	0.9	**1E-04**	0.9	**2E-04**	0.9	1E-01	0.7	**5E-03**	0.9	**2E-03**	Molecular function unknown	Cytoplasm	Unclassified
26276	**VPS33B**	**vacuolar protein sorting-associated protein 33B isoform 1**	13	51	13	0.9	**5E-04**	1.1	**1E-06**	1.0	**3E-03**	1.0	**1E-06**	1.0	4E-01	Transporter activity	Cytoplasm	Transport/cargo protein
54165	**DCUN1D1**	**DCN1-like protein 1**	7	37	7	0.9	**1E-03**	1.0	**8E-05**	1.1	**8E-03**	1.2	**7E-05**	1.0	9E-02	Molecular function unknown	-	Unclassified
1398	**CRK**	**adapter molecule crk isoform a**	8	50	3	0.9	**7E-03**	0.9	**3E-04**	1.0	8E-01	1.0	**5E-04**	0.9	4E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
4204	**MECP2**	**methyl-CpG-binding protein 2 isoform 2**	5	20	5	0.9	9E-02	1.1	**1E-02**	1.2	**6E-04**	**1.6**	**8E-03**	1.0	9E-02	DNA binding	Nucleus	DNA binding protein
2288	**FKBP4**	**peptidyl-prolyl cis-trans isomerase FKBP4**	29	240	29	0.9	**1E-11**	0.8	**6E-16**	1.1	**2E-06**	1.0	**2E-16**	0.9	**5E-02**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
8452	**CUL3**	**cullin-3 isoform 3**	24	112	23	0.9	**6E-09**	1.0	**4E-11**	1.1	**4E-09**	1.3	**2E-12**	1.0	2E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
24139	**EML2**	**echinoderm microtubule-associated protein-like 2 isoform 1**	18	124	18	0.9	**1E-05**	1.2	**2E-11**	1.2	**3E-10**	1.4	**4E-11**	0.9	**4E-03**	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein
2803	**GOLGA4**	**Golgin subfamily A member 4 isoform 1**	38	132	36	0.9	**2E-04**	1.1	**8E-09**	0.9	**6E-07**	1.1	**1E-09**	1.0	**4E-02**	Transporter activity	Golgi apparatus;Nucleus	Transport/cargo protein
128866	**CHMP4B**	**charged multivesicular body protein 4b**	8	55	7	0.9	**5E-04**	1.0	**6E-10**	1.1	2E-01	1.2	**5E-09**	1.0	5E-01	Transporter activity	Cytoplasm	Transport/cargo protein
3028	**HSD17B10**	**3-hydroxyacyl-CoA dehydrogenase type-2 isoform 1**	10	71	10	0.9	**6E-04**	1.1	**1E-06**	1.0	**3E-06**	1.0	**1E-08**	1.0	**5E-02**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
55681	**SCYL2**	**SCY1-like protein 2**	13	51	13	0.9	**3E-03**	0.9	**1E-04**	0.9	7E-01	1.0	**2E-04**	0.9	**1E-02**	Kinase activity	Perinuclear region	Serine/threonine kinase
9907	**AP5Z1**	**AP-5 complex subunit zeta-1**	3	9	3	0.9	6E-02	0.7	**1E-02**	1.0	1E-01	0.7	7E-01	0.8	1E-01	#N/A	#N/A	#N/A
55773	**TBC1D23**	**TBC1 domain family member 23 isoform 1**	5	14	5	0.9	9E-02	0.9	**1E-02**	0.9	6E-01	1.4	**5E-03**	1.3	1E-01	Molecular function unknown	-	Unclassified
8826	**IQGAP1**	**ras GTPase-activating-like protein IQGAP1**	75	757	71	0.9	**2E-16**	0.9	**2E-16**	1.0	9E-02	1.1	**2E-16**	0.9	**2E-05**	GTPase activator activity	Cytoplasm	GTPase activating protein
1606	**DGKA**	**diacylglycerol kinase alpha**	23	115	23	0.9	**3E-09**	1.0	**2E-12**	1.0	**7E-07**	1.0	**3E-11**	0.9	**4E-02**	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
22919	**MAPRE1**	**microtubule-associated protein RP/EB family member 1**	10	86	8	0.9	**5E-05**	0.8	**1E-07**	0.9	**3E-03**	0.8	**2E-03**	0.9	**4E-04**	Protein binding	Centrosome	Cell cycle control protein
6715	**SRD5A1**	**3-oxo-5-alpha-steroid 4-dehydrogenase 1**	1	4	1	0.9	**2E-03**	1.7	2E-01	0.8	**3E-02**	1.0	**3E-03**	1.1	**1E-02**	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase
8443	**GNPAT**	**dihydroxyacetone phosphate acyltransferase**	8	32	8	0.9	**3E-02**	1.0	**3E-07**	1.0	**2E-02**	1.1	**1E-05**	1.0	9E-01	Acyltransferase activity	Peroxisome	Enzyme: Acyltransferase
162	**AP1B1**	**AP-1 complex subunit beta-1 isoform b**	31	187	15	0.9	**2E-12**	1.0	**4E-15**	1.0	**7E-08**	1.0	**1E-13**	0.9	**7E-03**	Transporter activity	Golgi apparatus	Transport/cargo protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8065	**CUL5**	**cullin-5**	17	71	17	0.9	**8E-10**	1.0	**1E-10**	1.0	**2E-04**	1.1	**6E-12**	1.0	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55907	**CMAS**	**N-acylneuraminate cytidylyltransferase**	13	62	13	0.9	**6E-03**	1.1	**1E-05**	1.3	**5E-05**	**1.5**	**2E-06**	1.0	2E-01	Ligase activity	Nucleus	Enzyme: Ligase
26058	**GIGYF2**	**PERQ amino acid-rich with GYF domain-containing protein 2 isoform a**	7	33	7	0.9	6E-02	1.1	**7E-04**	0.8	**3E-02**	0.8	**5E-03**	1.0	2E-01	Molecular function unknown	Nucleus	Unclassified
2677	**GGCX**	**vitamin K-dependent gamma-carboxylase isoform 1**	2	13	2	0.9	7E-02	1.0	**2E-02**	0.9	5E-02	1.1	**3E-02**	1.1	7E-02	Ligase activity	Endoplasmic reticulum	Enzyme: Carboxylase
3320	**HSP90AA1**	**heat shock protein HSP 90-alpha isoform 1**	44	894	27	0.9	**2E-16**	0.7	**2E-16**	1.0	**2E-16**	0.9	**2E-16**	1.0	**1E-02**	Chaperone activity	Cytoplasm	Chaperone
3849	**KRT2**	**keratin, type II cytoskeletal 2 epidermal**	35	4415	19	0.9	**1E-08**	1.2	1E-01	0.7	**2E-16**	0.7	**2E-16**	**1.5**	**2E-16**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
10109	**ARPC2**	**actin-related protein 2/3 complex subunit 2**	16	153	16	0.9	**5E-12**	1.0	**2E-16**	0.9	**7E-04**	1.0	**2E-16**	0.9	**1E-03**	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein
3309	**HSPA5**	**78 kDa glucose-regulated protein**	42	766	39	0.9	**1E-08**	0.7	**2E-16**	1.0	**1E-08**	1.1	**2E-16**	1.1	**3E-03**	Chaperone activity	Endoplasmic reticulum	Chaperone
439	**ASNA1**	**ATPase ASNA1**	11	66	11	0.9	**3E-05**	1.0	**9E-07**	1.0	**3E-06**	1.2	**3E-07**	0.9	7E-02	ATPase activity	Cytoplasm	ATPase
8874	**ARHGEF7**	**rho guanine nucleotide exchange factor 7 isoform a*gi|4505573|ref|NP_003890.1| rho guanine nucleotide exchange factor 7 isoform a**	12	44	12	0.9	**3E-03**	1.0	**2E-04**	1.1	2E-01	1.1	**4E-06**	1.0	7E-01	Guanyl-nucleotide exchange factor activity;Molecular function unknown	Cytoplasm	Guanine nucleotide exchange factor
79073	**TMEM109**	**transmembrane protein 109**	5	23	5	0.9	**4E-03**	1.2	**4E-05**	1.0	**2E-03**	1.1	**1E-04**	1.1	6E-02	Molecular function unknown	-	Unclassified
54987	**C1orf123**	**UPF0587 protein C1orf123 isoform 1**	6	30	6	0.9	**1E-02**	1.0	**4E-04**	1.2	8E-02	1.1	**2E-04**	1.0	5E-01	Molecular function unknown	-	Unclassified
4854	**NOTCH3**	**neurogenic locus notch homolog protein 3**	7	25	4	0.9	8E-02	1.1	5E-02	0.9	**4E-03**	0.9	1E-01	0.8	4E-01	Receptor activity	Plasma membrane	Cell surface receptor
2632	**GBE1**	**1,4-alpha-glucan-branching enzyme**	18	91	18	0.9	**7E-06**	0.9	**2E-02**	0.8	9E-01	0.9	**7E-06**	1.0	9E-01	Transferase activity	-	Enzyme: Glycosyltransferase
5119	**CHMP1A**	**charged multivesicular body protein 1a isoform 2**	8	53	8	0.9	**1E-04**	0.9	**1E-08**	1.0	6E-01	1.0	**9E-09**	0.9	**2E-03**	Metallopeptidase activity	-	Metallo protease
5814	**PURB**	**transcriptional activator protein Pur-beta**	7	34	7	0.9	7E-02	1.1	**2E-03**	1.0	**1E-03**	1.4	**2E-04**	1.0	1E+00	Transcription regulator activity	Nucleus	Transcription regulatory protein
401494	**PTPLAD2; HACD4**	**very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 4**	1	6	1	0.9	1E-01	0.8	3E-01	0.8	3E-01	0.6	2E-01	0.9	8E-02	#N/A	#N/A	#N/A
6651	**SON**	**protein SON isoform F**	12	62	11	0.9	7E-01	0.7	4E-01	1.0	1E-01	0.7	4E-01	0.7	1E-01	Transcription factor activity	Nucleus	Transcription factor
10484	**SEC23A**	**protein transport protein Sec23A**	17	105	14	0.9	**3E-07**	0.9	**2E-05**	1.1	8E-01	1.2	**4E-07**	1.0	9E-01	Transporter activity	Cytoplasm	Transport/cargo protein
4125	**MAN2B1**	**lysosomal alpha-mannosidase isoform 1**	7	38	7	0.9	**7E-05**	1.2	**2E-03**	1.0	**3E-03**	1.2	**2E-04**	1.0	5E-01	Catalytic activity	Lysosome	Enzyme: Glycosidase
5825	**ABCD3**	**ATP-binding cassette sub-family D member 3 isoform a**	12	49	11	0.9	**3E-04**	1.4	**3E-06**	1.0	**4E-06**	1.2	**1E-07**	1.0	4E-01	ATP binding	Peroxisome	Integral membrane protein
57103	**C12orf5; TIGAR**	**fructose-2,6-bisphosphatase TIGAR**	9	59	9	0.9	**6E-04**	0.9	**5E-06**	1.0	2E-01	0.9	**2E-07**	0.8	**9E-05**	#N/A	#N/A	#N/A
9380	**GRHPR**	**glyoxylate reductase/hydroxypyruvate reductase**	8	38	8	0.9	**2E-02**	1.1	**1E-04**	1.0	**1E-02**	1.1	**2E-04**	1.0	1E+00	Catalytic activity	Cytoplasm	Enzyme: Reductase
55856	**ACOT13**	**acyl-coenzyme A thioesterase 13 isoform 1**	2	12	2	0.9	**3E-02**	1.2	**4E-03**	1.3	**1E-02**	**1.6**	**5E-03**	1.1	2E-01	Hydrolase activity	-	Enzyme: Hydrolase
11218	**DDX20**	**probable ATP-dependent RNA helicase DDX20**	4	14	4	0.9	5E-02	0.9	**2E-02**	0.9	9E-01	0.9	**3E-03**	0.9	3E-01	ATPase activity	Nucleus	ATPase
140576	**S100A16**	**PREDICTED: protein S100-A16 isoform X1**	6	199	6	0.9	**2E-12**	1.1	**2E-16**	1.1	**4E-13**	1.0	**2E-16**	1.0	2E-01	Calcium ion binding	Nucleolus	Calcium binding protein
5875	**RABGGTA**	**geranylgeranyl transferase type-2 subunit alpha**	16	97	16	0.9	**1E-09**	0.9	**3E-10**	1.0	8E-01	1.0	**5E-10**	1.0	5E-01	Transferase activity	Cytoplasm	Enzyme: Prenyltransferase
55313	**CPPED1**	**serine/threonine-protein phosphatase CPPED1 isoform a**	4	18	4	0.9	**3E-03**	0.9	**1E-03**	1.0	7E-01	1.0	**4E-05**	0.9	4E-01	Molecular function unknown	-	Unclassified
80331	**DNAJC5**	**PREDICTED: dnaJ homolog subfamily C member 5 isoform X1**	6	33	6	0.9	**7E-03**	1.0	**1E-03**	1.0	**3E-03**	1.3	**4E-07**	1.0	4E-01	Chaperone activity	Cytoplasmic vesicle	Chaperone
81555	**YIPF5**	**protein YIPF5 isoform a**	2	18	2	0.9	**4E-02**	1.0	**3E-02**	0.9	1E-01	1.0	**3E-02**	1.0	8E-01	Molecular function unknown	Golgi apparatus	Unclassified
51699	**VPS29**	**vacuolar protein sorting-associated protein 29 isoform 3**	6	66	6	0.9	**9E-08**	0.9	**1E-10**	1.0	3E-01	1.0	**1E-10**	0.9	**6E-03**	Hydrolase activity;Protein binding	Endosome	Transport/cargo protein;Enzyme: Hydrolase
4598	**MVK**	**mevalonate kinase isoform a**	7	38	7	0.9	**2E-04**	1.1	**1E-05**	1.3	**1E-05**	1.3	**3E-06**	1.0	4E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
397	**ARHGDIB**	**rho GDP-dissociation inhibitor 2**	7	33	7	0.9	**9E-04**	0.8	**2E-02**	0.8	1E-01	**0.6**	**5E-04**	0.9	**6E-03**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
253959	**RALGAPA1**	**ral GTPase-activating protein subunit alpha-1 isoform 2**	6	23	6	0.9	**1E-03**	1.2	**1E-04**	1.1	**7E-03**	1.2	**3E-04**	1.1	**6E-03**	GTPase activator activity	Nucleus;Cytoplasm	GTPase activating protein
29978	**UBQLN2**	**ubiquilin-2**	10	61	5	0.9	**3E-03**	0.8	**3E-04**	0.9	7E-01	0.7	3E-01	0.9	**5E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55760	**DHX32**	**putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX32**	10	34	10	0.9	**1E-02**	1.2	**2E-03**	1.2	7E-02	**1.7**	**2E-04**	1.0	8E-01	ATPase activity	Nucleus	ATPase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
147965	**FAM98C**	**protein FAM98C**	2	7	2	0.9	**1E-02**	1.0	**2E-02**	1.0	1E-01	1.2	7E-02	1.0	4E-01	Molecular function unknown	-	Unclassified
9325	**TRIP4**	**activating signal cointegrator 1**	8	34	8	0.9	1E-01	1.0	**8E-03**	0.9	**3E-02**	0.9	6E-02	0.9	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
23412	**COMMD3**	**COMM domain-containing protein 3**	3	12	3	0.9	2E-01	0.9	8E-02	1.0	3E-01	1.0	2E-01	0.9	4E-01	Molecular function unknown	-	Unclassified
6647	**SOD1**	**superoxide dismutase [Cu-Zn]**	8	83	8	0.9	**1E-06**	1.0	**1E-06**	1.0	**4E-03**	0.9	**1E-08**	1.0	9E-01	Superoxide dismutase activity	Cytoplasm	Enzyme: Superoxide dismutase
6845	**VAMP7**	**vesicle-associated membrane protein 7 isoform 1**	6	55	6	0.9	**3E-05**	1.0	**3E-06**	1.0	**5E-04**	1.1	**1E-07**	1.0	5E-01	Transporter activity	Plasma membrane;Cell surface;Lysosome	Transport/cargo protein
5516	**PPP2CB**	**serine/threonine-protein phosphatase 2A catalytic subunit beta isoform**	12	84	1	0.9	**3E-05**	1.0	**8E-08**	1.2	2E-01	1.0	**1E-08**	1.0	**3E-02**	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
9636	**ISG15**	**ubiquitin-like protein ISG15**	7	48	7	0.9	**2E-04**	**0.7**	**6E-06**	**0.3**	**4E-06**	**0.3**	**3E-06**	0.9	6E-02	Cytokine activity	Extracellular	Cytokine
6237	**RRAS**	**ras-related protein R-Ras**	11	60	9	0.9	**4E-04**	0.9	**1E-07**	1.0	7E-01	1.0	**1E-08**	1.0	3E-01	GTPase activity	Plasma membrane	GTPase
5504	**PPP1R2**	**protein phosphatase inhibitor 2 isoform 1**	5	18	5	0.9	**1E-03**	0.9	**8E-04**	1.2	6E-01	1.1	**2E-04**	1.0	9E-01	Protein binding	Cytoplasm	Cell cycle control protein
5170	**PDPK1**	**3-phosphoinositide-dependent protein kinase 1 isoform 1**	3	20	3	0.9	**4E-02**	0.9	**1E-04**	0.9	2E-01	1.1	**2E-03**	0.9	5E-01	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase
9144	**SYNGR2**	**synaptogyrin-2**	3	21	3	0.9	1E-01	1.5	3E-01	0.8	**4E-03**	1.1	**2E-02**	1.3	**1E-02**	Molecular function unknown	Plasma membrane	Integral membrane protein
54677	**CROT**	**peroxisomal carnitine O-octanoyltransferase isoform 1**	3	9	3	0.9	1E-01	1.4	8E-02	0.9	2E-01	1.0	1E-01	0.9	9E-02	Acyltransferase activity	Peroxisome	Enzyme: Acyltransferase
122553	**TRAPPC6B**	**trafficking protein particle complex subunit 6B isoform 1**	6	20	6	0.9	2E-01	0.9	**2E-04**	1.1	2E-01	1.2	**4E-06**	0.9	**3E-02**	Molecular function unknown	-	Unclassified
6709	**SPTAN1**	**spectrin alpha chain, non-erythrocytic 1 isoform 2**	123	931	123	0.9	**2E-16**	1.1	**2E-16**	0.9	**2E-16**	0.9	**2E-16**	1.0	**3E-05**	Structural constituent of cytoskeleton	Cytoplasm;Nucleus	Cytoskeletal protein;Structural protein
23071	**ERP44**	**endoplasmic reticulum resident protein 44**	11	112	10	0.9	**2E-11**	0.9	**3E-12**	0.9	6E-02	1.0	**6E-12**	1.0	1E-01	Molecular function unknown	Endoplasmic reticulum	Unclassified
286077	**FAM83H**	**protein FAM83H**	34	201	34	0.9	**1E-09**	1.1	**4E-16**	1.0	**2E-14**	1.0	**2E-16**	1.0	1E-01	Molecular function unknown	Nucleus	Unclassified
3419	**IDH3A**	**isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial**	13	101	13	0.9	**5E-08**	1.1	**5E-12**	1.0	**2E-08**	1.4	**2E-10**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
8078	**USP5**	**ubiquitin carboxyl-terminal hydrolase 5 isoform 1**	21	127	21	0.9	**2E-07**	1.0	**2E-08**	1.0	**2E-04**	0.9	**3E-09**	1.0	6E-01	Ubiquitin-specific protease activity	Extracellular	Ubiquitin proteasome system protein
7001	**PRDX2**	**peroxiredoxin-2**	9	194	8	0.9	**8E-05**	1.0	**2E-11**	1.0	**2E-02**	0.9	**3E-08**	0.9	7E-02	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase
5694;	**PSMB6**	**proteasome subunit beta type-6 isoform 1 proprotein**	5	15	5	0.9	**4E-02**	1.0	**7E-03**	1.0	5E-01	1.1	4E-01	0.9	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
4734	**NEDD4**	**E3 ubiquitin-protein ligase NEDD4 isoform 1**	7	31	3	0.9	**4E-04**	0.9	**2E-03**	0.9	8E-01	0.9	**4E-02**	1.0	1E+00	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10755	**GIPC1**	**PDZ domain-containing protein GIPC1 isoform 1**	10	56	10	0.9	**6E-04**	1.0	**2E-05**	1.0	**3E-03**	1.1	**4E-07**	0.9	1E-01	Binding	Cytoplasm	Unclassified
8615	**USO1**	**general vesicular transport factor p115 isoform 1**	24	146	24	0.9	**3E-03**	0.9	**5E-10**	1.0	1E-01	1.3	**2E-16**	1.0	9E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
51368	**TEX264**	**testis-expressed sequence 264 protein isoform 1**	9	32	9	0.9	**4E-03**	1.0	**5E-03**	0.9	**3E-02**	1.4	**5E-04**	1.0	**6E-03**	Molecular function unknown	Extracellular	Secreted polypeptide
6449	**SGTA**	**PREDICTED: small glutamine-rich tetratricopeptide repeat-containing protein alpha isoform X1**	6	41	6	0.9	**4E-03**	0.8	**1E-04**	0.9	**2E-02**	0.9	**4E-04**	0.9	1E-01	Chaperone activity	Cytoplasm	Chaperone
369	**ARAF**	**serine/threonine-protein kinase A-Raf isoform 2**	7	41	5	0.9	**3E-02**	0.9	**2E-03**	1.0	9E-01	0.9	**6E-03**	0.9	**1E-02**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
6396	**SEC13**	**protein SEC13 homolog isoform 3**	10	67	10	0.9	**4E-02**	1.0	**5E-03**	1.0	6E-01	1.1	**3E-02**	1.0	5E-01	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
1545	**CYP1B1**	**cytochrome P450 1B1**	4	12	4	0.9	1E-01	1.3	**1E-02**	1.7	1E-01	1.3	**5E-03**	1.0	5E-01	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase
2739	**GLO1**	**lactoylglutathione lyase**	12	172	12	0.9	**8E-13**	0.8	**2E-16**	1.0	**7E-04**	1.0	**2E-16**	0.9	**5E-03**	Lyase activity	Cytoplasm	Enzyme: Lyase
29766	**TMOD3**	**tropomodulin-3**	17	130	16	0.9	**4E-11**	0.8	**3E-14**	0.9	**3E-04**	1.3	**2E-16**	1.0	**1E-02**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
10094	**ARPC3**	**actin-related protein 2/3 complex subunit 3 isoform 1**	7	97	7	0.9	**6E-08**	0.9	**1E-06**	1.0	5E-01	1.0	**3E-07**	0.9	**1E-02**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
4199	**ME1**	**NADP-dependent malic enzyme**	17	144	17	0.9	**2E-06**	1.0	**1E-12**	1.4	**2E-04**	**1.5**	**3E-11**	0.9	**5E-02**	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase
84299	**MIEN1**	**migration and invasion enhancer 1**	3	24	3	0.9	**9E-04**	1.0	**3E-05**	1.1	**2E-04**	1.0	**3E-04**	0.9	1E-01	#N/A	#N/A	#N/A
5520	**PPP2R2A**	**serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform isoform 2**	16	96	12	0.9	**2E-02**	0.9	**8E-05**	1.1	7E-01	**1.5**	**6E-06**	0.9	3E-01	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
140775	**SMCR8**	**Smith-Magenis syndrome chromosomal region candidate gene 8 protein**	2	8	2	0.9	**4E-02**	1.0	**2E-02**	1.1	1E-01	1.0	**1E-02**	1.0	2E-01	Molecular function unknown	-	Unclassified
2280	**FKBP1A**	**peptidyl-prolyl cis-trans isomerase FKBP1A isoform a**	4	33	4	0.9	**4E-02**	0.7	**8E-04**	1.0	**3E-02**	**0.6**	**1E-02**	0.9	**1E-02**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
84376	**HOOK3**	**protein Hook homolog 3**	10	38	9	0.9	**5E-02**	0.9	**8E-05**	1.1	**3E-02**	1.0	**1E-04**	0.9	3E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
2064	ERBB2	receptor tyrosine-protein kinase erbB-2 isoform a	3	12	2	0.9	7E-02	0.8	**3E-03**	1.1	5E-02	1.9	1E+00	1.4	8E-02	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase
90407	TMEM41A	transmembrane protein 41A	2	8	2	0.9	9E-02	1.1	**2E-02**	1.1	3E-01	1.2	**2E-02**	0.9	8E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
10298	PAK4	serine/threonine-protein kinase PAK 4 isoform 1*gi|62422554|ref|NP_001014831.1| serine/threonine-protein kinase PAK 4 isoform 1*gi|62422557|ref|NP_001014832.1| serine/threonine-protein kinase PAK 4 isoform 1	2	8	2	0.9	1E-01	0.8	**2E-02**	1.2	1E-01	1.0	5E-02	1.0	7E-01	Cytoskeletal protein binding	Golgi membrane;Nucleus;Cytoplasm	Cytoskeletal associated protein
23299	BICD2	protein bicaudal D homolog 2 isoform 1	33	171	33	0.9	**6E-11**	1.0	7E-01	0.7	**3E-04**	0.8	**1E-08**	0.8	**5E-13**	Protein binding	Golgi apparatus;Nucleus;Cytoplasm	Structural protein
3958	LGALS3	galectin-3 isoform 1	8	171	8	0.9	**2E-10**	1.0	**2E-16**	1.0	**3E-09**	1.1	**2E-16**	1.0	**5E-03**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
1465	CSRP1	cysteine and glycine-rich protein 1 isoform 1	10	67	10	0.9	**1E-06**	0.9	**1E-10**	0.9	4E-01	1.1	**4E-07**	1.0	5E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
10269	ZMPSTE24	CAAX prenyl protease 1 homolog	10	77	10	0.9	**2E-06**	1.0	**4E-12**	1.0	**9E-06**	1.2	**3E-10**	1.0	1E-01	Metallopeptidase activity	Endoplasmic reticulum	Metallo protease
2052	EPHX1	epoxide hydrolase 1*gi|4503583|ref|NP_000111.1| epoxide hydrolase 1*gi|600971691|ref|NP_001278092.1| epoxide hydrolase 1	9	42	9	0.9	**2E-03**	1.4	**3E-04**	1.4	**4E-03**	**2.0**	**9E-04**	1.0	5E-01	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase
56898	BDH2	3-hydroxybutyrate dehydrogenase type 2	4	18	3	0.9	**2E-03**	1.2	**2E-03**	1.1	**3E-03**	1.2	**3E-03**	0.9	3E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
51596	CUTA	protein CutA isoform 1	3	19	3	0.9	**7E-03**	0.8	**1E-04**	1.0	5E-01	0.7	3E-01	0.9	3E-01	Molecular function unknown	Plasma membrane	Unclassified
3908	LAMA2	laminin subunit alpha-2 isoform a	1	14	1	0.9	7E-02	1.3	**2E-02**	0.8	**3E-03**	0.9	**2E-02**	1.1	2E-01	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
23443	SLC35A3	UDP-N-acetylglucosamine transporter isoform 3	1	6	1	0.9	2E-01	1.0	**2E-02**	1.0	1E-01	1.4	**1E-02**	0.9	2E-01	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein
4758	NEU1	sialidase-1	1	6	1	0.9	4E-01	0.8	1E-01	1.3	1E+00	1.2	9E-02	1.2	4E-01	Hydrolase activity	Lysosome	Enzyme: Hydrolase
708	C1QBP	complement component 1 Q subcomponent-binding protein, mitochondrial	6	96	6	0.9	**1E-04**	1.3	**4E-07**	1.0	**6E-05**	1.3	**4E-07**	1.1	**2E-03**	Complement receptor activity	Mitochondrion;Nucleus	Complement receptor
10121	ACTR1A	alpha-centractin	11	77	6	0.9	**4E-03**	1.0	**3E-04**	1.0	**1E-06**	1.1	**3E-06**	0.9	4E-01	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein
23294	ANKS1A	ankyrin repeat and SAM domain-containing protein 1A	5	17	5	0.9	**5E-03**	0.9	**1E-03**	1.0	6E-02	1.1	**4E-03**	0.9	5E-02	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
23558	WBP2	WW domain-binding protein 2	2	12	2	0.9	**3E-02**	1.1	**1E-02**	1.0	**2E-02**	1.1	**3E-02**	1.0	3E-01	Receptor binding	-	Ligand
6665	SOX15	protein SOX-15	2	9	2	0.9	9E-01	0.8	6E-01	1.0	9E-01	0.9	2E-01	1.0	8E-01	Transcription factor activity	Nucleus	Transcription factor
27095	TRAPPC3	trafficking protein particle complex subunit 3 isoform 2	5	46	5	0.9	**5E-06**	0.9	**9E-09**	1.0	4E-01	1.1	**4E-08**	1.0	4E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
2778	GNAS	protein GNAS isoform GNASS	10	63	9	0.9	**1E-05**	0.9	**1E-04**	0.9	3E-01	1.1	**6E-05**	1.0	4E-01	GTPase activity	Plasma membrane	G protein
80308	FLAD1	FAD synthase isoform 1	12	55	12	0.9	**2E-04**	1.0	**2E-07**	1.0	**3E-03**	1.1	**9E-09**	0.9	**5E-02**	Molecular function unknown	-	Unclassified
79720	VPS37B	vacuolar protein sorting-associated protein 37B	5	29	5	0.9	**3E-03**	0.8	**9E-04**	1.1	**3E-02**	1.3	**6E-04**	0.9	**4E-03**	Protein transporter activity	Cytoplasm	Transport/cargo protein
22978	NT5C2	cytosolic purine 5'-nucleotidase	11	54	11	0.9	**4E-02**	0.9	**1E-04**	1.0	5E-01	**1.5**	**5E-06**	1.0	6E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
10540	DCTN2	dynactin subunit 2 isoform 1	16	122	16	0.9	**7E-08**	1.0	**7E-12**	1.0	**3E-07**	0.9	**2E-11**	0.9	**1E-04**	Motor activity	Cytoplasm	Motor protein
223	ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	14	102	14	0.9	**7E-07**	1.1	**5E-08**	0.9	**1E-08**	0.9	**6E-09**	0.9	**2E-03**	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
9685	CLINT1	clathrin interactor 1 isoform 2	16	90	16	0.9	**1E-06**	1.0	**3E-10**	1.0	**2E-09**	0.9	**2E-09**	1.0	6E-01	Transporter activity	Golgi apparatus;Nucleus;Cytoplasm	Transport/cargo protein
7264	TSTA3	PREDICTED: GDP-L-fucose synthase isoform X1	6	35	6	0.9	**2E-04**	1.0	**7E-05**	1.0	**5E-02**	1.0	**9E-05**	0.9	8E-02	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
6812	STXBP1	syntaxin-binding protein 1 isoform a	8	31	8	0.9	**8E-03**	0.8	**2E-05**	1.1	**3E-02**	1.2	**6E-05**	1.0	1E+00	Transporter activity	Plasma membrane;Cytosol	Transport/cargo protein
23077	MYCBP2	E3 ubiquitin-protein ligase MYCBP2	4	16	4	0.9	**2E-02**	1.3	**2E-02**	0.9	**1E-02**	0.9	7E-02	1.1	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
23271	CAMSAP2	calmodulin-regulated spectrin-associated protein 2 isoform 1	11	40	11	0.9	**4E-02**	0.9	**7E-04**	1.0	9E-01	1.0	**8E-04**	1.0	5E-01	#N/A	#N/A	#N/A
55108	BSDC1	BSD domain-containing protein 1 isoform b	3	10	3	0.9	**5E-02**	1.0	**9E-03**	1.1	2E-01	1.2	**1E-02**	0.9	8E-01	Molecular function unknown	-	Unclassified
9516	LITAF	PREDICTED: lipopolysaccharide-induced tumor necrosis factor-alpha factor isoform X1	1	6	1	0.9	1E-01	0.9	**2E-02**	0.7	1E-01	0.9	**3E-03**	0.9	2E-01	Transcription factor activity	Nucleus	Transcription factor
57130	ATP13A1	manganese-transporting ATPase 13A1	20	89	20	0.9	**4E-09**	1.1	**3E-08**	0.9	**2E-06**	1.0	**5E-12**	1.0	5E-01	ATPase activity	Integral to membrane	ATPase
50808	AK3	GTP:AMP phosphotransferase AK3, mitochondrial isoform a	13	91	13	0.9	**2E-05**	1.2	**6E-06**	1.1	**9E-06**	1.2	**3E-04**	1.0	6E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9644	SH3PXD2A	PREDICTED: SH3 and PX domain-containing protein 2A isoform X1	15	31	13	0.9	**5E-04**	1.2	**1E-04**	0.9	**4E-05**	1.2	**3E-06**	1.0	**4E-02**	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
8192	CLPP	ATP-dependent Clp protease proteolytic subunit, mitochondrial	5	32	5	0.9	**9E-04**	1.1	**3E-05**	1.0	**1E-03**	1.2	**7E-05**	0.9	3E-01	Peptidase activity	Mitochondrion	Protease
4817	NIT1	nitrilase homolog 1 isoform 1	7	42	7	0.9	**2E-03**	0.9	**6E-08**	1.0	8E-01	1.2	**1E-07**	1.0	4E-01	Molecular function unknown	-	Unclassified
10328	EMC8	ER membrane protein complex subunit 8 isoform 1	7	28	7	0.9	**1E-02**	1.0	**3E-04**	1.0	2E-01	1.2	**2E-05**	0.9	8E-01	#N/A	#N/A	#N/A
23011	RAB21	ras-related protein Rab-21	10	43	10	0.9	**1E-02**	1.0	**2E-03**	0.9	**1E-02**	1.1	**2E-03**	1.0	2E-01	GTPase activity	Endoplasmic reticulum	GTPase
7168	TPM1	tropomyosin alpha-1 chain isoform Tpm1.7cy	22	235	1	0.9	**2E-02**	0.9	**2E-02**	**0.6**	**3E-03**	**0.5**	**5E-05**	1.1	**4E-02**	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein
5315	PKM	pyruvate kinase PKM isoform a	40	1238	4	0.9	**2E-16**	0.8	**2E-16**	0.9	**7E-07**	0.9	**3E-07**	1.0	**4E-02**	#N/A	#N/A	#N/A
5594	MAPK1	mitogen-activated protein kinase 1	16	140	11	0.9	**6E-08**	0.9	**9E-13**	0.9	1E+00	0.7	4E-01	0.9	**8E-05**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
28952	CCDC22	coiled-coil domain-containing protein 22	14	54	14	0.9	**8E-04**	0.9	**3E-06**	1.0	1E-01	1.1	**4E-04**	1.0	8E-01	Molecular function unknown	-	Unclassified
4318;	MMP9	matrix metalloproteinase-9 preproprotein	7	18	1	0.9	**5E-02**	1.4	**1E-02**	1.0	**1E-02**	1.3	**1E-02**	1.0	5E-01	Metallopeptidase activity	Extracellular	Metallo protease
114789	SLC25A25	calcium-binding mitochondrial carrier protein SCaMC-2 isoform b	3	6	3	0.9	2E-01	1.1	**3E-02**	1.0	2E-01	1.3	**3E-02**	1.1	3E-01	Transporter activity	Mitochondrion	Transport/cargo protein
51247	PAIP2	polyadenylate-binding protein-interacting protein 2*gi|75677355|ref|NP_001028284.1| polyadenylate-binding protein-interacting protein 2	1	6	1	0.9	3E-01	0.8	3E-01	1.0	5E-01	1.0	2E-01	1.0	7E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
6281	S100A10	protein S100-A10	7	278	7	0.9	**8E-08**	0.9	**2E-14**	1.1	9E-01	1.1	**2E-16**	1.0	3E-01	Calcium ion binding	Plasma membrane	Calcium binding protein
9958	USP15	ubiquitin carboxyl-terminal hydrolase 15 isoform 2	22	95	20	0.9	**5E-07**	1.0	**2E-08**	1.0	**4E-07**	1.0	**6E-10**	0.9	**3E-04**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10342	TFG	protein TFG isoform 1*gi|306774087|ref|NP_001182407.1| protein TFG isoform 1*gi|56090139|ref|NP_001007566.1| protein TFG isoform 1	7	70	7	0.9	**1E-05**	0.8	**9E-07**	0.9	**9E-03**	0.8	**1E-06**	1.0	8E-01	Receptor regulator activity	Cytoplasm	Enzyme regulator
375	ARF1	ADP-ribosylation factor 1	10	193	4	0.9	**3E-04**	0.9	**5E-06**	1.0	2E-01	1.0	**2E-07**	1.0	2E-01	GTPase activity	Golgi apparatus	GTPase
3422	IDI1	isopentenyl-diphosphate Delta-isomerase 1	11	73	11	0.9	**3E-04**	0.8	**3E-07**	1.1	**1E-03**	0.9	**1E-03**	0.9	**5E-06**	Isomerase activity	Peroxisome	Enzyme: Isomerase
5494	PPM1A	protein phosphatase 1A isoform 3	7	20	5	0.9	**5E-04**	0.9	**9E-04**	1.1	7E-01	1.2	**4E-04**	0.9	3E-01	Protein serine/threonine phosphatase activity	Cytoplasm;Nucleus	Serine/threonine phosphatase
84164;	ASCC2	activating signal cointegrator 1 complex subunit 2 isoform 1	8	16	3	0.9	**4E-03**	0.9	**1E-05**	0.9	**6E-03**	0.9	**3E-04**	0.8	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
25865	PRKD2	serine/threonine-protein kinase D2 isoform A	7	30	5	0.9	6E-02	0.8	**4E-03**	1.1	2E-01	0.9	7E-02	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
51272;	BET1L	BET1-like protein isoform 2	4	12	4	0.9	2E-01	1.0	**1E-02**	1.0	**3E-02**	0.9	**1E-02**	1.0	5E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
8887	TAX1BP1	tax1-binding protein 1 isoform 1	10	35	10	0.9	7E-01	0.8	5E-01	0.7	3E-01	0.9	**1E-02**	1.0	1E+00	Transcription factor activity	Nucleus	Transcription factor
84790	TUBA1C	tubulin alpha-1C chain isoform a	22	893	2	0.9	**2E-16**	0.8	**2E-16**	0.9	**3E-15**	0.9	**1E-13**	0.9	**9E-07**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
5518	PPP2R1A	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	25	227	18	0.9	**5E-13**	0.9	**2E-16**	1.0	2E-01	1.2	**2E-16**	0.9	**4E-05**	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
5048	PAFAH1B1	platelet-activating factor acetylhydrolase IB subunit alpha	18	168	17	0.9	**4E-12**	1.0	**1E-15**	1.1	**2E-09**	1.4	**2E-16**	1.0	3E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
5693	PSMB5	proteasome subunit beta type-5 isoform 1	10	82	3	0.9	**1E-06**	0.9	**3E-07**	1.0	**3E-02**	1.1	**9E-09**	1.1	**5E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55770	EXOC2	exocyst complex component 2	16	68	15	0.9	**2E-06**	1.1	**1E-08**	1.0	**5E-06**	1.1	**2E-09**	1.0	5E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
51031	GLOD4	glyoxalase domain-containing protein 4	15	102	15	0.9	**3E-06**	1.0	**2E-08**	1.1	**1E-02**	1.0	**1E-04**	0.9	**3E-06**	Molecular function unknown	Mitochondrion	Unclassified
51164	DCTN4	dynactin subunit 4 isoform b	7	40	7	0.9	**4E-05**	1.0	**5E-07**	1.0	**3E-03**	1.0	**4E-06**	0.9	6E-02	Molecular function unknown	Cytoplasm	Unclassified
80765	STARD5	stAR-related lipid transfer protein 5	3	11	3	0.9	**7E-03**	1.2	3E-01	0.7	**1E-03**	1.0	**5E-04**	0.9	1E-01	Transporter activity;Lipid transporter activity	Cytoplasm	Transport/cargo protein
51501	C11orf73; HIKESHI	protein Hikeshi	2	11	2	0.9	7E-02	0.8	**1E-02**	0.9	1E-01	0.6	1E-01	1.0	4E-01	#N/A	#N/A	#N/A
201266	SLC39A11	PREDICTED: zinc transporter ZIP11 isoform X2	2	7	2	0.9	8E-02	1.0	8E-02	1.1	1E-01	1.1	5E-02	1.0	4E-01	Transporter activity	Integral to membrane	Membrane transport protein
51070	NOSIP	nitric oxide synthase-interacting protein*gi|7705716|ref|NP_057037.1| nitric oxide synthase-interacting protein	2	8	2	0.9	1E-01	0.8	7E-02	1.0	2E-01	0.7	7E-01	1.0	9E-01	Transporter activity	Cytoplasmic vesicle	Transport/cargo protein
56889	TM9SF3	transmembrane 9 superfamily member 3	9	42	9	0.9	2E-01	1.2	2E-01	0.8	**1E-02**	1.0	5E-02	1.0	4E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
23499	MACF1	PREDICTED: microtubule-actin cross-linking factor 1 isoform X16	179	477	7	0.9	**9E-15**	1.1	**2E-16**	1.1	**2E-16**	1.1	**2E-16**	1.1	**5E-14**	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein
60626	RIC8A	synembryn-A isoform 2	17	98	16	0.9	**5E-10**	0.8	**4E-11**	1.1	**8E-05**	1.1	**4E-11**	1.0	3E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
653145	ANXA8	PREDICTED: annexin A8 isoform X6	16	71	1	0.9	**2E-07**	0.9	**4E-03**	0.8	**2E-02**	0.6	7E-02	0.9	**8E-03**	Calcium ion binding	-	Calcium binding protein
9578	CDC42BPB	serine/threonine-protein kinase MRCK beta	27	84	26	0.9	**3E-04**	1.1	**1E-08**	1.1	**2E-06**	1.1	**2E-08**	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
23140	ZZEF1	zinc finger ZZ-type and EF-hand domain-containing protein 1	3	11	3	0.9	**3E-03**	1.0	**1E-02**	1.0	**3E-02**	0.9	**1E-02**	1.1	1E-01	Molecular function unknown	-	Unclassified
5223; 643576	PGAM1; LOC643576	phosphoglycerate mutase 1	12	164	12	0.9	**3E-03**	0.9	**7E-04**	0.9	2E-01	0.8	6E-01	0.9	**2E-03**	#N/A	#N/A	#N/A
9670	IPO13	importin-13	3	10	3	0.9	**1E-02**	0.9	**7E-03**	1.1	8E-01	1.0	**1E-02**	1.0	1E-01	Ligand-dependent nuclear receptor activity	Cytoplasm	Nuclear receptor
5373	PMM2	phosphomannomutase 2	8	52	8	0.9	**4E-03**	0.9	**4E-03**	0.9	5E-01	0.9	**2E-06**	1.0	6E-01	Catalytic activity	Cytoplasm	Enzyme: Mutase
83892	KCTD10	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3	5	16	5	0.9	**5E-03**	1.0	**2E-03**	1.0	9E-02	0.9	6E-02	1.1	6E-01	Ion channel activity	-	Ion channel
23172	FAM175B	BRISC complex subunit Abro1	3	14	3	0.9	6E-02	1.0	**2E-02**	1.0	3E-01	1.1	**2E-03**	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
55362	TMEM63B	PREDICTED: CSC1-like protein 2 isoform X2	5	13	5	0.9	#N/A	1.1	#N/A	0.9	#N/A	0.9	#N/A	1.0	#N/A	Molecular function unknown	Integral to membrane	Integral membrane protein
6767	ST13	hsc70-interacting protein isoform 1	12	101	12	0.9	**2E-08**	0.9	**3E-11**	0.9	4E-01	1.0	**3E-09**	1.0	2E-01	Receptor signaling complex scaffold activity	Lysosome	Adapter molecule
164	AP1G1	AP-1 complex subunit gamma-1 isoform a	20	116	19	0.9	**2E-06**	1.0	**1E-08**	1.1	**2E-05**	1.1	**5E-09**	0.9	**2E-03**	Transporter activity	Golgi apparatus	Transport/cargo protein
55288	RHOT1	mitochondrial Rho GTPase 1 isoform 1	5	25	4	0.9	**4E-03**	1.1	**3E-04**	1.0	**2E-03**	1.1	**5E-05**	1.0	1E-01	GTPase activity	Mitochondrion	GTPase
22876;	INPP5F	phosphatidylinositide phosphatase SAC2 isoform 2	4	9	3	0.9	**8E-03**	0.8	**3E-03**	1.0	2E-01	1.0	**8E-03**	1.0	3E-01	Lipid phosphatase activity	-	Lipid phosphatase
29097	CNIH4	protein cornichon homolog 4 isoform 1	1	6	1	0.9	1E-01	0.8	**4E-02**	1.1	2E-01	1.3	**2E-02**	0.9	**6E-03**	Molecular function unknown	Integral to membrane	Unclassified
60493	FASTKD5	FAST kinase domain-containing protein 5	7	16	7	0.9	2E-01	1.1	6E-02	1.2	2E-01	1.0	**3E-02**	1.1	6E-01	Molecular function unknown	-	Unclassified
29911	HOOK2	protein Hook homolog 2 isoform 1	5	14	5	0.9	3E-01	1.1	**3E-02**	1.0	2E-01	1.0	3E-01	1.0	7E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
8411	EEA1	early endosome antigen 1	61	297	60	0.9	**2E-16**	1.0	**2E-16**	0.9	**2E-11**	1.0	**2E-16**	0.9	**9E-04**	Auxiliary transport protein activity	Endosome	Membrane transport protein
7529	YWHAB	14-3-3 protein beta/alpha	14	995	7	0.9	**3E-10**	0.9	**6E-12**	1.1	8E-02	0.9	**4E-11**	0.9	8E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
832	CAPZB	F-actin-capping protein subunit beta isoform 4	22	228	21	0.9	**1E-08**	1.0	**2E-16**	1.0	**3E-07**	1.0	**2E-16**	0.9	**1E-03**	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
51552	RAB14	ras-related protein Rab-14	13	127	12	0.9	**1E-07**	1.0	**5E-08**	0.9	**5E-07**	1.2	**1E-13**	1.0	6E-01	GTPase activity	Integral to membrane	GTPase
6576	SLC25A1	tricarboxylate transport protein, mitochondrial isoform b	10	79	10	0.9	**3E-06**	1.1	**1E-07**	1.1	**7E-05**	1.3	**4E-07**	1.0	9E-01	Transporter activity	Mitochondrion	Transport/cargo protein
2931	GSK3A	glycogen synthase kinase-3 alpha	9	48	5	0.9	**6E-04**	0.9	**9E-05**	1.0	8E-01	0.9	**4E-05**	1.0	5E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
10006	ABI1	abl interactor 1 isoform a	7	31	4	0.9	**2E-03**	1.0	**3E-04**	1.0	**7E-06**	1.1	**1E-04**	0.8	**1E-02**	Binding	Cytosol	Adapter molecule
57132	CHMP1B	charged multivesicular body protein 1b	8	41	8	0.9	**5E-03**	0.8	**9E-05**	0.9	5E-01	1.0	**2E-06**	0.9	**2E-03**	Transporter activity	Endosome	Transport/cargo protein
9529	BAG5	BAG family molecular chaperone regulator 5 isoform a	5	19	4	0.9	2E-01	0.9	**3E-03**	1.0	6E-01	1.1	**1E-02**	1.0	3E-01	Molecular function unknown	-	Unclassified
288	ANK3	ankyrin-3 isoform 1	8	16	8	0.9	2E-01	1.2	**2E-03**	1.1	**9E-03**	1.0	**2E-04**	0.9	2E-01	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule
306	ANXA3	annexin A3	25	293	25	0.9	**1E-11**	0.7	**2E-16**	1.2	**9E-06**	**1.8**	**2E-16**	1.0	**6E-03**	Calcium ion binding	Cytoplasm	Calcium binding protein
26136	TES	testin isoform 1	20	132	20	0.9	**2E-08**	0.8	**3E-08**	0.9	**1E-02**	0.8	**2E-04**	1.0	1E-01	Molecular function unknown	Extracellular	Secreted polypeptide
1639	DCTN1	dynactin subunit 1 isoform 1	40	254	40	0.9	**2E-08**	1.1	**2E-16**	1.0	**3E-08**	1.1	**2E-16**	0.9	**2E-02**	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein
79837	PIP4K2C	phosphatidylinositol 5-phosphate 4-kinase type-2 gamma isoform a*gi|226371739|ref|NP_001139730.1| phosphatidylinositol 5-phosphate 4-kinase type-2 gamma isoform a	12	60	12	0.9	**8E-08**	0.9	**5E-06**	1.0	8E-01	1.1	**1E-05**	1.0	5E-01	Lipid kinase activity	-	Lipid Kinase
808; 805; 801	CALM3; CALM2; CALM1	calmodulin*gi|5901912|ref|NP_008819.1| calmodulin*gi|58218968|ref|NP_005175.2| calmodulin	11	200	9	0.9	**2E-06**	0.8	**3E-08**	1.1	**1E-02**	1.1	**2E-08**	1.0	9E-01	#N/A	#N/A	#N/A
10550	ARL6IP5	PRA1 family protein 3	4	48	4	0.9	**9E-05**	1.0	**3E-05**	1.0	**1E-03**	1.1	**1E-04**	0.9	**3E-02**	Molecular function unknown	Cytoplasm	Unclassified
2029	ENSA	alpha-endosulfine isoform 1	6	60	5	0.9	**2E-04**	1.0	**1E-06**	1.1	**2E-05**	0.8	2E-01	0.9	**1E-05**	Receptor binding	Nucleus	Ligand
9538	EI24	PREDICTED: etoposide-induced protein 2.4 homolog isoform X1	4	14	4	0.9	**4E-03**	1.0	**3E-03**	0.9	**3E-02**	0.8	**3E-02**	0.9	2E-01	Signal transducer activity	Integral to membrane	Integral membrane protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10564	ARFGEF2	brefeldin A-inhibited guanine nucleotide-exchange protein 2	11	32	4	0.9	**6E-03**	1.0	**2E-03**	1.1	**8E-03**	1.3	**1E-03**	0.9	3E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
137492	VPS37A	vacuolar protein sorting-associated protein 37A isoform 1	3	14	3	0.9	**8E-03**	0.9	**8E-03**	1.0	3E-01	1.1	**1E-02**	1.1	2E-01	Molecular function unknown	Nucleus	Growth inhibitory factor
5298	PI4KB	phosphatidylinositol 4-kinase beta isoform 1	3	11	3	0.9	**1E-02**	0.8	7E-01	0.7	3E-01	0.5	3E-01	0.7	2E-01	Lipid kinase activity	Cytoplasm	Lipid Kinase
55737	VPS35	vacuolar protein sorting-associated protein 35	27	234	27	0.9	**3E-13**	0.9	**7E-16**	1.0	2E-01	1.1	**2E-16**	1.0	**3E-03**	Transporter activity	Cytoplasm	Transport/cargo protein
2060	EPS15	epidermal growth factor receptor substrate 15 isoform A	17	42	17	0.9	**2E-06**	1.0	**2E-08**	1.0	**1E-03**	1.3	**2E-08**	1.1	**1E-03**	Calcium ion binding	Plasma membrane	Calcium binding protein
5898	RALA	ras-related protein Ral-A	7	64	4	0.9	**6E-03**	0.9	**6E-07**	1.0	8E-02	1.2	**1E-08**	1.1	**1E-02**	GTPase activity	Plasma membrane	GTPase
26031	OSBPL3	PREDICTED: oxysterol-binding protein-related protein 3 isoform X1	11	31	11	0.9	**5E-02**	0.8	1E-01	0.9	1E-01	1.0	**2E-02**	0.9	7E-02	Steroid binding	Endoplasmic reticulum membrane	Unclassified
55227	LRRC1	leucine-rich repeat-containing protein 1	8	16	7	0.9	#N/A	1.1	#N/A	1.1	#N/A	0.9	#N/A	1.0	#N/A	Molecular function unknown	-	Unclassified
10135	NAMPT	nicotinamide phosphoribosyltransferase	26	219	26	0.9	**2E-16**	1.0	**2E-16**	1.3	**1E-13**	1.3	**2E-16**	0.9	**1E-03**	Transferase activity	Extracellular	Cytokine
26973	CHORDC1	PREDICTED: cysteine and histidine-rich domain-containing protein 1 isoform X1	10	60	10	0.9	**2E-07**	0.8	**7E-09**	0.9	**1E-04**	0.8	6E-02	1.0	5E-01	Molecular function unknown	-	Unclassified
10092	ARPC5	actin-related protein 2/3 complex subunit 5 isoform 1	8	73	7	0.9	**2E-05**	1.0	**4E-05**	1.0	**3E-02**	1.0	**1E-03**	1.0	1E-01	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein
25796	PGLS	6-phosphogluconolactonase	10	92	10	0.9	**3E-05**	1.0	**3E-06**	1.0	**1E-04**	1.0	**1E-06**	0.9	**2E-02**	Hydrolase activity	-	Enzyme: Hydrolase
10163	WASF2	wiskott-Aldrich syndrome protein family member 2 isoform 1	10	55	10	0.9	**1E-04**	1.0	**1E-06**	1.1	**5E-04**	1.2	**5E-07**	0.9	**7E-03**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
85450	ITPRIP	inositol 1,4,5-trisphosphate receptor-interacting protein*gi|436408724|ref|NP_001258941.1| inositol 1,4,5-trisphosphate receptor-interacting protein*gi|436408726|ref|NP_001258942.1| inositol 1,4,5-trisphosphate receptor-interacting protein	6	19	6	0.9	**2E-03**	1.4	**2E-03**	1.0	**8E-04**	1.4	**2E-03**	1.1	9E-02	Molecular function unknown;Receptor regulator activity	Plasma membrane	Unclassified
11140	CDC37	hsp90 co-chaperone Cdc37	12	61	12	1.0	**2E-05**	0.8	**5E-07**	1.0	**2E-02**	1.0	**2E-08**	0.9	**4E-02**	Chaperone activity	Cytoplasm	Chaperone
2531	KDSR	3-ketodihydrosphingosine reductase	7	49	7	1.0	**7E-05**	1.1	**6E-08**	1.2	**1E-05**	1.4	**3E-08**	1.0	9E-02	Oxidoreductase activity	Extracellular	Secreted polypeptide
57826	RAP2C	ras-related protein Rap-2c isoform 1	5	40	2	1.0	**1E-04**	1.2	**2E-05**	1.0	**5E-03**	1.0	**2E-05**	1.0	**4E-02**	GTPase activity	-	GTPase
6768	ST14	suppressor of tumorigenicity 14 protein	5	16	5	1.0	**8E-03**	0.9	1E-01	0.8	9E-01	0.6	7E-02	0.8	8E-02	Serine-type peptidase activity	Plasma membrane	Serine protease
60560	NAA35	PREDICTED: N-alpha-acetyltransferase 35, NatC auxiliary subunit isoform X1	7	22	7	1.0	**1E-02**	1.0	**1E-02**	0.9	**4E-02**	0.9	**1E-02**	1.1	2E-01	Molecular function unknown	-	Unclassified
27032	ATP2C1	calcium-transporting ATPase type 2C member 1 isoform 1e	3	12	3	1.0	5E-02	1.1	**4E-02**	0.8	**1E-02**	1.0	**1E-02**	1.0	1E+00	ATPase activity	Golgi apparatus	ATPase
51714	SELT	selenoprotein T	2	10	2	1.0	1E-01	1.1	1E-01	1.0	7E-01	1.4	7E-02	1.0	2E-01	#N/A	#N/A	#N/A
84617	TUBB6	tubulin beta-6 chain isoform 6*gi|746816001|ref|NP_001290458.1| tubulin beta-6 chain isoform 6	17	471	1	1.0	**2E-16**	0.8	**2E-16**	0.9	**3E-05**	1.0	**2E-16**	0.9	4E-01	Structural constituent of cytoskeleton	-	Cytoskeletal protein
65125	WNK1	serine/threonine-protein kinase WNK1 isoform 4	21	96	21	1.0	**1E-07**	1.2	**5E-05**	0.8	**9E-08**	0.8	**3E-02**	0.9	7E-02	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
25923	ATL3	atlastin-3 isoform 1	17	129	16	1.0	**2E-06**	1.0	**1E-06**	0.9	**1E-04**	1.0	**4E-10**	1.0	9E-01	Molecular function unknown	Mitochondrion	Unclassified
60491	NIF3L1	PREDICTED: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform X1	7	40	4	1.0	**1E-03**	0.9	**2E-06**	1.2	7E-01	1.3	**7E-06**	1.0	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
8417	STX7	syntaxin-7	5	22	5	1.0	**4E-03**	1.0	**8E-03**	1.0	9E-01	1.1	**2E-03**	1.0	6E-01	Protein binding	Endosome	Integral membrane protein
29082	CHMP4A	charged multivesicular body protein 4a	7	34	6	1.0	**2E-02**	1.0	**2E-03**	1.0	**4E-02**	0.9	**9E-03**	1.1	2E-01	Molecular function unknown	Cytoplasmic vesicle	Unclassified
23370	ARHGEF18	rho guanine nucleotide exchange factor 18 isoform b	4	16	3	1.0	**3E-02**	0.9	**9E-03**	1.0	2E-01	1.2	**9E-03**	1.0	7E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
57148	RALGAPB	ral GTPase-activating protein subunit beta isoform 1	2	9	2	1.0	8E-02	1.2	**2E-02**	1.1	**2E-02**	1.2	7E-02	1.2	3E-01	GTPase activator activity	Smooth microsome	GTPase activating protein
22933	SIRT2	NAD-dependent protein deacetylase sirtuin-2 isoform 1	2	10	2	1.0	1E+00	1.2	9E-01	0.8	**4E-02**	1.0	5E-02	1.1	5E-01	Deacetylase activity	Cytoplasm	Cell cycle control protein
3861	KRT14	keratin, type I cytoskeletal 14	59	12403	22	1.0	**2E-16**	1.3	**2E-16**	0.8	**2E-16**	0.9	**2E-16**	1.2	**2E-16**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
55031	USP47	ubiquitin carboxyl-terminal hydrolase 47 isoform a	19	82	19	1.0	**7E-08**	1.0	**2E-11**	1.1	**4E-03**	1.0	**2E-12**	0.9	**1E-02**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
8453	CUL2	cullin-2 isoform a	20	99	20	1.0	**1E-04**	1.0	**3E-06**	1.0	**5E-02**	1.0	**1E-04**	1.0	1E+00	Ubiquitin binding	Cytoplasm	Ubiquitin proteasome system protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
54732	TMED9	transmembrane emp24 domain-containing protein 9	8	44	5	1.0	**5E-04**	1.0	**6E-04**	1.0	**3E-02**	1.0	**3E-05**	0.9	2E-01	Molecular function unknown	Endoplasmic reticulum	Unclassified
7347	UCHL3	ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 2	6	33	6	1.0	**7E-04**	1.0	**3E-04**	1.0	7E-02	1.0	**1E-03**	0.9	**2E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
6810	STX4	syntaxin-4 isoform 3	7	27	7	1.0	**1E-03**	1.1	**2E-03**	1.1	**8E-04**	1.4	**2E-03**	1.1	**3E-02**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
9545	RAB3D	ras-related protein Rab-3D	7	72	4	1.0	**1E-03**	1.1	**1E-04**	1.0	**4E-04**	0.9	**7E-03**	0.9	**4E-02**	GTPase activity	Secretory granule	GTPase
39	ACAT2	acetyl-CoA acetyltransferase, cytosolic isoform 1	9	63	9	1.0	**2E-02**	0.9	**9E-06**	1.2	9E-01	1.0	**7E-06**	1.0	5E-01	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
7164	TPD52L1	tumor protein D53 isoform 1	6	26	6	1.0	**4E-02**	1.1	**5E-03**	1.0	**8E-04**	1.0	**1E-03**	1.0	5E-01	Molecular function unknown	-	Unclassified
6674	SPAG1	PREDICTED: sperm-associated antigen 1 isoform X1	2	8	2	1.0	9E-02	1.3	**3E-02**	1.1	**4E-02**	1.1	**3E-02**	0.9	1E+00	GTPase activity	Cytoplasm	GTPase
8436	SDPR	serum deprivation-response protein	3	6	3	1.0	3E-01	0.7	2E-01	1.0	3E-01	0.9	3E-01	0.9	5E-01	Serine-type peptidase activity	Cytoplasm	Serine protease
84498	FAM120B	constitutive coactivator of peroxisome proliferator-activated receptor gamma isoform b	2	6	2	1.0	5E-01	0.9	1E-01	1.0	7E-01	0.9	1E-01	1.0	7E-01	Molecular function unknown	-	Unclassified
2108	ETFA	electron transfer flavoprotein subunit alpha, mitochondrial isoform a	14	117	14	1.0	**4E-11**	1.2	**5E-15**	1.2	**4E-12**	**1.5**	**2E-16**	1.0	8E-01	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
54520	CCDC93	coiled-coil domain-containing protein 93	12	38	12	1.0	**3E-03**	1.0	**5E-06**	1.1	**5E-03**	1.1	**2E-06**	1.0	7E-01	Molecular function unknown	-	Unclassified
55850	USE1	vesicle transport protein USE1	3	14	3	1.0	**2E-02**	0.9	**2E-02**	1.1	8E-01	1.1	**2E-02**	1.0	6E-01	Molecular function unknown	-	Unclassified
27348	TOR1B	torsin-1B	5	20	5	1.0	3E-01	0.9	2E-01	1.0	4E-01	0.8	4E-01	0.8	6E-02	Chaperone activity	Perinuclear region	Chaperone
2821	GPI	PREDICTED: glucose-6-phosphate isomerase isoform X2	20	278	20	1.0	**2E-16**	0.9	**2E-16**	0.9	7E-01	0.8	**1E-03**	1.0	**4E-02**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
30001	ERO1L; ERO1A	ERO1-like protein alpha	14	115	14	1.0	**7E-11**	0.7	**7E-15**	0.9	**6E-08**	1.1	**6E-14**	1.0	**5E-02**	#N/A	#N/A	#N/A
375449	MAST4	microtubule-associated serine/threonine-protein kinase 4 isoform c	19	77	18	1.0	**2E-04**	1.1	**1E-08**	1.3	**2E-03**	**1.6**	**4E-09**	1.1	9E-02	Molecular function unknown	-	Unclassified
55847	CISD1	CDGSH iron-sulfur domain-containing protein 1	4	19	4	1.0	**3E-03**	1.4	**1E-02**	1.2	**1E-03**	0.8	6E-01	1.0	8E-01	Molecular function unknown	-	Unclassified
9342	SNAP29	synaptosomal-associated protein 29	10	36	10	1.0	**6E-03**	0.9	**2E-04**	1.0	7E-01	**1.5**	**8E-05**	0.9	2E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
114294	LACTB	serine beta-lactamase-like protein LACTB, mitochondrial isoform a	11	48	11	1.0	**9E-03**	1.2	**5E-05**	1.2	**1E-04**	1.4	**5E-05**	1.1	**2E-02**	Structural constituent of ribosome	Mitochondrion;Cytoplasm	Ribosomal subunit
25896	INTS7	integrator complex subunit 7 isoform 1	1	6	1	1.0	1E-01	1.0	2E-01	1.1	5E-01	1.2	1E-01	0.9	3E-01	Structural molecule activity	-	Structural protein
1981	EIF4G1	eukaryotic translation initiation factor 4 gamma 1 isoform 1	48	379	41	1.0	**2E-16**	0.9	**2E-16**	0.9	5E-01	0.9	**2E-16**	0.9	**5E-06**	Translation regulator activity	Nucleus;Cytoplasm	Translation regulatory protein
2947	GSTM3	glutathione S-transferase Mu 3	15	94	14	1.0	**2E-07**	1.1	**1E-12**	1.2	**2E-07**	1.4	**2E-11**	0.9	**2E-05**	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase
84305	WIBG; PYM1	partner of Y14 and mago isoform 1	5	29	5	1.0	**6E-05**	1.0	**8E-05**	1.0	1E-01	0.9	**2E-05**	0.9	3E-01	#N/A	#N/A	#N/A
3692	EIF6	eukaryotic translation initiation factor 6 isoform a	7	42	7	1.0	**1E-04**	1.0	**5E-06**	1.0	**2E-02**	1.1	**5E-06**	0.9	5E-02	Translation regulator activity	Cytoplasm	Translation regulatory protein
6434	TRA2B	transformer-2 protein homolog beta isoform 1	3	29	2	1.0	**9E-04**	1.0	**2E-05**	1.0	2E-01	1.1	**1E-08**	1.1	**4E-03**	RNA binding	Nucleus	RNA binding protein
5899	RALB	PREDICTED: ras-related protein Ral-B isoform X1	7	62	4	1.0	**2E-03**	1.1	**2E-04**	1.1	**8E-05**	1.3	**2E-04**	1.1	**2E-03**	GTPase activity	Cytoplasm	GTPase
4152	MBD1	PREDICTED: methyl-CpG-binding domain protein 1 isoform X2	3	14	3	1.0	**4E-03**	1.1	**3E-03**	1.3	8E-02	**2.0**	**2E-02**	1.2	**1E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
5500	PPP1CB	serine/threonine-protein phosphatase PP1-beta catalytic subunit isoform 1	15	139	4	1.0	**1E-02**	0.8	**1E-03**	0.9	4E-01	0.9	**6E-04**	0.9	7E-02	Protein serine/threonine phosphatase activity	Nucleolus	Serine/threonine phosphatase
10614	HEXIM1	protein HEXIM1	3	14	3	1.0	**1E-02**	0.8	**9E-04**	1.2	9E-02	0.9	8E-02	1.0	7E-01	Transcription factor activity	Nucleus	Transcription factor
5238	PGM3	PREDICTED: phosphoacetylglucosamine mutase isoform X1	12	50	12	1.0	**2E-02**	0.9	**3E-07**	1.2	2E-01	1.2	**1E-07**	1.0	4E-01	Catalytic activity	Cytoplasm	Enzyme: Mutase
115548	FCHO2	FCH domain only protein 2 isoform a	10	31	10	1.0	**4E-02**	1.1	**1E-03**	1.1	9E-02	1.3	**7E-03**	1.0	2E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
5621	PRNP	major prion protein preproprotein	5	27	5	1.0	**5E-02**	0.8	**4E-02**	1.0	1E-01	0.5	9E-02	1.1	2E-01	Molecular function unknown	Plasma membrane	Membrane bound ligand
3068	HDGF	hepatoma-derived growth factor isoform a	13	124	2	1.0	**1E-11**	1.0	**8E-09**	1.0	**2E-05**	0.7	**3E-03**	1.0	2E-01	Growth factor activity	Nucleus	Growth factor
208	AKT2	PREDICTED: RAC-beta serine/threonine-protein kinase isoform X1	10	36	7	1.0	**3E-03**	1.0	**1E-04**	1.2	1E-01	1.1	**4E-02**	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
55275	VPS53	vacuolar protein sorting-associated protein 53 homolog isoform 1	7	19	7	1.0	**2E-02**	1.2	**2E-04**	1.0	**3E-02**	1.1	**1E-05**	1.0	**2E-02**	Molecular function unknown	-	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
26128	**KIAA1279; KIF1BP**	**KIF1-binding protein**	7	24	6	1.0	**3E-02**	0.8	**2E-02**	1.0	**1E-02**	0.8	2E-01	0.8	**2E-02**	#N/A	#N/A	#N/A
4848	**CNOT2**	**CCR4-NOT transcription complex subunit 2**	2	7	2	1.0	9E-02	1.1	**1E-02**	1.0	1E-01	0.9	1E-01	0.9	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
51506	**UFC1**	**ubiquitin-fold modifier-conjugating enzyme 1**	3	9	3	1.0	1E-01	0.8	9E-02	0.8	**3E-02**	0.8	3E-01	0.9	7E-02	Molecular function unknown	-	Unclassified
2710	**GK**	**glycerol kinase isoform d**	3	6	3	1.0	3E-01	0.8	2E-01	1.2	5E-01	1.1	4E-01	0.9	5E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
1213	**CLTC**	**clathrin heavy chain 1 isoform 2**	73	863	56	1.0	**2E-16**	1.0	**2E-16**	1.1	**2E-16**	1.3	**2E-16**	1.0	7E-01	Structural molecule activity	Cytoplasm	Structural protein
6711	**SPTBN1**	**spectrin beta chain, non-erythrocytic 1 isoform 1**	98	624	86	1.0	**2E-16**	1.0	**2E-16**	0.9	**5E-10**	0.8	**2E-16**	1.0	1E-01	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
4282	**MIF**	**macrophage migration inhibitory factor**	5	152	5	1.0	**9E-13**	0.8	**2E-12**	1.0	**2E-03**	0.8	5E-01	0.8	**4E-06**	Cytokine activity	Extracellular	Cytokine
85377	**MICALL1**	**MICAL-like protein 1**	24	113	24	1.0	**1E-08**	1.1	**5E-12**	1.3	**3E-07**	1.1	**3E-08**	0.9	**3E-02**	Structural constituent of cytoskeleton	-	Cytoskeletal protein
5007	**OSBP**	**oxysterol-binding protein 1**	18	72	18	1.0	**2E-06**	1.0	**1E-09**	1.0	**4E-02**	1.0	**1E-11**	1.0	9E-01	Transporter activity	Cytoplasm	Transport/cargo protein
54505	**DHX29**	**ATP-dependent RNA helicase DHX29**	23	88	21	1.0	**3E-05**	1.0	**4E-05**	0.9	**2E-02**	1.0	**2E-05**	1.0	1E-01	Helicase activity	-	RNA helicase
622	**BDH1**	**D-beta-hydroxybutyrate dehydrogenase, mitochondrial**	9	50	9	1.0	**4E-04**	1.3	**3E-06**	1.3	**4E-06**	**1.6**	**6E-06**	1.0	2E-01	Catalytic activity	Mitochondrial membrane	Enzyme: Dehydrogenase
10413	**YAP1**	**yorkie homolog isoform 9**	9	43	9	1.0	**5E-04**	1.0	**5E-06**	1.0	**1E-02**	1.1	**5E-07**	1.0	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
83752	**LONP2**	**lon protease homolog 2, peroxisomal isoform 1**	6	18	6	1.0	**2E-02**	1.0	**1E-02**	1.0	9E-01	1.2	**2E-02**	1.1	7E-01	Aminopeptidase activity	-	Aminopeptidase
50484	**RRM2B**	**ribonucleoside-diphosphate reductase subunit M2 B isoform 2**	6	19	6	1.0	6E-02	1.0	**3E-02**	1.2	9E-02	1.1	**4E-02**	0.8	7E-02	Catalytic activity	Nucleus	Enzyme: Reductase
2997	**GYS1**	**glycogen [starch] synthase, muscle isoform 1**	7	39	7	1.0	**2E-04**	1.0	**5E-05**	1.0	**4E-03**	1.1	**4E-04**	1.0	8E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
4791	**NFKB2**	**nuclear factor NF-kappa-B p100 subunit isoform b**	6	23	5	1.0	**2E-03**	0.9	**9E-05**	1.2	4E-01	1.1	**3E-04**	1.1	4E-01	Transcription factor activity	Cytoplasm	Transcription factor
55971	**BAIAP2L1**	**brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1**	15	60	15	1.0	**5E-03**	0.9	**1E-04**	1.0	8E-01	0.8	5E-01	0.9	**1E-02**	Molecular function unknown	-	Unclassified
81631	**MAP1LC3B**	**microtubule-associated proteins 1A/1B light chain 3B**	2	14	1	1.0	**6E-03**	**0.7**	**4E-02**	0.6	5E-02	1.0	**7E-04**	1.1	5E-02	Molecular function unknown	Integral to membrane	Unclassified
6879	**TAF7**	**transcription initiation factor TFIID subunit 7**	2	12	2	1.0	**8E-03**	**0.7**	**4E-02**	0.9	**3E-02**	0.8	1E+00	1.1	1E-01	Transcription factor activity	Nucleus	Transcription factor
4835	**NQO2**	**PREDICTED: ribosyldihydronicotinamide dehydrogenase [quinone] isoform X1**	5	21	5	1.0	**2E-02**	1.1	**1E-03**	1.3	**6E-03**	0.9	**1E-02**	0.9	8E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
8227	**AKAP17A**	**A-kinase anchor protein 17A isoform 1**	2	6	2	1.0	1E-01	0.8	1E-01	1.1	2E-01	0.6	8E-01	1.0	4E-01	#N/A	#N/A	#N/A
9266	**CYTH2**	**cytohesin-2 isoform 1**	2	8	2	1.0	2E-01	0.9	**3E-02**	1.0	8E-01	1.0	1E-01	1.0	4E-01	Guanyl-nucleotide exchange factor activity	Cytosol	Guanine nucleotide exchange factor
50814	**NSDHL**	**sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating**	14	148	14	1.0	**1E-12**	1.0	**3E-16**	1.1	**2E-09**	**1.6**	**2E-16**	1.0	**7E-06**	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
10130	**PDIA6**	**protein disulfide-isomerase A6 isoform a**	15	182	15	1.0	**6E-10**	0.9	**3E-15**	1.0	5E-01	0.9	**1E-11**	1.1	**2E-09**	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase
51119	**SBDS**	**ribosome maturation protein SBDS**	17	119	16	1.0	**3E-07**	0.9	**3E-09**	1.0	5E-01	1.1	**3E-11**	0.9	5E-02	Molecular function unknown	Nucleolus	Unclassified
5906	**RAP1A**	**ras-related protein Rap-1A*gi|58331202|ref|NP_001010935.1|ras-related protein Rap-1A*gi|631226406|ref|NP_001278825.1|ras-related protein Rap-1A**	5	63	1	1.0	**2E-06**	1.1	**1E-08**	1.1	4E-01	1.4	**8E-07**	1.0	**2E-02**	GTPase activity	Plasma membrane	GTPase
1200	**TPP1**	**tripeptidyl-peptidase 1 preproprotein**	7	42	7	1.0	**4E-06**	1.0	**1E-05**	1.0	**1E-02**	1.1	**2E-05**	1.1	**2E-02**	Serine-type peptidase activity	Lysosome	Serine protease
5184	**PEPD**	**xaa-Pro dipeptidase isoform 1**	7	50	7	1.0	**2E-05**	0.9	**8E-08**	1.0	1E-01	1.0	**1E-05**	1.0	5E-01	Peptidase activity	Cytoplasm	Protease
5912	**RAP2B**	**ras-related protein Rap-2b**	6	62	4	1.0	**1E-04**	1.0	**2E-05**	1.1	6E-02	1.3	**1E-05**	1.0	3E-01	GTPase activity	Plasma membrane	GTPase
4357	**MPST**	**3-mercaptopyruvate sulfurtransferase isoform 1**	9	52	9	1.0	**3E-03**	1.0	**7E-05**	0.9	5E-02	0.7	8E-02	0.9	1E-01	Sulfotransferase activity	Mitochondrion	Enzyme: Sulphotransferase
51614	**ERGIC3**	**endoplasmic reticulum-Golgi intermediate compartment protein 3 isoform a**	5	24	5	1.0	**2E-02**	1.0	**8E-03**	0.9	**2E-03**	0.9	**2E-04**	0.9	2E-01	Molecular function unknown	Golgi apparatus	Unclassified
3855	**KRT7**	**keratin, type II cytoskeletal 7**	33	2081	21	1.0	**1E-04**	0.8	1E+00	0.8	**2E-16**	**1.7**	**2E-16**	1.2	**2E-16**	Structural constituent of cytoskeleton	Cytoplasm;Plasma membrane	Cytoskeletal protein
475	**ATOX1**	**copper transport protein ATOX1**	4	35	4	1.0	**6E-04**	0.8	**1E-05**	1.1	7E-02	0.8	**3E-02**	0.9	**6E-03**	Chaperone activity	Cytoplasm	Chaperone
55004	**LAMTOR1**	**ragulator complex protein LAMTOR1**	2	12	2	1.0	**9E-03**	1.1	**1E-03**	1.1	**3E-03**	1.1	**6E-04**	1.0	7E-01	#N/A	#N/A	#N/A
54497	**HEATR5B**	**HEAT repeat-containing protein 5B**	7	22	7	1.0	**1E-02**	1.1	**2E-03**	1.1	**4E-03**	1.2	**7E-05**	1.0	7E-01	Molecular function unknown	-	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
163859	**SDE2**	protein SDE2 homolog	6	17	6	1.0	1E-01	0.8	**2E-02**	1.2	9E-01	0.8	3E-01	0.9	8E-01	#N/A	#N/A	#N/A
23230	**VPS13A**	vacuolar protein sorting-associated protein 13A isoform A	3	7	3	1.0	5E-01	1.0	1E-01	1.0	3E-01	1.0	**1E-02**	1.0	1E+00	Transporter activity	-	Transport/cargo protein
58472	**SQRDL**	sulfide:quinone oxidoreductase, mitochondrial	23	211	23	1.0	**5E-12**	1.1	**1E-15**	1.3	**1E-12**	**2.0**	**2E-15**	1.1	**7E-06**	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
9748	**SLK**	STE20-like serine/threonine-protein kinase isoform 1	39	194	36	1.0	**1E-10**	0.9	**2E-16**	1.0	3E-01	1.3	**2E-16**	0.9	**9E-03**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
52	**ACP1**	low molecular weight phosphotyrosine protein phosphatase isoform c	3	34	3	1.0	**5E-03**	0.9	**1E-03**	1.0	3E-01	1.0	**2E-03**	0.9	6E-02	Acid phosphatase activity	Cytoplasm	Enzyme: Acid phosphatase
9392	**TGFBRAP1**	transforming growth factor-beta receptor-associated protein 1	6	17	6	1.0	**1E-02**	1.0	**2E-02**	1.0	6E-02	1.1	**3E-02**	0.9	5E-01	Chaperone activity	Cytoplasm	Chaperone
2187	**FANCB**	Fanconi anemia group B protein	1	6	1	1.0	6E-02	0.8	5E-02	1.1	7E-02	0.9	**4E-02**	0.9	2E-01	Molecular function unknown	-	Unclassified
403313	**PPAPDC2; PLPP6**	presqualene diphosphate phosphatase	2	10	2	1.0	1E-01	1.3	1E-01	1.0	2E-01	1.4	**2E-02**	1.2	**4E-02**	#N/A	#N/A	#N/A
2806	**GOT2**	aspartate aminotransferase, mitochondrial isoform 1	22	238	22	1.0	**2E-09**	1.1	**6E-13**	1.0	**3E-14**	1.2	**2E-16**	1.0	**3E-02**	Transaminase activity	Mitochondrion	Enzyme: Aminotransferase
84516	**DCTN5**	dynactin subunit 5 isoform 1	2	15	2	1.0	**9E-03**	0.9	**4E-03**	1.0	2E-01	1.0	**4E-03**	0.9	**1E-02**	Molecular function unknown	-	Unclassified
10075	**HUWE1**	PREDICTED: E3 ubiquitin-protein ligase HUWE1 isoform X2	56	119	6	1.0	**2E-02**	1.0	**4E-02**	0.8	**6E-03**	1.0	**7E-03**	0.9	3E-01	DNA binding	Nucleus	DNA binding protein
201163	**FLCN**	folliculin isoform 1	2	6	2	1.0	**3E-02**	**0.7**	**5E-02**	1.2	3E-01	1.0	1E-01	1.0	9E-01	Molecular function unknown	Cytoplasm	Unclassified
57665	**RDH14**	retinol dehydrogenase 14	6	30	6	1.0	7E-02	1.0	**3E-03**	1.1	**2E-02**	1.3	**2E-03**	1.0	4E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
54897	**CASZ1**	PREDICTED: zinc finger protein castor homolog 1 isoform X1	6	17	6	1.0	1E-01	1.1	**6E-04**	1.0	**5E-02**	1.1	**5E-04**	1.1	2E-01	-	Cytoplasm	-
10312	**TCIRG1**	V-type proton ATPase 116 kDa subunit a isoform 3 isoform a	9	22	7	1.0	2E-01	1.1	**1E-02**	1.1	9E-02	**1.6**	**1E-03**	1.0	2E-01	Transporter activity	Integral to membrane	Unclassified
6595	**SMARCA2**	probable global transcription activator SNF2L2 isoform c	14	25	9	1.0	#N/A	1.0	#N/A	1.1	#N/A	1.3	#N/A	0.9	#N/A	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor
4128	**MAOA**	amine oxidase [flavin-containing] A isoform 1	15	95	15	1.0	**3E-12**	**1.6**	**1E-14**	1.2	**6E-14**	**1.9**	**7E-15**	1.0	**7E-03**	Catalytic activity	Mitochondrion	Enzyme: Oxidase
4190	**MDH1**	malate dehydrogenase, cytoplasmic isoform 1	15	194	15	1.0	**1E-10**	1.0	**2E-16**	1.0	**5E-09**	0.9	**2E-15**	0.9	**3E-02**	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
51652	**CHMP3**	charged multivesicular body protein 3 isoform 1	8	37	8	1.0	**8E-03**	1.0	7E-02	0.8	1E-01	0.8	9E-01	0.9	2E-01	#N/A	#N/A	#N/A
57213	**SPRYD7**	SPRY domain-containing protein 7 isoform 1	2	12	2	1.0	**1E-02**	1.1	**2E-02**	0.9	1E-01	1.1	**2E-02**	1.1	1E-01	#N/A	#N/A	#N/A
311	**ANXA11**	annexin A11 isoform 1	18	125	18	1.0	**9E-08**	0.9	**2E-11**	1.0	5E-02	1.3	**5E-12**	1.0	2E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
51100	**SH3GLB1**	endophilin-B1 isoform 1	9	47	8	1.0	**1E-04**	0.9	**3E-07**	1.0	2E-01	1.0	**4E-07**	1.0	7E-01	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
79443	**FYCO1**	FYVE and coiled-coil domain-containing protein 1	14	54	14	1.0	**4E-04**	1.0	**9E-05**	1.0	7E-02	1.1	**4E-06**	1.1	3E-01	Molecular function unknown	-	Unclassified
27336	**HTATSF1**	HIV Tat-specific factor 1*gi|253970456|ref|NP_001156752.1| HIV Tat-specific factor 1	8	33	8	1.0	**4E-03**	0.9	**2E-03**	0.9	3E-01	1.0	**1E-02**	0.9	9E-02	Transcription factor activity	Nucleus	Transcription factor
2035	**EPB41**	protein 4.1 isoform 1	6	13	6	1.0	**9E-03**	1.1	**4E-03**	1.1	**3E-02**	0.7	6E-01	1.0	8E-01	Structural molecule activity	Nucleus	Structural protein
90268	**FAM105B; OTULIN**	PREDICTED: ubiquitin thioesterase otulin isoform X1	6	28	6	1.0	**1E-02**	1.1	**1E-03**	1.0	**2E-03**	1.1	**3E-03**	1.0	9E-01	#N/A	#N/A	#N/A
7168	**TPM1**	PREDICTED: tropomyosin alpha-1 chain isoform X12	15	101	2	1.0	**2E-02**	1.0	**2E-02**	1.1	**3E-03**	1.3	**5E-05**	1.0	**4E-02**	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein
2783	**GNB2**	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	9	76	5	1.0	**2E-02**	1.0	**5E-04**	1.1	**3E-02**	1.0	**3E-06**	0.9	**2E-02**	GTPase activity	Cytoplasm	G protein
23527	**ACAP2**	arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	13	44	13	1.0	**4E-02**	0.9	**8E-03**	1.1	3E-01	1.4	**2E-03**	1.0	4E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
4258	**MGST2**	microsomal glutathione S-transferase 2 isoform 1	1	6	1	1.0	**4E-02**	1.3	4E-01	0.7	**4E-02**	1.1	**4E-02**	1.1	1E-01	Glutathione transferase activity	Endoplasmic reticulum	Enzyme: Glutathione transferase
51271	**UBAP1**	ubiquitin-associated protein 1 isoform 2	8	29	8	1.0	1E-01	0.8	7E-02	1.0	5E-01	1.0	6E-02	0.8	8E-02	Molecular function unknown	-	Unclassified
55326	**AGPAT5**	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	1	6	1	1.0	4E-01	**1.5**	**2E-02**	1.1	**1E-05**	**1.5**	**2E-02**	1.0	5E-01	Transferase activity	Integral to membrane	Enzyme: Transferase
286144	**TRIQK**	triple QxxK/R motif-containing protein	1	6	1	1.0	5E-01	**1.5**	**1E-02**	1.3	1E-01	1.4	9E-02	1.2	8E-01	#N/A	#N/A	#N/A
7531	**YWHAE**	14-3-3 protein epsilon	19	1146	16	1.0	**2E-16**	1.0	**2E-16**	1.1	**1E-08**	1.1	**2E-16**	1.0	5E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
5529	**PPP2R5E**	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform isoform a	7	36	4	1.0	**2E-03**	0.7	**3E-04**	0.9	2E-01	0.8	8E-01	0.8	1E-01	Molecular function unknown	Cytoplasm	Regulatory/other subunit
5692	**PSMB4**	proteasome subunit beta type-4	6	41	6	1.0	**2E-03**	0.9	**3E-04**	1.1	2E-01	1.0	**6E-05**	0.9	**1E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
318	**NUDT2**	bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]	4	21	4	1.0	**2E-02**	1.0	**3E-05**	1.2	**1E-02**	1.2	**8E-05**	1.0	7E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8790	FPGT	fucose-1-phosphate guanylyltransferase isoform 1	3	11	3	1.0	5E-02	0.8	1E-01	0.9	4E-01	0.9	1E-01	0.8	6E-02	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase
145173	B3GALTL; B3GLCT	beta-1,3-glucosyltransferase	1	6	1	1.0	3E-01	0.9	6E-02	1.1	8E-01	1.2	**4E-02**	1.2	6E-01	#N/A	#N/A	#N/A
10487	CAP1	adenylyl cyclase-associated protein 1	24	354	3	1.0	**5E-14**	0.7	**2E-16**	1.1	**1E-08**	1.1	**2E-16**	1.0	**2E-04**	Molecular function unknown	Cytoplasm	Unclassified
79098	C1orf116	PREDICTED: specifically androgen-regulated gene protein isoform X1	25	154	25	1.0	**8E-09**	0.9	**4E-16**	1.1	9E-01	1.4	**2E-16**	1.0	7E-01	Molecular function unknown	Cytoplasm	Unclassified
9043	SPAG9	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	23	117	20	1.0	**1E-06**	1.0	**4E-13**	1.0	**2E-02**	1.1	**1E-11**	0.9	**1E-02**	Molecular function unknown	Cytoplasm;Plasma membrane	Integral membrane protein
126353	C19orf21; MISP	PREDICTED: mitotic interactor and substrate of PLK1 isoform X1	11	48	11	1.0	**8E-06**	**0.6**	**1E-03**	**0.6**	**3E-04**	**0.7**	**8E-03**	1.0	**1E-03**	#N/A	#N/A	#N/A
1432	MAPK14	mitogen-activated protein kinase 14 isoform 2	10	49	9	1.0	**9E-05**	0.9	**2E-06**	1.1	2E-01	1.0	**6E-05**	0.9	**3E-02**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
51633	OTUD6B	OTU domain-containing protein 6B isoform 1	6	25	6	1.0	**2E-03**	0.8	**7E-05**	1.1	3E-01	1.1	**2E-03**	0.9	2E-01	Molecular function unknown	-	Unclassified
54521	WDR44	WD repeat-containing protein 44 isoform 1	12	41	12	1.0	**1E-02**	1.0	**2E-05**	1.0	5E-01	1.1	**4E-06**	1.1	3E-01	Transporter activity	Cytoplasm	Transport/cargo protein
85369	STRIP1	striatin-interacting protein 1 isoform 1	5	24	5	1.0	**2E-02**	1.0	**8E-03**	1.0	1E-01	1.1	**2E-02**	1.0	1E+00	#N/A	#N/A	#N/A
9871	SEC24D	protein transport protein Sec24D	6	33	5	1.0	4E-01	0.8	2E-01	1.0	2E-01	0.8	8E-01	1.0	4E-01	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
51719	CAB39	calcium-binding protein 39*gi|195927022|ref|NP_001124322.1| calcium-binding protein 39*gi|7706481|ref|NP_057373.1| calcium-binding protein 39	18	162	18	1.0	**2E-14**	0.9	**5E-14**	1.0	7E-02	0.9	**1E-09**	1.0	2E-01	Calcium ion binding	-	Calcium binding protein
10848	PPP1R13L	relA-associated inhibitor	23	112	23	1.0	**3E-07**	1.0	**7E-11**	1.1	**4E-03**	1.1	**1E-10**	0.9	**1E-03**	Translation regulator activity	Nucleus;Cytoplasm	Translation regulatory protein
9217	VAPB	vesicle-associated membrane protein-associated protein B/C isoform 1	13	71	12	1.0	**8E-06**	1.1	**1E-08**	1.1	**3E-06**	1.4	**1E-07**	1.0	3E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
51637	C14orf166	UPF0568 protein C14orf166	11	76	11	1.0	**1E-05**	1.0	**4E-07**	1.0	3E-01	0.9	**1E-04**	1.0	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
4677	NARS	asparagine--tRNA ligase, cytoplasmic	17	107	17	1.0	**5E-05**	1.0	**5E-10**	1.0	**2E-02**	1.0	**3E-11**	0.9	1E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
8802	SUCLG1	succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	7	35	7	1.0	**1E-02**	1.2	**2E-03**	1.0	**2E-03**	1.1	**8E-03**	1.0	1E+00	Ligase activity	Mitochondrion	Enzyme: Ligase
9798	IST1	IST1 homolog isoform c	8	67	8	1.0	**4E-08**	0.9	**8E-08**	1.1	9E-01	1.3	**1E-09**	0.9	**3E-03**	#N/A	#N/A	#N/A
29767	TMOD2	tropomodulin-2 isoform a	5	35	4	1.0	**7E-03**	1.0	**3E-05**	1.9	5E-01	**2.3**	**6E-05**	1.0	9E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
51128	SAR1B	GTP-binding protein SAR1b*gi|7705827|ref|NP_057187.1| GTP-binding protein SAR1b	6	73	3	1.0	6E-02	0.9	**4E-03**	1.0	6E-01	1.2	**5E-03**	0.8	8E-02	GTPase activity	Endoplasmic reticulum	GTPase
5780	PTPN9	tyrosine-protein phosphatase non-receptor type 9	2	5	2	1.0	2E-01	1.3	2E-01	1.1	3E-01	0.8	5E-01	1.0	6E-01	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase
23597	ACOT9	acyl-coenzyme A thioesterase 9, mitochondrial isoform a	15	82	15	1.0	**2E-06**	1.0	**5E-07**	1.0	**4E-04**	1.2	**3E-07**	1.1	**6E-03**	Hydrolase activity	Mitochondrion	Enzyme: Esterase
65124	SOWAHC	ankyrin repeat domain-containing protein SOWAHC	11	50	11	1.0	**7E-06**	1.0	**3E-05**	0.9	**5E-03**	1.0	**2E-05**	1.0	9E-01	#N/A	#N/A	#N/A
4257	MGST1	microsomal glutathione S-transferase 1 isoform a	3	28	3	1.0	**1E-04**	1.3	**9E-09**	1.3	**9E-07**	**1.8**	**5E-07**	1.0	4E-01	Glutathione transferase activity	Microsome	Enzyme: Glutathione transferase
60412	EXOC4	exocyst complex component 4 isoform a	21	89	21	1.0	**7E-04**	1.1	**1E-04**	0.9	**3E-06**	1.0	**3E-08**	1.0	1E+00	Transporter activity	Plasma membrane	Transport/cargo protein
90550	MCU	calcium uniporter protein, mitochondrial isoform 1	10	41	10	1.0	**4E-03**	1.0	**7E-04**	1.1	**8E-04**	1.3	**3E-04**	1.0	**2E-02**	#N/A	#N/A	#N/A
100	ADA	adenosine deaminase	6	30	6	1.0	**4E-03**	1.1	**1E-04**	1.3	**2E-03**	1.1	**2E-04**	1.0	4E-01	Deaminase activity	Plasma membrane	Enzyme: Deaminase
4673	NAP1L1	nucleosome assembly protein 1-like 1	7	73	6	1.0	**1E-02**	**0.6**	**1E-02**	0.8	**6E-04**	0.7	7E-02	0.8	**5E-03**	DNA binding	Nucleus	Transcription regulatory protein
70	ACTC1	actin, alpha cardiac muscle 1 proprotein	21	1435	2	1.0	**2E-02**	**0.7**	**1E-03**	1.1	**2E-04**	1.1	**5E-03**	1.1	1E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
80854	SETD7	histone-lysine N-methyltransferase SETD7	4	13	4	1.0	6E-02	0.8	5E-02	0.9	**3E-02**	0.8	1E+00	0.9	1E-01	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase
401152	C4orf3	uncharacterized protein C4orf3 isoform 1	1	9	1	1.0	8E-02	1.1	8E-02	0.9	1E-01	1.0	**5E-02**	1.0	7E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
131118	DNAJC19	mitochondrial import inner membrane translocase subunit TIM14 isoform 1	2	9	2	1.0	2E-01	1.1	**4E-02**	1.1	2E-01	1.2	1E-01	0.9	9E-01	Protein translocase activity	Mitochondrial membrane	Enzyme: Translocase
10476	ATP5H	ATP synthase subunit d, mitochondrial isoform a	13	125	13	1.0	4E-01	1.1	1E-01	1.1	9E-01	1.0	5E-01	1.0	2E-01	Transporter activity	Mitochondrial membrane	Transport/cargo protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
23170	TTLL12	tubulin--tyrosine ligase-like protein 12	16	95	16	1.0	**2E-09**	1.0	**4E-10**	1.1	**3E-02**	1.2	**9E-09**	1.0	2E-01	Ligase activity	Nucleus;Cytoplasm	Enzyme: Ligase
23	ABCF1	ATP-binding cassette sub-family F member 1 isoform a	18	98	18	1.0	**4E-05**	0.9	**6E-08**	0.9	1E-01	1.0	**1E-09**	1.0	6E-01	Translation regulator activity	Ribosome;Nucleus	Translation regulatory protein
1182	CLCN3	H(+)/Cl(-) exchange transporter 3 isoform b	5	24	5	1.0	**2E-04**	1.2	**1E-05**	0.9	**8E-04**	**1.5**	**2E-06**	1.1	2E-01	Voltage-gated ion channel activity	Endosome;Plasma membrane;Golgi apparatus	Voltage gated channel
10087;	COL4A3BP	collagen type IV alpha-3-binding protein isoform 3	22	46	22	1.0	**7E-04**	0.8	**9E-06**	1.1	1E-01	1.3	**5E-05**	0.9	**2E-02**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
4509	ATP8	ATP synthase F0 subunit 8 (mitochondrion)	2	10	2	1.0	**1E-03**	1.1	2E-01	0.8	**5E-04**	**0.5**	**2E-03**	0.9	1E-01	#N/A	#N/A	#N/A
80028	FBXL18	F-box/LRR-repeat protein 18	7	28	7	1.0	**5E-03**	0.8	**3E-04**	1.1	2E-01	1.1	**5E-05**	1.0	3E-01	Molecular function unknown	-	Unclassified
63898	SH2D4A	SH2 domain-containing protein 4A isoform a*gi|292658783|ref|NP_001167630.1|SH2 domain-containing protein 4A isoform a	7	21	7	1.0	**3E-02**	0.9	**8E-04**	1.2	4E-01	1.2	**9E-05**	1.0	5E-01	Molecular function unknown	Nucleus	Unclassified
22949	PTGR1	prostaglandin reductase 1 isoform 1*gi|226059159|ref|NP_001139580.1|prostaglandin reductase 1 isoform 1	10	73	10	1.0	**1E-06**	1.1	**7E-08**	1.4	**7E-06**	**1.9**	**3E-08**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
29079;	MED4	mediator of RNA polymerase II transcription subunit 4 isoform 1	14	121	14	1.0	**2E-06**	0.9	**1E-06**	1.0	2E-01	1.0	**1E-06**	1.1	**4E-03**	Translation regulator activity	Nucleus	Translation regulatory protein
2286	FKBP2	peptidyl-prolyl cis-trans isomerase FKBP2	4	24	4	1.0	**6E-05**	0.9	**4E-06**	1.1	6E-01	1.2	**4E-06**	1.0	3E-01	Isomerase activity	Endoplasmic reticulum lumen	Enzyme: Isomerase
26064	RAI14	ankycorbin isoform d	13	36	13	1.0	**9E-04**	0.9	**7E-05**	1.1	1E-01	1.2	**7E-05**	1.0	**4E-02**	Molecular function unknown	Cytoplasm	Unclassified
90639	COX19	cytochrome c oxidase assembly protein COX19	3	12	3	1.0	**2E-03**	0.9	**5E-04**	1.0	8E-01	1.0	**2E-02**	1.0	3E-01	Ion transporter activity	Cytosol	Chaperone
47	ACLY	ATP-citrate synthase isoform 4	49	474	1	1.0	**2E-16**	0.8	**2E-16**	1.1	**2E-16**	1.1	**2E-16**	0.9	**5E-04**	ATPase activity	Cytoplasm	ATPase
8533	COPS3	COP9 signalosome complex subunit 3 isoform 1	12	83	12	1.0	**1E-06**	1.0	**1E-08**	1.1	**3E-03**	1.1	**3E-10**	0.9	7E-02	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
26100	WIPI2	WD repeat domain phosphoinositide-interacting protein 2 isoform a	7	30	6	1.0	**5E-04**	1.2	**3E-05**	1.0	**1E-04**	**1.7**	**5E-05**	1.1	6E-02	Molecular function unknown	-	Unclassified
6548	SLC9A1	sodium/hydrogen exchanger 1	5	28	5	1.0	**5E-04**	0.9	**1E-04**	1.0	6E-02	1.0	**4E-05**	1.0	5E-02	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
3005	H1F0	histone H1.0	8	70	8	1.0	**6E-04**	**1.9**	**7E-09**	**1.6**	**2E-10**	**4.3**	**9E-11**	1.0	6E-02	DNA binding	Nucleus	DNA binding protein
64780	MICAL1	protein-methionine sulfoxide oxidase MICAL1 isoform 3	8	24	8	1.0	**9E-04**	0.9	**2E-04**	1.0	7E-01	0.8	**5E-03**	1.0	9E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
29924	EPN1	epsin-1 isoform a	7	30	7	1.0	**1E-03**	0.9	**3E-03**	1.1	7E-01	1.0	**2E-03**	1.0	9E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6714	SRC	proto-oncogene tyrosine-protein kinase Src	12	56	6	1.0	**7E-03**	0.9	**3E-03**	1.0	2E-01	0.9	5E-02	0.9	1E+00	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase
497661	C18orf32	UPF0729 protein C18orf32	2	10	2	1.0	**3E-02**	1.0	**1E-02**	1.1	1E-01	**1.6**	**3E-02**	1.2	1E-01	Molecular function unknown	-	Unclassified
9446	GSTO1	glutathione S-transferase omega-1 isoform 1	16	258	16	1.0	**2E-16**	0.9	**2E-16**	1.2	**4E-02**	1.2	**2E-16**	1.0	**1E-02**	Glutathione transferase activity	Nucleus	Enzyme: Glutathione transferase
5720	PSME1	proteasome activator complex subunit 1 isoform 1	12	111	12	1.0	**2E-09**	0.9	**7E-11**	1.0	7E-01	0.9	1E-01	0.9	**2E-03**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
552900; 654483; 102725214	LOC101060252; BOLA2; BOLA2B; LOC102725214	bolA-like protein 2	4	38	4	1.0	**4E-05**	0.8	**4E-06**	1.2	**2E-02**	1.0	**2E-06**	0.8	**1E-03**	#N/A	#N/A	#N/A
283638	CEP170B; KIAA0284	centrosomal protein of 170 kDa protein B isoform 1	8	16	8	1.0	**2E-02**	0.9	**4E-03**	1.1	9E-01	0.8	4E-01	0.8	8E-02	#N/A	#N/A	#N/A
2769	GNA15	guanine nucleotide-binding protein subunit alpha-15	5	22	4	1.0	**2E-02**	1.1	**4E-02**	1.0	**3E-02**	0.7	5E-01	1.0	9E-01	GTPase activity	Plasma membrane	G protein
65260	SELRC1; COA7	cytochrome c oxidase assembly factor 7	4	11	4	1.0	7E-02	1.0	2E-01	0.9	7E-01	0.9	1E-01	0.8	**5E-02**	#N/A	#N/A	#N/A
140809	SRXN1	sulfiredoxin-1	3	12	3	1.0	1E-01	1.0	**1E-02**	**1.6**	**3E-02**	**1.5**	**2E-02**	0.8	**1E-02**	Molecular function unknown	-	Unclassified
79966	SCD5	stearoyl-CoA desaturase 5 isoform a	3	9	3	1.0	2E-01	1.0	1E-01	0.6	3E-01	1.0	2E-01	1.0	4E-01	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase
51449	PCYOX1	prenylcysteine oxidase 1	12	114	12	1.0	**7E-13**	1.2	**1E-15**	1.2	**4E-13**	**1.6**	**3E-16**	1.0	8E-01	Catalytic activity	Lysosome	Enzyme: Oxidase
55763	EXOC1	exocyst complex component 1 isoform 1	18	78	18	1.0	**9E-09**	1.0	**9E-13**	1.0	**3E-07**	1.1	**7E-10**	1.0	6E-01	Transporter activity	Cytoplasm	Transport/cargo protein
55054	ATG16L1	autophagy-related protein 16-1 isoform 1	7	29	7	1.0	**2E-03**	0.9	**1E-04**	1.2	9E-01	1.2	**4E-04**	1.0	2E-01	Intracellular transporter activity	Integral to membrane	Integral membrane protein
7920	ABHD16A	abhydrolase domain-containing protein 16A isoform a	2	10	2	1.0	**1E-02**	1.3	**7E-03**	1.1	**6E-03**	1.4	**4E-03**	0.9	8E-01	#N/A	#N/A	#N/A
2517	FUCA1	tissue alpha-L-fucosidase	3	7	3	1.0	**4E-02**	1.1	**2E-02**	1.2	5E-02	1.4	**1E-04**	1.1	1E+00	Hydrolase activity	Lysosome	Enzyme: Hydrolase
7189	TRAF6	TNF receptor-associated factor 6	3	10	3	1.0	1E-01	0.9	3E-01	0.8	7E-01	0.8	6E-01	1.0	5E-01	Signal transducer activity	Cytoplasm	Adapter molecule

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3300	DNAJB2	dnaJ homolog subfamily B member 2 isoform b	9	30	8	1.0	3E-01	1.2	**3E-02**	0.9	**2E-03**	0.8	**5E-02**	0.8	3E-01	Heat shock protein activity	Cytoplasm	Heat shock protein
9632	SEC24C	protein transport protein Sec24C*gi|38373671|ref|NP_940999.1| protein transport protein Sec24C	21	128	20	1.0	**2E-10**	1.0	**7E-13**	1.1	**2E-04**	1.2	**6E-10**	1.0	7E-01	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
28976	ACAD9	acyl-CoA dehydrogenase family member 9, mitochondrial	17	95	17	1.0	**6E-09**	1.2	**9E-10**	1.0	**3E-07**	1.2	**1E-10**	1.0	4E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
56681	SAR1A	GTP-binding protein SAR1a	8	88	4	1.0	**3E-08**	0.9	**3E-09**	1.0	8E-01	1.1	**4E-10**	0.9	2E-01	GTPase activity	Endoplasmic reticulum	GTPase
7251	TSG101	tumor susceptibility gene 101 protein	9	54	9	1.0	**2E-05**	0.9	**3E-06**	1.1	6E-01	1.2	**3E-07**	0.9	**2E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55666	NPLOC4	nuclear protein localization protein 4 homolog	12	59	12	1.0	**6E-05**	1.0	**7E-06**	1.1	**2E-05**	1.3	**6E-07**	1.0	2E-01	Transporter activity	Nucleus	Transport/cargo protein
11021	RAB35	ras-related protein Rab-35 isoform 1	11	110	8	1.0	**2E-04**	1.0	**1E-04**	1.0	3E-01	1.1	**1E-04**	0.9	3E-01	GTPase activity	-	GTPase
2011	MARK2	serine/threonine-protein kinase MARK2 isoform d	17	64	12	1.0	**3E-04**	0.9	**1E-05**	1.0	2E-01	0.9	**5E-04**	0.9	**3E-02**	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase
51160	VPS28	vacuolar protein sorting-associated protein 28 homolog isoform 2	5	30	5	1.0	**2E-03**	0.9	**5E-06**	1.2	4E-01	1.3	**2E-06**	0.9	**4E-03**	Transporter activity	Cytoplasm	Transport/cargo protein
8500	PPFIA1	liprin-alpha-1 isoform b	5	12	5	1.0	1E-01	0.9	7E-02	1.0	8E-01	1.2	1E-01	1.0	5E-01	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein
9388	LIPG	endothelial lipase	4	14	4	1.0	4E-01	0.9	3E-01	1.0	4E-01	1.1	2E-01	1.2	2E-01	Lipase activity	Extracellular	Enzyme: Lipase
56243;	KIAA1217	sickle tail protein homolog isoform 4	14	25	6	1.0	7E-01	0.9	1E-01	1.1	**3E-02**	**2.0**	**2E-02**	1.1	2E-01	Molecular function unknown	-	Unclassified
9124	PDLIM1	PDZ and LIM domain protein 1	15	152	15	1.0	**2E-15**	0.9	6E-01	0.7	**4E-03**	**0.5**	**4E-14**	0.9	**5E-07**	Molecular function unknown	Cytoplasm	Unclassified
5879	RAC1	ras-related C3 botulinum toxin substrate 1 isoform Rac1b	8	69	4	1.0	**2E-08**	0.9	**1E-10**	1.0	1E+00	1.0	**5E-11**	1.0	2E-01	GTPase activity	Cytoplasm	GTPase
10016	PDCD6	programmed cell death protein 6 isoform 1	6	70	1	1.0	**2E-08**	1.0	**2E-08**	1.2	**5E-03**	1.2	**9E-09**	0.9	3E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
5685	PSMA4	proteasome subunit alpha type-4 isoform 1*gi|4506185|ref|NP_002780.1| proteasome subunit alpha type-4 isoform 1	10	94	10	1.0	**9E-07**	0.9	**2E-08**	1.1	9E-01	1.0	**2E-13**	0.9	**2E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
26118;	WSB1	WD repeat and SOCS box-containing protein 1 isoform 2	30	73	30	1.0	**2E-05**	0.9	**4E-12**	1.1	3E-01	1.2	**2E-13**	1.0	7E-02	Molecular function unknown	-	Unclassified
6652	SORD	sorbitol dehydrogenase	11	47	11	1.0	**2E-03**	1.0	**2E-04**	1.0	**4E-02**	0.9	**5E-03**	1.0	8E-01	Catalytic activity	Plasma membrane	Enzyme: Dehydrogenase
10490	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B	7	24	7	1.0	**2E-03**	1.0	**4E-03**	0.8	**4E-02**	1.0	**5E-04**	1.1	**1E-02**	Molecular function unknown	Cytoplasmic vesicle	Unclassified
10227	MFSD10	major facilitator superfamily domain-containing protein 10	5	26	5	1.0	**2E-02**	0.9	**1E-04**	1.1	2E-01	1.3	**7E-04**	1.1	5E-01	Molecular function unknown	-	Unclassified
156	ADRBK1; GRK2	beta-adrenergic receptor kinase 1	5	17	5	1.0	**3E-02**	1.1	**1E-02**	1.1	6E-02	0.8	**5E-02**	1.0	9E-02	#N/A	#N/A	#N/A
58497	PRUNE; PRUNE1	protein prune homolog isoform 1	2	10	2	1.0	1E-01	1.2	6E-02	1.3	**3E-02**	1.4	**4E-02**	0.9	**4E-02**	#N/A	#N/A	#N/A
83693	HSDL1	PREDICTED: inactive hydroxysteroid dehydrogenase-like protein 1 isoform X1	1	6	1	1.0	5E-01	0.9	**4E-02**	1.1	6E-01	1.1	**3E-02**	1.0	1E+00	Catalytic activity	-	Enzyme: Dehydrogenase
81	ACTN4	PREDICTED: alpha-actinin-4 isoform X2	54	633	3	1.0	**1E-03**	0.9	**4E-09**	1.0	5E-02	1.3	**2E-16**	1.0	6E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
1778	DYNC1H1	cytoplasmic dynein 1 heavy chain 1	166	1123	166	1.0	**2E-16**	1.0	**2E-16**	1.0	**2E-16**	1.1	**2E-16**	1.0	**1E-04**	ATPase activity	Cytoplasm	ATPase
833	CARS	cysteine--tRNA ligase, cytoplasmic isoform c	28	140	28	1.0	**1E-09**	0.9	**4E-10**	1.1	9E-01	1.1	**1E-10**	1.0	1E+00	Ligase activity	Cytoplasm	Enzyme: Ligase
5683	PSMA2	proteasome subunit alpha type-2	5	27	5	1.0	**8E-06**	1.0	**3E-06**	1.1	9E-02	1.1	**1E-06**	0.9	2E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
2287	FKBP3	peptidyl-prolyl cis-trans isomerase FKBP3	11	60	11	1.0	**7E-05**	1.1	**3E-06**	1.1	**3E-03**	1.0	**5E-05**	1.0	2E-01	Isomerase activity	Nucleus	Enzyme: Isomerase
5034	P4HB	protein disulfide-isomerase	38	579	38	1.0	**2E-16**	0.9	**2E-16**	1.0	1E-01	0.8	**3E-06**	1.0	**1E-03**	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase
51400	PPME1	protein phosphatase methylesterase 1 isoform a	13	88	13	1.0	**7E-07**	0.8	**1E-10**	1.0	**2E-04**	0.9	**5E-08**	0.9	**1E-04**	Methyltransferase activity	-	Enzyme: Methyltransferase
5860	QDPR	dihydropteridine reductase	6	41	6	1.0	**3E-03**	1.0	**3E-04**	1.0	**1E-02**	1.1	**3E-06**	1.0	8E-01	Catalytic activity	Extracellular	Enzyme: Reductase
102	ADAM10	disintegrin and metalloproteinase domain-containing protein 10	5	22	5	1.0	2E-01	0.9	6E-01	0.8	4E-01	0.9	2E-01	0.9	8E-01	Metallopeptidase activity	Plasma membrane	Metallo protease
2317	FLNB	filamin-B isoform 1	137	1803	125	1.0	**2E-16**	0.7	**2E-16**	1.2	**2E-16**	**1.5**	**2E-16**	1.0	**2E-16**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
8239	USP9X	probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 3	44	203	44	1.0	**1E-08**	1.0	**2E-16**	1.0	**7E-10**	1.3	**2E-16**	1.0	**3E-03**	Ubiquitin-specific protease activity	Cytoplasm;Nucleus	Ubiquitin proteasome system protein
54205	CYCS	cytochrome c	7	101	7	1.0	**5E-07**	**1.6**	**5E-14**	1.3	**3E-10**	**1.6**	**7E-11**	1.1	**9E-09**	Catalytic activity	Mitochondrion	Enzyme: Oxidase

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10133	OPTN	optineurin	18	89	18	1.0	**5E-07**	0.9	**6E-10**	1.0	2E-01	0.8	**5E-06**	0.9	7E-02	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein
11079;	RER1	protein RER1	2	7	2	1.0	**7E-04**	0.9	**1E-03**	0.9	**3E-02**	1.0	**8E-04**	0.9	7E-01	Molecular function unknown	Golgi apparatus	Integral membrane protein
147179	WIPF2	PREDICTED: WAS/WASL-interacting protein family member 2 isoform X1	8	28	8	1.0	**8E-03**	0.9	**7E-04**	1.1	4E-01	1.3	**4E-03**	1.0	8E-01	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein
81570	CLPB	caseinolytic peptidase B protein homolog isoform 1	7	23	7	1.0	2E-01	1.0	**2E-03**	1.2	9E-02	1.2	**7E-03**	1.0	3E-01	ATPase activity	Nucleus	ATPase
3840	KPNA4	importin subunit alpha-3	10	67	6	1.0	**1E-07**	0.9	**5E-09**	1.0	5E-02	0.9	**2E-06**	1.0	**1E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
224	ALDH3A2	fatty aldehyde dehydrogenase isoform 1	16	101	15	1.0	**4E-07**	**1.5**	**3E-09**	1.2	**4E-10**	**1.8**	**2E-10**	1.0	5E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
1727	CYB5R3	NADH-cytochrome b5 reductase 3 isoform 3	10	96	10	1.0	**9E-07**	1.1	**7E-08**	1.1	**2E-06**	1.3	**4E-08**	1.0	7E-02	Catalytic activity	Cytoplasm	Enzyme: Reductase
8890	EIF2B4	translation initiation factor eIF-2B subunit delta isoform 2	10	57	10	1.0	**2E-04**	1.0	**4E-07**	1.1	**1E-04**	1.2	**8E-11**	1.0	7E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
5878	RAB5C	ras-related protein Rab-5C isoform b	8	67	5	1.0	**5E-04**	0.9	**7E-05**	1.0	9E-01	1.0	**3E-04**	1.0	6E-01	GTPase activity	Endosome	GTPase
9950	GOLGA5	Golgin subfamily A member 5	7	29	7	1.0	**2E-03**	1.0	**9E-03**	1.0	7E-02	1.2	**1E-03**	1.0	7E-01	Auxiliary transport protein activity	Golgi apparatus;Nucleus;Cytoplasm	Membrane transport protein
230	ALDOC	PREDICTED: fructose-bisphosphate aldolase C isoform X1	22	280	15	1.0	**2E-02**	1.0	**1E-08**	1.2	**2E-02**	**1.8**	**1E-09**	0.9	**7E-04**	Lyase activity	Mitochondrion	Enzyme: Lyase
1939	EIF2D	eukaryotic translation initiation factor 2D isoform 1	5	18	5	1.0	6E-01	1.0	**5E-02**	1.0	1E-01	0.9	8E-02	0.9	5E-01	#N/A	#N/A	#N/A
1499	CTNNB1	catenin beta-1	32	323	25	1.0	**1E-12**	0.9	**2E-13**	0.9	**5E-03**	0.8	**1E-05**	1.0	**3E-04**	Cell adhesion molecule activity	Plasma membrane;Nucleus;Cytoplasm	Adhesion molecule
3710	ITPR3	inositol 1,4,5-trisphosphate receptor type 3	50	226	42	1.0	**1E-11**	1.1	**2E-16**	1.1	**5E-14**	1.2	**2E-16**	1.0	1E-01	Intracellular ligand-gated ion channel activity	Plasma membrane	Intracellular ligand gated channel
55970	GNG12	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	4	62	4	1.0	**1E-06**	1.0	**3E-09**	1.0	**2E-03**	0.9	**3E-04**	1.1	**1E-03**	GTPase activity	Cytoplasm	G protein
54344	DPM3	dolichol-phosphate mannosyltransferase subunit 3 isoform 1	2	18	2	1.0	**1E-03**	1.0	**3E-04**	1.0	**3E-02**	1.3	**3E-04**	1.0	8E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Synthase
60491	NIF3L1	putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform 3	4	32	1	1.0	**1E-03**	0.8	**2E-06**	0.9	7E-01	0.8	**7E-06**	0.8	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
130340	AP1S3	AP-1 complex subunit sigma-3	4	21	3	1.0	**4E-03**	1.1	**1E-03**	0.9	1E-01	1.4	**1E-02**	1.0	3E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
5495	PPM1B	PREDICTED: protein phosphatase 1B isoform X1	6	12	5	1.0	**4E-03**	1.0	**4E-02**	0.9	3E-01	1.0	3E-01	0.9	9E-01	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
4690	NCK1	cytoplasmic protein NCK1 isoform 1	9	36	8	1.0	**6E-03**	0.8	**9E-06**	1.0	3E-01	0.8	2E-01	0.9	**3E-03**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
55561	CDC42BPG	serine/threonine-protein kinase MRCK gamma	4	9	4	1.0	9E-02	0.9	6E-02	1.1	7E-01	1.0	**3E-02**	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
8518	IKBKAP	elongator complex protein 1	10	31	10	1.0	9E-01	0.8	**3E-02**	1.0	3E-01	0.9	**6E-04**	1.0	1E+00	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
5834	PYGB	glycogen phosphorylase, brain form	42	245	4	1.0	**2E-16**	0.7	**2E-16**	0.9	2E-01	**1.5**	**2E-16**	1.0	**2E-06**	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase
9948	WDR1	WD repeat-containing protein 1 isoform 1	28	211	28	1.0	**4E-13**	0.9	**5E-16**	0.9	8E-01	1.0	**2E-16**	0.9	**6E-08**	Molecular function unknown	Cytoplasm	Unclassified
3954	LETM1	LETM1 and EF-hand domain-containing protein 1, mitochondrial	22	151	22	1.0	**2E-09**	1.1	**2E-12**	1.1	**1E-11**	1.3	**9E-15**	1.0	4E-01	Calcium ion binding	Plasma membrane	Calcium binding protein
8724	SNX3	sorting nexin-3 isoform a	8	60	6	1.0	**9E-06**	0.8	**1E-05**	0.9	2E-01	0.6	2E-01	0.9	**4E-03**	Protein transporter activity	Endosome	Transport/cargo protein
3959	LGALS3BP	galectin-3-binding protein	6	32	6	1.0	**1E-04**	0.7	6E-02	0.8	**6E-04**	0.7	1E-01	0.9	2E-01	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
23358	USP24	ubiquitin carboxyl-terminal hydrolase 24	18	47	17	1.0	**3E-03**	0.9	**2E-04**	1.0	4E-01	1.0	**3E-05**	1.0	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
9382	COG1	conserved oligomeric Golgi complex subunit 1	9	36	9	1.0	**8E-03**	1.1	**1E-03**	1.0	**1E-02**	1.2	**2E-04**	1.1	1E-01	Structural molecule activity	Golgi apparatus	Structural protein
79135	APOO	apolipoprotein O	3	14	3	1.0	**3E-02**	1.0	**9E-03**	1.1	6E-02	1.2	**5E-02**	1.0	6E-01	Molecular function unknown	Mitochondrion	Unclassified
51780	KDM3B	lysine-specific demethylase 3B	3	8	3	1.0	**3E-02**	0.8	**2E-03**	1.1	9E-01	0.9	5E-02	0.9	2E-01	Molecular function unknown	Nucleus	Unclassified
9564	BCAR1	breast cancer anti-estrogen resistance protein 1 isoform 1	2	8	2	1.0	2E-01	1.0	**3E-02**	1.1	7E-01	1.1	5E-02	1.1	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
22948	CCT5	T-complex protein 1 subunit epsilon	34	419	33	1.0	**2E-16**	0.8	**2E-16**	1.0	**2E-03**	1.0	**3E-13**	0.9	**3E-04**	Chaperone activity	Centrosome	Chaperone
7415	VCP	transitional endoplasmic reticulum ATPase	43	463	43	1.0	**2E-16**	1.0	**2E-16**	1.1	**2E-16**	1.3	**2E-16**	1.0	9E-01	ATPase activity	Cytoplasm;Nucleus;Nucleolus;Perinuclear region	ATPase
5702	PSMC3	26S protease regulatory subunit 6A	25	178	25	1.0	**7E-12**	1.0	**2E-16**	1.1	**1E-02**	1.3	**2E-16**	0.9	**6E-06**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	**p-value**	**Median Fold change**	**p-value**	**Median Fold change**	**p-value**	**Median Fold change**	**p-value**	**Median Fold change**	**p-value**			
353	**APRT**	**adenine phosphoribosyltransferase isoform a**	9	63	9	1.0	**8E-08**	1.1	**4E-09**	1.2	**1E-08**	1.2	**5E-11**	0.9	1E-01	Transferase activity	-	Enzyme: Ribosyltransferase
1819	**DRG2**	**developmentally-regulated GTP-binding protein 2**	13	90	12	1.0	**6E-07**	0.9	**8E-08**	1.1	7E-01	1.0	**2E-09**	0.9	**4E-03**	Molecular function unknown	-	Unclassified
5498	**PPOX**	**protoporphyrinogen oxidase**	4	22	4	1.0	**1E-04**	1.0	**2E-04**	1.1	**1E-02**	1.3	**6E-05**	0.9	7E-01	Catalytic activity	Mitochondrion	Enzyme: Oxidase
9652	**TTC37**	**tetratricopeptide repeat protein 37**	12	63	12	1.0	**3E-04**	1.1	**2E-05**	1.0	**9E-05**	1.0	**3E-07**	1.0	9E-01	Molecular function unknown	-	Unclassified
1159; 548596	**CKMT1B; CKMT1A**	**creatine kinase U-type, mitochondrial**	13	129	13	1.0	**4E-07**	1.2	**5E-09**	0.9	**3E-09**	0.8	**1E-06**	1.0	7E-01	#N/A	#N/A	#N/A
9218	**VAPA**	**vesicle-associated membrane protein-associated protein A isoform 2**	10	98	9	1.0	**6E-07**	1.1	**2E-08**	1.1	**2E-04**	**1.6**	**4E-08**	1.1	**2E-02**	Auxiliary transport protein activity	Endoplasmic reticulum membrane;Golgi membrane	Membrane transport protein
5711	**PSMD5**	**26S proteasome non-ATPase regulatory subunit 5 isoform 1**	13	90	13	1.0	**1E-04**	1.0	**3E-07**	1.0	**3E-02**	1.1	**3E-08**	1.0	9E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
14	**AAMP**	**angio-associated migratory cell protein isoform 1**	6	26	6	1.0	**2E-04**	1.0	**2E-04**	1.0	6E-02	1.1	**2E-03**	1.0	9E-01	Cell adhesion molecule activity	Extracellular	Adhesion molecule
5813	**PURA**	**transcriptional activator protein Pur-alpha**	8	36	8	1.0	**2E-03**	1.1	**9E-06**	1.2	**1E-02**	**1.6**	**2E-05**	0.9	4E-01	Transcription factor activity	Nucleus	Transcription factor
60559	**SPCS3**	**signal peptidase complex subunit 3**	4	22	4	1.0	**4E-03**	1.1	**1E-03**	1.0	**4E-05**	1.2	**1E-04**	1.0	9E-02	Protease activator activity	-	Protease
53349	**ZFYVE1**	**zinc finger FYVE domain-containing protein 1 isoform 1**	4	11	4	1.0	6E-02	0.9	7E-02	1.0	4E-01	1.3	**4E-03**	1.1	5E-01	Lipid binding	Golgi apparatus	Unclassified
800	**CALD1**	**caldesmon isoform 2**	23	135	23	1.0	**7E-08**	0.9	**7E-06**	0.8	4E-01	**0.5**	**3E-07**	1.0	3E-01	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein
5447	**POR**	**NADPH--cytochrome P450 reductase**	19	120	19	1.0	**1E-07**	1.1	**7E-09**	1.2	**2E-08**	**1.7**	**2E-09**	1.0	**3E-04**	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase
55361	**PI4K2A**	**phosphatidylinositol 4-kinase type 2-alpha**	21	125	21	1.0	**3E-06**	1.1	**5E-15**	1.1	**3E-05**	**1.7**	**2E-16**	1.1	**6E-05**	Lipid kinase activity	Golgi apparatus	Lipid Kinase
10577	**NPC2**	**epididymal secretory protein E1**	5	54	5	1.0	**9E-06**	1.0	**3E-10**	1.2	**4E-02**	1.1	**4E-08**	1.0	1E-01	Transporter activity	Lysosome	Transport/cargo protein
55177	**FAM82A2; RMDN3**	**PREDICTED: regulator of microtubule dynamics protein 3 isoform X1**	8	17	8	1.0	#N/A	1.1	#N/A	1.3	#N/A	1.5	#N/A	1.1	#N/A	#N/A	#N/A	#N/A
10787	**NCKAP1**	**nck-associated protein 1 isoform 2**	33	241	33	1.0	**7E-14**	1.0	**2E-16**	1.0	**6E-06**	1.1	**2E-16**	1.0	1E-01	Protein binding	Cytoplasm	Integral membrane protein
4218	**RAB8A**	**ras-related protein Rab-8A**	10	138	4	1.0	**1E-07**	0.9	**1E-08**	1.0	6E-02	1.0	**7E-07**	1.0	9E-01	GTPase activity	Nucleus	GTPase
10165	**SLC25A13**	**calcium-binding mitochondrial carrier protein Aralar2 isoform 1**	19	84	12	1.0	**6E-07**	1.0	**2E-07**	0.9	**1E-05**	1.0	**1E-06**	1.1	**4E-03**	Transporter activity;Carrier activity	Mitochondrion	Calcium binding protein;Transport/cargo protein
80279	**CDK5RAP3**	**PREDICTED: CDK5 regulatory subunit-associated protein 3 isoform X1**	10	70	10	1.0	**9E-05**	1.0	**2E-06**	1.0	**8E-05**	1.1	**3E-07**	1.0	5E-01	Molecular function unknown	-	Cell cycle control protein
2580	**GAK**	**cyclin-G-associated kinase isoform 1**	13	52	13	1.0	**7E-04**	0.9	**2E-04**	1.0	**1E-02**	1.0	**2E-04**	0.9	**2E-02**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
4351	**MPI**	**mannose-6-phosphate isomerase isoform 1**	6	21	6	1.0	**2E-02**	1.0	**2E-03**	1.1	2E-01	1.1	**2E-03**	1.0	9E-01	Isomerase activity	Cytoplasm	Enzyme: Isomerase
81027	**TUBB1**	**tubulin beta-1 chain**	8	208	3	1.0	**4E-02**	0.9	6E-02	1.1	5E-01	1.0	2E-01	1.0	5E-01	Structural constituent of cytoskeleton	Nucleolus	Cytoskeletal protein
27309	**ZNF330**	**zinc finger protein 330 isoform 1**	2	6	2	1.0	2E-01	1.0	1E-01	1.3	2E-01	1.1	2E-01	1.1	9E-01	Molecular function unknown	Nucleolus	Unclassified
10576	**CCT2**	**T-complex protein 1 subunit beta isoform 1**	30	376	30	1.0	**2E-16**	0.9	**2E-16**	1.0	**4E-02**	1.0	**2E-16**	0.9	9E-02	Chaperone activity	Cytoplasm	Chaperone
501	**ALDH7A1**	**alpha-aminoadipic semialdehyde dehydrogenase isoform 1**	25	208	25	1.0	**1E-15**	1.3	**2E-16**	1.0	**2E-16**	1.1	**2E-16**	1.0	**5E-02**	Oxidoreductase activity	-	Enzyme: Oxidoreductase
2314	**FLII**	**protein flightless-1 homolog isoform 1**	34	223	34	1.0	**3E-13**	0.8	**2E-16**	1.0	**1E-05**	1.3	**2E-16**	1.0	**4E-02**	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein
4597	**MVD**	**diphosphomevalonate decarboxylase**	13	91	13	1.0	**5E-07**	0.9	**2E-11**	1.4	5E-01	1.2	**2E-06**	0.9	**3E-02**	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase
4191	**MDH2**	**malate dehydrogenase, mitochondrial isoform 1**	18	318	18	1.0	**1E-06**	1.1	**2E-15**	1.1	**8E-09**	1.3	**2E-16**	0.9	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
373156	**GSTK1**	**glutathione S-transferase kappa 1 isoform b**	7	80	7	1.0	**4E-06**	1.1	**1E-07**	1.1	**3E-08**	1.1	**1E-08**	1.0	7E-01	Glutathione transferase activity	Peroxisome;Mitochondrion	Enzyme: Glutathione transferase
11316	**COPE**	**coatomer subunit epsilon isoform a**	6	57	6	1.0	**9E-06**	0.9	**2E-06**	1.0	3E-01	1.0	**3E-07**	1.0	5E-01	Transporter activity	Cytoplasm	Transport/cargo protein
53916	**RAB4B**	**ras-related protein Rab-4B**	6	67	3	1.0	9E-02	1.0	7E-02	1.0	3E-01	1.2	**5E-03**	1.0	1E+00	GTPase activity	-	GTPase
5092	**PCBD1**	**pterin-4-alpha-carbinolamine dehydratase isoform 1**	3	16	2	1.0	2E-01	0.9	**3E-02**	1.0	9E-01	0.8	7E-01	1.0	6E-01	Hydro-lyase activity	Cytoplasm	Enzyme: Dehydratase
488	**ATP2A2**	**sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform b**	35	282	35	1.0	**2E-16**	1.0	**2E-16**	1.0	**8E-12**	1.3	**2E-16**	1.0	**9E-04**	Auxiliary transport protein activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Membrane transport protein
55699	**IARS2**	**isoleucine--tRNA ligase, mitochondrial**	29	195	29	1.0	**2E-16**	1.3	**2E-16**	1.1	**2E-16**	1.3	**2E-16**	1.0	2E-01	TRNA ligase activity	Mitochondrion	-

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
5862	RAB2A	ras-related protein Rab-2A isoform a	11	110	11	1.0	**1E-08**	1.0	**1E-11**	1.0	**7E-04**	1.1	**2E-10**	1.0	4E-01	GTPase activity	Endoplasmic reticulum	GTPase
29979	UBQLN1	ubiquilin-1 isoform 1	7	47	2	1.0	**4E-06**	0.9	**7E-08**	1.1	7E-02	0.8	2E-01	0.9	**1E-04**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
1783	DYNC1LI2	cytoplasmic dynein 1 light intermediate chain 2 isoform 1	14	62	13	1.0	**1E-05**	0.9	**1E-04**	0.9	2E-01	0.8	**3E-04**	0.9	**2E-02**	Molecular function unknown	Cytoplasm	Unclassified
8562;	DENR	density-regulated protein	3	18	3	1.0	**2E-05**	0.9	**1E-07**	1.0	6E-01	1.0	**6E-07**	0.9	2E-01	Molecular function unknown	Nucleus	Unclassified
2184	FAH	fumarylacetoacetase	3	22	3	1.0	**3E-03**	1.1	**1E-03**	1.1	**9E-03**	1.1	**1E-02**	1.1	1E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
132789	GNPDA2	glucosamine-6-phosphate isomerase 2 isoform 1	7	47	4	1.0	**6E-03**	1.0	**4E-03**	1.1	8E-02	0.9	**1E-02**	1.0	2E-01	Deaminase activity	-	Enzyme: Deaminase
51762	RAB8B	ras-related protein Rab-8B	9	119	3	1.0	**3E-02**	0.9	**2E-02**	0.9	9E-01	1.1	6E-02	1.0	2E-01	GTPase activity	Cytoplasmic vesicle	GTPase
506	ATP5B	ATP synthase subunit beta, mitochondrial	19	422	19	1.0	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	1.3	**2E-16**	1.1	**5E-03**	Transporter activity	Mitochondrion	Transport/cargo protein
3895	KTN1	PREDICTED: kinectin isoform X1	60	318	60	1.0	**2E-16**	1.0	**2E-16**	1.0	**3E-11**	0.9	**2E-16**	1.0	9E-01	Cytoskeletal anchoring activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Anchor protein
10213	PSMD14	26S proteasome non-ATPase regulatory subunit 14	10	68	10	1.0	**3E-09**	0.9	**7E-08**	1.1	**2E-02**	1.2	**1E-09**	1.0	4E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
5706	PSMC6	26S protease regulatory subunit 10B	18	143	18	1.0	**1E-08**	0.9	**1E-11**	1.1	7E-02	1.3	**9E-13**	1.0	6E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
5321	PLA2G4A	cytosolic phospholipase A2	16	94	16	1.0	**6E-08**	0.7	**2E-07**	0.9	**3E-06**	**0.6**	**3E-07**	0.9	**2E-02**	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase
310	ANXA7	annexin A7 isoform 2	16	120	16	1.0	**9E-07**	1.0	**2E-10**	1.0	**6E-03**	0.9	**4E-04**	0.9	5E-01	Calcium ion binding	Nucleus	Calcium binding protein
51290	ERGIC2	endoplasmic reticulum-Golgi intermediate compartment protein 2	5	22	5	1.0	**3E-03**	0.9	**1E-03**	0.9	8E-01	1.0	**5E-03**	0.9	2E-01	Molecular function unknown	Nucleus	Unclassified
81855	SFXN3	sideroflexin-3	7	26	5	1.0	**2E-02**	1.0	**2E-04**	0.9	1E-01	1.2	**2E-04**	**1.5**	**3E-02**	Molecular function unknown	Integral to membrane	Integral membrane protein
60386	SLC25A19	PREDICTED: mitochondrial thiamine pyrophosphate carrier isoform X1	1	6	1	1.0	2E-01	1.0	8E-02	1.0	4E-01	1.3	**2E-02**	0.9	8E-01	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
374395	TMEM179B	transmembrane protein 179B	1	6	1	1.0	3E-01	1.3	5E-02	0.9	4E-01	0.7	6E-01	1.0	9E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
5684	PSMA3	proteasome subunit alpha type-3 isoform 1	12	125	12	1.0	**6E-11**	0.9	**1E-13**	1.1	1E-01	1.0	**1E-14**	0.9	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10598	AHSA1	activator of 90 kDa heat shock protein ATPase homolog 1	13	96	13	1.0	**6E-08**	0.8	**8E-09**	1.0	**5E-02**	0.9	**2E-06**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
6416	MAP2K4	dual specificity mitogen-activated protein kinase kinase 4 isoform 2	9	44	9	1.0	**1E-06**	1.0	**3E-06**	1.0	**1E-02**	1.1	**6E-07**	0.9	1E-01	Protein threonine/tyrosine kinase activity	Cytoplasm;Plasma membrane	Dual specificity kinase
8496	PPFIBP1	liprin-beta-1 isoform 2	10	35	10	1.0	**1E-04**	0.9	**9E-05**	1.0	1E-01	1.0	**1E-03**	1.0	2E-01	Cytoskeletal anchoring activity	Plasma membrane	Anchor protein
10695	CNPY3	protein canopy homolog 3	3	11	3	1.0	**8E-04**	0.8	**3E-03**	1.2	**1E-02**	0.8	**2E-03**	0.9	3E-01	Molecular function unknown	-	Unclassified
6876	TAGLN	transgelin*gi|48255907|ref|NP_001001522.1| transgelin	7	17	7	1.0	**1E-02**	1.0	4E-01	0.7	**2E-02**	0.7	8E-01	1.0	9E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
56270	WDR45B; WDR45L	WD repeat domain phosphoinositide-interacting protein 3	4	21	3	1.0	**3E-02**	1.1	**3E-03**	1.2	1E-01	1.0	**2E-02**	0.9	6E-01	#N/A	#N/A	#N/A
116150	NUS1	nogo-B receptor	1	5	1	1.0	5E-02	1.0	**2E-03**	1.3	2E-01	1.2	**9E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
1678	TIMM8A	mitochondrial import inner membrane translocase subunit Tim8 A isoform 1	4	16	4	1.0	5E-02	1.1	**2E-02**	1.1	**5E-02**	1.3	**3E-02**	1.1	9E-01	Catalytic activity	Mitochondrion	Enzyme: Translocase
55578	FAM48A; SUPT20H	transcription factor SPT20 homolog isoform c	1	8	1	1.0	3E-01	1.0	5E-02	0.9	5E-01	0.8	2E-01	1.0	4E-01	#N/A	#N/A	#N/A
1666	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	12	68	12	1.0	**5E-08**	1.3	**3E-10**	1.1	**3E-08**	1.3	**6E-10**	1.0	3E-01	Catalytic activity	Mitochondrion	Enzyme: Reductase
63893	UBE2O	ubiquitin-conjugating enzyme E2 O	10	44	10	1.0	**2E-03**	0.9	**1E-03**	1.1	2E-01	1.0	**3E-04**	0.9	**2E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55486	PARL	presenilins-associated rhomboid-like protein, mitochondrial isoform 1 preproprotein	2	12	2	1.0	**3E-03**	1.3	**9E-04**	1.4	**2E-04**	**1.6**	**3E-04**	1.0	2E-01	Metallopeptidase activity	Mitochondrion	Metallo protease
10294	DNAJA2	dnaJ homolog subfamily A member 2	8	58	8	1.0	**6E-03**	0.8	7E-02	0.9	2E-01	1.0	2E-01	0.9	**3E-03**	Chaperone activity	Cytoplasm	Chaperone
10058	ABCB6	ATP-binding cassette sub-family B member 6, mitochondrial	5	14	5	1.0	**1E-02**	1.4	**2E-02**	1.3	**2E-02**	1.3	**2E-02**	1.0	1E+00	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
83862	TMEM120A	transmembrane protein 120A	2	11	2	1.0	**2E-02**	1.1	**2E-03**	1.5	7E-02	**1.6**	**2E-02**	0.9	5E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
1.01E+08	SYNJ2BP-COX16	SYNJ2BP-COX16 protein isoform 1	2	14	2	1.0	#N/A	0.9	#N/A	0.9	#N/A	0.9	#N/A	1.0	#N/A	#N/A	#N/A	#N/A
498	ATP5A1	ATP synthase subunit alpha, mitochondrial isoform a*gi|50345984|ref|NP_001001937.1| ATP synthase subunit alpha, mitochondrial isoform a	28	433	28	1.0	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	1.2	**2E-16**	1.0	**3E-05**	Transporter activity	Mitochondrion	Transport/cargo protein
6923	TCEB2	transcription elongation factor B polypeptide 2 isoform b	5	55	5	1.0	**4E-08**	1.0	**2E-11**	1.1	**1E-02**	1.2	**1E-10**	0.9	6E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10724	**MGEA5**	**protein O-GlcNAcase isoform a**	25	112	25	1.0	**1E-07**	1.0	**2E-10**	1.2	**3E-04**	**1.5**	**2E-12**	0.9	**2E-02**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
23197	**FAF2**	**FAS-associated factor 2**	11	71	11	1.0	**2E-07**	1.0	**1E-08**	1.0	**1E-03**	**1.5**	**1E-07**	1.0	7E-01	Molecular function unknown	Cytoplasm	Unclassified
7511	**XPNPEP1**	**xaa-Pro aminopeptidase 1 isoform 1**	15	85	15	1.0	**6E-07**	1.0	**4E-07**	1.0	**2E-05**	1.1	**2E-08**	0.9	**7E-03**	Aminopeptidase activity	Cytoplasm	Aminopeptidase
9131	**AIFM1**	**apoptosis-inducing factor 1, mitochondrial isoform 1**	12	63	12	1.0	**2E-05**	1.1	**2E-08**	1.2	**2E-05**	1.3	**1E-09**	1.1	8E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
1.03E+08	**LOC102723897**	**PREDICTED: LOW QUALITY PROTEIN: WAS protein family homolog 2-like isoform X7**	3	6	3	1.0	**5E-03**	0.9	**2E-03**	1.0	8E-01	0.9	1E+00	0.9	4E-01	#N/A	#N/A	#N/A
5831	**PYCR1**	**pyrroline-5-carboxylate reductase 1, mitochondrial isoform 5**	1	6	1	1.0	**8E-03**	1.2	**4E-03**	1.0	2E-01	1.0	1E-01	1.0	2E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
2475	**MTOR**	**serine/threonine-protein kinase mTOR**	14	41	14	1.0	**2E-02**	0.9	**6E-04**	1.0	1E-01	1.0	**8E-03**	1.0	9E-01	Kinase activity	Nucleus	Cell cycle control protein
2952	**GSTT1**	**glutathione S-transferase theta-1 isoform a**	3	16	3	1.0	**2E-02**	1.0	**5E-03**	1.0	2E-01	1.2	**3E-03**	1.1	3E-01	Glutathione transferase activity	Nucleus	Enzyme: Glutathione transferase
6293	**VPS52**	**vacuolar protein sorting-associated protein 52 homolog isoform 1**	4	12	4	1.0	3E-01	0.9	1E-01	0.8	3E-01	1.0	**9E-03**	1.1	2E-01	Transporter activity	Cytoplasm	Transport/cargo protein
5870	**RAB6A**	**ras-related protein Rab-6A isoform a**	13	149	12	1.0	**1E-13**	1.0	**2E-16**	1.1	**7E-08**	1.1	**2E-16**	1.0	7E-01	GTPase activity	Golgi apparatus	GTPase
7353	**UFD1L**	**ubiquitin fusion degradation protein 1 homolog isoform A**	12	61	12	1.0	**2E-08**	0.9	**2E-08**	1.1	7E-01	1.0	**3E-08**	0.9	**3E-05**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
522	**ATP5J**	**ATP synthase-coupling factor 6, mitochondrial isoform b**	3	35	3	1.0	**5E-06**	1.1	**1E-07**	1.1	**2E-06**	1.0	**8E-07**	1.0	9E-01	ATPase activity;Protein binding	Mitochondrion	ATPase;Transport/cargo protein
55506	**H2AFY2**	**core histone macro-H2A.2**	15	90	13	1.0	**6E-05**	1.2	**2E-04**	1.0	**4E-03**	1.4	**2E-03**	1.1	**3E-02**	DNA binding	Nucleus	DNA binding protein
92421	**CHMP4C**	**charged multivesicular body protein 4c**	3	13	2	1.0	**2E-02**	0.8	**3E-02**	1.1	1E-01	1.2	**4E-02**	1.2	8E-01	Molecular function unknown	-	Unclassified
51399	**TRAPPC4**	**trafficking protein particle complex subunit 4**	4	22	4	1.0	5E-02	0.9	**6E-03**	1.1	1E+00	0.9	**1E-03**	1.0	2E-01	Transporter activity	Cytoplasm	Transport/cargo protein
272	**AMPD3**	**AMP deaminase 3 isoform 1A**	5	15	4	1.0	1E-01	1.1	**4E-02**	1.1	2E-01	1.4	**6E-03**	0.9	2E-01	Deaminase activity	Cytoplasm	Enzyme: Deaminase
4048	**LTA4H**	**leukotriene A-4 hydrolase isoform 1**	25	213	25	1.0	**2E-16**	0.9	**2E-16**	1.0	**1E-03**	1.0	**2E-16**	0.9	**2E-08**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
5611	**DNAJC3**	**dnaJ homolog subfamily C member 3**	19	94	18	1.0	**9E-09**	0.9	**4E-10**	1.1	8E-01	1.1	**2E-10**	1.1	**1E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
2193	**FARSA**	**phenylalanine--tRNA ligase alpha subunit**	13	100	13	1.0	**4E-07**	1.0	**9E-09**	1.0	**2E-05**	1.1	**6E-10**	1.0	8E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
30849	**PIK3R4**	**phosphoinositide 3-kinase regulatory subunit 4**	8	33	8	1.0	**3E-05**	0.8	**6E-05**	1.0	6E-01	1.0	**4E-04**	0.9	2E-01	Receptor signaling complex scaffold activity	-	Adapter molecule
25934	**NIPSNAP3A**	**protein NipSnap homolog 3A**	6	32	6	1.0	**6E-05**	1.2	**1E-03**	1.2	**1E-03**	1.3	**8E-04**	1.0	9E-02	Transporter activity	Plasma membrane	Transport/cargo protein
54464	**XRN1**	**5'-3' exoribonuclease 1 isoform a**	8	28	8	1.0	**2E-04**	1.0	**3E-05**	1.1	**1E-02**	1.0	**3E-05**	0.9	8E-01	Ribonuclease activity	Cytoplasm	Ribonuclease
84301;	**DDI2**	**protein DDI1 homolog 2**	9	18	9	1.0	**2E-04**	1.0	**1E-05**	1.0	**1E-03**	1.2	**1E-07**	1.0	6E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
8799	**LOC101060567; PEX11B**	**peroxisomal membrane protein 11B isoform 1**	7	40	7	1.0	**2E-03**	1.1	**1E-04**	1.0	**2E-04**	1.4	**2E-04**	1.0	9E-01	#N/A	#N/A	#N/A
56893	**UBQLN4**	**ubiquilin-4 isoform 1**	5	24	3	1.0	9E-02	0.9	9E-02	0.9	7E-01	0.7	3E-01	0.8	9E-02	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
25771	**TBC1D22A**	**TBC1 domain family member 22A isoform a**	4	14	4	1.0	9E-02	1.1	**8E-03**	1.0	**6E-03**	1.0	**4E-03**	0.9	8E-01	GTPase activator activity	Nucleus	GTPase activating protein
9445	**ITM2B**	**integral membrane protein 2B**	3	21	3	1.0	1E-01	0.9	**3E-03**	0.5	5E-01	0.5	1E-01	0.9	5E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
3326	**HSP90AB1**	**heat shock protein HSP 90-beta isoform a**	41	824	24	1.0	**2E-16**	0.8	**2E-16**	0.9	**2E-16**	0.8	**2E-02**	0.9	**6E-03**	Chaperone activity	Cytoplasm	Chaperone
1892	**ECHS1**	**enoyl-CoA hydratase, mitochondrial**	14	104	14	1.0	**3E-11**	1.2	**2E-11**	1.1	**9E-11**	1.3	**3E-11**	1.0	4E-01	Catalytic activity	Mitochondrion	Enzyme: Hydratase
23164	**MPRIP**	**PREDICTED: myosin phosphatase Rho-interacting protein isoform X1**	21	41	20	1.0	**1E-06**	1.0	**3E-09**	1.2	**5E-03**	**1.7**	**7E-08**	1.0	1E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
55229	**PANK4**	**pantothenate kinase 4**	12	46	12	1.0	**3E-06**	1.0	**3E-08**	1.3	**5E-03**	**1.9**	**5E-07**	1.0	5E-01	Catalytic activity	-	Enzyme: Phosphotransferase
1459	**CSNK2A2**	**casein kinase II subunit alpha'**	9	52	8	1.0	**5E-06**	0.9	**4E-05**	1.0	4E-01	1.0	**2E-05**	0.9	**3E-02**	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
5747	**PTK2**	**focal adhesion kinase 1 isoform b**	11	53	11	1.0	**1E-05**	0.9	**1E-05**	1.0	1E-01	0.9	**2E-02**	0.9	**4E-03**	Protein-tyrosine kinase activity	Cytoplasm;Nucleus	Tyrosine kinase
8604	**SLC25A12**	**calcium-binding mitochondrial carrier protein Aralar1**	15	61	8	1.0	**3E-05**	1.2	**4E-07**	1.0	**6E-05**	1.2	**8E-07**	1.0	1E-01	Transporter activity	Mitochondrion	Transport/cargo protein
8673	**VAMP8**	**vesicle-associated membrane protein 8**	4	26	4	1.0	**7E-05**	1.0	**1E-05**	1.1	**6E-04**	1.0	**9E-05**	0.9	**2E-02**	Auxiliary transport protein activity	Endosome	Membrane transport protein
51608	**GET4**	**Golgi to ER traffic protein 4 homolog**	7	27	7	1.0	**3E-03**	1.0	**8E-03**	1.1	**7E-03**	1.3	**5E-04**	1.0	7E-01	#N/A	#N/A	#N/A
80777	**CYB5B**	**cytochrome b5 type B**	5	26	5	1.0	**7E-03**	1.2	**2E-02**	1.1	**8E-05**	1.4	**2E-04**	1.1	**3E-03**	Transporter activity	Mitochondrion	Transport/cargo protein
92689	**FAM114A1**	**protein NOXP20**	5	20	5	1.0	**8E-03**	0.8	**6E-03**	1.3	1E-01	1.2	**2E-03**	1.1	**9E-03**	Molecular function unknown	Cytoplasm	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
26115	**TANC2**	**protein TANC2**	1	6	1	1.0	1E-01	0.9	**9E-03**	1.1	5E-01	1.1	**2E-02**	1.2	1E-01	Molecular function unknown	-	Unclassified
403	**ARL3**	**ADP-ribosylation factor-like protein 3**	9	47	9	1.0	5E-01	1.0	1E-01	1.0	7E-01	1.0	2E-01	0.9	2E-01	GTPase activity	Cytoplasm	GTPase
6950	**TCP1**	**T-complex protein 1 subunit alpha isoform a**	27	391	27	1.0	**2E-16**	0.9	**2E-16**	1.0	7E-01	1.1	**2E-16**	1.0	4E-01	Chaperone activity	Cytoplasm	Chaperone
5550	**PREP**	**prolyl endopeptidase**	27	182	27	1.0	**6E-13**	1.0	**1E-13**	1.0	**1E-05**	1.0	**1E-13**	0.9	**1E-05**	Serine-type peptidase activity	Cytoplasm	Serine protease
3416	**IDE**	**insulin-degrading enzyme isoform 1**	19	100	19	1.0	**6E-09**	1.0	**1E-09**	0.9	**8E-05**	1.0	**3E-11**	0.9	4E-01	Metallopeptidase activity	Cytoplasm	Metallo protease
5195	**PEX14**	**peroxisomal membrane protein PEX14**	6	41	6	1.0	**3E-05**	1.0	**8E-07**	1.1	**1E-06**	1.4	**3E-07**	1.0	8E-01	Protein binding	Peroxisome	Integral membrane protein
8573	**CASK**	**peripheral plasma membrane protein CASK isoform 1**	13	46	13	1.0	**1E-03**	1.1	**5E-04**	1.0	**3E-03**	0.8	**1E-02**	1.0	7E-01	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase
53343	**NUDT9**	**ADP-ribose pyrophosphatase, mitochondrial isoform a**	5	21	5	1.0	**8E-03**	0.9	**5E-03**	1.0	8E-01	0.8	2E-01	0.8	**6E-03**	Catalytic activity	Mitochondrion;Cytoplasm	Enzyme: Phosphatase
23731	**TMEM245**	**transmembrane protein 245**	6	15	6	1.0	**2E-02**	1.2	**1E-02**	1.0	1E-01	1.3	7E-02	1.3	9E-02	#N/A	#N/A	#N/A
1.01E+08	**ATP5J2-PTCD1**	**ATP5J2-PTCD1 fusion protein**	6	49	4	1.0	#N/A	1.0	#N/A	1.1	#N/A	1.0	#N/A	1.1	#N/A	#N/A	#N/A	#N/A
22820	**COPG1**	**coatomer subunit gamma-1**	23	170	20	1.0	**2E-16**	0.8	**2E-16**	1.0	**9E-05**	0.9	**2E-08**	0.9	**3E-03**	#N/A	#N/A	#N/A
4659	**PPP1R12A**	**protein phosphatase 1 regulatory subunit 12A isoform a**	24	105	24	1.0	**1E-11**	0.9	**6E-12**	1.0	6E-02	1.1	**6E-11**	1.0	5E-01	Phosphatase regulator activity	Cytoplasm	Regulatory/other subunit
8813	**DPM1**	**dolichol-phosphate mannosyltransferase subunit 1**	8	36	8	1.0	**5E-04**	1.1	**4E-04**	1.0	**3E-04**	1.3	**9E-05**	1.0	7E-02	Mannosyltransferase activity	Plasma membrane	Enzyme: Synthase
9690	**UBE3C**	**ubiquitin-protein ligase E3C**	9	39	9	1.0	**1E-03**	0.9	**1E-05**	1.0	1E-01	0.8	**4E-02**	0.9	**1E-02**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
7466	**WFS1**	**wolframin*gi|224994205|ref|NP_001139325.1| wolframin**	6	17	6	1.0	**2E-03**	0.9	**9E-04**	1.1	**2E-02**	1.1	**4E-03**	1.1	**3E-02**	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein
4358	**MPV17**	**PREDICTED: protein Mpv17 isoform X1**	2	12	2	1.0	**2E-02**	1.2	**1E-02**	1.2	**1E-02**	1.2	**7E-03**	1.0	9E-01	Molecular function unknown	Peroxisome;Mitochondrion	Integral membrane protein
7114	**TMSB4X**	**thymosin beta-4**	6	76	4	1.0	5E-02	**0.4**	**7E-03**	1.2	**3E-03**	0.5	1E-01	0.8	5E-02	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
8853	**ASAP2**	**arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2 isoform a**	8	37	7	1.0	7E-02	1.0	8E-02	0.9	2E-01	1.3	**6E-03**	1.1	2E-01	GTPase activator activity	Golgi apparatus;Cytoplasm	GTPase activating protein
3551	**IKBKB**	**inhibitor of nuclear factor kappa-B kinase subunit beta isoform 1**	3	12	2	1.0	1E-01	1.0	1E-01	0.9	3E-01	1.0	**2E-03**	0.9	1E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
54503	**ZDHHC13**	**palmitoyltransferase ZDHHC13 isoform 1**	2	8	2	1.0	1E-01	1.2	5E-02	0.9	**2E-02**	1.4	**3E-02**	1.2	7E-02	Molecular function unknown	Integral to membrane	Unclassified
51397	**COMMD10**	**COMM domain-containing protein 10**	2	11	2	1.0	1E-01	1.0	**2E-02**	1.0	2E-01	1.1	**2E-02**	0.9	5E-01	Molecular function unknown	-	Unclassified
55832	**CAND1**	**cullin-associated NEDD8-dissociated protein 1**	48	379	48	1.0	**2E-16**	0.9	**2E-16**	1.1	**2E-06**	1.0	**2E-16**	0.9	**9E-05**	Transcription regulator activity	Nucleus	Transcription regulatory protein
10961	**ERP29**	**endoplasmic reticulum resident protein 29 isoform 1**	9	89	9	1.0	**1E-07**	0.9	**7E-10**	1.1	**1E-02**	0.9	**7E-09**	0.9	1E-01	Chaperone activity	Endoplasmic reticulum	Chaperone
5573	**PRKAR1A**	**cAMP-dependent protein kinase type I-alpha regulatory subunit isoform a**	12	67	12	1.0	**5E-05**	0.9	**2E-06**	1.0	4E-01	0.9	**1E-08**	0.9	9E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
1635	**DCTD**	**deoxycytidylate deaminase isoform a**	4	29	4	1.0	**1E-04**	1.0	**8E-06**	1.4	8E-02	1.2	**3E-05**	1.0	5E-01	Deaminase activity	-	Enzyme: Deaminase
6737	**TRIM21**	**E3 ubiquitin-protein ligase TRIM21**	8	28	8	1.0	**1E-02**	0.7	5E-02	0.8	5E-02	0.7	5E-01	0.9	6E-02	Ribonucleoprotein	Plasma membrane	Ribonucleoprotein
55697	**VAC14**	**protein VAC14 homolog**	9	41	9	1.0	6E-02	1.3	**1E-03**	1.1	**7E-04**	**1.5**	**1E-07**	1.0	2E-01	Molecular function unknown	Microsome;Centrosome	Unclassified
10527	**IPO7**	**importin-7**	21	134	21	1.0	**4E-10**	0.8	**2E-13**	1.1	1E-01	1.0	**8E-10**	0.9	**1E-03**	Transporter activity	Nucleus	Transport/cargo protein
9861	**PSMD6**	**26S proteasome non-ATPase regulatory subunit 6 isoform 1**	21	146	21	1.0	**5E-10**	1.1	**3E-13**	1.0	**5E-04**	1.2	**2E-16**	1.0	1E-01	Ubiquitin-specific protease activity	Peroxisome	Ubiquitin proteasome system protein
539	**ATP5O**	**ATP synthase subunit O, mitochondrial**	9	92	9	1.0	**4E-08**	1.1	**2E-09**	1.1	**1E-07**	1.1	**2E-11**	1.0	9E-01	Transporter activity	Mitochondrion	Transport/cargo protein
8402	**SLC25A11**	**mitochondrial 2-oxoglutarate/malate carrier protein isoform 1**	8	78	8	1.0	**5E-07**	1.3	**7E-07**	1.2	**3E-06**	1.4	**5E-10**	1.1	**1E-05**	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
51429	**SNX9**	**sorting nexin-9**	7	40	7	1.0	**1E-06**	0.8	**6E-10**	1.1	**1E-03**	1.4	**9E-09**	0.9	**2E-02**	Receptor signaling complex scaffold activity	-	Adapter molecule
5921	**RASA1**	**ras GTPase-activating protein 1 isoform 1**	10	44	10	1.0	**1E-05**	0.8	**9E-08**	1.1	**4E-03**	1.3	**2E-08**	1.0	8E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
6601	**SMARCC2**	**SWI/SNF complex subunit SMARCC2 isoform a**	13	46	8	1.0	**2E-04**	1.1	**1E-05**	1.2	**2E-02**	1.0	**2E-05**	1.2	9E-01	Transcription factor activity	Nucleus	Transcription factor
10449	**ACAA2**	**3-ketoacyl-CoA thiolase, mitochondrial**	8	45	8	1.0	**3E-04**	1.3	**3E-07**	1.5	**8E-06**	**2.2**	**1E-07**	1.0	9E-01	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
23589	**CARHSP1**	**calcium-regulated heat stable protein 1**	5	34	5	1.0	**4E-03**	0.8	**2E-04**	1.2	1E-01	1.4	**1E-06**	1.0	4E-01	Calcium ion binding	Cytoplasm	Calcium binding protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
90809	**TMEM55B**	**type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase isoform 1**	3	9	3	1.0	**3E-02**	0.9	**2E-02**	1.1	9E-01	1.0	**1E-02**	1.0	1E+00	Molecular function unknown	Integral to membrane	Unclassified
64900	**LPIN3**	**phosphatidate phosphatase LPIN3**	3	8	3	1.0	1E-01	0.9	2E-01	3.0	9E-01	1.2	**5E-03**	1.1	7E-01	Molecular function unknown	Nucleus	Unclassified
51493	**C22orf28; RTCB**	**tRNA-splicing ligase RtcB homolog**	19	143	19	1.0	**9E-13**	1.0	**2E-13**	1.1	**1E-06**	1.1	**5E-12**	1.0	2E-01	#N/A	#N/A	#N/A
53905	**DUOX1**	**dual oxidase 1*gi|28872751|ref|NP_787954.1| dual oxidase 1**	12	43	12	1.0	**1E-04**	1.8	2E-01	**0.7**	**9E-06**	**0.5**	**4E-03**	0.9	2E-01	Catalytic activity	Plasma membrane	Enzyme: Peroxidase
4850	**CNOT4**	**CCR4-NOT transcription complex subunit 4 isoform f**	3	18	3	1.0	**2E-04**	0.7	**1E-05**	1.0	**3E-03**	0.7	7E-01	0.9	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
7542	**ZFPL1**	**zinc finger protein-like 1**	6	22	6	1.0	**8E-04**	1.1	**1E-04**	1.2	**2E-02**	**1.5**	**9E-04**	1.1	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
51569	**UFM1**	**ubiquitin-fold modifier 1 isoform 1**	2	11	2	1.0	**4E-02**	0.8	**2E-02**	1.0	5E-01	0.8	8E-01	1.0	8E-01	Molecular function unknown	-	Unclassified
124808	**CCDC43**	**coiled-coil domain-containing protein 43 isoform 1**	4	14	4	1.0	9E-02	1.0	5E-02	1.1	4E-01	1.0	**2E-02**	0.9	**2E-02**	Molecular function unknown	-	Unclassified
1495	**CTNNA1**	**PREDICTED: catenin alpha-1 isoform X2**	37	299	27	1.0	**2E-16**	1.0	**2E-16**	1.1	**5E-14**	0.8	**6E-04**	0.9	**8E-05**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
7533	**YWHAH**	**14-3-3 protein eta**	14	955	10	1.0	**1E-11**	0.8	**1E-10**	1.0	**7E-06**	0.9	**2E-11**	1.0	2E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6891	**TAP2**	**antigen peptide transporter 2 isoform 1**	8	25	8	1.0	**8E-04**	1.0	**1E-03**	1.0	**2E-03**	1.0	**2E-03**	1.0	4E-01	Transporter activity	Endoplasmic reticulum;Integral to membrane	Transport/cargo protein
51072	**MEMO1**	**PREDICTED: protein MEMO1 isoform X1**	8	37	8	1.0	**1E-02**	1.0	**6E-03**	0.9	1E-01	0.8	**2E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
10049	**DNAJB6**	**dnaJ homolog subfamily B member 6 isoform b**	7	44	6	1.0	**1E-02**	1.0	**6E-06**	1.0	6E-02	1.2	**2E-07**	1.3	**4E-02**	Chaperone activity	Cytoplasm;Nucleus	Chaperone
23306	**TMEM194A; NEMP1**	**transmembrane protein 194A isoform a**	3	10	3	1.0	**2E-02**	0.9	**1E-03**	1.2	7E-01	1.2	**2E-03**	1.1	3E-01	#N/A	#N/A	#N/A
5305;	**PIP4K2A**	**phosphatidylinositol 5-phosphate 4-kinase type-2 alpha**	6	12	4	1.0	6E-02	1.0	**5E-02**	1.2	7E-01	1.3	**3E-02**	1.0	3E-01	Lipid kinase activity	-	Lipid Kinase
908	**CCT6A**	**T-complex protein 1 subunit zeta isoform a**	25	242	25	1.0	**2E-16**	0.9	**2E-16**	1.0	**7E-03**	1.0	**2E-16**	1.0	5E-01	Chaperone activity	Cytoplasm	Chaperone
5887	**RAD23B**	**UV excision repair protein RAD23 homolog B isoform 1**	14	133	12	1.0	**3E-08**	0.9	**4E-11**	1.1	**4E-02**	1.0	**3E-09**	1.0	1E+00	DNA binding	Nucleus	DNA repair protein
30844	**EHD4**	**EH domain-containing protein 4**	20	127	14	1.0	**3E-08**	0.9	**4E-12**	1.1	9E-02	1.2	**6E-10**	1.0	**1E-02**	Calcium ion binding	Extracellular	Calcium binding protein
5037	**PEBP1**	**phosphatidylethanolamine-binding protein 1 preproprotein**	8	93	8	1.0	**2E-06**	1.0	**1E-11**	1.1	**8E-03**	0.9	**3E-05**	0.9	**2E-07**	Protease inhibitor activity	Cytoplasm	Protease inhibitor
7334	**UBE2N**	**ubiquitin-conjugating enzyme E2 N**	9	92	9	1.0	**9E-06**	0.8	**4E-06**	1.1	**2E-02**	0.8	**2E-05**	0.9	**9E-03**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
255520	**ELMOD2**	**PREDICTED: ELMO domain-containing protein 2 isoform X1**	8	40	8	1.0	**2E-05**	1.3	**1E-07**	1.2	**2E-05**	**1.5**	**4E-06**	1.0	5E-01	Molecular function unknown	-	Unclassified
9454	**HOMER3**	**PREDICTED: homer protein homolog 3 isoform X1**	8	32	8	1.0	**3E-05**	0.9	**3E-06**	1.1	1E-01	1.2	**3E-05**	1.0	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
8634	**RTCA**	**RNA 3'-terminal phosphate cyclase isoform a**	6	31	6	1.0	**1E-03**	0.8	**5E-04**	1.0	**2E-02**	1.0	**4E-05**	1.0	8E-01	#N/A	#N/A	#N/A
27236	**ARFIP1**	**PREDICTED: arfaptin-1 isoform X1**	10	63	9	1.0	**3E-03**	1.0	**7E-05**	1.1	**2E-03**	1.2	**2E-06**	0.9	3E-01	Regulator of G-protein signaling activity	Cytoplasm	Unclassified
85365	**ALG2**	**alpha-1,3/1,6-mannosyltransferase ALG2**	4	22	4	1.0	**5E-03**	1.0	**3E-04**	1.2	**3E-02**	1.4	**1E-03**	1.0	9E-01	Mannosyltransferase activity	Endoplasmic reticulum	Enzyme: Mannosyltransferase
5688	**PSMA7**	**proteasome subunit alpha type-7**	11	77	11	1.0	**1E-09**	0.9	**1E-10**	1.1	**3E-02**	1.1	**9E-11**	0.9	**3E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55075	**UACA**	**uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 2**	17	53	17	1.0	**1E-05**	1.1	**1E-08**	1.0	**1E-06**	1.2	**1E-09**	1.1	**1E-02**	Molecular function unknown	Nucleus	Unclassified
8904	**CPNE1**	**copine-1 isoform b**	9	49	9	1.0	**2E-04**	1.0	**6E-06**	1.0	**2E-02**	1.1	**7E-06**	0.9	3E-01	Transporter activity	Cytoplasm	Transport/cargo protein
9522	**SCAMP1**	**secretory carrier-associated membrane protein 1 isoform 1**	5	33	5	1.0	**2E-03**	1.1	**2E-04**	1.1	**7E-04**	1.1	**2E-05**	1.0	1E+00	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
27342	**RABGEF1**	**rab5 GDP/GTP exchange factor isoform b**	7	25	5	1.0	**4E-03**	0.9	**1E-03**	1.1	9E-01	0.9	**3E-02**	0.9	**1E-02**	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
91298	**C12orf29**	**uncharacterized protein C12orf29**	2	8	2	1.0	1E-01	0.9	9E-02	0.9	4E-01	0.9	4E-01	0.8	2E-01	Molecular function unknown	-	Unclassified
4627	**MYH9**	**PREDICTED: myosin-9 isoform X1**	133	2064	105	1.0	**2E-16**	0.9	**2E-16**	1.0	**1E-03**	1.0	**2E-16**	1.0	**7E-05**	Structural molecule activity	Cytoplasm	Structural protein
1937	**EEF1G**	**elongation factor 1-gamma**	25	310	25	1.0	**2E-16**	0.9	**2E-16**	0.9	**6E-05**	1.0	**2E-16**	0.9	**9E-04**	Translation regulator activity	Cytoplasm	Translation regulatory protein
5682	**PSMA1**	**proteasome subunit alpha type-1 isoform 1**	16	127	16	1.0	**1E-11**	0.9	**1E-14**	1.1	**1E-03**	1.1	**1E-13**	0.9	**4E-03**	Peptidase activity	Cytoplasm	Protease
7408	**VASP**	**vasodilator-stimulated phosphoprotein**	17	144	1	1.0	**1E-10**	0.8	**2E-11**	1.2	3E-01	1.3	**7E-11**	0.9	5E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
4676	**NAP1L4**	**nucleosome assembly protein 1-like 4**	11	79	10	1.0	**2E-08**	0.9	**3E-09**	1.0	5E-01	1.0	**5E-09**	0.9	**1E-03**	Chaperone activity	Nucleus	Chaperone
79188	**TMEM43**	**transmembrane protein 43**	13	82	13	1.0	**4E-07**	1.1	**6E-11**	1.0	**4E-08**	1.1	**1E-09**	1.0	8E-02	Molecular function unknown	Integral to membrane	Integral membrane protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6836	SURF4	surfeit locus protein 4 isoform 1	5	46	5	1.0	**3E-05**	0.9	**2E-05**	1.1	4E-01	1.3	**2E-04**	1.0	7E-01	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein
51122	COMMD2	COMM domain-containing protein 2	4	17	4	1.0	**2E-04**	0.9	**2E-03**	1.1	9E-01	1.0	**2E-04**	0.9	8E-01	Molecular function unknown	-	Unclassified
9320	TRIP12	E3 ubiquitin-protein ligase TRIP12 isoform a	16	60	16	1.0	**3E-04**	0.8	**2E-06**	1.0	**8E-03**	1.1	**1E-04**	1.0	6E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
8776	MTMR1	myotubularin-related protein 1	6	20	6	1.0	**1E-03**	1.0	**1E-03**	1.1	**4E-02**	1.1	**4E-03**	0.9	3E-01	Protein tyrosine/serine/threonine phosphatase activity;Lipid phosphatase activity	-	Lipid phosphatase;Dual specificity phosphatase
1155	TBCB	tubulin-folding cofactor B isoform 1	7	38	7	1.0	**2E-03**	0.9	**3E-03**	1.0	**2E-02**	0.8	7E-01	0.9	**4E-02**	Chaperone activity	Cytoplasm	Chaperone
10311	DSCR3	Down syndrome critical region protein 3	5	28	5	1.0	**4E-03**	1.1	**2E-03**	1.1	**3E-02**	1.1	**5E-03**	1.0	7E-01	Molecular function unknown	-	Unclassified
55831	EMC3	ER membrane protein complex subunit 3	4	10	4	1.0	**9E-03**	1.0	**6E-03**	1.1	**2E-02**	1.1	**8E-03**	0.9	4E-01	#N/A	#N/A	#N/A
598	BCL2L1	bcl-2-like protein 1 isoform 1	4	15	4	1.0	8E-01	0.9	1E-01	1.4	3E-01	**2.1**	**1E-02**	1.2	5E-02	Receptor signaling complex scaffold activity	Mitochondrial membrane	Adapter molecule
5917	RARS	arginine--tRNA ligase, cytoplasmic	32	246	32	1.0	**2E-15**	0.9	**2E-16**	1.1	**4E-03**	1.2	**2E-16**	0.9	**3E-06**	Ligase activity	Cytoplasm	Enzyme: Ligase
1687	DFNA5	non-syndromic hearing impairment protein 5 isoform a	17	119	17	1.0	**7E-11**	1.0	**2E-14**	1.1	**2E-04**	0.9	**7E-12**	0.9	5E-02	Molecular function unknown	-	Unclassified
10987	COPS5	COP9 signalosome complex subunit 5	9	70	9	1.0	**4E-06**	0.9	**2E-08**	1.1	**1E-02**	1.0	**8E-08**	0.9	6E-02	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
5584	PRKCI	protein kinase C iota type	5	24	5	1.0	**1E-04**	0.9	**3E-05**	1.0	1E-01	1.2	**2E-04**	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
5355	PLP2	proteolipid protein 2	1	12	1	1.0	**2E-04**	1.0	**4E-04**	1.0	3E-01	0.9	**1E-02**	1.1	3E-01	Ion channel activity	Endoplasmic reticulum	Ion channel
439921	MXRA7	matrix-remodeling-associated protein 7 isoform 3	3	14	1	1.0	**4E-02**	0.9	**6E-03**	1.0	4E-01	1.0	**4E-03**	0.7	8E-01	Molecular function unknown	-	Unclassified
9678	PHF14	PHD finger protein 14	1	4	1	1.0	1E-01	0.9	6E-02	1.1	7E-01	0.8	3E-01	1.0	7E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
58506	SCAF1	splicing factor, arginine/serine-rich 19	2	9	1	1.0	4E-01	0.9	2E-01	1.3	7E-01	1.0	4E-01	0.9	6E-01	RNA binding	Nucleus	RNA binding protein
23039	XPO7	exportin-7	20	122	20	1.0	**2E-12**	0.9	**5E-13**	1.2	**3E-04**	1.2	**9E-14**	0.9	**2E-03**	Transporter activity	Nucleus	Transport/cargo protein
4580	MTX1	metaxin-1 isoform 1	6	27	6	1.0	**1E-04**	1.0	**8E-06**	1.0	**7E-03**	1.1	**7E-04**	1.0	2E-01	Auxiliary transport protein activity;Transporter activity	Mitochondrion	Membrane transport protein
55572	FOXRED1	FAD-dependent oxidoreductase domain-containing protein 1	4	15	4	1.0	**2E-03**	1.2	**1E-03**	1.2	**4E-03**	1.1	**1E-03**	1.0	6E-01	Molecular function unknown	Mitochondrion	Unclassified
54832	VPS13C	vacuolar protein sorting-associated protein 13C isoform 2A	8	20	8	1.0	**5E-03**	1.1	**1E-02**	1.0	**1E-02**	0.9	**4E-02**	1.0	4E-01	Molecular function unknown	Nucleus	Unclassified
8976; 142685	WASL; ASB15	neural Wiskott-Aldrich syndrome protein	6	28	6	1.0	**1E-02**	1.0	**5E-04**	1.1	2E-01	1.3	**2E-04**	1.0	9E-01	#N/A	#N/A	#N/A
127018	LYPLAL1	lysophospholipase-like protein 1 isoform a	6	30	6	1.0	**2E-02**	1.1	**7E-03**	1.1	**4E-03**	1.1	**6E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
57506	MAVS	mitochondrial antiviral-signaling protein isoform 1	4	16	4	1.0	5E-02	1.0	**2E-02**	1.2	1E-01	1.1	**8E-03**	0.9	5E-02	Molecular function unknown	-	Unclassified
6838	SURF6	surfeit locus protein 6 isoform 1	7	25	7	1.0	7E-02	1.0	5E-01	0.7	9E-02	**0.6**	**3E-02**	1.0	5E-01	RNA binding	Nucleolus	RNA binding protein
51135	IRAK4	PREDICTED: interleukin-1 receptor-associated kinase 4 isoform X1	3	9	3	1.0	8E-02	0.8	**1E-02**	0.9	5E-01	0.8	**3E-02**	0.8	**5E-02**	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase
4710	NDUFB4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 isoform 1	2	14	2	1.0	1E-01	**0.7**	**4E-03**	1.0	**2E-02**	0.7	3E-01	1.0	6E-01	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase
23395	LARS2	PREDICTED: probable leucine--tRNA ligase, mitochondrial isoform X1	12	23	12	1.0	3E-01	1.1	**4E-03**	1.1	**2E-02**	1.2	**1E-03**	1.0	4E-01	Transferase activity	Mitochondrion	Enzyme: Transferase
10959	TMED2	transmembrane emp24 domain-containing protein 2	5	81	5	1.0	**8E-09**	1.1	**8E-09**	1.0	**3E-05**	1.3	**5E-07**	1.1	9E-02	Transporter activity	Golgi apparatus	Transport/cargo protein
5905	RANGAP1	PREDICTED: ran GTPase-activating protein 1 isoform X1	15	82	15	1.0	**2E-07**	0.8	**5E-08**	0.9	**2E-03**	1.1	**8E-09**	0.9	**4E-04**	GTPase activator activity	Cytoplasm	GTPase activating protein
6251	RSU1	ras suppressor protein 1 isoform 1	11	57	11	1.0	**8E-06**	0.9	**1E-06**	1.0	3E-01	0.8	5E-01	0.9	**3E-03**	Molecular function unknown	-	Unclassified
2040	STOM	erythrocyte band 7 integral membrane protein isoform a	9	93	9	1.0	**1E-05**	0.8	**1E-11**	1.1	**2E-02**	1.2	**7E-14**	1.0	7E-01	Channel regulator activity	Cytoplasmic vesicle	Integral membrane protein
9581	PREPL	prolyl endopeptidase-like isoform 1*gi|284172420|ref|NP_001165077.1| prolyl endopeptidase-like isoform 1*gi|70778815|ref|NP_006027.2| prolyl endopeptidase-like isoform 1	4	18	4	1.0	**2E-02**	0.7	5E-02	1.0	**1E-02**	0.9	7E-02	0.8	**2E-02**	Serine-type peptidase activity	-	Serine protease
122830	NAA30	N-alpha-acetyltransferase 30	2	8	2	1.0	**4E-02**	0.9	6E-02	1.0	9E-01	1.1	7E-02	1.1	2E-01	Transferase activity	-	Enzyme: Transferase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
388962	**BOLA3**	**bolA-like protein 3 isoform 1**	3	8	3	1.0	1E-01	0.7	9E-02	1.0	7E-01	0.7	7E-01	1.0	8E-01	Molecular function unknown	-	Unclassified
23274	**CLEC16A**	**protein CLEC16A isoform 2**	2	8	2	1.0	4E-01	0.9	1E-01	0.9	2E-01	1.1	1E-01	1.3	7E-02	Molecular function unknown	-	Unclassified
56243	**KIAA1217**	**sickle tail protein homolog isoform 1**	10	32	4	1.0	7E-01	1.1	1E-01	1.0	**3E-02**	0.8	**2E-02**	1.0	2E-01	Molecular function unknown	-	Unclassified
10575	**CCT4**	**T-complex protein 1 subunit delta isoform a**	31	353	30	1.0	**2E-16**	0.9	**2E-16**	1.0	**1E-02**	1.0	**2E-16**	1.0	4E-01	Chaperone activity	Cytoplasm	Chaperone
7416	**VDAC1**	**voltage-dependent anion-selective channel protein 1**	14	290	13	1.0	**2E-16**	1.1	**2E-16**	1.1	**7E-12**	1.3	**2E-16**	1.0	**2E-02**	Voltage-gated ion channel activity	Mitochondrion	Voltage gated channel
51143	**DYNC1LI1**	**cytoplasmic dynein 1 light intermediate chain 1**	15	109	14	1.0	**3E-09**	1.0	**3E-11**	1.1	**7E-05**	1.3	**2E-13**	1.0	5E-01	Motor activity	Cytoskeleton	Motor protein
25932	**CLIC4**	**chloride intracellular channel protein 4**	9	62	9	1.0	**2E-06**	0.8	**2E-08**	1.0	**2E-03**	1.2	**4E-10**	0.9	6E-01	Intracellular ligand-gated ion channel activity	Cytoplasm	Intracellular ligand gated channel
8575	**PRKRA**	**interferon-inducible double-stranded RNA-dependent protein kinase activator A isoform 1**	7	46	7	1.0	**2E-04**	1.3	**3E-06**	1.2	**9E-04**	1.3	**2E-05**	1.0	3E-01	RNA binding	Cytoplasm	RNA binding protein
9230	**RAB11B**	**ras-related protein Rab-11B**	13	173	2	1.0	**2E-03**	0.9	**2E-03**	1.0	4E-01	1.0	**6E-03**	0.9	6E-01	GTPase activator activity	Nucleus	GTPase activating protein
54812	**AFTPH**	**aftiphilin isoform a**	3	14	3	1.0	**4E-02**	1.0	**3E-02**	1.0	1E-01	1.0	8E-02	1.0	9E-01	Molecular function unknown	Cytoplasm	Unclassified
326625	**MMAB**	**cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial**	3	16	3	1.0	6E-02	1.1	**2E-02**	1.1	**2E-03**	1.2	**1E-02**	0.9	6E-01	Catalytic activity	Mitochondrion	Enzyme: Adenosyltransferase
1938	**EEF2**	**elongation factor 2**	49	859	48	1.0	**2E-16**	0.9	**2E-16**	0.9	**2E-02**	0.9	**2E-16**	0.9	**7E-04**	Translation regulator activity	Cytoplasm	Translation regulatory protein
821	**CANX**	**calnexin**	26	308	26	1.0	**2E-16**	1.0	**2E-16**	1.0	**5E-14**	1.1	**2E-16**	1.1	**2E-05**	Chaperone activity	Endoplasmic reticulum membrane	Chaperone
3035	**HARS**	**histidine--tRNA ligase, cytoplasmic isoform 3**	24	146	17	1.0	**9E-13**	0.9	**6E-16**	1.0	**2E-04**	0.9	**5E-09**	0.9	**3E-03**	Ligase activity	Cytoplasm	Enzyme: Ligase
11311	**VPS45**	**vacuolar protein sorting-associated protein 45 isoform 1**	14	78	14	1.0	**5E-10**	1.1	**6E-14**	1.1	**6E-10**	1.2	**4E-15**	1.0	3E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
79944	**L2HGDH**	**L-2-hydroxyglutarate dehydrogenase, mitochondrial**	8	35	8	1.0	**4E-07**	1.1	**3E-09**	1.1	**4E-05**	1.3	**1E-07**	1.0	**4E-02**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
11235	**PDCD10**	**PREDICTED: programmed cell death protein 10 isoform X1**	9	54	9	1.0	**7E-04**	0.9	**8E-06**	1.1	4E-01	1.1	**8E-04**	1.1	4E-01	Molecular function unknown	-	Unclassified
201475	**RAB12**	**ras-related protein Rab-12**	11	83	10	1.0	**3E-02**	1.1	**6E-03**	0.9	**2E-05**	1.0	**2E-02**	1.0	9E-01	GTP binding	-	G protein
50813	**COPS7A**	**COP9 signalosome complex subunit 7a*gi|255760064|ref|NP_001157565.1| COP9 signalosome complex subunit 7a*gi|255760066|ref|NP_001157566.1| COP9 signalosome complex subunit 7a*gi|7705330|ref|NP_057403.1| COP9 signalosome complex subunit 7a**	3	14	3	1.0	**4E-02**	1.0	**4E-02**	1.1	1E-01	1.0	**3E-02**	0.9	6E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
374882	**TMEM205**	**transmembrane protein 205**	3	11	3	1.0	5E-01	1.3	4E-01	1.0	**5E-02**	1.2	2E-01	1.1	8E-01	Molecular function unknown	Integral to membrane	Unclassified
2058	**EPRS**	**bifunctional glutamate/proline--tRNA ligase**	51	338	50	1.0	**2E-16**	0.9	**2E-16**	1.0	**1E-04**	1.1	**2E-16**	0.9	**2E-03**	Ligase activity	Cytoplasm	Enzyme: Ligase
7170	**TPM3**	**PREDICTED: tropomyosin alpha-3 chain isoform X3**	21	150	4	1.0	**2E-16**	1.0	**2E-16**	1.1	**2E-03**	1.2	**2E-16**	1.0	4E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein;Structural protein
3068;	**HDGF**	**hepatoma-derived growth factor isoform b**	14	59	4	1.0	**1E-11**	1.3	**8E-09**	1.3	**2E-05**	**1.6**	**3E-03**	1.0	2E-01	Growth factor activity	Nucleus	Growth factor
4301	**MLLT4**	**PREDICTED: afadin isoform X1**	34	78	2	1.0	**1E-11**	1.0	**2E-16**	1.0	**6E-12**	1.1	**2E-16**	1.0	**8E-04**	Cell adhesion molecule activity	Cytoplasm	Cell junction protein
4641	**MYO1C**	**unconventional myosin-Ic isoform b**	36	214	36	1.0	**2E-11**	0.9	**2E-16**	1.0	**6E-03**	1.1	**4E-11**	1.0	**3E-02**	Motor activity	Plasma membrane	Motor protein
65264	**UBE2Z**	**ubiquitin-conjugating enzyme E2 Z**	9	43	9	1.0	**1E-05**	0.8	**3E-06**	1.1	1E-01	0.9	**2E-03**	0.8	**1E-04**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
6305	**SBF1**	**myotubularin-related protein 5**	12	38	12	1.0	**1E-04**	1.0	**1E-06**	1.1	**3E-02**	1.0	**2E-07**	1.0	1E+00	Molecular function unknown	Cytoplasm	Unclassified
5930	**RBBP6**	**E3 ubiquitin-protein ligase RBBP6 isoform 1**	9	29	9	1.0	**5E-04**	1.1	**1E-05**	1.2	**2E-03**	**1.5**	**3E-05**	1.1	**8E-03**	Ubiquitin-specific protease activity	Nucleus;Cytoplasm	Ubiquitin proteasome system protein
11261	**CHP1**	**calcineurin B homologous protein 1**	5	30	5	1.0	**5E-04**	1.0	**3E-05**	1.0	**4E-02**	**1.5**	**8E-05**	1.0	9E-02	#N/A	#N/A	#N/A
1207	**CLNS1A**	**methylosome subunit pICln**	3	22	3	1.0	**7E-04**	0.9	**2E-04**	1.1	4E-01	1.0	**7E-03**	0.9	3E-01	Transporter activity	Plasma membrane	Transport/cargo protein
6903	**TBCC**	**tubulin-specific chaperone C**	4	14	4	1.0	**8E-04**	1.0	**4E-02**	1.0	8E-01	0.9	8E-02	0.9	5E-01	Chaperone activity	Cytoplasm	Chaperone
51571	**FAM49B**	**protein FAM49B**	13	69	13	1.0	**2E-03**	0.8	**2E-05**	1.1	2E-01	0.9	**8E-06**	0.9	3E-01	Molecular function unknown	-	Unclassified
10228	**STX6**	**syntaxin-6 isoform 1**	8	38	7	1.0	**2E-03**	1.0	**5E-04**	1.0	**1E-02**	1.2	**4E-05**	1.0	8E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
1992	**SERPINB1**	**PREDICTED: leukocyte elastase inhibitor isoform X1**	17	122	17	1.0	**3E-03**	0.8	**2E-13**	**2.0**	**6E-03**	**2.5**	**5E-16**	1.1	**3E-04**	Protease inhibitor activity	Cytoplasm	Protease inhibitor
23670	**TMEM2**	**transmembrane protein 2 isoform b**	2	5	2	1.0	**8E-03**	0.9	**2E-03**	0.9	1E+00	1.1	**2E-02**	1.0	9E-01	Molecular function unknown	-	Integral membrane protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9647	PPM1F	protein phosphatase 1F	7	30	7	1.0	**1E-02**	1.0	**5E-03**	1.1	**4E-02**	1.1	**4E-03**	1.0	4E-01	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
79888	LPCAT1	lysophosphatidylcholine acyltransferase 1	9	24	9	1.0	**4E-02**	0.9	**1E-02**	1.1	6E-01	0.9	5E-01	1.1	**1E-02**	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase
90441	ZNF622	zinc finger protein 622	6	20	6	1.0	6E-02	0.9	7E-02	1.0	5E-01	0.9	9E-02	1.0	8E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
5709	PSMD3	26S proteasome non-ATPase regulatory subunit 3	29	194	29	1.0	8E-02	1.0	**1E-02**	1.1	9E-01	1.2	**9E-03**	0.9	**2E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
7178	TPT1	translationally-controlled tumor protein isoform 1	6	96	6	1.0	**2E-08**	0.8	**4E-06**	0.9	**1E-03**	1.1	**7E-13**	1.0	3E-01	Calcium ion binding	Nucleus	Calcium binding protein
23633	KPNA6	importin subunit alpha-7	17	124	10	1.0	**2E-07**	1.0	**5E-07**	1.0	**1E-03**	1.0	**5E-06**	0.9	1E+00	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
998	CDC42	cell division control protein 42 homolog isoform 1	8	69	7	1.0	**7E-06**	0.9	**3E-06**	1.0	**4E-02**	1.0	**4E-05**	0.9	**1E-03**	GTPase activity	Cytoplasm	GTPase
8031	NCOA4	nuclear receptor coactivator 4 isoform 1	9	38	9	1.0	**1E-05**	0.9	**3E-02**	0.8	5E-01	0.9	**6E-03**	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
57674	RNF213	E3 ubiquitin-protein ligase RNF213 isoform 3	18	48	18	1.0	**4E-04**	1.0	**1E-06**	1.0	2E-01	0.9	**2E-03**	1.0	5E-01	Molecular function unknown	-	Unclassified
7322	UBE2D2	ubiquitin-conjugating enzyme E2 D2 isoform 1	3	40	2	1.0	**7E-03**	0.8	**2E-03**	1.1	**4E-02**	0.8	4E-01	0.8	**7E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
387522	TMEM189-UBE2V1	TMEM189-UBE2V1 fusion protein	8	95	3	1.0	#N/A	1.0	#N/A	1.0	#N/A	1.0	#N/A	1.1	#N/A	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
7414	VCL	vinculin isoform meta-VCL	60	463	60	1.0	**2E-16**	0.8	**2E-16**	1.0	**7E-03**	0.9	**9E-06**	0.9	**9E-05**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
8301	PICALM	phosphatidylinositol-binding clathrin assembly protein isoform 1	13	68	13	1.0	**6E-06**	0.9	**2E-06**	0.9	1E+00	1.0	**2E-05**	0.9	3E-01	Clathrin binding	Plasma membrane	Transport/cargo protein
51181	DCXR	L-xylulose reductase isoform 1	8	42	8	1.0	**2E-04**	**1.5**	**3E-04**	1.4	**6E-04**	1.2	**2E-04**	0.9	7E-02	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase
55573	CDV3	protein CDV3 homolog isoform b	7	42	4	1.0	**3E-04**	0.8	**2E-05**	0.9	7E-02	0.7	3E-01	0.9	1E-01	Molecular function unknown	Nucleus	Unclassified
3612	IMPA1	inositol monophosphatase 1 isoform 2	10	46	10	1.0	**2E-03**	0.8	**2E-03**	1.1	3E-01	0.9	**2E-06**	0.9	1E-01	Phosphoprotein phosphatase activity	Cytoplasm	Enzyme: Phosphatase
58478	ENOPH1	enolase-phosphatase E1 isoform 1	4	24	4	1.0	**4E-02**	0.9	**6E-03**	1.2	2E-01	**1.5**	**9E-04**	1.0	1E-01	Molecular function unknown	-	Unclassified
5863	RGL2	ral guanine nucleotide dissociation stimulator-like 2 isoform 1	2	6	2	1.0	2E-01	0.9	**6E-03**	1.1	9E-01	1.1	2E-01	1.0	1E+00	GTPase activity	-	GTPase
7879	RAB7A	ras-related protein Rab-7a	15	187	15	1.0	**5E-15**	0.9	**2E-16**	1.2	3E-01	1.4	**2E-16**	1.0	3E-01	GTPase activity	Endosome	GTPase
9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	16	108	16	1.0	**5E-11**	1.0	**7E-13**	1.1	**8E-08**	1.0	**4E-10**	0.9	9E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
10910	SUGT1	suppressor of G2 allele of SKP1 homolog isoform SGT1B	14	66	14	1.0	**2E-09**	0.8	**3E-08**	1.0	**2E-02**	0.8	**2E-02**	0.9	**5E-05**	Ubiquitin-specific protease activity	Nucleus	Cell cycle control protein;Ubiquitin proteasome system protein
7332	UBE2L3	ubiquitin-conjugating enzyme E2 L3 isoform 4	8	64	8	1.0	**4E-09**	0.9	**1E-10**	1.1	2E-01	1.0	**5E-08**	0.9	**6E-04**	Ubiquitin-specific protease activity;Ubiquitin binding	Cytoplasm	Ubiquitin proteasome system protein
5571	PRKAG1	5'-AMP-activated protein kinase subunit gamma-1 isoform 3	10	47	10	1.0	**3E-06**	0.9	**4E-06**	1.0	2E-01	1.0	**3E-06**	0.9	**4E-04**	Molecular function unknown	-	Regulatory/other subunit
6814	STXBP3	syntaxin-binding protein 3	14	61	14	1.0	**2E-05**	1.1	**3E-06**	1.2	**5E-05**	1.3	**3E-07**	1.0	7E-01	Transporter activity	Cytoplasmic vesicle	Transport/cargo protein
247	ALOX15B	arachidonate 15-lipoxygenase B isoform d	12	59	12	1.0	**4E-05**	1.3	**3E-08**	1.7	**3E-06**	1.4	**1E-06**	1.0	7E-01	Catalytic activity	Cytoplasm	Enzyme: Oxygenase
29880	ALG5	dolichyl-phosphate beta-glucosyltransferase isoform 1	6	27	6	1.0	**5E-05**	1.1	**2E-05**	1.0	**4E-03**	1.3	**3E-04**	1.0	5E-02	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase
10330	CNPY2	protein canopy homolog 2 isoform 1	7	34	7	1.0	**6E-04**	1.0	**6E-05**	1.1	**8E-03**	1.1	**3E-03**	1.0	6E-01	Protein binding	Integral to membrane	Integral membrane protein
143098	MPP7	PREDICTED: MAGUK p55 subfamily member 7 isoform X1	5	20	5	1.0	**6E-03**	1.3	**5E-04**	1.0	**1E-03**	0.8	**4E-02**	0.9	8E-01	Receptor signaling complex scaffold activity	-	Adapter molecule
55833	UBAP2	ubiquitin-associated protein 2 isoform 1	4	14	4	1.0	**2E-02**	0.9	**1E-02**	1.0	2E-01	0.9	6E-02	1.0	8E-01	Molecular function unknown	-	Unclassified
140735	DYNLL2	dynein light chain 2, cytoplasmic	3	32	1	1.0	**3E-02**	1.1	**9E-03**	1.3	**1E-02**	1.3	**1E-03**	1.0	8E-01	Motor activity	Cytoplasm	Motor protein
1965	EIF2S1	eukaryotic translation initiation factor 2 subunit 1	18	127	18	1.0	**4E-11**	0.9	**2E-13**	1.0	2E-01	1.0	**3E-15**	0.9	**3E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
9255	AIMP1	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 isoform b	12	64	12	1.0	**1E-07**	1.0	**1E-08**	1.1	**1E-03**	1.1	**2E-10**	0.9	1E-01	Cytokine activity	Extracellular	Cytokine
4507	MTAP	S-methyl-5'-thioadenosine phosphorylase	14	84	14	1.0	**3E-06**	0.8	**8E-07**	1.1	**6E-03**	0.9	**1E-06**	0.9	**4E-03**	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase
56954	NIT2	omega-amidase NIT2	11	63	11	1.0	**1E-05**	1.0	**3E-09**	1.2	5E-01	1.3	**4E-06**	0.9	**4E-02**	Hydrolase activity	-	Enzyme: Hydrolase
28985	MCTS1	malignant T-cell-amplified sequence 1 isoform 2	9	52	9	1.0	**3E-05**	0.9	**9E-05**	1.1	7E-01	1.1	**2E-06**	0.9	2E-01	DNA binding	Cytoplasm	Cell cycle control protein
30851	TAX1BP3	tax1-binding protein 3 isoform 1	1	31	1	1.0	**5E-05**	0.9	**5E-06**	1.0	3E-01	0.8	1E-01	0.7	**1E-05**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
10671	DCTN6	dynactin subunit 6	2	9	2	1.0	**8E-04**	1.0	**3E-03**	1.2	**5E-02**	1.1	**1E-02**	0.9	1E-01	Molecular function unknown	Mitochondrion	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
84233	**TMEM126A**	**transmembrane protein 126A isoform 1**	5	28	5	1.0	**2E-03**	1.0	**6E-04**	1.1	**3E-03**	1.3	**5E-04**	1.0	8E-02	Molecular function unknown	-	Unclassified
3476	**IGBP1**	**immunoglobulin-binding protein 1**	6	22	6	1.0	**3E-03**	0.9	**1E-03**	1.0	9E-01	1.0	**1E-02**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
54863	**TOR4A**	**torsin-4A**	4	12	4	1.0	9E-02	1.1	1E-01	1.0	7E-01	0.8	5E-01	1.0	4E-01	#N/A	#N/A	#N/A
9868	**TOMM70A; TOMM70**	**mitochondrial import receptor subunit TOM70**	24	155	24	1.0	**2E-16**	1.1	**2E-16**	1.1	**3E-14**	1.1	**2E-16**	1.0	4E-01	#N/A	#N/A	#N/A
10972	**TMED10**	**transmembrane emp24 domain-containing protein 10**	8	102	8	1.0	**5E-08**	1.1	**2E-09**	1.1	**1E-08**	1.3	**2E-08**	1.0	4E-01	Transporter activity	Integral to membrane	Integral membrane protein
1962	**EHHADH**	**peroxisomal bifunctional enzyme isoform 1**	15	60	15	1.0	**1E-07**	1.1	**3E-08**	1.1	**6E-04**	1.3	**4E-08**	1.0	5E-01	Catalytic activity	Peroxisome	Enzyme: Hydratase
9138	**ARHGEF1**	**rho guanine nucleotide exchange factor 1 isoform 1**	23	98	23	1.0	**3E-07**	0.8	**4E-09**	1.1	**1E-04**	1.2	**7E-08**	1.0	4E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
23607	**CD2AP**	**CD2-associated protein**	20	87	20	1.0	**5E-06**	0.9	**2E-07**	1.0	1E-01	1.1	**2E-09**	1.0	7E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
27183	**VPS4A**	**vacuolar protein sorting-associated protein 4A**	15	87	9	1.0	**4E-05**	0.9	**4E-05**	1.1	4E-01	1.0	**3E-05**	0.9	**4E-03**	ATPase activity	Cytoplasm	ATPase
64135	**IFIH1**	**interferon-induced helicase C domain-containing protein 1**	4	20	4	1.0	**8E-03**	0.7	3E-01	**0.7**	**6E-03**	0.7	2E-01	0.9	**4E-03**	ATPase activity	Cytoplasm	ATPase
57819	**LSM2**	**U6 snRNA-associated Sm-like protein LSm2**	3	15	3	1.0	**5E-02**	0.9	5E-02	1.1	5E-01	0.9	7E-02	0.9	8E-02	RNA binding	Cytoplasm	RNA binding protein
950	**SCARB2**	**lysosome membrane protein 2 isoform 1**	12	91	12	1.0	**2E-11**	1.1	**3E-13**	1.1	**4E-09**	1.2	**5E-12**	1.0	9E-01	Receptor activity	Plasma membrane	Cell surface receptor
515	**ATP5F1**	**ATP synthase F(0) complex subunit B1, mitochondrial**	8	72	8	1.0	**4E-07**	1.1	**3E-07**	1.1	**1E-05**	1.2	**5E-07**	1.0	1E-01	Transporter activity	Mitochondrion	Transport/cargo protein
5710	**PSMD4**	**26S proteasome non-ATPase regulatory subunit 4**	10	79	10	1.0	**2E-05**	1.0	**9E-07**	1.1	**1E-02**	1.1	**7E-07**	0.9	**2E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
7917	**BAG6**	**large proline-rich protein BAG6 isoform a**	11	55	11	1.0	**1E-04**	1.0	**4E-08**	1.0	**3E-02**	1.1	**6E-06**	1.2	1E-01	#N/A	#N/A	#N/A
58513	**EPS15L1**	**epidermal growth factor receptor substrate 15-like 1 isoform 1**	11	58	11	1.0	**2E-04**	1.1	**2E-07**	1.1	**5E-04**	1.1	**2E-06**	1.0	3E-01	Calcium ion binding	Nucleus	Calcium binding protein
51067	**YARS2**	**tyrosine--tRNA ligase, mitochondrial**	8	40	8	1.0	**4E-04**	1.0	**1E-04**	1.1	**1E-02**	1.1	**2E-04**	1.0	5E-01	Molecular function unknown	-	Unclassified
1174	**AP1S1**	**AP-1 complex subunit sigma-1A**	5	32	4	1.0	**1E-03**	1.1	**8E-05**	1.0	8E-02	0.9	**1E-03**	1.0	1E+00	Transporter activity	Golgi apparatus	Transport/cargo protein
5096	**PCCB**	**propionyl-CoA carboxylase beta chain, mitochondrial isoform 2**	6	21	6	1.0	**2E-02**	1.3	**1E-04**	1.1	**2E-03**	1.1	**2E-04**	1.1	8E-02	Ligase activity	Mitochondrion	Enzyme: Carboxylase
54471	**SMCR7L; MIEF1**	**mitochondrial dynamics protein MID51 isoform 2**	2	7	2	1.0	**5E-02**	1.2	**3E-02**	1.2	4E-01	1.2	5E-02	1.0	5E-01	#N/A	#N/A	#N/A
102157402; 6880	**AK6; TAF9**	**adenylate kinase isoenzyme 6 isoform b**	2	6	2	1.0	8E-01	1.0	6E-01	1.3	6E-01	0.8	2E-01	1.1	8E-01	#N/A	#N/A	#N/A
1654	**DDX3X**	**ATP-dependent RNA helicase DDX3X isoform 1**	36	302	35	1.0	**2E-16**	1.0	**2E-16**	1.0	**2E-08**	0.9	**2E-16**	1.0	1E-01	RNA binding	Nucleus	RNA helicase
7171	**TPM4**	**tropomyosin alpha-4 chain isoform Tpm4.2cy**	20	342	4	1.0	**2E-11**	0.7	**7E-15**	1.0	7E-01	0.9	**5E-08**	0.9	8E-02	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
10434	**LYPLA1**	**acyl-protein thioesterase 1 isoform 1**	8	52	8	1.0	**6E-08**	0.9	**5E-08**	1.2	2E-01	1.3	**8E-08**	1.0	6E-01	Phospholipase activity	Endoplasmic reticulum	Enzyme: Phospholipase
80184	**CEP290**	**centrosomal protein of 290 kDa**	3	12	2	1.0	**7E-04**	0.9	**5E-07**	1.1	5E-02	1.0	**1E-04**	1.0	6E-01	#N/A	#N/A	#N/A
5537	**PPP6C**	**serine/threonine-protein phosphatase 6 catalytic subunit isoform a**	6	32	6	1.0	**9E-04**	0.9	**5E-04**	1.0	8E-01	1.1	**1E-04**	0.9	2E-01	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase
10211	**FLOT1**	**PREDICTED: flotillin-1 isoform X1**	6	20	6	1.0	**5E-03**	1.0	**1E-03**	1.3	**2E-02**	1.4	**4E-03**	0.8	**3E-02**	Molecular function unknown	Plasma membrane	Unclassified
55336	**FBXL8**	**F-box/LRR-repeat protein 8**	1	6	1	1.0	**1E-02**	1.4	**2E-02**	1.2	**2E-03**	1.2	**1E-02**	1.0	6E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
114790	**STK11IP**	**serine/threonine-protein kinase 11-interacting protein**	6	21	6	1.0	**1E-02**	1.1	**1E-02**	1.0	**7E-03**	1.1	**1E-02**	1.0	6E-01	Molecular function unknown	Cytoplasm	Unclassified
51322	**WAC**	**WW domain-containing adapter protein with coiled-coil isoform 1**	2	7	2	1.0	**2E-02**	0.8	**1E-03**	1.1	4E-01	0.6	1E-01	0.8	1E-01	Pre-mRNA splicing factor activity	Nucleus;Cytoplasm	Unclassified
55829	**VIMP**	**selenoprotein S isoform 2**	1	6	1	1.0	**3E-02**	0.8	**2E-03**	0.9	1E-01	0.8	5E-01	1.1	**2E-02**	#N/A	#N/A	#N/A
57590	**WDFY1**	**WD repeat and FYVE domain-containing protein 1**	3	18	3	1.0	**5E-03**	1.2	**3E-03**	1.1	**1E-03**	1.1	**3E-03**	0.9	3E-01	Molecular function unknown	Endosome	Unclassified
84687	**PPP1R9B**	**neurabin-2**	7	33	7	1.0	**1E-02**	1.0	**6E-03**	1.1	1E-01	0.9	**2E-03**	1.0	2E-01	Phosphatase regulator activity	Cytoplasm	Regulatory/other subunit
5977	**DPF2**	**zinc finger protein ubi-d4**	4	18	4	1.0	**3E-02**	1.0	**8E-04**	1.0	**4E-02**	1.0	**7E-03**	0.9	5E-01	DNA binding	Nucleus	DNA binding protein
83737	**ITCH**	**PREDICTED: E3 ubiquitin-protein ligase Itchy homolog isoform X1**	4	13	4	1.0	**3E-02**	1.0	**3E-03**	1.3	1E-01	1.1	**8E-03**	1.2	1E-01	Ubiquitin-specific protease activity	Endosome	Ubiquitin proteasome system protein
26292	**MYCBP**	**C-Myc-binding protein**	3	14	3	1.0	7E-02	0.9	7E-02	1.0	6E-01	0.9	7E-02	0.9	5E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
5708	**PSMD2**	**26S proteasome non-ATPase regulatory subunit 2 isoform 1**	34	270	34	1.0	**1E-15**	0.9	**2E-16**	1.1	6E-01	1.2	**2E-16**	0.9	**1E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7965	**AIMP2**	**aminoacyl tRNA synthase complex-interacting multifunctional protein 2**	6	42	6	1.0	**7E-05**	0.9	**1E-04**	1.0	9E-01	1.1	**1E-04**	0.9	**4E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
23770	**FKBP8**	**peptidyl-prolyl cis-trans isomerase FKBP8**	8	23	8	1.0	**2E-03**	1.0	5E-02	0.9	**4E-02**	**0.6**	**4E-03**	0.9	1E-01	Receptor signaling complex scaffold activity;Protease inhibitor activity	Mitochondrion	Adapter molecule
121512	**FGD4**	**FYVE, RhoGEF and PH domain-containing protein 4 isoform 1**	6	15	6	1.0	**8E-03**	0.9	**8E-04**	1.2	3E-01	**1.5**	**3E-02**	1.0	4E-01	Guanyl-nucleotide exchange factor activity	Cytoskeleton	Guanine nucleotide exchange factor
26093	**CCDC9**	**coiled-coil domain-containing protein 9**	6	27	6	1.0	**9E-03**	0.9	**1E-03**	1.0	4E-01	1.0	**8E-04**	0.9	4E-01	Molecular function unknown	Nucleus	Unclassified
10489	**LRRC41**	**leucine-rich repeat-containing protein 41**	3	9	3	1.0	**3E-02**	1.0	**2E-02**	1.1	**4E-03**	1.4	**2E-02**	1.1	6E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
509	**ATP5C1**	**ATP synthase subunit gamma, mitochondrial isoform L (liver)**	13	99	13	1.0	**6E-11**	1.2	**5E-13**	1.1	**6E-11**	1.2	**3E-12**	1.1	5E-01	Transporter activity	Mitochondrion	Transport/cargo protein
56061	**UBFD1**	**ubiquitin domain-containing protein UBFD1**	5	26	5	1.0	**1E-05**	0.9	**2E-05**	1.0	2E-01	0.8	3E-01	0.9	**2E-03**	Molecular function unknown	-	Unclassified
50999	**TMED5**	**transmembrane emp24 domain-containing protein 5 isoform 1**	5	46	5	1.0	**3E-05**	0.9	**3E-05**	1.3	6E-02	**1.6**	**2E-06**	1.1	**3E-02**	Molecular function unknown	Membrane fraction	Unclassified
10190	**TXNDC9**	**thioredoxin domain-containing protein 9**	6	31	5	1.0	**3E-05**	**0.7**	**4E-04**	1.0	**3E-03**	0.7	1E-01	0.8	**3E-02**	Molecular function unknown	Cytoplasm	Unclassified;Cell cycle control protein
65992	**DDRGK1**	**DDRGK domain-containing protein 1**	6	41	5	1.0	**1E-03**	1.0	**9E-05**	1.0	**4E-02**	1.1	**2E-04**	1.0	1E+00	Molecular function unknown	-	Unclassified
10565	**ARFGEF1**	**brefeldin A-inhibited guanine nucleotide-exchange protein 1**	14	52	7	1.0	**2E-03**	1.0	**1E-03**	1.0	**8E-03**	1.0	**4E-04**	1.0	9E-01	Guanyl-nucleotide exchange factor activity	Golgi apparatus	Guanine nucleotide exchange factor
80005	**DOCK5**	**dedicator of cytokinesis protein 5**	11	38	11	1.0	**1E-02**	0.8	**1E-03**	0.9	3E-01	0.9	**9E-06**	1.0	6E-01	Molecular function unknown	-	Unclassified
71	**ACTG1**	**actin, cytoplasmic 2**	24	2382	8	1.0	**2E-16**	0.8	**2E-16**	1.1	**2E-06**	1.1	**2E-16**	1.0	8E-02	Structural constituent of cytoskeleton	Cytoplasm	Structural protein
10694	**CCT8**	**T-complex protein 1 subunit theta isoform 1**	33	413	33	1.0	**2E-16**	0.9	**2E-16**	1.1	**1E-04**	1.0	**2E-16**	0.9	**4E-08**	Chaperone activity	Cytoplasm	Chaperone
5110	**PCMT1**	**protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 2**	13	115	13	1.0	**9E-10**	1.0	**8E-11**	1.2	**2E-04**	1.2	**1E-11**	0.9	**1E-02**	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase
9919	**SEC16A**	**protein transport protein Sec16A isoform 1**	20	67	20	1.0	**3E-08**	1.0	**4E-10**	1.0	**2E-02**	1.1	**5E-09**	1.0	8E-01	Molecular function unknown	Endoplasmic reticulum	Unclassified
128240	**APOA1BP; NAXE**	**NAD(P)H-hydrate epimerase**	8	50	8	1.0	**1E-05**	1.1	**2E-05**	1.1	**4E-04**	1.1	**7E-06**	0.9	**2E-02**	#N/A	#N/A	#N/A
114883	**OSBPL9**	**oxysterol-binding protein-related protein 9 isoform f**	8	42	7	1.0	**3E-04**	1.0	**2E-04**	1.2	1E-01	1.3	**5E-05**	1.0	**2E-02**	Transporter activity	Cytoplasm;Nucleus	Transport/cargo protein
23446	**SLC44A1**	**choline transporter-like protein 1 isoform b**	8	45	8	1.0	**5E-04**	1.1	**7E-04**	0.9	**1E-02**	1.0	**2E-02**	1.0	4E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
57606	**SLAIN2**	**PREDICTED: SLAIN motif-containing protein 2 isoform X1**	8	18	2	1.0	**7E-04**	1.0	**4E-03**	1.0	2E-01	0.7	6E-01	1.1	**3E-03**	Molecular function unknown	-	Unclassified
22818	**COPZ1**	**coatomer subunit zeta-1 isoform 4**	3	20	3	1.0	**1E-03**	0.8	**1E-05**	1.0	**7E-03**	0.9	**4E-03**	0.9	**2E-03**	Transporter activity	Cytoplasm	Transport/cargo protein
1021	**CDK6**	**cyclin-dependent kinase 6*gi|4502741|ref|NP_001250.1| cyclin-dependent kinase 6**	5	35	4	1.0	**1E-03**	0.9	**6E-03**	0.9	4E-01	0.8	5E-01	1.0	4E-01	Protein binding	Nucleus	Cell cycle control protein
6575	**SLC20A2**	**sodium-dependent phosphate transporter 2*gi|380503862|ref|NP_001244110.1| sodium-dependent phosphate transporter 2*gi|5803173|ref|NP_006740.1| sodium-dependent phosphate transporter 2**	8	47	8	1.0	**5E-03**	0.9	**9E-07**	1.1	1E-01	**1.6**	**2E-05**	1.3	**2E-04**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
22837	**COBLL1**	**cordon-bleu protein-like 1 isoform 1**	7	23	7	1.0	**2E-02**	1.2	5E-01	0.7	**3E-03**	**0.6**	**6E-03**	0.9	5E-01	Molecular function unknown	-	Unclassified
10430	**TMEM147**	**transmembrane protein 147 isoform 1**	1	6	1	1.0	**2E-02**	1.2	5E-02	1.0	6E-02	1.3	**2E-02**	1.1	3E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
79415	**C17orf62**	**uncharacterized protein C17orf62 isoform a**	4	13	4	1.0	5E-02	1.0	**3E-03**	1.0	2E-01	1.4	**1E-03**	1.1	3E-01	Molecular function unknown	Nucleus	Unclassified
10238	**DCAF7**	**DDB1- and CUL4-associated factor 7**	3	14	3	1.0	9E-02	0.9	5E-02	1.0	4E-01	1.0	**2E-02**	0.9	3E-01	Molecular function unknown	Cytoplasm	Unclassified
231	**AKR1B1**	**aldose reductase**	13	123	12	1.0	**7E-13**	1.1	**7E-16**	1.4	**5E-13**	**1.6**	**2E-15**	1.0	**2E-02**	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
5605	**MAP2K2**	**dual specificity mitogen-activated protein kinase kinase 2**	13	86	8	1.0	**6E-08**	1.1	**5E-06**	1.0	3E-01	1.1	**4E-09**	1.1	2E-01	Protein threonine/tyrosine kinase activity	Cytoplasm	Dual specificity kinase
6611	**SMS**	**spermine synthase isoform 1**	12	57	12	1.0	**7E-08**	0.8	**1E-07**	1.0	**1E-02**	1.2	**8E-08**	1.0	1E+00	Transferase activity	-	Enzyme: Synthase
54867	**TMEM214**	**transmembrane protein 214 isoform 1**	10	56	10	1.0	**2E-04**	1.0	**6E-05**	1.2	**3E-02**	0.9	**1E-05**	1.1	**2E-02**	Molecular function unknown	-	Unclassified
55325	**UFSP2**	**ufm1-specific protease 2**	6	31	6	1.0	**5E-04**	0.9	**5E-05**	1.1	2E-01	1.1	**3E-04**	0.9	8E-02	Peptidase activity	-	Protease
9040	**UBE2M**	**NEDD8-conjugating enzyme Ubc12**	8	53	8	1.0	**6E-04**	1.0	**2E-05**	1.1	**6E-03**	1.2	**1E-06**	1.0	1E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
27248	**ERLEC1**	**endoplasmic reticulum lectin 1 isoform 1**	4	9	4	1.0	**3E-02**	1.0	1E-01	1.1	2E-01	1.2	**2E-02**	1.0	7E-01	Molecular function unknown	-	Unclassified
8454	**CUL1**	**PREDICTED: cullin-1 isoform X1**	22	92	22	1.0	**4E-13**	0.9	**6E-15**	1.1	8E-01	1.0	**1E-13**	0.9	**2E-02**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
10611	**PDLIM5**	**PDZ and LIM domain protein 5 isoform a**	20	141	20	1.0	**5E-13**	0.9	**2E-13**	0.9	2E-01	0.9	**3E-10**	0.9	**4E-04**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
4940	**OAS3**	**PREDICTED: 2'-5'-oligoadenylate synthase 3 isoform X1**	21	63	21	1.0	**2E-11**	0.8	**1E-04**	0.8	**2E-06**	**0.7**	**3E-03**	0.9	**3E-03**	Ligase activity	Cytoplasm	Enzyme: Ligase
1967	**EIF2B1**	**translation initiation factor eIF-2B subunit alpha**	9	72	9	1.0	**2E-07**	1.0	**7E-11**	1.1	**1E-07**	1.2	**4E-14**	0.9	**2E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
27335	**EIF3K**	**eukaryotic translation initiation factor 3 subunit K isoform 1**	3	38	3	1.0	**1E-05**	0.9	**2E-05**	0.9	4E-01	0.9	**5E-04**	0.9	2E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
10166	**SLC25A15**	**mitochondrial ornithine transporter 1**	2	16	2	1.0	**2E-03**	1.0	**5E-03**	1.0	5E-01	1.1	**1E-04**	1.0	8E-01	Transporter activity	Mitochondrion	Transport/cargo protein
513	**ATP5D**	**ATP synthase subunit delta, mitochondrial*gi|50345991|ref|NP_001001975.1| ATP synthase subunit delta, mitochondrial**	2	12	2	1.0	**5E-03**	1.2	**7E-03**	1.1	**6E-03**	1.2	**3E-03**	1.0	4E-01	ATPase activity	Mitochondrial membrane	ATPase
83640	**FAM103A1**	**RNMT-activating mini protein**	2	8	2	1.0	**6E-03**	0.8	**4E-03**	1.1	6E-01	0.9	6E-01	1.1	8E-01	Molecular function unknown	-	Unclassified
1716	**DGUOK**	**deoxyguanosine kinase, mitochondrial isoform a**	2	10	2	1.0	**1E-02**	1.1	**9E-03**	1.2	**3E-02**	1.3	**1E-02**	1.1	5E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
23130	**ATG2A**	**autophagy-related protein 2 homolog A**	2	8	2	1.0	**3E-02**	1.1	**5E-03**	0.9	1E-01	1.2	**6E-03**	1.1	**4E-02**	Molecular function unknown	-	Unclassified
6603	**SMARCD2**	**SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2**	3	14	3	1.0	1E-01	1.1	**6E-03**	1.0	1E-01	1.1	1E-01	1.2	**3E-02**	DNA binding	Nucleus	DNA binding protein
27243	**CHMP2A**	**charged multivesicular body protein 2a**	7	31	7	1.0	1E-01	0.9	**1E-02**	1.0	8E-01	1.0	**2E-03**	0.9	**1E-03**	Transporter activity	Cytoplasm	Transport/cargo protein
4735	**SEPT2**	**septin-2 isoform b**	15	128	15	1.0	**1E-10**	0.9	**7E-11**	1.1	**1E-02**	0.9	**6E-10**	0.9	**5E-03**	#N/A	#N/A	#N/A
824	**CAPN2**	**calpain-2 catalytic subunit isoform 1**	24	163	24	1.0	**2E-16**	0.9	**2E-16**	1.0	2E-01	1.0	**2E-16**	1.0	8E-01	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
51144	**HSD17B12**	**estradiol 17-beta-dehydrogenase 12**	13	108	13	1.0	**5E-11**	1.1	**2E-16**	1.2	**7E-10**	**1.5**	**5E-16**	1.0	**3E-02**	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
10483	**SEC23B**	**protein transport protein Sec23B isoform 1**	14	89	11	1.0	**6E-11**	0.9	**1E-13**	1.0	9E-01	0.9	**7E-09**	0.9	**6E-03**	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
6723	**SRM**	**spermidine synthase**	5	57	5	1.0	**4E-10**	0.8	**4E-11**	1.0	**4E-03**	0.9	**7E-07**	1.0	3E-01	Transferase activity;Methyltransferase activity	Cytoplasm	Enzyme: Synthase
10327	**AKR1A1**	**alcohol dehydrogenase [NADP(+)]**	18	163	17	1.0	**1E-09**	1.1	**2E-13**	1.2	**8E-16**	1.1	**8E-14**	0.9	**5E-04**	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
10901	**DHRS4**	**dehydrogenase/reductase SDR family member 4 isoform 1**	9	59	9	1.0	**7E-06**	1.1	**7E-08**	1.1	**6E-03**	1.3	**3E-07**	1.0	4E-01	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase
706	**TSPO**	**translocator protein**	2	28	2	1.0	**3E-05**	1.2	**7E-07**	1.2	**4E-05**	1.3	**9E-06**	1.0	**3E-02**	Receptor activity	Mitochondrion	Integral membrane protein
64087	**MCCC2**	**methylcrotonoyl-CoA carboxylase beta chain, mitochondrial**	13	57	13	1.0	**2E-04**	1.1	**2E-05**	1.1	**3E-05**	1.1	**1E-04**	1.0	1E-01	Ligase activity	Mitochondrion	Enzyme: Carboxylase
114131;	**UCN3**	**urocortin-3 preproprotein**	5	12	5	1.0	**3E-04**	0.9	**5E-02**	0.8	3E-01	0.6	3E-01	0.9	4E-01	Receptor binding	-	Ligand
9197	**SLC33A1**	**acetyl-coenzyme A transporter 1*gi|4757708|ref|NP_004724.1| acetyl-coenzyme A transporter 1**	4	20	4	1.0	**2E-03**	1.0	**1E-03**	1.2	1E-01	1.1	**7E-03**	1.1	**4E-02**	Transferase activity	Endoplasmic reticulum	Enzyme: Transferase
51441	**YTHDF2**	**YTH domain-containing family protein 2 isoform 1**	7	35	4	1.0	**4E-03**	0.9	**2E-03**	1.0	6E-01	0.8	5E-01	1.0	8E-01	Molecular function unknown	-	Unclassified
284361	**EMC10**	**ER membrane protein complex subunit 10 isoform 2**	2	16	2	1.0	**6E-03**	1.1	**1E-02**	1.1	**1E-02**	1.2	**5E-03**	0.9	7E-01	#N/A	#N/A	#N/A
5738	**PTGFRN**	**prostaglandin F2 receptor negative regulator**	20	108	20	1.0	**2E-12**	1.0	5E-01	0.7	**4E-03**	**0.5**	**3E-07**	0.9	**8E-03**	Protein binding	Golgi apparatus	Integral membrane protein
8943	**AP3D1**	**AP-3 complex subunit delta-1 isoform 3**	26	133	26	1.0	**2E-11**	0.9	**5E-16**	1.0	7E-01	0.9	**2E-05**	1.0	**3E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
64225	**ATL2**	**atlastin-2 isoform 2**	7	57	5	1.0	**2E-06**	1.0	**1E-08**	1.2	**9E-05**	**1.5**	**1E-05**	0.9	7E-01	Molecular function unknown	Nucleus	Unclassified
25874	**MPC2**	**mitochondrial pyruvate carrier 2*gi|7661602|ref|NP_056230.1| mitochondrial pyruvate carrier 2**	3	15	3	1.0	**1E-03**	1.1	**3E-04**	1.4	**3E-02**	**1.5**	**2E-03**	1.0	2E-01	#N/A	#N/A	#N/A
57410	**SCYL1**	**N-terminal kinase-like protein isoform A**	5	28	5	1.0	**3E-03**	0.9	**5E-04**	1.1	3E-01	1.1	**4E-04**	1.0	1E+00	Transcription regulator activity	Centrosome	Cell cycle control protein
80207	**OPA3**	**optic atrophy 3 protein isoform b**	3	10	3	1.0	**1E-02**	1.1	**8E-03**	1.1	5E-02	1.4	**5E-03**	1.1	2E-01	Molecular function unknown	Mitochondrion	Unclassified
670	**BPHL**	**valacyclovir hydrolase isoform 1**	5	23	5	1.0	1E-01	1.2	**2E-03**	1.2	5E-02	1.2	**5E-03**	1.0	8E-01	Hydrolase activity	-	Enzyme: Hydrolase
3918	**LAMC2**	**laminin subunit gamma-2 isoform a**	42	304	42	1.0	**2E-16**	0.8	**2E-16**	1.2	**1E-08**	1.3	**2E-16**	1.4	**2E-16**	Structural molecule activity	Cytoplasm	Structural protein
8662	**EIF3B**	**PREDICTED: eukaryotic translation initiation factor 3 subunit B isoform X1**	23	170	23	1.0	**6E-14**	0.8	**1E-11**	0.9	**2E-02**	0.8	1E-01	0.9	**7E-09**	Translation regulator activity	Ribosome	Translation regulatory protein
1431	**CS**	**citrate synthase, mitochondrial**	12	128	12	1.0	**1E-13**	1.1	**2E-13**	1.1	**3E-10**	1.2	**7E-15**	1.0	6E-01	Acyltransferase activity	Mitochondrial matrix	Enzyme: Acyltransferase

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
4637	**MYL6**	**myosin light polypeptide 6 isoform 2**	12	229	7	1.0	**3E-13**	0.8	**4E-13**	1.1	**2E-02**	1.0	**5E-12**	0.9	2E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
5962	**RDX**	**radixin isoform 1*gi|386781571|ref|NP_001247422.1|radixin isoform 1**	34	467	16	1.0	**1E-09**	0.9	**2E-16**	1.0	6E-01	0.9	**4E-03**	0.9	1E-01	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
285527	**FRYL**	**protein furry homolog-like**	24	101	24	1.0	**9E-08**	1.0	**2E-07**	1.0	**5E-04**	1.1	**2E-09**	1.0	9E-01	Molecular function unknown	-	Unclassified
79084	**WDR77**	**methylosome protein 50**	6	46	6	1.0	**4E-06**	0.9	**2E-08**	1.0	2E-01	1.2	**2E-08**	1.0	9E-01	Molecular function unknown	Nucleus	Unclassified
64077	**LHPP**	**phospholysine phosphohistidine inorganic pyrophosphate phosphatase isoform 1**	3	14	3	1.0	**2E-04**	1.3	**1E-03**	1.2	**2E-05**	1.0	**3E-03**	0.9	6E-02	Molecular function unknown	-	Unclassified
5217	**PFN2**	**profilin-2 isoform a**	4	21	2	1.0	**3E-04**	1.0	**3E-04**	1.3	3E-01	1.1	**8E-05**	0.9	5E-01	Structural molecule activity	Cytoplasm	Structural protein
4682	**NUBP1**	**cytosolic Fe-S cluster assembly factor NUBP1 isoform 1**	4	20	4	1.0	**4E-04**	0.8	**3E-05**	1.1	2E-01	1.3	**2E-04**	0.9	**6E-03**	DNA binding	Nucleus	DNA binding protein
26073	**POLDIP2**	**polymerase delta-interacting protein 2 isoform 1**	8	30	8	1.0	**4E-04**	1.0	**2E-05**	1.2	2E-01	1.0	**3E-04**	1.0	7E-01	Molecular function unknown	Nucleus	Unclassified
340543	**TCEAL5**	**transcription elongation factor A protein-like 5**	2	8	2	1.0	**5E-02**	1.0	8E-02	1.0	2E-01	0.8	6E-01	1.0	8E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
54914	**FOCAD**	**focadhesin**	5	10	5	1.0	#N/A	1.0	#N/A	1.0	#N/A	1.0	#N/A	1.0	#N/A	#N/A	#N/A	#N/A
55245	**UQCC; UQCC1**	**ubiquinol-cytochrome-c reductase complex assembly factor 1 isoform a**	1	12	1	1.0	3E-01	0.9	5E-02	1.1	5E-01	1.1	**3E-03**	1.1	3E-01	#N/A	#N/A	#N/A
87	**ACTN1**	**alpha-actinin-1 isoform b**	52	1096	30	1.0	**2E-16**	**0.7**	**2E-16**	1.0	**2E-16**	0.9	**2E-16**	1.0	**5E-04**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein;Structural protein
7203	**CCT3**	**T-complex protein 1 subunit gamma isoform a**	33	459	33	1.0	**2E-16**	0.9	**2E-16**	1.0	**2E-02**	1.0	**2E-16**	0.9	**2E-04**	Chaperone activity	Cytoplasm	Chaperone
3098	**HK1**	**PREDICTED: hexokinase-1 isoform X2**	42	398	37	1.0	**2E-16**	1.3	**2E-16**	1.3	**2E-16**	1.3	**2E-16**	1.0	3E-01	Catalytic activity	Cytoplasm	Enzyme: Sugar phosphotransferase
10056	**FARSB**	**phenylalanine--tRNA ligase beta subunit**	22	202	22	1.0	**4E-09**	1.0	**1E-12**	1.0	**7E-11**	1.2	**2E-14**	1.0	4E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
3927	**LASP1**	**LIM and SH3 domain protein 1 isoform a**	14	103	13	1.0	**5E-06**	0.7	**2E-06**	1.0	**6E-06**	1.0	**5E-07**	1.0	9E-01	Cytoskeletal protein binding	Focal adhesion	Cytoskeletal associated protein
5130	**PCYT1A**	**choline-phosphate cytidylyltransferase A**	11	49	11	1.0	**9E-06**	1.0	**8E-06**	1.0	**1E-02**	0.9	**5E-06**	1.0	2E-01	Nucleotidyltransferase activity	Nucleus	Enzyme: Nucleotidyltransferase
84896	**ATAD1**	**PREDICTED: ATPase family AAA domain-containing protein 1 isoform X1**	8	41	8	1.0	**2E-05**	1.0	**3E-05**	1.0	**4E-04**	0.9	1E-01	1.0	7E-01	ATPase activity	Mitochondrion;Nucleus	ATPase
25909	**AHCTF1**	**protein ELYS**	14	44	14	1.0	**8E-05**	1.1	**8E-04**	1.2	8E-02	1.1	**6E-05**	1.1	1E-01	Transcription factor activity	Nucleus	Transcription factor
4650	**MYO9B**	**unconventional myosin-IXb isoform 1**	12	42	12	1.0	**1E-03**	0.9	**5E-04**	1.1	2E-01	1.0	**6E-05**	1.0	8E-01	Motor activity	Cytoplasm	Motor protein
7110	**TMF1**	**TATA element modulatory factor**	6	18	6	1.0	**2E-03**	0.9	**3E-03**	1.0	9E-01	1.2	**2E-04**	1.1	3E-01	Transcription factor activity	Nucleus	Transcription factor
88455	**ANKRD13A**	**ankyrin repeat domain-containing protein 13A**	6	18	6	1.0	**2E-02**	0.9	**4E-02**	1.0	5E-01	1.0	**2E-03**	1.0	5E-01	Molecular function unknown	-	Unclassified
90580	**C19orf52**	**uncharacterized protein C19orf52**	4	18	4	1.0	**3E-02**	0.9	**3E-02**	1.0	2E-01	1.2	**3E-02**	0.9	2E-01	Molecular function unknown	-	Unclassified
10116	**FEM1B**	**protein fem-1 homolog B**	6	15	6	1.0	**4E-02**	1.1	6E-02	1.1	2E-01	1.0	**2E-02**	1.0	3E-01	Molecular function unknown	-	Unclassified
1175	**AP2S1**	**AP-2 complex subunit sigma isoform 3**	2	12	2	1.0	8E-02	0.9	**3E-02**	1.0	1E-01	1.0	6E-02	0.9	4E-01	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule
84617	**TUBB6**	**tubulin beta-6 chain isoform 3**	28	247	9	1.0	#N/A	1.0	#N/A	1.1	#N/A	1.2	#N/A	1.0	#N/A	#N/A	#N/A	#N/A
3852	**KRT5**	**keratin, type II cytoskeletal 5**	68	15218	37	1.0	**2E-16**	1.2	**2E-16**	0.9	**2E-16**	0.9	**1E-12**	1.2	**2E-16**	Structural molecule activity	Cytoplasm	Structural protein
3308	**HSPA4**	**heat shock 70 kDa protein 4**	48	384	47	1.0	**2E-16**	0.9	**2E-16**	1.1	4E-01	1.0	**2E-16**	0.9	**1E-09**	Chaperone activity	Golgi apparatus;Cytoplasm	Chaperone
37	**ACADVL**	**very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 3**	24	164	24	1.0	**1E-09**	1.3	**2E-12**	1.5	**2E-16**	**2.1**	**1E-14**	1.0	**2E-03**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
5604	**MAP2K1**	**dual specificity mitogen-activated protein kinase kinase 1**	15	99	10	1.0	**2E-08**	0.8	**4E-09**	1.1	**1E-03**	1.2	**1E-09**	1.0	2E-01	Protein threonine/tyrosine kinase activity	Cytoplasm	Dual specificity kinase
11112	**HIBADH**	**3-hydroxyisobutyrate dehydrogenase, mitochondrial**	6	38	6	1.0	**9E-05**	1.1	**8E-05**	1.2	**1E-06**	1.3	**1E-05**	1.0	**3E-02**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
292	**SLC25A5**	**ADP/ATP translocase 2**	18	326	5	1.0	**3E-04**	1.3	**7E-07**	1.1	**3E-07**	1.2	**2E-08**	1.0	8E-01	ATP binding	Mitochondrion	Integral membrane protein
493856	**CISD2**	**CDGSH iron-sulfur domain-containing protein 2**	6	22	6	1.0	**5E-04**	0.9	**2E-03**	1.1	2E-01	1.3	**5E-03**	1.0	4E-01	Molecular function unknown	Integral to membrane	Unclassified
55163	**PNPO**	**pyridoxine-5'-phosphate oxidase**	6	32	6	1.0	**6E-04**	1.2	**5E-04**	0.9	**3E-04**	0.8	2E-01	0.9	**1E-02**	Catalytic activity	Cytoplasm	Enzyme: Oxidase
55677	**IWS1**	**protein IWS1 homolog**	5	18	5	1.0	**1E-03**	0.9	**3E-03**	1.1	3E-01	1.0	**5E-04**	0.9	**5E-02**	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
159013	**CXorf38**	**uncharacterized protein CXorf38**	2	10	2	1.0	**4E-03**	0.8	**5E-04**	1.2	2E-01	1.1	**3E-03**	0.9	8E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
29888	**STRN4**	**striatin-4 isoform 2**	6	29	4	1.0	**1E-02**	1.0	**7E-03**	1.0	2E-01	1.0	**3E-02**	0.9	4E-01	Molecular function unknown	Cytoplasm	Unclassified
80700	**UBXN6**	**UBX domain-containing protein 6 isoform 1**	3	12	3	1.0	5E-02	1.1	6E-02	1.1	**8E-03**	1.0	**4E-02**	0.9	3E-01	Molecular function unknown	Cytoplasm;Membrane fraction	Unclassified
29062	**WDR91**	**WD repeat-containing protein 91**	2	6	2	1.0	1E-01	1.1	1E-01	1.0	4E-01	0.9	3E-01	1.1	4E-01	Molecular function unknown	-	Unclassified
51371	**POMP**	**proteasome maturation protein**	3	10	3	1.0	2E-01	0.7	**4E-02**	1.1	**3E-02**	0.7	5E-01	0.8	1E-01	Molecular function unknown	-	Unclassified
23001	**WDFY3**	**WD repeat and FYVE domain-containing protein 3**	2	8	2	1.0	2E-01	0.9	1E-01	1.1	4E-01	1.1	2E-01	0.9	3E-01	Molecular function unknown	-	Unclassified
84514	**GHDC**	**GH3 domain-containing protein isoform 3**	2	8	2	1.0	2E-01	0.8	1E-01	1.0	7E-01	1.3	1E-01	1.1	1E-01	Molecular function unknown	-	Unclassified
9601	**PDIA4**	**protein disulfide-isomerase A4**	38	363	38	1.0	**2E-16**	0.9	**2E-16**	1.1	**3E-02**	0.9	**2E-15**	1.1	**2E-07**	Chaperone activity	Endoplasmic reticulum	Chaperone

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
57470	**LRRC47**	**leucine-rich repeat-containing protein 47**	19	122	19	1.0	**3E-15**	1.0	**2E-16**	1.2	**2E-04**	1.1	**3E-16**	0.9	**2E-03**	Molecular function unknown	Cytoplasm	Unclassified
822	**CAPG**	**PREDICTED: macrophage-capping protein isoform X1**	9	115	9	1.0	**5E-10**	1.0	**2E-16**	1.3	**9E-10**	1.3	**2E-16**	0.9	**4E-02**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
308	**ANXA5**	**annexin A5**	23	305	22	1.0	**4E-09**	0.8	**3E-12**	1.2	**4E-05**	1.0	**1E-07**	1.0	3E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
5631	**PRPS1**	**ribose-phosphate pyrophosphokinase 1 isoform 1**	10	65	4	1.0	**1E-08**	0.9	**7E-09**	1.3	1E+00	0.9	**1E-07**	1.0	8E-02	Ligase activity	-	Enzyme: Ligase
1968	**EIF2S3**	**eukaryotic translation initiation factor 2 subunit 3**	19	116	19	1.0	**3E-08**	1.0	**4E-11**	1.0	2E-01	1.0	**9E-10**	1.0	2E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
5269	**SERPINB6**	**serpin B6 isoform d**	12	91	11	1.0	**8E-06**	0.9	**2E-06**	1.1	6E-01	1.3	**1E-06**	0.9	**2E-03**	Protease inhibitor activity	Cytoplasm	Protease inhibitor
5204	**PFDN5**	**prefoldin subunit 3 isoform 1**	17	54	12	1.0	**1E-05**	0.9	**7E-06**	1.1	**3E-02**	1.0	**2E-05**	0.9	8E-01	Chaperone activity	Nucleus	Chaperone
662	**BNIP1**	**vesicle transport protein SEC20 isoform BNIP1**	5	28	5	1.0	**1E-04**	1.1	**5E-06**	1.0	**2E-02**	1.1	**6E-05**	0.9	6E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6309	**SC5D; SC5DL**	**lathosterol oxidase**	2	14	2	1.0	**4E-03**	1.0	**3E-03**	1.3	6E-02	1.2	**4E-03**	1.0	9E-01	#N/A	#N/A	#N/A
8508	**NIPSNAP1**	**protein NipSnap homolog 1 isoform 1**	8	42	6	1.0	**6E-03**	1.4	**5E-03**	1.2	**6E-03**	1.4	**1E-02**	1.1	7E-02	Molecular function unknown	Mitochondrion	Unclassified
92521	**SPECC1**	**cytospin-B isoform 1**	10	32	9	1.0	1E-01	0.9	**2E-02**	1.1	8E-01	0.9	**2E-02**	1.0	9E-01	#N/A	#N/A	#N/A
11154	**AP4S1**	**AP-4 complex subunit sigma-1 isoform 2**	2	10	2	1.0	2E-01	0.8	8E-02	1.1	7E-01	1.0	1E-01	0.8	3E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
4123	**MAN2C1**	**alpha-mannosidase 2C1 isoform 2**	2	10	2	1.0	2E-01	1.0	2E-01	1.1	4E-01	1.4	**4E-02**	1.0	8E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
2617	**GARS**	**glycine--tRNA ligase**	28	207	28	1.0	**2E-16**	0.8	**2E-16**	1.0	**2E-07**	1.1	**2E-16**	1.0	8E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
11315	**PARK7**	**protein DJ-1**	13	156	13	1.0	**1E-11**	0.9	**4E-14**	1.1	8E-01	0.9	**7E-08**	1.0	2E-01	RNA binding	Cytoplasm	RNA binding protein
3093	**UBE2K**	**ubiquitin-conjugating enzyme E2 K isoform 1**	9	79	9	1.0	**8E-07**	0.9	**3E-07**	1.1	**1E-03**	0.9	**4E-07**	0.9	**7E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
2339	**FNTA**	**protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha**	6	36	6	1.0	**2E-05**	0.9	**1E-05**	1.0	3E-01	0.9	**1E-03**	0.9	**1E-02**	Transferase activity	Cytoplasm	Enzyme: Transferase
23307	**FKBP15**	**FK506-binding protein 15**	11	39	11	1.0	**2E-05**	1.0	**2E-05**	1.1	**4E-02**	1.1	**2E-05**	1.0	4E-01	Isomerase activity	Axon	Enzyme: Isomerase
29966	**STRN3**	**striatin-3 isoform 1**	9	42	7	1.0	**3E-04**	1.0	**7E-05**	1.1	1E-01	1.2	**6E-04**	1.0	**4E-02**	Calcium ion binding	Nucleus	Calcium binding protein
125963	**OR1M1**	**olfactory receptor 1M1**	1	10	1	1.0	**8E-04**	0.8	**3E-03**	1.5	**4E-03**	1.0	**2E-03**	1.0	9E-01	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor
1203	**CLN5**	**ceroid-lipofuscinosis neuronal protein 5**	5	24	5	1.0	**2E-03**	1.0	**6E-04**	1.0	2E-01	1.1	**4E-04**	1.0	2E-01	Molecular function unknown	Lysosome	Unclassified
5565	**LOC101060511; PRKAB2**	**5'-AMP-activated protein kinase subunit beta-2**	1	6	1	1.0	1E-01	0.8	8E-02	1.3	5E-01	1.3	**3E-02**	1.1	1E-01	#N/A	#N/A	#N/A
10428	**CFDP1**	**craniofacial development protein 1**	4	11	4	1.0	2E-01	0.9	**2E-02**	1.0	7E-01	0.8	4E-01	1.0	5E-01	Molecular function unknown	Cytoplasm	Unclassified
54475	**NLE1**	**notchless protein homolog 1 isoform a**	2	6	2	1.0	3E-01	1.3	7E-02	1.0	2E-01	1.3	4E-01	1.1	4E-01	Molecular function unknown	Nucleolus	Unclassified
64837	**KLC2**	**kinesin light chain 2 isoform 1**	16	72	9	1.0	**1E-05**	0.9	**2E-04**	1.1	2E-01	1.1	**5E-04**	0.9	7E-02	Motor activity	Cytoplasm	Motor protein
79751	**SLC25A22**	**PREDICTED: mitochondrial glutamate carrier 1 isoform X1**	9	40	9	1.0	**5E-05**	1.0	**4E-05**	1.1	**1E-02**	1.2	**5E-05**	1.1	**4E-03**	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
7265	**TTC1**	**tetratricopeptide repeat protein 1*gi|543173164|ref|NP_001269429.1| tetratricopeptide repeat protein 1**	9	36	9	1.0	**6E-05**	0.9	**3E-06**	1.1	4E-01	0.9	**1E-03**	1.0	9E-01	Receptor signaling complex scaffold activity	-	Adapter molecule
5566	**PRKACA**	**cAMP-dependent protein kinase catalytic subunit alpha isoform Calpha1**	14	57	14	1.0	**8E-05**	1.1	**2E-06**	1.2	**1E-06**	1.3	**4E-06**	1.0	7E-01	Protein serine/threonine kinase activity	Golgi apparatus;Nucleus;Cytoplasm	Serine/threonine kinase
57488	**ESYT2**	**extended synaptotagmin-2**	14	47	13	1.0	**2E-04**	1.0	**8E-05**	1.0	**8E-03**	1.0	**2E-06**	1.0	1E+00	Molecular function unknown	Mitochondrion	Unclassified
10067	**SCAMP3**	**secretory carrier-associated membrane protein 3 isoform 1**	8	31	8	1.0	**1E-03**	1.0	**3E-04**	1.1	**2E-02**	1.2	**7E-04**	1.1	6E-02	Auxiliary transport protein activity	Plasma membrane;Nucleus	Membrane transport protein
26993	**AKAP8L**	**A-kinase anchor protein 8-like isoform 1**	7	34	7	1.0	**7E-03**	1.0	**6E-04**	1.2	**1E-02**	1.1	**5E-04**	0.9	1E-01	DNA binding	Nucleus	DNA binding protein
84447	**SYVN1**	**E3 ubiquitin-protein ligase synoviolin isoform b**	3	11	3	1.0	**1E-02**	1.1	**9E-04**	1.2	8E-02	1.4	**7E-04**	1.0	3E-01	Ubiquitin-specific protease activity;Ligase activity	Endoplasmic reticulum	Ubiquitin proteasome system protein
10651	**MTX2**	**metaxin-2**	6	14	6	1.0	**1E-02**	1.0	**5E-03**	1.1	3E-01	1.2	**3E-02**	0.9	9E-01	Molecular function unknown	Mitochondrion	Unclassified
112724	**RDH13**	**PREDICTED: retinol dehydrogenase 13 isoform X1**	3	10	3	1.0	**4E-02**	1.0	**3E-02**	0.9	8E-02	1.0	**7E-03**	0.9	6E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
65244	**SPATS2**	**PREDICTED: spermatogenesis-associated serine-rich protein 2 isoform X1**	2	9	2	1.0	8E-02	0.9	1E-01	1.1	6E-01	1.0	2E-01	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
57553	**MICAL3**	**PREDICTED: protein-methionine sulfoxide oxidase MICAL3 isoform X1**	7	16	7	1.0	1E-01	0.9	**2E-02**	1.1	6E-01	0.8	5E-02	1.1	7E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
55193	**PBRM1**	**protein polybromo-1**	10	25	10	1.0	1E-01	1.1	1E-01	0.9	**1E-02**	0.8	6E-01	1.0	8E-01	Chromatin binding	Nucleus	Regulatory/other subunit
5687	**PSMA6**	**proteasome subunit alpha type-6 isoform a**	13	152	13	1.0	**2E-15**	1.0	**2E-16**	1.1	**1E-03**	1.1	**2E-16**	0.9	**2E-04**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10419	**PRMT5**	**protein arginine N-methyltransferase 5 isoform a**	18	99	18	1.0	**2E-11**	0.9	**4E-12**	1.0	3E-01	1.1	**2E-12**	1.0	6E-01	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6730	SRP68	signal recognition particle subunit SRP68 isoform 1	24	145	24	1.0	**4E-11**	1.0	**7E-14**	1.1	**8E-04**	1.2	**2E-13**	1.0	2E-01	RNA binding	Nucleolus	RNA binding protein
26015	RPAP1	RNA polymerase II-associated protein 1	4	11	4	1.0	**5E-02**	0.8	**4E-02**	1.1	3E-01	0.8	1E-01	1.0	9E-01	Molecular function unknown	-	Unclassified
11070	TMEM115	transmembrane protein 115	1	6	1	1.0	8E-02	1.0	7E-02	1.0	3E-01	1.3	9E-02	1.0	5E-01	Molecular function unknown	Plasma membrane	Unclassified
9092	SART1	U4/U6.U5 tri-snRNP-associated protein 1	9	28	9	1.0	2E-01	1.0	6E-02	1.1	**3E-02**	0.9	**2E-03**	0.9	4E-01	Molecular function unknown	Nucleus	Unclassified
4670	HNRNPM	heterogeneous nuclear ribonucleoprotein M isoform a	40	313	5	1.0	**2E-16**	1.0	**2E-16**	1.0	**2E-07**	1.0	**2E-16**	1.2	**9E-03**	Ribonucleoprotein	Nucleolus;Nucleus	Ribonucleoprotein
5530	PPP3CA	serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 2	12	79	7	1.0	**5E-08**	0.9	**3E-08**	1.2	9E-02	1.0	**3E-06**	1.0	1E+00	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
1376	CPT2	carnitine O-palmitoyltransferase 2, mitochondrial	20	85	20	1.0	**8E-07**	1.3	**3E-08**	1.1	**1E-09**	1.3	**2E-08**	1.0	4E-01	Palmitoyltransferase activity	Mitochondrion	Enzyme: Palmitoyltransferase
23386	NUDCD3	nudC domain-containing protein 3	9	52	9	1.0	**4E-06**	0.9	**1E-06**	1.1	1E-01	**0.6**	**3E-04**	0.9	**3E-02**	Molecular function unknown	-	Unclassified
26273	FBXO3	F-box only protein 3 isoform 1	5	10	5	1.0	**4E-03**	1.0	**4E-03**	1.0	3E-01	1.1	**2E-02**	0.9	9E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
97	ACYP1	acylphosphatase-1 isoform c	2	12	2	1.0	**6E-03**	0.9	**3E-04**	1.3	7E-01	1.0	**2E-04**	0.9	8E-02	Hydrolase activity	Cytoplasm	Enzyme: Phosphatase
9821	RB1CC1	RB1-inducible coiled-coil protein 1 isoform 1	5	9	5	1.0	7E-02	1.1	6E-02	1.0	7E-02	**1.5**	**1E-02**	1.3	6E-02	Transcription factor activity	Nucleus	Transcription factor
54939	COMMD4	COMM domain-containing protein 4 isoform 1	2	12	2	1.0	1E-01	0.9	**4E-02**	0.9	7E-01	0.8	7E-02	1.0	5E-01	Molecular function unknown	-	Unclassified
10574	CCT7	T-complex protein 1 subunit eta isoform a	29	298	29	1.0	**2E-16**	0.9	**2E-16**	1.1	**3E-05**	1.1	**2E-16**	0.9	**1E-10**	Chaperone activity	Cytoplasm	Chaperone
56005	C19orf10; MYDGF	UPF0556 protein C19orf10	5	41	5	1.0	**2E-09**	0.9	**3E-08**	1.2	1E+00	1.1	**9E-06**	1.1	**5E-03**	#N/A	#N/A	#N/A
7336	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	7	91	2	1.0	**2E-09**	0.8	**3E-11**	1.0	2E-01	0.9	**3E-10**	0.9	**3E-03**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
8665	EIF3F	eukaryotic translation initiation factor 3 subunit F	11	83	11	1.0	**9E-08**	0.9	**3E-09**	1.0	1E+00	0.9	**4E-09**	0.9	7E-02	Translation regulator activity	Cytoplasm	Translation regulatory protein
2764	GMFB	glia maturation factor beta	4	26	4	1.0	**4E-05**	1.0	**3E-04**	1.2	**1E-02**	1.0	**3E-05**	1.0	4E-01	Growth factor activity	Cytoplasm	Growth factor
84962	AJUBA	LIM domain-containing protein ajuba isoform 1	7	27	7	1.0	**6E-05**	0.8	**1E-04**	1.0	2E-01	0.9	1E-01	1.0	9E-01	#N/A	#N/A	#N/A
5162	PDHB	pyruvate dehydrogenase E1 component subunit beta, mitochondrial isoform 1	12	81	12	1.0	**2E-04**	1.1	**3E-06**	1.2	**5E-06**	1.4	**4E-07**	1.1	**1E-02**	Carboxy-lyase activity	Mitochondrion	Enzyme: Decarboxylase
5791	PTPRE	receptor-type tyrosine-protein phosphatase epsilon isoform 2	8	31	8	1.0	**2E-04**	0.9	**1E-04**	1.2	4E-01	1.1	**1E-04**	1.1	**2E-03**	Receptor signaling protein tyrosine phosphatase activity	Plasma membrane	Receptor tyrosine phosphatase
389541	LAMTOR4	ragulator complex protein LAMTOR4	1	12	1	1.0	**2E-03**	1.1	**2E-04**	1.2	**6E-03**	1.1	**1E-04**	0.9	4E-01	#N/A	#N/A	#N/A
8463	TEAD2	transcriptional enhancer factor TEF-4 isoform 2	1	6	1	1.0	**3E-03**	0.9	**1E-03**	1.2	9E-01	1.1	**4E-02**	1.1	1E-01	Transcription factor activity	Nucleus	Transcription factor
6206	RPS12	40S ribosomal protein S12	7	97	7	1.0	**1E-02**	0.9	4E-01	0.8	4E-01	0.6	9E-02	0.9	**3E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
79672	FN3KRP	ketosamine-3-kinase	6	21	6	1.0	**2E-02**	0.9	**3E-04**	1.0	9E-01	1.0	**1E-02**	0.9	**3E-02**	Catalytic activity	-	Enzyme: Phosphotransferase
81490	PTDSS2	phosphatidylserine synthase 2	3	16	3	1.0	**5E-02**	1.0	**3E-02**	1.0	3E-01	1.1	**6E-03**	1.0	8E-01	Transferase activity	Mitochondrion	Enzyme: Synthase
23038	WDTC1	PREDICTED: WD and tetratricopeptide repeats protein 1 isoform X1	2	6	2	1.0	2E-01	0.9	6E-02	1.2	3E-01	1.1	4E-01	0.8	**6E-03**	Molecular function unknown	-	Unclassified
1.01E+08	CORO7-PAM16	CORO7-PAM16 protein	7	41	7	1.0	#N/A	1.0	#N/A	1.1	#N/A	1.1	#N/A	1.0	#N/A	#N/A	#N/A	#N/A
5859	QARS	glutamine--tRNA ligase isoform a	33	189	32	1.0	**2E-09**	1.0	**2E-11**	1.1	**1E-05**	1.3	**3E-11**	0.9	2E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
7419	VDAC3	voltage-dependent anion-selective channel protein 3 isoform 2	8	142	7	1.0	**3E-09**	1.1	**1E-12**	1.1	**1E-08**	1.4	**1E-11**	1.0	1E-01	Voltage-gated ion channel activity	Mitochondrion	Voltage gated channel
3881	KRT31	keratin, type I cuticular Ha1	13	626	4	1.0	8E-02	0.8	**2E-02**	0.9	4E-01	**2.9**	**4E-09**	**1.7**	**4E-05**	Structural molecule activity	-	Structural protein
115209	OMA1	metalloendopeptidase OMA1, mitochondrial	3	14	3	1.0	1E-01	1.0	**3E-02**	1.0	3E-01	1.0	**2E-05**	1.0	3E-01	Metallopeptidase activity	Endoplasmic reticulum	Metallo protease
85865	GTPBP10	GTP-binding protein 10 isoform 2	4	11	4	1.0	7E-01	1.0	9E-01	1.0	9E-01	0.9	1E+00	1.1	2E-01	RNA binding	Nucleus	RNA binding protein
5717	PSMD11	26S proteasome non-ATPase regulatory subunit 11	22	152	22	1.0	**1E-12**	1.0	**2E-15**	1.1	**2E-05**	1.3	**5E-16**	0.9	**7E-05**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
6731	SRP72	signal recognition particle subunit SRP72 isoform 1	23	104	23	1.0	**3E-09**	1.0	**3E-12**	1.1	**2E-05**	1.2	**6E-10**	1.0	1E-01	RNA binding	Nucleolus	RNA binding protein
23616	SH3BP1	SH3 domain-binding protein 1	13	87	13	1.0	**5E-09**	1.0	**9E-09**	1.1	**2E-05**	1.1	**1E-04**	0.9	9E-02	GTPase activator activity	-	GTPase activating protein
826	CAPNS1	PREDICTED: calpain small subunit 1 isoform X1	7	47	5	1.0	**2E-07**	0.9	**1E-08**	1.1	**5E-03**	1.1	**6E-09**	0.9	5E-01	Peptide binding	Cytoplasm	Regulatory/other subunit
51138	COPS4	COP9 signalosome complex subunit 4 isoform 1	17	89	17	1.0	**2E-05**	1.0	**6E-07**	1.2	**1E-02**	1.1	**2E-04**	1.0	1E-01	Molecular function unknown	-	Unclassified
8892	EIF2B2	translation initiation factor eIF-2B subunit beta	8	48	8	1.0	**2E-05**	1.0	**3E-06**	1.2	**2E-03**	1.3	**5E-06**	0.9	1E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3420	**IDH3B**	**isocitrate dehydrogenase [NAD] subunit beta, mitochondrial isoform a**	11	54	11	1.0	**8E-05**	1.2	**8E-05**	1.1	**5E-05**	1.3	**1E-05**	1.1	**3E-04**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
152579	**SCFD2**	**sec1 family domain-containing protein 2**	7	25	7	1.0	**3E-03**	1.0	**6E-04**	0.9	8E-02	0.9	**1E-03**	1.0	6E-01	Transporter activity	-	Transport/cargo protein
84656	**GLYR1**	**putative oxidoreductase GLYR1**	6	16	6	1.0	**7E-03**	1.0	**6E-03**	1.2	2E-01	1.3	**1E-03**	1.1	**3E-02**	Catalytic activity	Nucleus	Enzyme: Dehydrogenase
10555	**AGPAT2**	**1-acyl-sn-glycerol-3-phosphate acyltransferase beta isoform a**	2	11	2	1.0	**9E-03**	1.1	**2E-02**	1.3	**7E-03**	**1.5**	**2E-02**	1.1	6E-02	Acyltransferase activity	-	Enzyme: Acyltransferase
55037	**PTCD3**	**pentatricopeptide repeat domain-containing protein 3, mitochondrial**	10	60	10	1.0	**5E-02**	1.4	**2E-03**	1.0	**3E-03**	1.1	**9E-06**	1.1	4E-01	Protein binding	-	Unclassified
83657	**DYNLRB2**	**dynein light chain roadblock-type 2 isoform 2**	1	6	1	1.0	6E-02	1.0	**3E-02**	1.0	2E-01	0.9	1E-01	0.9	3E-01	Molecular function unknown	-	Unclassified
54951	**COMMD8**	**COMM domain-containing protein 8**	3	8	3	1.0	9E-02	0.8	5E-02	1.0	5E-01	0.9	**3E-02**	0.9	3E-01	Molecular function unknown	-	Unclassified
22950	**SLC4A1AP**	**kanadaptin**	5	10	5	1.0	**3E-02**	0.8	**2E-02**	1.2	6E-01	1.0	**2E-02**	1.0	1E+00	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
5718	**PSMD12**	**26S proteasome non-ATPase regulatory subunit 12 isoform 1**	17	158	17	1.0	**2E-11**	1.0	**1E-13**	1.1	**9E-06**	1.3	**4E-13**	1.0	9E-02	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10617	**STAMBP**	**PREDICTED: STAM-binding protein isoform X1**	11	55	11	1.0	**3E-08**	1.0	**6E-09**	1.0	**6E-05**	1.0	**2E-08**	0.9	2E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
396	**ARHGDIA**	**rho GDP-dissociation inhibitor 1 isoform e**	9	89	9	1.0	**1E-06**	0.9	**4E-07**	1.1	2E-01	1.0	**7E-08**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
26275	**HIBCH**	**3-hydroxyisobutyryl-CoA hydrolase, mitochondrial isoform 1**	12	53	12	1.0	**1E-06**	1.2	**3E-06**	1.1	**7E-07**	1.1	**3E-07**	1.0	2E-01	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase
553115	**PEF1**	**peflin**	6	38	6	1.0	**4E-05**	1.0	**2E-04**	1.1	**3E-02**	1.2	**5E-04**	1.0	9E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
79587	**CARS2**	**probable cysteine--tRNA ligase, mitochondrial**	8	29	8	1.0	**2E-04**	1.0	**1E-03**	1.0	1E-01	1.0	**7E-05**	1.0	2E-01	Ligase activity	Mitochondrion	Enzyme: Ligase
51084	**CRYL1**	**lambda-crystallin homolog**	4	22	4	1.0	**4E-04**	1.1	**3E-03**	1.3	**5E-03**	1.4	**2E-03**	0.9	**2E-02**	Oxidoreductase activity	-	Enzyme: Oxidoreductase
9819	**TSC22D2**	**TSC22 domain family protein 2 isoform 1**	5	23	5	1.0	**3E-03**	0.8	**8E-04**	1.2	5E-01	1.4	**4E-05**	0.9	9E-01	Molecular function unknown	-	Unclassified
6231; 101929876; 728937	**RPS26; LOC101929876; RPS26P25**	**PREDICTED: 40S ribosomal protein S26**	4	49	4	1.0	**2E-02**	0.9	**1E-09**	1.1	6E-02	0.9	**2E-04**	0.8	9E-02	#N/A	#N/A	#N/A
79778	**MICALL2**	**MICAL-like protein 2**	6	18	6	1.0	**3E-02**	1.3	**1E-02**	1.2	**4E-02**	1.2	**1E-02**	1.0	6E-01	Molecular function unknown	-	Unclassified
6645	**SNTB2**	**beta-2-syntrophin**	10	36	10	1.0	5E-02	1.0	**1E-02**	1.0	**6E-03**	0.8	3E-01	1.0	9E-01	Receptor signaling complex scaffold activity	Cytoplasm;Nucleus	Adapter molecule
4000	**LMNA**	**lamin isoform C**	45	986	1	1.0	**2E-16**	1.0	**2E-16**	1.2	**2E-16**	**1.5**	**2E-16**	1.1	**2E-03**	Structural molecule activity	Nucleus;Cytoplasm	Structural protein
1314	**COPA**	**coatomer subunit alpha isoform 2**	54	379	54	1.0	**2E-16**	0.9	**2E-16**	1.1	**2E-02**	1.0	**2E-16**	1.0	2E-01	Transporter activity	Cytoplasm	Transport/cargo protein
5690	**PSMB2**	**proteasome subunit beta type-2 isoform 1**	10	80	9	1.0	**2E-05**	0.9	**4E-07**	1.2	4E-01	1.1	**5E-07**	1.0	1E+00	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
4043	**LRPAP1**	**alpha-2-macroglobulin receptor-associated protein**	16	72	16	1.0	**4E-05**	1.0	**1E-05**	1.4	**4E-04**	1.2	**2E-06**	0.9	**9E-04**	Chaperone activity	Endoplasmic reticulum	Chaperone
23325	**KIAA1033**	**WASH complex subunit 7 isoform 1**	15	43	15	1.0	**2E-04**	0.9	**3E-04**	1.1	8E-02	1.0	**2E-04**	1.0	9E-01	Molecular function unknown	-	Unclassified
93343	**FAM125A; MVB12A**	**multivesicular body subunit 12A isoform 1**	1	6	1	1.0	**4E-02**	1.0	**3E-02**	1.2	1E-01	1.4	**3E-02**	0.9	3E-01	#N/A	#N/A	#N/A
114971	**PTPMT1**	**phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 isoform 1**	3	11	3	1.0	7E-02	1.0	**5E-02**	1.5	2E-01	**1.8**	**4E-02**	1.0	5E-01	Protein tyrosine/serine/threonine phosphatase activity	-	Dual specificity phosphatase
57448	**BIRC6**	**baculoviral IAP repeat-containing protein 6**	3	6	3	1.0	2E-01	1.1	**2E-02**	1.1	1E-01	1.0	**2E-02**	0.8	4E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6233	**RPS27A**	**ubiquitin-40S ribosomal protein S27a**	12	358	12	1.0	**4E-16**	0.9	**2E-16**	1.1	2E-01	0.9	**3E-07**	1.0	**4E-04**	Ubiquitin-specific protease activity	Ribosome	Ubiquitin proteasome system protein
4942	**OAT**	**PREDICTED: ornithine aminotransferase, mitochondrial isoform X1**	13	148	13	1.0	**1E-11**	0.9	**6E-13**	1.3	9E-02	1.0	**1E-15**	1.1	**2E-08**	Transaminase activity	Mitochondrion	Enzyme: Aminotransferase
5781	**PTPN11**	**tyrosine-protein phosphatase non-receptor type 11 isoform 1**	19	130	18	1.0	**1E-07**	1.0	**5E-08**	1.1	**4E-03**	1.0	**3E-08**	1.0	1E-01	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase
85021	**REPS1**	**ralBP1-associated Eps domain-containing protein 1 isoform c**	11	38	11	1.0	**8E-04**	1.0	**3E-05**	1.1	**5E-03**	1.4	**1E-05**	1.0	9E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
6427	**SRSF2**	**serine/arginine-rich splicing factor 2**	5	26	5	1.0	**1E-02**	1.0	**2E-03**	1.0	**7E-03**	1.0	**2E-04**	1.1	**4E-02**	#N/A	#N/A	#N/A
79139	**DERL1**	**derlin-1 isoform a**	5	15	5	1.0	**1E-02**	0.9	**5E-03**	1.2	6E-01	**1.5**	**8E-03**	1.1	**4E-02**	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
23198	**PSME4**	**proteasome activator complex subunit 4**	6	19	6	1.0	**2E-02**	1.0	**8E-03**	1.0	2E-01	1.0	**3E-03**	1.0	1E+00	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
91869	**RFT1**	**protein RFT1 homolog**	4	17	4	1.0	**3E-02**	0.9	**3E-02**	1.0	4E-01	1.2	**2E-02**	1.0	4E-01	Molecular function unknown	-	Integral membrane protein
121260	**SLC15A4**	**solute carrier family 15 member 4**	2	10	2	1.0	8E-02	1.0	**3E-02**	1.1	4E-01	1.2	7E-02	1.1	3E-01	Auxiliary transport protein activity	Integral to membrane	Membrane transport protein
9276	**COPB2**	**coatomer subunit beta'**	34	211	34	1.0	**2E-16**	0.8	**2E-16**	1.0	**2E-06**	1.0	**2E-16**	0.9	**2E-03**	Transporter activity	Cytoplasm	Transport/cargo protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
1615	**DARS**	**aspartate--tRNA ligase, cytoplasmic isoform 1**	31	239	31	1.0	**1E-14**	0.9	**2E-13**	1.1	**6E-03**	1.2	**3E-16**	0.9	**2E-02**	ATPase activity	Cytoplasm	ATPase
5562	**PRKAA1**	**5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform 2**	11	47	10	1.0	**7E-09**	1.0	**2E-09**	1.1	**4E-02**	1.1	**1E-08**	1.0	9E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
5936	**RBM4**	**RNA-binding protein 4 isoform 1**	11	54	11	1.0	**5E-06**	0.9	**3E-07**	1.0	8E-01	0.8	**2E-03**	0.8	**4E-05**	RNA binding	Nucleus	RNA binding protein
261726	**TIPRL**	**TIP41-like protein isoform 1**	10	55	10	1.0	**8E-06**	0.8	**4E-04**	1.1	2E-01	0.9	9E-01	0.9	**4E-03**	Molecular function unknown	-	Unclassified
66036	**MTMR9**	**myotubularin-related protein 9**	9	42	9	1.0	**2E-04**	1.0	**1E-04**	1.2	**4E-02**	1.1	**6E-03**	0.9	**7E-03**	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase
23786	**BCL2L13**	**bcl-2-like protein 13 isoform b**	10	44	10	1.0	**2E-03**	1.0	**6E-04**	1.0	1E-01	0.9	**2E-05**	1.0	9E-01	Molecular function unknown	Mitochondrion	Integral membrane protein
1121	**CHM**	**rab proteins geranylgeranyltransferase component A 1 isoform a**	2	10	2	1.0	**4E-03**	0.7	**3E-03**	0.9	3E-01	0.8	9E-01	1.0	8E-01	Transaminase activity	Cytoplasm	Enzyme: Prenyltransferase
2954	**GSTZ1**	**maleylacetoacetate isomerase isoform 1**	3	18	3	1.0	**5E-03**	1.2	**7E-04**	1.1	**5E-03**	1.2	**8E-04**	0.9	**1E-02**	Glutathione transferase activity	-	Enzyme: Glutathione transferase
4893	**NRAS**	**GTPase NRas**	6	33	1	1.0	**1E-02**	1.0	**1E-02**	1.1	5E-01	1.1	**7E-05**	1.2	5E-01	GTPase activity	Plasma membrane	GTPase
5335	**PLCG1**	**1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 isoform a**	7	30	7	1.0	**2E-02**	0.9	**1E-02**	0.9	3E-01	0.8	2E-01	0.9	2E-01	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase
55669	**MFN1**	**mitofusin-1**	5	16	4	1.0	**3E-02**	1.0	**6E-03**	1.2	1E-01	0.9	7E-02	0.9	6E-01	GTPase activity	Mitochondrion	GTPase
169714	**QSOX2**	**sulfhydryl oxidase 2**	5	14	5	1.0	**5E-02**	1.0	**2E-02**	1.2	1E-01	1.2	**3E-02**	1.2	3E-01	Molecular function unknown	Plasma membrane	Unclassified
2909	**ARHGAP35**	**rho GTPase-activating protein 35**	5	16	5	1.0	7E-02	0.9	**2E-02**	0.9	2E-01	0.8	7E-01	0.9	9E-02	#N/A	#N/A	#N/A
23376	**UFL1**	**E3 UFM1-protein ligase 1**	22	95	21	1.0	**3E-10**	1.1	**3E-14**	1.0	**3E-06**	1.1	**9E-12**	1.1	**3E-02**	#N/A	#N/A	#N/A
8907	**AP1M1**	**AP-1 complex subunit mu-1 isoform 1**	18	107	14	1.0	**1E-09**	1.1	**3E-13**	1.2	**1E-05**	1.3	**1E-11**	1.0	6E-01	Receptor signaling complex scaffold activity	Golgi apparatus	Adapter molecule
51068	**NMD3**	**60S ribosomal export protein NMD3**	6	36	6	1.0	**1E-04**	0.9	**7E-06**	1.0	**3E-02**	0.7	1E-01	0.9	**1E-02**	Molecular function unknown	Nucleolus	Unclassified
1975	**EIF4B**	**eukaryotic translation initiation factor 4B isoform 1**	20	118	20	1.0	**7E-04**	0.8	**6E-04**	0.9	**2E-02**	0.7	2E-01	0.8	**2E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
27109	**ATP5S**	**ATP synthase subunit s, mitochondrial isoform a**	2	9	2	1.0	**3E-02**	1.2	5E-02	1.1	7E-02	1.4	**3E-02**	1.1	7E-02	Molecular function unknown	Mitochondrion	Unclassified
7867	**MAPKAPK3**	**MAP kinase-activated protein kinase 3**	9	44	5	1.0	2E-01	0.9	**9E-03**	1.1	3E-01	0.9	4E-01	0.9	3E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
4259	**MGST3**	**microsomal glutathione S-transferase 3**	2	14	2	1.0	4E-01	1.1	2E-01	1.0	**9E-03**	1.1	8E-02	1.2	4E-01	Glutathione transferase activity	Endoplasmic reticulum	Enzyme: Glutathione transferase
5701	**PSMC2**	**26S protease regulatory subunit 7 isoform 1**	26	220	26	1.0	**2E-16**	0.9	**2E-16**	1.1	**2E-02**	1.2	**2E-16**	1.0	**3E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
4628	**MYH10**	**PREDICTED: myosin-10 isoform X1**	69	561	44	1.0	**2E-13**	1.1	**2E-16**	1.1	**3E-14**	1.2	**2E-16**	1.0	3E-01	Structural molecule activity	Cytoplasm	Structural protein
80273	**GRPEL1**	**grpE protein homolog 1, mitochondrial**	12	97	11	1.0	**1E-09**	1.1	**2E-13**	1.3	**5E-09**	**1.5**	**5E-13**	1.1	**2E-05**	Chaperone activity	Mitochondrion	Chaperone
79735	**TBC1D17**	**TBC1 domain family member 17 isoform 1**	5	20	4	1.0	**2E-04**	1.1	**1E-03**	0.9	**1E-03**	0.9	**3E-04**	1.0	5E-01	GTPase activator activity	-	GTPase activating protein
55707	**NECAP2**	**adaptin ear-binding coat-associated protein 2 isoform 2**	4	11	4	1.0	1E-01	1.0	1E-01	1.2	4E-01	1.0	1E-01	1.0	1E+00	Molecular function unknown	-	Unclassified
22908	**SACM1L**	**phosphatidylinositide phosphatase SAC1**	15	68	15	1.0	**5E-06**	1.0	**6E-07**	1.1	**7E-05**	1.3	**3E-05**	1.0	**8E-03**	Lipid phosphatase activity	Endoplasmic reticulum	Lipid phosphatase
79956	**ERMP1**	**endoplasmic reticulum metallopeptidase 1**	13	58	13	1.0	**7E-06**	1.1	**1E-07**	1.1	**2E-06**	1.1	**3E-08**	1.0	9E-02	Molecular function unknown	Integral to membrane	Integral membrane protein
134266	**GRPEL2**	**grpE protein homolog 2, mitochondrial**	4	13	4	1.0	**1E-02**	1.3	**8E-03**	1.4	**7E-03**	1.2	**8E-03**	1.1	6E-02	Chaperone activity	Mitochondrion	Chaperone
1861	**TOR1A**	**torsin-1A**	5	21	5	1.0	**4E-02**	0.9	**8E-03**	1.1	2E-01	1.1	**3E-02**	1.0	5E-01	Chaperone activity	Endoplasmic reticulum	Chaperone
7171	**TPM4**	**tropomyosin alpha-4 chain isoform Tpm4.1cy**	25	353	5	1.0	**2E-11**	1.1	**7E-15**	1.1	7E-01	1.3	**5E-08**	1.1	8E-02	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
2801	**GOLGA2**	**Golgin subfamily A member 2**	16	60	16	1.0	**1E-06**	1.1	**2E-07**	1.1	**1E-04**	1.4	**6E-09**	1.0	7E-02	Structural molecule activity	Golgi apparatus;Golgi membrane	Structural protein
26043	**UBXN7**	**UBX domain-containing protein 7**	12	50	11	1.0	**3E-06**	1.1	**4E-06**	1.3	**1E-05**	1.3	**8E-08**	1.0	6E-01	Molecular function unknown	-	Unclassified
3040; 3039	**HBA2; HBA1**	**hemoglobin subunit alpha**	4	54	4	1.0	**8E-06**	1.2	**4E-10**	2.3	**8E-09**	**3.2**	**2E-11**	1.0	4E-01	#N/A	#N/A	#N/A
5832	**ALDH18A1**	**PREDICTED: delta-1-pyrroline-5-carboxylate synthase isoform X1**	21	136	21	1.0	**8E-06**	1.0	**8E-12**	1.0	**1E-04**	0.8	**1E-02**	1.0	1E-01	Ligase activity	Mitochondrion	Enzyme: Phosphotransferase;Enzyme: Ligase;Enzyme: Reductase
375790	**AGRN**	**agrin**	12	48	12	1.0	**2E-04**	0.7	**8E-06**	0.9	**1E-02**	0.9	**1E-03**	1.1	**4E-03**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
196527	**ANO6**	**anoctamin-6 isoform d**	9	34	9	1.0	**8E-04**	1.0	**5E-05**	1.0	**1E-02**	0.9	**9E-04**	1.1	**2E-02**	Molecular function unknown	Integral to membrane	Integral membrane protein
10920	**COPS8**	**COP9 signalosome complex subunit 8 isoform 1**	5	29	5	1.0	**6E-03**	0.9	**4E-03**	1.1	4E-01	1.1	**4E-03**	0.9	**5E-02**	Molecular function unknown	Cytoplasm	Regulatory/other subunit
6525	**SMTN**	**PREDICTED: smoothelin isoform X1**	7	23	7	1.0	**2E-02**	0.8	**5E-03**	1.1	2E-01	1.1	**1E-03**	1.0	7E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
11101	**ATE1**	**arginyl-tRNA--protein transferase 1 isoform 2**	4	17	4	1.0	2E-01	1.1	2E-01	1.2	1E-01	1.4	2E-01	1.0	1E-01	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
161	**AP2A2**	**AP-2 complex subunit alpha-2 isoform 1**	23	131	10	1.0	**2E-16**	1.0	**2E-16**	1.1	5E-01	0.8	**1E-04**	1.1	8E-01	Transporter activity	Plasma membrane	Transport/cargo protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10989	**IMMT**	**MICOS complex subunit MIC60 isoform 1**	31	194	1	1.0	**2E-16**	1.1	**2E-16**	1.1	**2E-16**	1.4	**2E-16**	1.2	**8E-03**	Motor activity	Mitochondrion	Motor protein
8895	**CPNE3**	**copine-3**	17	135	16	1.0	**1E-10**	0.9	**1E-10**	1.1	1E-01	1.0	**3E-09**	1.0	9E-01	Transporter activity	Cytoplasm	Transport/cargo protein
6642	**SNX1**	**sorting nexin-1 isoform a**	15	100	13	1.0	**4E-07**	1.1	**1E-10**	1.0	**6E-03**	0.8	**8E-03**	1.0	9E-01	Transporter activity	Endosome;Plasma membrane	Transport/cargo protein
10020	**GNE**	**bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase isoform 1**	4	13	4	1.0	**3E-05**	0.7	**4E-03**	1.1	8E-02	0.9	**2E-03**	1.1	1E-01	Racemase and epimerase activity	Cytoplasm	Enzyme: Epimerase
9527	**GOSR1**	**Golgi SNAP receptor complex member 1 isoform 1**	6	28	6	1.0	**5E-04**	1.0	**2E-04**	1.1	**1E-02**	1.1	**7E-04**	1.1	**1E-02**	Auxiliary transport protein activity	Golgi apparatus;Nucleus	Membrane transport protein
867	**CBL**	**E3 ubiquitin-protein ligase CBL**	9	37	8	1.0	**8E-04**	0.9	**5E-05**	1.1	7E-01	1.1	**8E-04**	1.0	6E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
27352	**SGSM3**	**small G protein signaling modulator 3 isoform 1**	1	7	1	1.0	**3E-02**	0.9	**9E-03**	1.1	3E-01	1.2	**2E-02**	1.1	2E-01	Molecular function unknown	Plasma membrane	Unclassified
23275	**POFUT2**	**GDP-fucose protein O-fucosyltransferase 2 isoform C**	3	11	3	1.0	**4E-02**	0.9	**4E-02**	1.3	4E-01	1.1	1E-01	1.0	3E-01	Fucosyltransferase activity	Cytoplasm	Enzyme: Fucosyltransferase
3709	**ITPR2**	**inositol 1,4,5-trisphosphate receptor type 2**	12	60	4	1.0	**4E-02**	1.1	**7E-04**	1.1	**4E-02**	1.0	**2E-02**	1.2	8E-01	Transporter activity	Plasma membrane	Transport/cargo protein
6897	**TARS**	**threonine--tRNA ligase, cytoplasmic isoform 2**	32	207	31	1.0	**2E-16**	0.7	**2E-16**	0.9	**2E-12**	0.8	9E-01	0.9	**2E-02**	Ligase activity	Cytoplasm	Enzyme: Ligase
2771	**GNAI2**	**guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 1**	13	112	7	1.0	**2E-12**	0.9	**4E-16**	1.0	**5E-04**	0.9	**4E-06**	1.0	7E-02	GTPase activity;G-protein-coupled receptor binding	Plasma membrane	GTPase;G protein
83939	**EIF2A**	**eukaryotic translation initiation factor 2A**	16	92	16	1.0	**2E-06**	0.8	**9E-09**	1.0	**3E-02**	0.7	4E-01	0.9	**3E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
2633	**GBP1**	**interferon-induced guanylate-binding protein 1**	11	48	11	1.0	**2E-05**	0.9	9E-01	0.7	6E-01	**0.6**	**4E-03**	0.8	**7E-05**	GTPase activity	Cytoplasm	GTPase
10243	**GPHN**	**gephyrin isoform 1**	7	19	7	1.0	**3E-03**	1.0	**1E-03**	1.1	**3E-02**	0.9	7E-02	1.0	9E-01	Molecular function unknown;Receptor binding	Cytosol	Anchor protein;Unclassified
6732	**SRPK1**	**SRSF protein kinase 1**	10	43	6	1.0	**4E-03**	0.9	**1E-03**	1.1	3E-01	0.8	**2E-02**	0.9	4E-01	Protein threonine/tyrosine kinase activity	Nucleus	Dual specificity kinase
64149	**C17orf75**	**protein Njmu-R1**	5	12	5	1.0	**1E-02**	0.8	**1E-02**	1.0	3E-01	1.2	**2E-02**	1.0	1E+00	Molecular function unknown	-	Unclassified
89796	**NAV1**	**neuron navigator 1 isoform 1**	5	14	5	1.0	**2E-02**	0.9	**1E-02**	0.9	6E-01	1.1	2E-01	1.1	1E-01	Molecular function unknown	Nucleus	Unclassified
26065	**LSM14A**	**protein LSM14 homolog A isoform b**	4	15	4	1.0	**3E-02**	1.0	**3E-02**	1.1	3E-01	0.8	8E-01	0.8	1E-01	Molecular function unknown	-	Unclassified
10935	**PRDX3**	**thioredoxin-dependent peroxide reductase, mitochondrial isoform a**	9	148	9	1.0	**4E-12**	1.1	**2E-16**	1.1	**1E-10**	1.3	**2E-16**	1.0	**7E-03**	Peroxidase activity	Mitochondrion	Enzyme: Peroxidase
23256	**SCFD1**	**sec1 family domain-containing protein 1 isoform a**	17	80	17	1.0	**6E-11**	0.9	**4E-11**	1.1	3E-01	1.1	**3E-13**	1.0	9E-02	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
8801	**SUCLG2**	**succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial isoform 2**	18	114	17	1.0	**2E-09**	1.4	**2E-13**	1.2	**1E-11**	1.2	**3E-13**	1.0	5E-01	Ligase activity	Mitochondrion	Enzyme: Ligase
5782	**PTPN12**	**tyrosine-protein phosphatase non-receptor type 12 isoform 1**	15	49	15	1.0	**3E-05**	0.8	**1E-05**	1.2	**5E-03**	1.2	**2E-04**	1.0	4E-01	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase
10447; 51384	**FAM3C; WNT16**	**PREDICTED: protein FAM3C isoform X1**	7	38	7	1.0	**1E-03**	1.1	**2E-04**	1.0	**3E-02**	1.1	**3E-04**	1.0	5E-01	#N/A	#N/A	#N/A
7257	**TSNAX**	**translin-associated protein X**	3	15	3	1.0	**4E-03**	0.9	**2E-03**	1.2	8E-01	0.9	**4E-03**	0.9	7E-01	Transporter activity	Cytoplasm	Transport/cargo protein
394	**ARHGAP5**	**rho GTPase-activating protein 5 isoform b**	5	13	5	1.0	**6E-03**	0.9	**5E-03**	1.1	5E-01	1.0	**1E-02**	0.9	2E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
91949	**COG7**	**conserved oligomeric Golgi complex subunit 7**	7	30	7	1.0	**1E-02**	1.0	**1E-02**	1.1	**9E-03**	1.0	**2E-03**	1.0	1E+00	Structural molecule activity	Golgi apparatus	Structural protein
5777	**PTPN6**	**tyrosine-protein phosphatase non-receptor type 6 isoform 3**	6	17	6	1.0	**1E-02**	1.2	**5E-03**	1.0	1E-01	1.3	**9E-03**	1.1	3E-01	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase
51019	**CCDC53**	**WASH complex subunit CCDC53 isoform 1**	4	9	4	1.0	1E-01	0.9	6E-02	1.1	5E-01	1.1	**4E-02**	1.0	7E-01	Molecular function unknown	-	Unclassified
23568	**ARL2BP**	**ADP-ribosylation factor-like protein 2-binding protein**	2	8	2	1.0	1E-01	0.7	**2E-02**	1.4	**3E-02**	0.8	7E-01	0.9	2E-01	GTPase activator activity	-	GTPase activating protein
10726	**NUDC**	**nuclear migration protein nudC**	20	185	19	1.0	**2E-15**	0.8	**2E-16**	1.1	**3E-04**	0.9	**8E-09**	0.9	**6E-07**	Protein binding	Cytoplasm	Cell cycle control protein
7372	**UMPS**	**uridine 5'-monophosphate synthase**	19	108	19	1.0	**2E-10**	0.9	**2E-10**	1.0	2E-01	0.8	**6E-04**	0.9	**6E-03**	Transferase activity	Nucleus	Enzyme: Synthase
9989	**PPP4R1**	**serine/threonine-protein phosphatase 4 regulatory subunit 1 isoform a**	15	65	15	1.0	**1E-08**	0.9	**2E-08**	1.2	6E-01	1.1	**1E-10**	0.9	7E-01	Enzyme regulator activity	Centrosome	Enzyme regulator
23065	**EMC1**	**ER membrane protein complex subunit 1 isoform 1**	17	92	17	1.0	**3E-07**	1.1	**8E-07**	1.1	**8E-05**	1.2	**4E-07**	1.0	7E-01	#N/A	#N/A	#N/A
54947	**LPCAT2**	**lysophosphatidylcholine acyltransferase 2**	8	43	8	1.0	**4E-07**	1.0	**1E-06**	1.0	**5E-02**	1.1	**1E-06**	1.1	**1E-02**	Molecular function unknown	-	Unclassified
55631	**LRRC40**	**leucine-rich repeat-containing protein 40**	15	50	15	1.0	**2E-06**	0.9	**1E-06**	1.0	5E-01	0.9	**5E-03**	1.0	6E-01	Molecular function unknown	-	Unclassified
11333	**PDAP1**	**28 kDa heat- and acid-stable phosphoprotein**	11	55	11	1.0	**5E-04**	1.0	**3E-04**	1.1	**4E-02**	0.8	8E-01	1.0	6E-02	Growth factor binding	Extracellular	Secreted polypeptide

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6905	TBCE	tubulin-specific chaperone E isoform b	10	39	9	1.0	**1E-03**	0.9	**2E-04**	1.1	7E-01	1.0	**5E-05**	1.0	7E-01	Chaperone activity	Cytoplasm	Chaperone
285590	SH3PXD2B	SH3 and PX domain-containing protein 2B	12	52	10	1.0	**2E-03**	1.1	**1E-03**	1.0	**6E-04**	0.9	**2E-03**	0.9	6E-01	Molecular function unknown	-	Unclassified
28957	MRPS28	28S ribosomal protein S28, mitochondrial	4	15	4	1.0	**1E-02**	1.1	**2E-03**	1.2	**8E-03**	1.0	**3E-03**	1.0	4E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
64976	MRPL40	39S ribosomal protein L40, mitochondrial	4	13	4	1.0	**4E-02**	1.0	**1E-02**	1.1	**3E-02**	0.9	**2E-02**	0.8	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
5700	PSMC1	26S protease regulatory subunit 4	28	222	26	1.0	**5E-14**	1.0	**2E-16**	1.1	**5E-04**	1.2	**2E-16**	1.0	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10207	INADL; PATJ	inaD-like protein	7	22	7	1.0	**2E-04**	0.9	**3E-04**	1.0	4E-01	0.9	**2E-03**	1.0	7E-02	#N/A	#N/A	#N/A
170954	PPP1R18	phostensin	11	41	11	1.0	**5E-04**	**0.6**	**1E-03**	1.0	**6E-04**	0.9	6E-02	1.0	6E-01	#N/A	#N/A	#N/A
23095	KIF1B	kinesin-like protein KIF1B isoform b	16	54	3	1.0	**1E-03**	1.1	**1E-04**	1.2	**7E-04**	**1.5**	**2E-04**	1.0	4E-01	Motor activity	Cytoplasmic vesicle	Motor protein
55627	SMPD4	sphingomyelin phosphodiesterase 4 isoform 2	6	14	6	1.0	**6E-03**	0.9	**4E-04**	1.0	2E-01	1.1	**8E-04**	1.0	6E-01	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein
1453	CSNK1D	casein kinase I isoform delta isoform 1	8	33	7	1.0	**1E-02**	1.0	**5E-03**	1.2	2E-01	1.0	**4E-03**	1.0	5E-01	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase
10256	CNKSR1	connector enhancer of kinase suppressor of ras 1 isoform 2	2	4	2	1.0	2E-01	0.9	2E-01	1.0	4E-01	0.9	6E-01	1.1	8E-01	Kinase binding	Cytoplasm	Unclassified
2023	ENO1	alpha-enolase isoform 1	24	1017	21	1.0	**2E-16**	0.8	**2E-16**	1.0	**7E-09**	0.8	**3E-02**	1.0	3E-01	Catalytic activity	Cytoplasm	Enzyme: Hydratase
7184	HSP90B1	endoplasmin	40	562	39	1.1	**2E-16**	0.8	**2E-16**	1.0	**3E-10**	1.1	**2E-16**	1.1	**3E-09**	Heat shock protein activity	Endoplasmic reticulum	Heat shock protein
984	CDK11B	cyclin-dependent kinase 11B isoform 1	17	84	17	1.1	**7E-08**	1.0	**6E-15**	1.2	**7E-07**	1.2	**2E-13**	1.1	**4E-02**	Protein serine/threonine kinase activity	Nucleus;Cytoplasm	Cell cycle control protein
23085	ERC1	ELKS/Rab6-interacting/CAST family member 1 isoform epsilon	33	152	33	1.1	**1E-07**	1.0	**5E-08**	1.0	**4E-03**	0.9	**2E-08**	1.0	4E-01	Protein binding	Cytoplasm	Regulatory/other subunit
11252	PACSIN2	protein kinase C and casein kinase substrate in neurons protein 2 isoform A	13	65	13	1.1	**7E-06**	0.8	**4E-07**	1.0	6E-02	0.8	**3E-02**	0.9	**3E-02**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
54926	UBE2R2	ubiquitin-conjugating enzyme E2 R2	6	29	5	1.1	**2E-05**	1.0	**1E-06**	1.2	**3E-02**	1.1	**2E-06**	0.9	**2E-02**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
79631	EFTUD1; EFL1	elongation factor Tu GTP-binding domain-containing protein 1 isoform 2	18	87	17	1.1	**2E-05**	0.9	**3E-11**	1.2	6E-01	1.4	**5E-12**	0.9	**1E-02**	#N/A	#N/A	#N/A
4644	MYO5A	unconventional myosin-Va isoform 1	34	101	29	1.1	**8E-05**	1.2	**4E-06**	1.1	**2E-06**	1.2	**2E-06**	1.0	**4E-03**	Structural molecule activity	Cytoplasm	Structural protein
55139	ANKZF1	ankyrin repeat and zinc finger domain-containing protein 1 isoform 1	6	22	6	1.1	**3E-04**	0.9	**4E-05**	1.0	5E-01	0.9	**3E-03**	0.9	7E-01	Molecular function unknown	Cytoplasm	Unclassified
4285	MIPEP	mitochondrial intermediate peptidase	11	52	11	1.1	**8E-04**	1.1	**4E-06**	1.0	**4E-04**	0.8	4E-01	1.0	1E+00	Metallopeptidase activity	Mitochondrion	Metallo protease
51071	DERA	deoxyribose-phosphate aldolase isoform 1	5	20	5	1.1	**1E-03**	0.9	**4E-03**	1.1	5E-01	1.0	**4E-03**	0.9	2E-01	Lyase activity	-	Enzyme: Lyase
84193	SETD3	PREDICTED: histone-lysine N-methyltransferase setd3 isoform X1	7	24	7	1.1	**4E-03**	1.1	**4E-03**	1.0	1E-01	0.7	5E-01	1.0	8E-01	Methyltransferase activity	-	Enzyme: Methyltransferase
130617	ZFAND2B	AN1-type zinc finger protein 2B isoform 1	1	6	1	1.1	**1E-02**	0.9	**3E-02**	1.0	8E-01	1.0	**2E-02**	0.9	9E-01	Molecular function unknown	-	Unclassified
51715	RAB23	ras-related protein Rab-23	2	10	2	1.1	**2E-02**	1.0	**1E-03**	1.1	6E-01	1.0	1E-01	1.3	1E-01	Transporter activity	Plasma membrane	Transport/cargo protein
26000	TBC1D10B	TBC1 domain family member 10B	6	18	6	1.1	**2E-02**	1.0	**2E-03**	1.2	3E-01	1.4	**3E-03**	1.0	5E-01	GTPase activator activity	-	GTPase activating protein
7518	XRCC4	PREDICTED: DNA repair protein XRCC4 isoform X1	4	12	4	1.1	**3E-02**	0.9	**2E-02**	1.1	5E-01	0.9	**7E-03**	0.9	4E-01	DNA repair protein	Nucleus	DNA repair protein
5163	PDK1	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial isoform 2	2	7	2	1.1	6E-02	0.9	**1E-02**	1.0	6E-01	0.7	3E-01	0.9	2E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
38	ACAT1	acetyl-CoA acetyltransferase, mitochondrial	17	121	17	1.1	**2E-12**	1.2	**7E-15**	1.1	**3E-10**	1.0	**1E-10**	1.0	6E-01	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
5686	PSMA5	proteasome subunit alpha type-5 isoform 1	9	98	9	1.1	**1E-11**	1.0	**6E-13**	1.2	**8E-05**	1.2	**4E-11**	0.9	**2E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
351	APP	amyloid beta A4 protein isoform a	15	98	14	1.1	**4E-08**	0.8	8E-01	0.7	**2E-03**	0.9	**4E-04**	1.0	**3E-03**	Receptor activity	Cell surface;Plasma membrane	Cell surface receptor
1075	CTSC	dipeptidyl peptidase 1 isoform a preproprotein	9	30	9	1.1	**4E-07**	1.0	**2E-09**	1.3	**2E-02**	1.3	**5E-08**	1.1	**2E-03**	Cysteine-type peptidase activity	Lysosome	Cysteine protease
80347	COASY	PREDICTED: bifunctional coenzyme A synthase isoform X2	7	40	7	1.1	**9E-05**	1.1	**2E-05**	1.1	**2E-03**	1.1	**4E-05**	0.9	3E-01	Transferase activity	Cytoplasm	Enzyme: Transferase
374354	NHLRC2	NHL repeat-containing protein 2	8	32	8	1.1	**1E-04**	1.0	**9E-08**	1.2	**1E-02**	1.3	**6E-07**	1.0	9E-01	Molecular function unknown	-	Unclassified
84328	LZIC	protein LZIC	6	39	6	1.1	**2E-04**	0.9	**3E-04**	1.2	4E-01	1.1	**3E-04**	1.0	5E-01	Molecular function unknown	-	Unclassified
6234	RPS28	40S ribosomal protein S28	3	33	3	1.1	**3E-04**	1.0	1E-01	0.8	**2E-02**	**0.6**	**3E-03**	1.2	**3E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
4141	MARS	methionine--tRNA ligase, cytoplasmic	23	172	23	1.1	**2E-02**	1.0	**8E-11**	1.1	**4E-03**	1.3	**2E-16**	1.0	2E-01	Ligase activity	Cytoplasm	Enzyme: Ligase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
55909	BIN3	bridging integrator 3	3	6	3	1.1	3E-01	1.1	6E-01	0.8	1E-01	0.8	5E-01	0.8	2E-01	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule
3329	HSPD1	60 kDa heat shock protein, mitochondrial	34	553	34	1.1	**2E-16**	1.0	**2E-16**	1.0	**1E-13**	1.1	**2E-16**	1.1	**7E-08**	Heat shock protein activity	Mitochondrial matrix	Heat shock protein
5976	UPF1	regulator of nonsense transcripts 1 isoform 1	33	191	33	1.1	**2E-16**	0.9	**2E-16**	1.1	2E-01	0.9	**7E-12**	0.9	**8E-04**	Helicase activity	Cytoplasm;Nucleus	RNA binding protein
6218	RPS17; RPS17L	40S ribosomal protein S17	4	94	4	1.1	**4E-09**	1.0	**4E-05**	0.9	**2E-02**	0.7	1E-01	1.0	5E-01	#N/A	#N/A	#N/A
8669	EIF3J	eukaryotic translation initiation factor 3 subunit J isoform 1	10	63	10	1.1	**4E-07**	0.8	**4E-08**	1.0	**1E-02**	0.8	**9E-03**	0.9	**2E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
9318	COPS2	COP9 signalosome complex subunit 2 isoform 2	13	67	13	1.1	**9E-06**	1.0	**6E-06**	1.2	**8E-03**	1.1	**7E-06**	0.9	**3E-03**	Transcription regulator activity	Nucleus	Transcription regulatory protein
80124	VCPIP1	deubiquitinating protein VCIP135	9	31	9	1.1	**1E-05**	0.9	**3E-07**	1.0	1E-01	0.9	**6E-05**	0.9	6E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
10367	MICU1	calcium uptake protein 1, mitochondrial isoform 1	8	34	8	1.1	**1E-04**	1.1	**1E-07**	1.2	**4E-03**	1.4	**2E-06**	1.1	2E-01	#N/A	#N/A	#N/A
54820	NDE1	nuclear distribution protein nudE homolog 1	10	37	8	1.1	**8E-03**	1.0	**1E-03**	1.1	8E-02	1.0	**4E-02**	1.0	8E-02	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein
5528	PPP2R5D	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform isoform 1	10	34	7	1.1	**1E-02**	0.8	**8E-03**	1.0	**1E-02**	0.9	**1E-02**	0.9	1E-01	Protein serine/threonine phosphatase activity	Nucleus;Cytoplasm	Serine/threonine phosphatase
196463	PLBD2	putative phospholipase B-like 2 isoform 1	8	39	8	1.1	**5E-02**	1.1	**2E-04**	1.2	**2E-02**	1.1	**5E-05**	1.0	1E-01	Molecular function unknown	Lysosome	Unclassified
3888	KRT82	keratin, type II cuticular Hb2	3	1196	3	1.1	1E-01	0.9	5E-01	0.7	9E-01	0.6	7E-01	1.0	8E-01	Structural molecule activity	-	Structural protein
1.01E+08	NEDD8-MDP1	NEDD8-MDP1 protein	6	30	6	1.1	#N/A	1.0	#N/A	1.1	#N/A	0.8	#N/A	1.0	#N/A	#N/A	#N/A	#N/A
5719	PSMD13	26S proteasome non-ATPase regulatory subunit 13 isoform 1	22	180	22	1.1	**2E-16**	1.0	**2E-16**	1.1	**1E-06**	1.2	**2E-16**	1.0	1E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
1315	COPB1	coatomer subunit beta	33	237	33	1.1	**3E-15**	0.9	**2E-16**	1.0	**5E-05**	1.0	**2E-16**	0.9	**1E-04**	Transporter activity	Cytoplasm	Transport/cargo protein
1936	EEF1D	elongation factor 1-delta isoform 1*gi|304555583|ref|NP_001123525.2| elongation factor 1-delta isoform 1	14	235	2	1.1	**4E-12**	0.9	**2E-14**	0.9	6E-02	1.0	**3E-13**	0.9	**4E-03**	Guanyl-nucleotide exchange factor activity	Endoplasmic reticulum	Guanine nucleotide exchange factor
9537	TP53I11	tumor protein p53-inducible protein 11	4	20	4	1.1	**6E-04**	0.9	**6E-05**	1.0	2E-01	0.9	**3E-03**	1.1	4E-01	Molecular function unknown	Cytoplasm	Unclassified
79624	C6orf211; ARMT1	UPF0364 protein C6orf211 isoform a	9	42	9	1.1	**8E-04**	0.9	**4E-07**	1.0	6E-01	1.1	**4E-07**	0.9	**6E-03**	#N/A	#N/A	#N/A
26286	ARFGAP3	ADP-ribosylation factor GTPase-activating protein 3 isoform 1	6	37	6	1.1	**2E-03**	0.8	**3E-04**	1.3	1E-01	1.0	**4E-03**	1.0	7E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
5501	PPP1CC	serine/threonine-protein phosphatase PP1-gamma catalytic subunit isoform 2	13	130	2	1.1	**5E-03**	1.0	**2E-02**	1.1	2E-01	1.3	**2E-02**	1.0	5E-01	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase
131076	CCDC58	coiled-coil domain-containing protein 58	4	22	4	1.1	**3E-02**	1.0	**1E-02**	1.1	**1E-02**	1.0	**4E-02**	1.0	5E-01	Molecular function unknown	-	Unclassified
1798;	DPAGT1	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase	2	7	2	1.1	**3E-02**	1.1	**2E-02**	1.2	**1E-04**	1.4	**9E-03**	1.1	**7E-03**	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase
644815	FAM83G	protein FAM83G	14	60	14	1.1	**5E-02**	1.4	**5E-03**	1.1	**3E-03**	1.0	**1E-02**	0.9	**2E-02**	Molecular function unknown	-	Unclassified
23760	PITPNB	phosphatidylinositol transfer protein beta isoform isoform 3	17	126	13	1.1	**4E-08**	0.9	**2E-10**	1.1	4E-01	0.9	**2E-03**	1.0	8E-02	Transporter activity	Cytoplasm	Transport/cargo protein
10767	HBS1L	HBS1-like protein isoform 1	14	55	14	1.1	**1E-07**	1.0	**8E-09**	1.0	6E-02	1.0	**2E-07**	1.0	7E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
6921	TCEB1	transcription elongation factor B polypeptide 1 isoform a	6	56	6	1.1	**3E-06**	0.9	**3E-07**	1.1	7E-01	1.2	**1E-06**	0.9	**3E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
7337	UBE3A	ubiquitin-protein ligase E3A isoform 2	13	50	13	1.1	**5E-05**	1.0	**1E-04**	1.1	**6E-03**	1.0	**4E-04**	0.9	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
55620	STAP2	signal-transducing adaptor protein 2 isoform 1	6	21	6	1.1	**2E-02**	1.1	**4E-03**	1.2	**2E-02**	1.2	**1E-02**	0.9	6E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6782	HSPA13	heat shock 70 kDa protein 13	4	14	4	1.1	**2E-02**	0.7	**2E-03**	1.0	**4E-02**	0.9	**5E-02**	1.1	2E-01	Chaperone activity	Endoplasmic reticulum	Chaperone
51234	EMC4	ER membrane protein complex subunit 4 isoform a	3	14	3	1.1	9E-02	1.1	6E-02	1.1	5E-02	1.2	7E-02	1.0	6E-01	#N/A	#N/A	#N/A
23411	SIRT1	NAD-dependent protein deacetylase sirtuin-1 isoform a	1	5	1	1.1	1E-01	0.9	8E-02	1.2	9E-01	1.1	**5E-02**	0.8	5E-01	Deacetylase activity	Nucleus	Enzyme: Deacetylase
118987	PDZD8	PDZ domain-containing protein 8	2	7	2	1.1	2E-01	1.0	2E-01	1.1	1E-01	1.2	**2E-02**	0.9	5E-01	Molecular function unknown	Nucleus	Unclassified
404734	ANKHD1-EIF4EBP3	ANKHD1-EIF4EBP3 protein	16	67	9	1.1	#N/A	0.9	#N/A	1.0	#N/A	0.9	#N/A	0.9	#N/A	Molecular function unknown	-	Unclassified
1653	DDX1	ATP-dependent RNA helicase DDX1	28	204	28	1.1	**2E-16**	1.0	**2E-16**	1.1	**5E-11**	1.0	**2E-16**	1.0	7E-02	RNA binding	Nucleus	RNA binding protein
5704	PSMC4	26S protease regulatory subunit 6B isoform 1	19	132	18	1.1	**2E-16**	1.0	**2E-16**	1.1	**6E-07**	1.2	**5E-15**	0.9	**1E-03**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
192111	PGAM5	serine/threonine-protein phosphatase PGAM5, mitochondrial isoform 1	10	75	10	1.1	**4E-09**	1.0	**3E-10**	1.2	**5E-05**	1.1	**6E-09**	1.0	2E-01	Catalytic activity	Cytosol	Enzyme: Mutase
3949	LDLR	low-density lipoprotein receptor isoform 1	16	83	16	1.1	**9E-07**	0.9	**7E-09**	1.3	4E-01	1.1	**2E-09**	1.1	**2E-04**	Receptor activity	Plasma membrane	Cell surface receptor
29925	GMPPB	mannose-1-phosphate guanyltransferase beta isoform 1	7	34	7	1.1	**2E-06**	0.9	**1E-07**	1.1	9E-01	1.2	**7E-07**	1.0	8E-01	Phosphorylase activity	-	Enzyme: Phosphorylase
2879	GPX4	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform C	7	33	7	1.1	**2E-05**	1.0	**7E-06**	1.2	**4E-03**	1.3	**5E-07**	1.0	2E-01	Peroxidase activity	Mitochondrion	Enzyme: Peroxidase
642	BLMH	bleomycin hydrolase	9	34	9	1.1	**2E-03**	1.2	**2E-03**	1.0	**5E-04**	1.0	**4E-03**	1.1	**2E-02**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
91663;	MYADM	myeloid-associated differentiation marker*gi|589058153|ref|NP_001277119.1| myeloid-associated differentiation marker*gi|589058155|ref|NP_001277122.1| myeloid-associated differentiation marker*gi|589269113|ref|NP_001277123.1| myeloid-associated differentiation marker*gi|589269118|ref|NP_001277120.1| myeloid-associated differentiation marker*gi|589269122|ref|NP_001277121.1| myeloid-associated differentiation marker*gi|589269136|ref|NP_001277118.1| myeloid-associated differentiation marker*gi|589269138|ref|NP_001277117.1| myeloid-associated differentiation marker*gi|66932923|ref|NP_001018654.1| myeloid-associated differentiation marker*gi|66932925|ref|NP_001018655.1| myeloid-associated differentiation marker*gi|66932927|ref|NP_001018656.1| myeloid-associated differentiation marker*gi|66932929|ref|NP_001018657.1| myeloid-associated differentiation marker	5	14	4	1.1	**7E-03**	1.0	**3E-03**	1.1	1E+00	1.0	**6E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
9054	NFS1	cysteine desulfurase, mitochondrial isoform a	5	20	5	1.1	**7E-03**	0.8	**3E-03**	1.3	5E-01	1.4	**5E-02**	1.0	5E-01	Sulfotransferase activity	Mitochondrion	Enzyme: Sulphotransferase
55020	TTC38	tetratricopeptide repeat protein 38	6	16	6	1.1	**3E-02**	1.0	**1E-03**	1.2	5E-02	1.2	**2E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
64221	ROBO3	PREDICTED: roundabout homolog 3 isoform X1	1	3	1	1.1	6E-02	1.0	8E-02	1.0	2E-01	0.9	1E-01	0.9	5E-01	Molecular function unknown	-	Unclassified
10454	TAB1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 isoform alpha	4	14	4	1.1	8E-02	0.9	**4E-02**	1.0	9E-01	0.9	6E-02	1.0	6E-01	#N/A	#N/A	#N/A
5236	PGM1	phosphoglucomutase-1 isoform 1	23	187	23	1.1	**2E-16**	0.9	**2E-16**	1.1	**4E-03**	0.9	**2E-16**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Mutase
1737	DLAT	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	13	90	13	1.1	**2E-14**	1.1	**5E-14**	1.2	**9E-10**	1.4	**5E-14**	1.0	1E-01	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
2539	G6PD	glucose-6-phosphate 1-dehydrogenase isoform a	26	178	1	1.1	**7E-11**	1.0	**4E-12**	1.3	**8E-10**	1.4	**1E-12**	0.7	**3E-03**	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
6717	SRI	sorcin isoform A	7	79	7	1.1	**5E-09**	0.9	**5E-10**	1.1	1E-01	1.1	**3E-08**	0.9	**6E-03**	Calcium ion binding	Cytoplasm	Calcium binding protein
5713	PSMD7	26S proteasome non-ATPase regulatory subunit 7	9	91	9	1.1	**1E-07**	1.0	**8E-09**	1.1	**5E-04**	1.2	**2E-08**	0.9	**2E-02**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
5058	PAK1	PREDICTED: serine/threonine-protein kinase PAK 1 isoform X1	10	45	6	1.1	**2E-05**	0.8	**4E-06**	1.0	**1E-02**	1.0	**2E-03**	1.0	3E-01	Protein serine/threonine kinase activity	Plasma membrane;Cytoplasm	Serine/threonine kinase
10728	PTGES3	prostaglandin E synthase 3 isoform a	8	84	8	1.1	**4E-05**	0.8	**2E-06**	1.1	**4E-02**	0.8	3E-01	0.9	**7E-03**	Chaperone activity	Cytoplasm	Chaperone
788	SLC25A20	mitochondrial carnitine/acylcarnitine carrier protein	6	24	6	1.1	**7E-05**	1.3	**1E-04**	1.4	**4E-05**	**2.0**	**6E-04**	1.1	**2E-02**	Catalytic activity	Mitochondrion	Enzyme: Translocase
7375	USP4	ubiquitin carboxyl-terminal hydrolase 4 isoform a	15	44	13	1.1	**1E-04**	1.1	**2E-04**	1.1	**2E-04**	1.2	**1E-05**	1.0	3E-01	Ubiquitin-specific protease activity	Cytoplasm;Nucleus	Ubiquitin proteasome system protein
9321	TRIP11	thyroid receptor-interacting protein 11	19	63	18	1.1	**2E-04**	0.9	**6E-05**	1.1	**5E-02**	0.9	**2E-03**	0.9	**5E-03**	Receptor binding	Golgi apparatus	Ligand
64746	ACBD3	Golgi resident protein GCP60	9	45	9	1.1	**2E-03**	0.9	**6E-04**	1.1	5E-01	1.1	**5E-03**	1.1	4E-01	Transporter activity	Golgi apparatus	Transport/cargo protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7871	**SLMAP**	**PREDICTED: sarcolemmal membrane-associated protein isoform X5**	6	9	6	1.1	**4E-03**	1.1	**3E-03**	1.1	**3E-02**	1.1	**1E-03**	1.1	4E-01	Molecular function unknown	Plasma membrane	Unclassified
26985	**AP3M1**	**PREDICTED: AP-3 complex subunit mu-1 isoform X1**	8	32	5	1.1	**1E-02**	0.9	**2E-02**	0.9	6E-01	0.9	**2E-03**	1.0	7E-01	Protein transporter activity	Golgi apparatus	Transport/cargo protein
8780	**RIOK3**	**serine/threonine-protein kinase RIO3**	5	26	5	1.1	**2E-02**	0.9	**2E-02**	1.1	9E-01	0.8	**9E-03**	0.9	3E-01	Protein kinase activity	-	Cell cycle control protein
8933;	**FAM127A**	**protein FAM127A**	3	5	3	1.1	**2E-02**	0.9	**3E-02**	0.9	7E-01	0.7	1E+00	1.1	9E-01	Molecular function unknown	-	Unclassified
147007	**TMEM199**	**transmembrane protein 199**	1	6	1	1.1	**3E-02**	0.8	**3E-02**	1.1	9E-01	**1.6**	**1E-02**	1.1	2E-01	Molecular function unknown	-	Unclassified
10897	**YIF1A**	**protein YIF1A isoform 1**	1	6	1	1.1	2E-01	1.7	2E-01	1.2	2E-01	2.1	2E-01	1.4	2E-01	Protein binding;Transporter activity	Golgi apparatus	Integral membrane protein
8546	**AP3B1**	**AP-3 complex subunit beta-1 isoform 1**	29	146	29	1.1	**1E-11**	0.9	**4E-15**	1.0	3E-01	0.9	**2E-07**	1.0	**3E-02**	Receptor signaling complex scaffold activity	Plasma membrane;Nucleus;Cytoplasm	Adapter molecule
10204	**NUTF2**	**PREDICTED: nuclear transport factor 2 isoform X1**	6	79	5	1.1	**1E-07**	1.0	**2E-10**	1.2	1E-01	1.1	**7E-09**	0.9	**4E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
10007	**GNPDA1**	**glucosamine-6-phosphate isomerase 1**	11	70	8	1.1	**1E-05**	1.0	**7E-07**	1.2	**1E-02**	1.2	**3E-07**	1.0	9E-01	Deaminase activity	-	Enzyme: Deaminase
152137	**CCDC50**	**coiled-coil domain-containing protein 50 long isoform**	9	44	9	1.1	**8E-05**	1.0	**2E-04**	0.9	8E-01	0.9	1E-01	0.9	3E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
133619	**PRRC1**	**PREDICTED: protein PRRC1 isoform X1**	4	22	4	1.1	**3E-04**	0.9	**5E-05**	1.1	**5E-02**	1.0	**1E-03**	1.0	3E-01	Molecular function unknown	Golgi apparatus	Unclassified
63971	**KIF13A**	**kinesin-like protein KIF13A isoform a**	14	43	13	1.1	**3E-04**	0.9	2E-01	0.8	8E-01	0.7	6E-01	0.9	4E-01	Motor activity	Golgi apparatus	Motor protein
55585	**UBE2Q1**	**ubiquitin-conjugating enzyme E2 Q1**	5	14	5	1.1	**1E-02**	1.0	5E-02	0.9	1E-01	1.0	1E-01	1.0	4E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
91875	**TTC5**	**tetratricopeptide repeat protein 5**	1	6	1	1.1	3E-01	0.8	6E-02	1.1	2E-01	0.8	7E-01	1.1	1E+00	Molecular function unknown	-	Unclassified
3850	**KRT3**	**keratin, type II cytoskeletal 3**	26	3357	5	1.1	9E-01	1.5	9E-01	0.9	**9E-06**	1.0	**6E-05**	1.2	**9E-03**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
1627	**DBN1**	**drebrin isoform a**	13	82	13	1.1	**2E-09**	0.7	**5E-10**	0.9	**3E-06**	0.8	**2E-02**	1.0	9E-02	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
5770	**PTPN1**	**tyrosine-protein phosphatase non-receptor type 1 isoform 1**	17	106	17	1.1	**9E-09**	0.9	**4E-09**	0.9	8E-02	1.0	**9E-11**	1.0	**7E-03**	Protein tyrosine phosphatase activity	Endoplasmic reticulum	Tyrosine phosphatase
115098	**CCDC124**	**coiled-coil domain-containing protein 124**	14	69	14	1.1	**4E-06**	0.9	**1E-06**	1.0	4E-01	0.8	**1E-02**	0.9	**1E-02**	Molecular function unknown	-	Unclassified
79031	**PDCL3**	**phosducin-like protein 3**	6	29	6	1.1	**3E-05**	**0.7**	**1E-05**	0.9	**2E-05**	**0.6**	**2E-04**	0.9	**3E-04**	Molecular function unknown	Cytoplasm	Unclassified
10542	**LAMTOR5**	**ragulator complex protein LAMTOR5**	3	29	3	1.1	**8E-04**	1.1	**2E-05**	1.2	**1E-04**	1.1	**2E-06**	0.9	7E-02	#N/A	#N/A	#N/A
113178;	**SCAMP4**	**secretory carrier-associated membrane protein 4**	3	9	3	1.1	**1E-03**	1.0	**1E-03**	0.9	**5E-03**	1.1	**3E-04**	1.0	1E-01	Auxiliary transport protein activity	Cytoplasmic vesicle	Membrane transport protein
10534	**SSSCA1**	**Sjoegren syndrome/scleroderma autoantigen 1 isoform 1**	2	12	2	1.1	**3E-03**	0.8	**5E-03**	1.0	**4E-02**	0.9	**4E-02**	0.9	1E-01	Molecular function unknown	Centrosome	Cell cycle control protein
79874	**RABEP2**	**rab GTPase-binding effector protein 2**	11	31	11	1.1	**4E-03**	0.9	**3E-04**	1.1	2E-01	1.1	**1E-05**	1.0	8E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
8517	**IKBKG**	**NF-kappa-B essential modulator isoform b**	6	23	6	1.1	**1E-02**	1.0	**1E-02**	1.1	1E-01	1.1	**2E-02**	0.9	1E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
80227	**PAAF1**	**proteasomal ATPase-associated factor 1 isoform 2**	6	23	6	1.1	**1E-02**	1.0	**1E-03**	1.0	3E-01	0.9	**2E-02**	1.0	8E-01	Protein binding	-	Ubiquitin proteasome system protein
2958	**GTF2A2**	**PREDICTED: transcription initiation factor IIA subunit 2 isoform X1**	2	6	2	1.1	**2E-02**	0.9	2E-01	1.1	7E-01	0.7	8E-01	1.1	6E-01	Transcription factor activity	Nucleus	Transcription factor
26173	**INTS1**	**integrator complex subunit 1**	6	13	6	1.1	**2E-02**	0.9	**7E-03**	1.1	1E+00	0.8	2E-01	0.9	3E-01	Molecular function unknown	Nucleus	Unclassified
387	**RHOA**	**transforming protein RhoA**	10	88	4	1.1	**3E-02**	1.0	**2E-02**	1.2	**4E-02**	1.2	**3E-03**	0.9	1E-01	GTPase activity	Cytoplasm	GTPase
1487	**CTBP1**	**C-terminal-binding protein 1 isoform 1**	8	38	5	1.1	1E-01	1.1	2E-01	1.1	7E-02	0.8	2E-01	1.2	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9793;	**CKAP5**	**cytoskeleton-associated protein 5 isoform b**	68	156	60	1.1	**2E-16**	1.0	**2E-16**	1.0	**7E-05**	0.9	**3E-08**	1.0	1E-01	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein
9588	**PRDX6**	**peroxiredoxin-6**	14	189	14	1.1	**2E-16**	1.0	**2E-16**	1.2	**8E-13**	1.0	**2E-16**	0.9	**1E-07**	Peroxidase activity	Lysosome	Enzyme: Peroxidase
3032	**HADHB**	**PREDICTED: trifunctional enzyme subunit beta, mitochondrial isoform X1**	20	157	20	1.1	**4E-10**	1.3	**6E-12**	1.2	**5E-13**	1.4	**9E-14**	1.0	1E+00	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
84817	**TXNDC17**	**thioredoxin domain-containing protein 17**	6	100	6	1.1	**9E-10**	0.8	**5E-10**	1.0	**1E-05**	0.8	**2E-04**	0.9	**3E-04**	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
7045	**TGFBI**	**transforming growth factor-beta-induced protein ig-h3**	16	87	16	1.1	**9E-10**	**1.6**	**2E-11**	1.1	**9E-11**	1.1	**4E-12**	1.4	**1E-09**	Receptor binding	Extracellular	Ligand
6392	**SDHD**	**succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial isoform a**	1	6	1	1.1	**7E-03**	1.1	**1E-03**	1.1	**1E-02**	0.8	9E-01	0.8	1E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
23224	**SYNE2**	**nesprin-2 isoform 5**	18	40	16	1.1	**5E-02**	1.0	**4E-02**	1.0	**4E-02**	1.1	**2E-04**	1.1	8E-02	Structural constituent of cytoskeleton	Nucleus;Cytoplasm	Cytoskeletal protein
51379	**CRLF3**	**cytokine receptor-like factor 3**	6	20	6	1.1	1E-01	0.9	**5E-03**	1.2	7E-01	**1.5**	**5E-03**	1.0	5E-01	Molecular function unknown	-	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7284	**TUFM**	**elongation factor Tu, mitochondrial**	25	239	25	1.1	**2E-16**	1.1	**2E-16**	1.2	**2E-16**	1.4	**2E-16**	1.0	**2E-02**	Translation regulator activity	Mitochondrion	Translation regulatory protein
327	**APEH**	**PREDICTED: acylamino-acid-releasing enzyme isoform X1**	17	122	17	1.1	**2E-09**	1.1	**7E-12**	1.2	**1E-06**	1.1	**2E-09**	1.0	4E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
23203	**PMPCA**	**mitochondrial-processing peptidase subunit alpha isoform 1**	12	78	12	1.1	**2E-07**	1.0	**1E-08**	1.0	**9E-05**	1.0	**1E-09**	1.0	1E-01	Peptidase activity	Mitochondrion	Protease
2794	**GNL1**	**PREDICTED: guanine nucleotide-binding protein-like 1 isoform X1**	11	48	11	1.1	**3E-07**	0.9	**3E-08**	1.0	2E-01	1.2	**1E-08**	1.0	1E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
23637	**RABGAP1**	**PREDICTED: rab GTPase-activating protein 1 isoform X1**	20	68	17	1.1	**4E-07**	1.0	**1E-07**	1.0	**3E-04**	1.3	**9E-10**	1.0	1E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
9260	**PDLIM7**	**PDZ and LIM domain protein 7 isoform 1**	12	64	12	1.1	**5E-07**	0.9	**3E-07**	1.0	1E-01	0.8	4E-01	1.0	3E-01	Receptor signaling complex scaffold activity	Cytoskeleton	Adapter molecule
55357	**TBC1D2**	**TBC1 domain family member 2A isoform 1**	14	69	14	1.1	**4E-06**	0.9	**4E-07**	1.1	2E-01	1.0	**3E-05**	1.1	2E-01	GTPase activator activity	-	GTPase activating protein
25940	**FAM98A**	**protein FAM98A isoform 1**	10	49	8	1.1	**5E-05**	1.0	**1E-04**	1.1	2E-01	0.9	**1E-03**	0.9	6E-02	Molecular function unknown	-	Unclassified
2332	**FMR1**	**fragile X mental retardation protein 1 isoform ISO1**	10	62	7	1.1	**4E-04**	1.0	**2E-03**	1.1	**3E-02**	1.0	**3E-02**	1.0	5E-01	RNA binding	Cytoplasm;Nucleus	RNA binding protein
5203	**PFDN4**	**prefoldin subunit 4**	2	19	2	1.1	**3E-03**	0.8	**2E-03**	1.2	5E-01	1.0	**9E-04**	1.0	9E-01	Chaperone activity	Cytoplasm	Chaperone
57085	**AGTRAP**	**type-1 angiotensin II receptor-associated protein isoform a**	3	24	1	1.1	**3E-03**	1.1	**3E-05**	1.2	**2E-03**	**1.5**	**6E-05**	1.3	**4E-02**	Molecular function unknown	Integral to membrane	Unclassified
23328	**SASH1**	**SAM and SH3 domain-containing protein 1**	3	8	3	1.1	**2E-02**	1.1	6E-02	1.0	2E-01	1.4	**2E-02**	1.0	8E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
253558	**LCLAT1**	**PREDICTED: lysocardiolipin acyltransferase 1 isoform X1**	6	17	6	1.1	**3E-02**	1.2	8E-02	1.1	**9E-03**	1.3	**4E-02**	1.0	1E+00	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase
3188	**HNRNPH2**	**heterogeneous nuclear ribonucleoprotein H2**	8	110	3	1.1	6E-02	1.0	**2E-02**	1.1	**2E-02**	1.3	**2E-02**	0.8	1E-01	RNA binding	Nucleus	Ribonucleoprotein
10295	**BCKDK**	**[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial isoform a**	1	6	1	1.1	1E-01	1.5	1E-01	1.3	2E-01	1.4	2E-01	1.1	2E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
989	**SEPT7**	**septin-7 isoform 1**	20	136	18	1.1	**2E-13**	1.1	**6E-12**	1.1	**5E-06**	1.0	**5E-12**	0.9	**1E-03**	#N/A	#N/A	#N/A
9694	**EMC2**	**ER membrane protein complex subunit 2**	10	59	10	1.1	**2E-07**	1.1	**4E-07**	1.1	**4E-05**	1.2	**2E-06**	1.1	1E-01	#N/A	#N/A	#N/A
55816	**DOK5**	**docking protein 5 isoform c**	7	18	7	1.1	**2E-05**	1.1	**1E-05**	1.1	**2E-05**	1.3	**5E-05**	1.0	2E-01	Receptor signaling complex scaffold activity	Integral to membrane	Adapter molecule
4528	**MTIF2**	**translation initiation factor IF-2, mitochondrial**	11	15	11	1.1	**4E-03**	1.2	**3E-04**	1.2	**6E-03**	1.4	**2E-03**	1.0	8E-01	Translation regulator activity	Mitochondrion	Translation regulatory protein
23214	**XPO6**	**exportin-6 isoform 2**	3	13	3	1.1	**1E-02**	1.0	**1E-03**	1.1	1E-01	0.8	2E-01	1.0	1E-01	Transporter activity	Nucleus	Transport/cargo protein
23141	**ANKLE2**	**ankyrin repeat and LEM domain-containing protein 2**	6	22	6	1.1	**2E-02**	1.1	**5E-03**	1.0	6E-02	1.2	**3E-02**	1.4	1E-01	Molecular function unknown	-	Unclassified
23193	**GANAB**	**neutral alpha-glucosidase AB isoform 3**	25	205	1	1.1	**1E-10**	1.1	**7E-12**	1.2	**2E-03**	1.2	**2E-16**	1.3	**2E-02**	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase
6780	**STAU1**	**double-stranded RNA-binding protein Staufen homolog 1 isoform b**	14	103	11	1.1	**7E-10**	0.8	**2E-10**	1.0	8E-02	0.8	**6E-04**	0.9	**3E-04**	RNA binding;Transporter activity	Endoplasmic reticulum	RNA binding protein;Transport/cargo protein
1460	**CSNK2B**	**casein kinase II subunit beta isoform 2**	6	48	6	1.1	**2E-06**	0.9	**3E-07**	1.1	8E-01	1.1	**2E-06**	0.9	**6E-03**	Protein serine/threonine kinase activity	-	Serine/threonine kinase
4836	**NMT1**	**glycylpeptide N-tetradecanoyltransferase 1**	15	99	9	1.1	**1E-04**	1.0	**1E-05**	1.1	**4E-02**	1.0	**3E-04**	1.0	4E-01	Molecular function unknown;Acyltransferase activity	Ribosome	Enzyme: Acyltransferase;Unclassified
6613	**SUMO2**	**small ubiquitin-related modifier 2 isoform a**	2	56	1	1.1	**2E-04**	1.0	**1E-04**	1.2	3E-01	1.0	**4E-04**	1.0	8E-01	Molecular function unknown	Nucleus	Unclassified
51035	**UBXN1**	**UBX domain-containing protein 1 isoform 1**	7	35	7	1.1	**6E-04**	1.0	**1E-05**	1.1	2E-01	1.1	**7E-08**	0.9	**4E-02**	Ubiquitin binding	-	Ubiquitin proteasome system protein
79571	**GCC1**	**GRIP and coiled-coil domain-containing protein 1**	6	17	6	1.1	**9E-04**	1.1	**1E-02**	1.1	2E-01	1.0	**6E-03**	0.9	2E-01	Structural molecule activity	Golgi apparatus	Structural protein
8893	**EIF2B5**	**translation initiation factor eIF-2B subunit epsilon**	6	43	6	1.1	**2E-03**	1.0	**7E-04**	1.2	**2E-04**	1.3	**2E-03**	1.0	5E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
51015	**ISOC1**	**isochorismatase domain-containing protein 1**	3	21	3	1.1	**2E-03**	1.0	**2E-04**	1.2	6E-01	0.9	**1E-03**	1.0	1E-01	Molecular function unknown	-	Unclassified
64802	**NMNAT1**	**nicotinamide mononucleotide adenylyltransferase 1 isoform 1*gi|663071195|ref|NP_001284707.1| nicotinamide mononucleotide adenylyltransferase 1 isoform 1**	2	8	2	1.1	1E-01	1.0	1E-01	1.1	3E-01	0.8	2E-01	0.9	8E-01	Nucleotidyltransferase activity	Nucleus	Enzyme: Nucleotidyltransferase
50	**ACO2**	**aconitate hydratase, mitochondrial**	33	198	33	1.1	**9E-13**	1.3	**6E-15**	1.1	**8E-15**	0.9	**4E-14**	0.9	**3E-02**	Catalytic activity	Mitochondrion	Enzyme: Hydratase
10053	**AP1M2**	**AP-1 complex subunit mu-2 isoform 2**	15	72	11	1.1	**4E-07**	1.0	**2E-09**	1.0	**3E-03**	0.9	**2E-07**	1.0	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
8623	**ASMTL**	**N-acetylserotonin O-methyltransferase-like protein isoform 3**	11	46	11	1.1	**3E-06**	1.2	**3E-06**	1.2	**1E-05**	1.2	**4E-05**	0.9	**6E-03**	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
644	**BLVRA**	**PREDICTED: biliverdin reductase A isoform X1**	10	67	10	1.1	**3E-05**	1.0	**1E-04**	1.2	**4E-04**	1.0	**5E-05**	1.0	3E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
5300	**PIN1**	peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	5	30	5	1.1	**2E-04**	1.0	**2E-04**	1.0	1E-01	0.8	4E-01	0.8	**4E-04**	Isomerase activity	Nucleus	Enzyme: Isomerase
84061	**MAGT1**	magnesium transporter protein 1	5	32	5	1.1	**8E-04**	1.1	**1E-05**	1.0	**2E-03**	1.0	**5E-06**	1.1	5E-01	Molecular function unknown	-	Unclassified
6429	**SRSF4**	serine/arginine-rich splicing factor 4	12	86	7	1.1	**1E-03**	1.2	**5E-05**	1.2	**2E-04**	1.2	**3E-05**	1.0	2E-01	#N/A	#N/A	#N/A
90233	**ZNF551**	zinc finger protein 551 isoform 1	1	6	1	1.1	**9E-03**	0.9	**1E-02**	1.1	1E-01	1.0	5E-02	1.0	7E-01	DNA binding	-	DNA binding protein
51765	**MST4; STK26**	serine/threonine-protein kinase 26 isoform 1	13	79	6	1.1	**1E-02**	1.0	**8E-03**	1.1	2E-01	0.9	**3E-03**	1.1	7E-02	#N/A	#N/A	#N/A
5705	**PSMC5**	26S protease regulatory subunit 8 isoform 1	22	186	20	1.1	**1E-14**	1.0	**1E-15**	1.1	**4E-06**	1.3	**8E-13**	0.9	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
4599	**MX1**	interferon-induced GTP-binding protein Mx1 isoform a	28	215	27	1.1	**4E-14**	**0.6**	**4E-07**	**0.3**	**2E-05**	**0.1**	**8E-08**	0.8	**4E-09**	GTPase activity	Cytoplasm	GTPase
7150	**TOP1**	DNA topoisomerase 1	27	176	27	1.1	**3E-13**	0.9	**4E-15**	1.2	3E-01	1.3	**3E-15**	1.0	**2E-02**	DNA topoisomerase activity	Nucleus	Enzyme: Topoisomerase
3417	**IDH1**	isocitrate dehydrogenase [NADP] cytoplasmic	25	245	24	1.1	**8E-13**	0.9	**2E-16**	1.2	**2E-05**	1.2	**2E-16**	0.9	**3E-05**	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
8663	**EIF3C**	eukaryotic translation initiation factor 3 subunit C isoform a	30	219	30	1.1	**4E-11**	1.0	**1E-14**	0.9	**4E-02**	0.9	**2E-10**	1.0	7E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
9373	**PLAA**	phospholipase A-2-activating protein	16	84	16	1.1	**2E-09**	0.9	**1E-10**	1.1	8E-01	1.1	**2E-08**	0.8	**4E-05**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6778	**STAT6**	signal transducer and activator of transcription 6 isoform 1	12	55	11	1.1	**8E-06**	1.0	**2E-06**	1.1	9E-02	0.8	**3E-04**	0.9	1E-01	Transcription factor activity	Cytoplasm	Transcription factor
8668	**EIF3I**	eukaryotic translation initiation factor 3 subunit I	13	93	13	1.1	**4E-05**	0.9	**2E-05**	1.0	7E-01	0.9	**5E-06**	0.9	2E-01	Translation regulator activity	Ribosome	Translation regulatory protein
54187	**NANS**	sialic acid synthase	11	44	11	1.1	**6E-05**	0.9	**7E-06**	1.3	**9E-03**	**1.5**	**5E-05**	1.0	7E-01	Catalytic activity	Cytoplasm	Enzyme: Synthase
9375	**TM9SF2**	transmembrane 9 superfamily member 2	10	42	10	1.1	**1E-04**	1.0	**3E-04**	1.0	3E-01	0.9	**4E-04**	1.0	**2E-02**	Molecular function unknown	Endosome	Integral membrane protein
3267	**AGFG1**	arf-GAP domain and FG repeat-containing protein 1 isoform 1	4	30	4	1.1	**3E-04**	1.0	**4E-04**	1.1	**2E-02**	1.0	**2E-04**	1.0	7E-01	RNA binding	Nucleus	RNA binding protein
64422	**ATG3**	ubiquitin-like-conjugating enzyme ATG3 isoform 1	5	23	5	1.1	**9E-03**	1.0	**1E-03**	1.1	**3E-02**	0.9	**1E-03**	1.0	1E+00	Molecular function unknown	Cytoplasm	Unclassified
54585	**LZTFL1**	leucine zipper transcription factor-like protein 1 isoform 1	4	14	4	1.1	3E-01	0.9	9E-02	0.9	2E-01	0.9	1E-01	1.1	2E-01	Molecular function unknown	-	Unclassified
3336;	**HSPE1**	10 kDa heat shock protein, mitochondrial	47	170	42	1.1	**2E-16**	0.9	**2E-16**	1.1	1E-01	1.0	**5E-15**	1.0	**7E-05**	Heat shock protein activity	Mitochondrion	Heat shock protein
79026	**AHNAK**	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X1	264	1416	15	1.1	**6E-15**	1.0	**1E-15**	1.1	**6E-11**	1.0	**4E-16**	0.9	1E-01	Protein binding	Nucleus	Unclassified
10914	**PAPOLA**	poly(A) polymerase alpha isoform 1	11	43	11	1.1	**9E-05**	0.9	**4E-05**	1.1	4E-01	1.0	6E-02	1.0	6E-01	RNA binding	-	RNA binding protein
5357	**PLS1**	plastin-1*gi|223718250|ref|NP_001138791.1|plastin-1*gi|288915536|ref|NP_001165783.1|plastin-1	15	174	10	1.1	**3E-04**	0.8	**1E-11**	1.0	**6E-05**	1.1	**2E-16**	1.0	7E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
64689	**GORASP1**	Golgi reassembly-stacking protein 1 isoform 1	3	13	2	1.1	**9E-03**	1.0	**3E-03**	1.1	6E-02	1.1	**5E-03**	1.0	8E-01	Structural molecule activity	Golgi apparatus	Structural protein
9683	**N4BP1**	NEDD4-binding protein 1	6	13	6	1.1	2E-01	1.1	**1E-02**	1.1	**2E-02**	1.2	**5E-02**	0.9	1E-01	#N/A	#N/A	#N/A
9716	**AQR**	intron-binding protein aquarius	5	13	4	1.1	2E-01	0.8	1E-01	1.0	5E-01	0.8	3E-01	0.9	5E-01	Molecular function unknown	Nucleus	Unclassified
3691;	**ITGB4**	integrin beta-4 isoform 1	61	201	5	1.1	**2E-16**	1.1	**2E-16**	1.1	**2E-16**	1.3	**2E-05**	1.1	**2E-16**	Cell adhesion molecule activity	Integral to membrane;Nucleus	Adhesion molecule
2923	**PDIA3**	protein disulfide-isomerase A3	29	412	29	1.1	**2E-16**	0.9	**2E-16**	1.1	7E-01	1.0	**2E-16**	1.0	**4E-04**	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase
5091	**PC**	PREDICTED: pyruvate carboxylase, mitochondrial isoform X1	35	185	35	1.1	**8E-14**	0.9	**3E-13**	1.2	**2E-02**	1.2	**2E-16**	1.0	**4E-03**	Ligase activity	Mitochondrion	Enzyme: Carboxylase
7283	**TUBG1**	tubulin gamma-1 chain	9	46	9	1.1	**1E-07**	0.9	**9E-10**	1.1	3E-01	1.0	**4E-07**	0.9	3E-01	Structural constituent of cytoskeleton	Nucleus	Cytoskeletal protein
94056	**SYAP1**	synapse-associated protein 1	8	48	8	1.1	**1E-05**	0.9	**1E-05**	1.0	7E-01	0.9	**7E-04**	0.9	**5E-02**	Transporter activity	Nucleus;Cytoplasm	Transport/cargo protein
2799	**GNS**	N-acetylglucosamine-6-sulfatase	9	66	9	1.1	**3E-05**	1.1	**8E-09**	1.2	**1E-02**	1.4	**3E-05**	1.0	1E-01	Catalytic activity	Lysosome	Enzyme: Sulphatase
8891	**EIF2B3**	translation initiation factor eIF-2B subunit gamma isoform 1	8	42	8	1.1	**2E-04**	1.0	**5E-05**	1.2	**9E-04**	1.3	**1E-05**	0.9	**4E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
3837	**KPNB1**	importin subunit beta-1 isoform 1	28	356	28	1.1	**2E-16**	0.9	**2E-16**	1.1	3E-01	1.1	**2E-16**	0.9	**8E-04**	Transporter activity	Cytoplasm	Transport/cargo protein
8565	**YARS**	tyrosine--tRNA ligase, cytoplasmic	32	214	32	1.1	**2E-16**	0.9	**2E-16**	1.1	2E-01	1.1	**2E-16**	1.0	3E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
10531	**PITRM1**	presequence protease, mitochondrial isoform 1	24	120	24	1.1	**2E-12**	1.1	**8E-14**	1.1	**6E-09**	0.9	**9E-15**	1.0	**3E-02**	Metallopeptidase activity	Extracellular	Metallo protease
2181	**ACSL3**	long-chain-fatty-acid--CoA ligase 3	21	172	18	1.1	**5E-08**	1.1	**4E-15**	1.4	**2E-06**	**2.1**	**2E-16**	1.0	5E-01	CoA-ligase activity	Peroxisome	Enzyme: Ligase
6745	**SSR1**	translocon-associated protein subunit alpha isoform 1	3	28	3	1.1	**1E-04**	0.9	**5E-06**	1.1	7E-01	1.0	**5E-07**	1.0	8E-01	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein
23131	**GPATCH8**	G patch domain-containing protein 8 isoform 1	4	12	4	1.1	**3E-03**	1.0	**3E-03**	1.2	1E-01	1.0	**4E-02**	0.9	2E-01	Molecular function unknown	Nucleus	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
339122	RAB43	ras-related protein Rab-43 isoform a	5	54	4	1.1	**3E-03**	0.7	1E-01	0.9	6E-02	1.0	**5E-03**	1.2	**3E-03**	GTPase activity	-	GTPase
55914	ERBB2IP; ERBIN	protein LAP2 isoform 8	9	20	9	1.1	**1E-02**	1.2	**3E-02**	1.1	6E-02	**1.5**	**6E-03**	1.4	**3E-02**	#N/A	#N/A	#N/A
345757	FAM174A	membrane protein FAM174A	1	6	1	1.1	**3E-02**	1.2	**1E-02**	1.0	**1E-03**	1.0	7E-02	1.2	**2E-02**	Molecular function unknown	Integral to membrane	Integral membrane protein
10970	CKAP4	cytoskeleton-associated protein 4	30	227	29	1.1	**2E-16**	0.9	**2E-16**	1.1	**3E-04**	1.0	**2E-16**	1.0	**8E-05**	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
5707	PSMD1	26S proteasome non-ATPase regulatory subunit 1 isoform 1	37	256	37	1.1	**2E-16**	1.0	**2E-16**	1.1	**4E-11**	1.3	**2E-16**	0.9	**2E-04**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
29789	OLA1	obg-like ATPase 1 isoform 1	19	132	19	1.1	**6E-10**	1.0	**3E-10**	1.1	**2E-05**	1.1	**3E-11**	1.0	1E+00	Molecular function unknown	Nucleolus	Unclassified
7841	MOGS	mannosyl-oligosaccharide glucosidase isoform 1	17	107	17	1.1	**3E-07**	1.0	**2E-08**	1.1	**3E-07**	1.2	**2E-10**	1.1	**6E-05**	Glucosidase activity	Endoplasmic reticulum	Enzyme: Glucosidase
91408	BTF3L4	transcription factor BTF3 homolog 4 isoform 1	8	55	6	1.1	**5E-06**	1.2	**2E-09**	1.2	**2E-06**	1.1	**2E-07**	1.0	2E-01	Molecular function unknown	-	Unclassified
5876	RABGGTB	geranylgeranyl transferase type-2 subunit beta	3	20	3	1.1	**7E-06**	0.9	**2E-05**	1.0	9E-01	1.0	**8E-05**	1.0	2E-01	Transferase activity	Cytoplasm	Enzyme: Prenyltransferase
55604	LRRC16A	leucine-rich repeat-containing protein 16A isoform 1	12	34	12	1.1	**1E-04**	0.9	**7E-04**	1.1	9E-01	1.1	**2E-04**	1.0	5E-01	Molecular function unknown	-	Unclassified
51112	TRAPPC12	PREDICTED: trafficking protein particle complex subunit 12 isoform X1	8	30	8	1.1	**1E-04**	1.0	**1E-05**	1.0	3E-01	0.9	**6E-05**	1.0	4E-01	#N/A	#N/A	#N/A
8027	STAM	signal transducing adapter molecule 1	7	35	7	1.1	**5E-04**	1.0	**1E-06**	1.2	**1E-02**	1.2	**2E-05**	1.0	8E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
7268	TTC4	tetratricopeptide repeat protein 4 isoform 1	5	24	5	1.1	**1E-03**	0.7	**7E-04**	1.1	**9E-03**	0.7	2E-01	0.9	1E-01	Molecular function unknown	-	Unclassified
2959	GTF2B	transcription initiation factor IIB	5	16	5	1.1	**2E-03**	0.8	**2E-03**	0.9	**2E-02**	0.8	1E+00	0.9	5E-01	Transcription factor activity	Nucleus	Transcription factor
7260	TSSC1	protein TSSC1	3	18	3	1.1	**2E-02**	1.0	**5E-04**	1.1	**2E-02**	1.1	**9E-04**	1.0	5E-01	Molecular function unknown	-	Unclassified
2015;	ADGRE1	EGF-like module-containing mucin-like hormone receptor-like 1 isoform 1	6	15	3	1.1	**3E-02**	0.9	**4E-02**	1.1	7E-01	0.9	5E-02	1.0	3E-01	#N/A	#N/A	#N/A
55860	ACTR10	actin-related protein 10	5	13	5	1.1	**4E-02**	1.0	**2E-02**	1.1	9E-02	1.1	**3E-02**	0.9	2E-01	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein
83858	ATAD3B	ATPase family AAA domain-containing protein 3B	17	92	3	1.1	9E-02	1.0	8E-02	0.9	1E-01	1.0	**4E-02**	1.4	**1E-02**	ATPase activity	Mitochondrion	ATPase
2804	GOLGB1	PREDICTED: golgin subfamily B member 1 isoform X1	61	204	60	1.1	**3E-11**	1.1	**3E-16**	1.1	**2E-06**	1.1	**1E-11**	1.0	**4E-02**	Structural molecule activity	Golgi apparatus	Structural protein
5954	RCN1	reticulocalbin-1	8	67	8	1.1	**2E-09**	0.9	**2E-08**	1.1	5E-01	1.2	**1E-11**	1.0	5E-01	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein
203068	TUBB	tubulin beta chain isoform b	23	1078	4	1.1	**4E-07**	0.7	**3E-05**	1.1	**4E-04**	0.8	**2E-02**	0.9	**3E-03**	Structural constituent of cytoskeleton	Cytoplasm;Plasma membrane	Cytoskeletal protein
25828	TXN2	thioredoxin, mitochondrial	1	18	1	1.1	**1E-04**	1.1	**2E-04**	1.3	**8E-03**	1.0	**2E-03**	1.0	4E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
5049	PAFAH1B2	platelet-activating factor acetylhydrolase IB subunit beta isoform a	5	57	5	1.1	**2E-04**	1.0	**3E-07**	1.3	1E-01	1.2	**4E-08**	1.0	**3E-02**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
1073	CFL2	cofilin-2 isoform 1	10	97	5	1.1	**5E-04**	0.8	**4E-04**	1.0	2E-01	1.0	**6E-03**	1.0	4E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
23761	PISD	PREDICTED: phosphatidylserine decarboxylase proenzyme isoform X1	5	18	5	1.1	**2E-03**	1.2	**3E-04**	1.2	**8E-03**	1.2	**5E-03**	0.9	3E-01	Carboxy-lyase activity	Mitochondrion	Enzyme: Decarboxylase
11176	BAZ2A	bromodomain adjacent to zinc finger domain protein 2A isoform 1	5	14	4	1.1	**3E-03**	1.1	**6E-03**	1.1	**3E-02**	1.0	**3E-03**	1.1	2E-01	Transcription regulator activity	Nucleolus	Transcription regulatory protein
9616	RNF7	RING-box protein 2 isoform 1	1	6	1	1.1	**8E-03**	1.0	**4E-02**	1.1	4E-01	1.0	**5E-02**	0.8	1E-01	Ligase activity	Nucleus	Enzyme: Ligase
9765	ZFYVE16	zinc finger FYVE domain-containing protein 16 isoform a*gi|157426866|ref|NP_001098721.1|zinc finger FYVE domain-containing protein 16 isoform a*gi|546232057|ref|NP_001271165.1|zinc finger FYVE domain-containing protein 16 isoform a	8	23	7	1.1	**8E-03**	1.0	**4E-03**	1.1	**2E-02**	1.0	**3E-04**	1.0	7E-01	Auxiliary transport protein activity	Endosome	Membrane transport protein
3798	KIF5A	kinesin heavy chain isoform 5A	11	85	2	1.1	**4E-02**	1.0	**4E-08**	1.0	**7E-03**	0.8	**7E-08**	1.1	**3E-05**	Motor activity	Cytoplasm	Motor protein
132	ADK	adenosine kinase isoform b	16	161	16	1.1	**3E-15**	1.0	**2E-16**	1.0	**6E-09**	1.1	**2E-16**	0.9	**6E-03**	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
7296	TXNRD1	thioredoxin reductase 1, cytoplasmic isoform 3	17	90	16	1.1	**1E-08**	1.0	**3E-09**	1.9	**2E-03**	**2.7**	**6E-09**	0.9	1E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
23348	DOCK9	PREDICTED: dedicator of cytokinesis protein 9 isoform X1	10	15	6	1.1	**6E-04**	0.9	**1E-04**	1.0	1E-01	1.2	**3E-05**	1.0	4E-01	Guanyl-nucleotide exchange factor activity	Plasma membrane	Guanine nucleotide exchange factor
24145	PANX1	pannexin-1	7	29	7	1.1	**2E-03**	0.7	**3E-03**	1.0	**4E-04**	**0.7**	**7E-03**	1.0	3E-01	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
4253	CTAGE5	cTAGE family member 5 isoform 6	9	34	9	1.1	**2E-03**	1.1	**2E-04**	1.0	**5E-03**	1.2	**9E-05**	1.0	2E-01	Molecular function unknown	Cytoplasm	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
50848	**F11R**	**junctional adhesion molecule A**	7	34	7	1.1	**2E-03**	1.0	**3E-03**	0.9	**4E-03**	**0.6**	**2E-03**	1.0	9E-01	Cell adhesion molecule activity	Cell junction	Adhesion molecule
381	**ARF5**	**ADP-ribosylation factor 5**	9	140	3	1.1	**3E-03**	1.0	**3E-04**	1.2	5E-01	1.0	5E-02	0.8	5E-02	GTPase activity	Cytoplasm	G protein
23729	**SHPK**	**sedoheptulokinase**	2	12	2	1.1	**5E-03**	1.0	**4E-03**	1.3	**1E-02**	1.2	**1E-02**	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
8754	**ADAM9**	**disintegrin and metalloproteinase domain-containing protein 9**	3	8	3	1.1	7E-02	0.8	2E-01	0.7	8E-02	0.9	9E-02	1.1	6E-02	Metallopeptidase activity	Plasma membrane;Nucleus;Cytoplasm	Metallo protease
90459	**ERI1**	**3'-5' exoribonuclease 1**	2	8	2	1.1	1E-01	0.9	**2E-02**	1.2	6E-01	1.0	**1E-02**	1.1	5E-01	Ribonuclease activity	-	Ribonuclease
4976	**OPA1**	**dynamin-like 120 kDa protein, mitochondrial isoform 8**	23	110	23	1.1	**8E-11**	1.0	**6E-12**	1.2	**4E-07**	1.1	**7E-11**	1.0	3E-01	GTPase activity	Mitochondrion	GTPase
27101	**CACYBP**	**calcyclin-binding protein isoform 1**	8	60	8	1.1	**2E-07**	0.7	**9E-09**	1.1	**2E-05**	0.8	2E-01	0.9	3E-01	Molecular function unknown	Cytoplasm	Ubiquitin proteasome system protein
10632	**ATP5L**	**ATP synthase subunit g, mitochondrial**	5	34	5	1.1	**2E-07**	1.1	**2E-06**	1.2	**6E-04**	1.2	**2E-07**	1.0	**6E-03**	ATPase activity	Mitochondrion	ATPase
285148	**IAH1**	**isoamyl acetate-hydrolyzing esterase 1 homolog**	7	34	7	1.1	**5E-04**	1.0	**4E-05**	1.2	**6E-03**	1.1	**9E-05**	1.0	1E+00	Hydrolase activity	-	Enzyme: Esterase
53918	**PELO**	**protein pelota homolog**	4	16	4	1.1	**4E-03**	0.9	**2E-03**	1.1	9E-01	0.9	**6E-03**	1.0	9E-01	Molecular function unknown	Nucleus	Cell cycle control protein
55802	**DCP1A**	**mRNA-decapping enzyme 1A isoform a**	3	12	3	1.1	**2E-02**	0.9	**3E-02**	1.0	4E-01	1.1	**2E-02**	0.9	6E-01	Transcription factor activity	Nucleus	Transcription factor
7090	**TLE3**	**transducin-like enhancer protein 3 isoform b**	6	12	6	1.1	**4E-02**	1.0	**3E-02**	1.1	4E-01	1.0	**3E-02**	1.1	8E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
27068	**PPA2**	**inorganic pyrophosphatase 2, mitochondrial isoform 1**	16	161	15	1.1	**2E-15**	1.4	**2E-16**	1.2	**4E-16**	1.4	**2E-16**	1.0	**2E-03**	Catalytic activity	Mitochondrion;Cytoplasm	Enzyme: Phosphatase
4924	**NUCB1**	**nucleobindin-1**	18	112	17	1.1	**7E-09**	1.1	**2E-10**	1.0	**2E-07**	**0.6**	**2E-06**	0.9	**8E-05**	Calcium ion binding	Golgi apparatus	Calcium binding protein
25839	**COG4**	**conserved oligomeric Golgi complex subunit 4 isoform 1**	13	64	13	1.1	**4E-07**	1.0	**5E-09**	1.1	5E-01	1.2	**1E-08**	1.0	4E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
5691	**PSMB3**	**proteasome subunit beta type-3**	8	56	8	1.1	**1E-06**	1.0	**2E-07**	1.3	1E-01	1.1	**5E-08**	1.0	5E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
22907	**DHX30**	**putative ATP-dependent RNA helicase DHX30 isoform 1**	17	67	17	1.1	**4E-06**	1.0	**2E-08**	1.2	2E-01	0.9	**2E-03**	1.0	4E-01	RNA binding	Nucleus	RNA binding protein
29109	**FHOD1**	**FH1/FH2 domain-containing protein 1**	6	23	6	1.1	**4E-05**	**0.7**	**2E-04**	1.2	**5E-03**	0.9	**3E-03**	0.9	**5E-02**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
57648	**KIAA1522**	**uncharacterized protein KIAA1522 isoform 1**	9	35	9	1.1	**5E-05**	1.0	**2E-05**	1.2	**5E-03**	0.9	**5E-05**	1.0	7E-01	Molecular function unknown	-	Unclassified
11258	**DCTN3**	**dynactin subunit 3 isoform 1**	8	37	8	1.1	**1E-03**	1.1	**1E-04**	1.1	**8E-04**	1.1	**7E-05**	1.0	4E-01	Cytoskeletal protein binding	Centrosome	Cell cycle control protein
84747	**UNC119B**	**protein unc-119 homolog B**	1	5	1	1.1	**3E-02**	1.0	**3E-02**	1.4	3E-01	1.0	1E-01	0.9	6E-01	Molecular function unknown	-	Unclassified
3914	**LAMB3**	**laminin subunit beta-3**	48	396	48	1.1	**2E-16**	0.8	**2E-16**	1.2	**1E-15**	1.2	**2E-16**	1.4	**2E-16**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
9181	**ARHGEF2**	**rho guanine nucleotide exchange factor 2 isoform 1**	19	67	19	1.1	**3E-05**	0.7	**6E-05**	1.2	**1E-04**	1.0	**2E-04**	1.0	3E-01	Guanyl-nucleotide exchange factor activity	Cytoskeleton	Guanine nucleotide exchange factor
50865	**HEBP1**	**heme-binding protein 1**	6	40	6	1.1	**1E-04**	1.1	**3E-05**	1.2	**3E-03**	1.1	**1E-04**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
54834	**GDAP2**	**ganglioside-induced differentiation-associated protein 2 isoform a**	3	13	3	1.1	**7E-04**	0.9	**9E-04**	1.3	9E-01	1.0	**1E-02**	1.1	**3E-02**	Molecular function unknown	-	Unclassified
55602	**CDKN2AIP**	**CDKN2A-interacting protein**	7	27	7	1.1	**1E-03**	1.0	**3E-05**	1.3	6E-01	1.0	**9E-04**	1.0	3E-01	RNA binding	Nucleus	RNA binding protein
22905	**EPN2**	**epsin-2 isoform b**	4	24	4	1.1	**6E-03**	1.0	**3E-03**	1.0	**6E-03**	0.9	**4E-02**	1.0	2E-01	Receptor signaling complex scaffold activity;Molecular function unknown	Cytoplasmic vesicle	Unclassified;Adapter molecule
26580	**BSCL2**	**seipin isoform 1**	2	6	2	1.1	1E-01	1.3	**4E-02**	1.1	2E-01	1.1	9E-02	1.2	4E-01	Molecular function unknown	Plasma membrane	Unclassified
10048	**RANBP9**	**ran-binding protein 9**	3	8	3	1.1	3E-01	1.0	2E-01	0.8	3E-01	**1.5**	**1E-02**	1.1	5E-01	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein
10985	**GCN1L1; GCN1**	**translational activator GCN1**	78	485	78	1.1	**2E-16**	1.0	**2E-16**	1.1	**2E-13**	1.0	**2E-16**	1.0	1E-01	#N/A	#N/A	#N/A
25782	**RAB3GAP2**	**rab3 GTPase-activating protein non-catalytic subunit**	19	89	19	1.1	**3E-11**	0.9	**5E-11**	1.0	9E-02	1.0	**6E-10**	1.0	9E-01	GTPase activator activity	Cytoplasmic vesicle	GTPase activating protein
9897	**KIAA0196**	**WASH complex subunit strumpellin**	20	97	20	1.1	**6E-11**	1.0	**4E-15**	1.1	**6E-04**	1.0	**2E-16**	1.0	1E+00	Molecular function unknown	-	Unclassified
8664	**EIF3D**	**PREDICTED: eukaryotic translation initiation factor 3 subunit D isoform X1**	17	90	17	1.1	**9E-11**	0.9	**1E-12**	1.0	**2E-02**	0.9	**6E-08**	0.9	**3E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
91039	**DPP9**	**dipeptidyl peptidase 9**	15	76	15	1.1	**9E-07**	0.9	**6E-08**	1.3	5E-01	1.3	**5E-09**	1.0	9E-01	Aminopeptidase activity	Cytoplasm	Aminopeptidase
56616	**DIABLO**	**diablo homolog, mitochondrial isoform 1**	8	48	8	1.1	**5E-06**	1.0	**8E-07**	1.2	**2E-05**	1.4	**1E-07**	1.0	8E-01	Caspase activator activity	Mitochondrion	Cell cycle control protein
9973	**CCS**	**copper chaperone for superoxide dismutase**	5	25	5	1.1	**1E-04**	1.0	**3E-04**	1.1	5E-02	1.2	**7E-04**	0.9	2E-01	Chaperone activity	Cytoplasm	Chaperone
5970	**RELA**	**transcription factor p65 isoform 2**	5	28	5	1.1	**1E-04**	0.9	**1E-04**	1.1	6E-01	1.1	**7E-04**	0.9	4E-01	Transcription factor activity	Nucleus	Transcription factor
23654	**PLXNB2**	**PREDICTED: plexin-B2 isoform X1**	16	64	14	1.1	**3E-04**	1.1	**4E-07**	1.1	**1E-03**	0.8	**4E-02**	1.0	6E-01	Receptor activity	Plasma membrane	Cell surface receptor
56947	**MFF**	**mitochondrial fission factor isoform a**	3	10	3	1.1	**1E-02**	1.0	**3E-03**	1.2	6E-02	1.0	**3E-02**	1.0	5E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
112464	**PRKCDBP**	**protein kinase C delta-binding protein**	4	26	4	1.1	**4E-02**	0.9	**1E-02**	1.0	8E-01	0.9	**4E-04**	1.1	7E-02	Molecular function unknown	Nucleus	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
2935	**GSPT1**	**eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 1**	19	122	19	1.1	**2E-13**	0.8	**7E-13**	1.0	**5E-04**	0.9	**2E-12**	0.9	**2E-06**	GTPase activity	Cytoplasm	Cell cycle control protein
2665	**GDI2**	**rab GDP dissociation inhibitor beta isoform 1**	25	296	18	1.1	**3E-11**	0.9	**3E-12**	1.1	1E-01	0.9	**2E-11**	0.9	**5E-03**	Auxiliary transport protein activity	Cytoplasm	Membrane transport protein
5331	**PLCB3**	**PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 isoform X1**	20	91	20	1.1	**2E-08**	0.9	**1E-10**	1.1	3E-01	0.9	**3E-02**	1.0	7E-01	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase
9125	**RQCD1; CNOT9**	**cell differentiation protein RCD1 homolog isoform 2**	9	46	9	1.1	**4E-06**	1.0	**1E-06**	1.1	**3E-02**	1.0	**1E-05**	1.0	5E-01	#N/A	#N/A	#N/A
10980	**COPS6**	**COP9 signalosome complex subunit 6**	8	37	8	1.1	**2E-04**	1.0	**1E-05**	1.2	**4E-03**	1.1	**3E-06**	0.9	4E-01	Protein binding	Cytoplasm	Cell cycle control protein
23348;	**DOCK9**	**dedicator of cytokinesis protein 9 isoform d**	10	18	6	1.1	**6E-04**	0.9	**1E-04**	1.1	1E-01	0.9	**3E-05**	1.0	4E-01	Guanyl-nucleotide exchange factor activity	Plasma membrane	Guanine nucleotide exchange factor
400	**ARL1**	**ADP-ribosylation factor-like protein 1 isoform 1**	5	35	5	1.1	**7E-04**	0.9	**5E-04**	1.0	6E-01	1.0	**2E-04**	1.0	4E-01	GTPase activity	Golgi apparatus	GTPase
84844	**PHF5A**	**PHD finger-like domain-containing protein 5A**	4	20	4	1.1	**4E-03**	0.9	**2E-06**	1.2	8E-01	0.9	**6E-03**	1.0	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
8936	**WASF1**	**wiskott-Aldrich syndrome protein family member 1**	2	8	2	1.1	**1E-02**	0.9	5E-02	1.1	5E-01	0.9	3E-01	1.1	4E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
2733	**GLE1**	**nucleoporin GLE1 isoform 1**	4	11	4	1.1	**2E-02**	0.9	**2E-02**	1.2	2E-01	1.2	**2E-02**	1.0	5E-01	Transporter activity	Nuclear membrane	Transport/cargo protein
23564	**DDAH2**	**PREDICTED: N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 isoform X1**	5	21	5	1.1	**3E-02**	**1.6**	**4E-04**	1.4	**2E-02**	1.4	**1E-03**	1.2	**3E-02**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
92259	**MRPS36**	**28S ribosomal protein S36, mitochondrial**	3	20	3	1.1	**3E-02**	1.0	**5E-03**	1.2	**3E-02**	1.3	**7E-03**	0.9	7E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
28511	**NKIRAS2**	**NF-kappa-B inhibitor-interacting Ras-like protein 2 isoform a**	1	6	1	1.1	6E-02	0.9	**5E-02**	1.1	9E-01	1.7	2E-01	1.4	1E-01	GTPase activity	-	GTPase
153364	**MBLAC2**	**metallo-beta-lactamase domain-containing protein 2**	2	8	2	1.1	8E-02	1.0	7E-02	1.3	6E-01	1.2	6E-02	1.0	6E-01	Molecular function unknown	-	Unclassified
8772	**FADD**	**FAS-associated death domain protein**	2	10	2	1.1	1E-01	0.8	**8E-03**	1.1	2E-01	0.8	9E-02	0.9	**2E-02**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
23474	**ETHE1**	**persulfide dioxygenase ETHE1, mitochondrial**	8	74	8	1.1	**4E-10**	1.1	**2E-11**	1.2	**3E-08**	1.4	**1E-10**	1.0	3E-01	Molecular function unknown	Mitochondrion	Unclassified
27131	**SNX5**	**sorting nexin-5 isoform a**	10	49	9	1.1	**5E-08**	1.1	**1E-07**	1.0	**3E-04**	0.7	3E-01	0.9	**1E-03**	Transporter activity	Endosome	Transport/cargo protein
5250	**SLC25A3**	**phosphate carrier protein, mitochondrial isoform a**	13	174	13	1.1	**7E-08**	1.2	**6E-14**	1.2	**2E-16**	1.3	**2E-16**	1.2	**4E-03**	Transporter activity	Mitochondrial membrane	Transport/cargo protein
23640	**HSPBP1**	**hsp70-binding protein 1 isoform 1**	8	49	8	1.1	**2E-06**	0.9	**2E-08**	1.1	5E-01	0.8	**1E-02**	1.0	9E-01	Molecular function unknown	-	Unclassified
5481	**PPID**	**peptidyl-prolyl cis-trans isomerase D**	12	75	11	1.1	**1E-05**	0.7	**3E-07**	1.0	**3E-05**	0.7	4E-01	0.9	3E-01	Isomerase activity	Nucleolus	Enzyme: Isomerase
6634	**SNRPD3**	**small nuclear ribonucleoprotein Sm D3**	3	53	3	1.1	**2E-04**	0.7	**7E-03**	1.0	6E-02	0.7	3E-01	1.0	9E-01	RNA binding	Nucleus	RNA binding protein
6632	**SNRPD1**	**small nuclear ribonucleoprotein Sm D1 isoform 1**	4	28	4	1.1	**5E-04**	0.9	**6E-05**	1.0	2E-01	0.9	**3E-04**	1.2	1E-01	RNA binding	Nucleus	RNA binding protein
55684	**RABL6**	**rab-like protein 6 isoform 3**	6	28	6	1.1	**2E-03**	1.0	**2E-04**	1.1	**1E-02**	1.1	**5E-05**	0.9	**5E-04**	#N/A	#N/A	#N/A
81562	**LMAN2L**	**VIP36-like protein isoform 1**	2	10	2	1.1	**6E-03**	1.1	**6E-04**	1.2	**7E-03**	**1.5**	**2E-05**	1.4	**5E-02**	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
26057	**ANKRD17**	**ankyrin repeat domain-containing protein 17 isoform a**	16	59	7	1.1	**1E-02**	1.0	**9E-04**	0.9	6E-01	1.2	3E-01	0.9	**2E-02**	Molecular function unknown	Nucleus	Unclassified
4782	**NFIC**	**nuclear factor 1 C-type isoform 1**	4	17	3	1.1	**1E-02**	**1.8**	**6E-03**	1.1	**4E-02**	0.9	8E-01	1.2	5E-01	Transcription factor activity	Nucleus	Transcription factor
90507	**SCRN2**	**PREDICTED: secernin-2 isoform X1**	5	16	5	1.1	**2E-02**	1.1	**9E-03**	1.2	**7E-03**	1.3	**2E-02**	1.0	3E-01	Aminopeptidase activity	Cytoplasm	Aminopeptidase
256987	**SERINC5**	**serine incorporator 5 isoform 1**	1	6	1	1.1	**2E-02**	0.9	8E-02	0.8	8E-01	0.7	9E-02	1.0	6E-01	Molecular function unknown	-	Unclassified
92935	**MARS2**	**methionine--tRNA ligase, mitochondrial**	3	10	3	1.1	**4E-02**	1.3	**2E-02**	1.3	1E-01	1.1	**2E-02**	1.0	9E-01	Ligase activity	-	Enzyme: Synthase
63905	**MANBAL**	**protein MANBAL**	1	6	1	1.1	7E-02	1.1	**3E-02**	1.0	**4E-02**	0.8	2E-01	1.0	7E-01	Molecular function unknown	Integral to membrane	Integral membrane protein;Unclassified
3550	**IK**	**protein Red**	8	33	8	1.1	2E-01	0.8	**4E-02**	1.1	1E-01	0.7	2E-01	0.9	1E-01	Molecular function unknown	Nucleus	Unclassified
93380	**MMGT1**	**membrane magnesium transporter 1**	2	8	2	1.1	2E-01	1.1	5E-02	1.2	8E-02	1.2	**3E-02**	0.9	4E-01	Molecular function unknown	-	Unclassified
3646	**EIF3E**	**eukaryotic translation initiation factor 3 subunit E**	17	138	17	1.1	**8E-14**	1.0	**9E-12**	1.0	**4E-02**	0.9	**7E-14**	1.0	2E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
55968;	**NSFL1C**	**NSFL1 cofactor p47 isoform a**	26	74	1	1.1	**5E-07**	1.1	**2E-08**	1.1	**1E-08**	0.9	**6E-06**	1.0	6E-02	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
54881	**TEX10**	**testis-expressed sequence 10 protein isoform 1**	17	66	17	1.1	**1E-03**	0.9	**4E-04**	1.1	6E-01	1.0	**1E-04**	1.0	3E-01	Molecular function unknown	-	Unclassified
50619	**DEF6**	**differentially expressed in FDCP 6 homolog**	6	23	5	1.1	**6E-03**	0.9	**7E-04**	1.4	6E-01	1.2	**4E-02**	1.0	5E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
1662	**DDX10**	**probable ATP-dependent RNA helicase DDX10**	5	12	5	1.1	**8E-03**	0.8	**3E-03**	1.2	2E-01	1.1	2E-01	0.9	2E-01	RNA binding	Nucleus	RNA binding protein
7024	**TFCP2**	**alpha-globin transcription factor CP2 isoform 1**	2	10	2	1.1	8E-02	0.9	2E-01	1.0	3E-01	0.8	9E-01	0.8	**2E-02**	Transcription factor activity	Nucleus	Transcription factor

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
64761	PARP12	poly [ADP-ribose] polymerase 12	2	7	2	1.1	2E-01	0.9	1E-01	1.0	3E-01	0.9	2E-01	1.0	8E-01	DNA binding	-	DNA binding protein
1973	EIF4A1	eukaryotic initiation factor 4A-I isoform 1	21	399	10	1.1	**2E-16**	0.9	**2E-16**	1.0	**8E-04**	0.9	**2E-16**	0.9	**2E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
51386	EIF3L	eukaryotic translation initiation factor 3 subunit L isoform 1	21	158	21	1.1	**5E-10**	0.9	**2E-10**	0.9	2E-01	0.9	**3E-13**	1.0	9E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
653145	ANXA8	annexin A8 isoform 2	16	136	1	1.1	**2E-07**	1.1	**4E-03**	0.9	**2E-02**	0.7	7E-02	1.0	**8E-03**	Calcium ion binding	-	Calcium binding protein
148362	BROX	BRO1 domain-containing protein BROX isoform a	8	30	8	1.1	**1E-06**	0.9	**1E-05**	1.1	1E-01	1.2	**4E-05**	1.0	2E-01	#N/A	#N/A	#N/A
1445	CSK	tyrosine-protein kinase CSK	12	57	12	1.1	**3E-06**	0.9	**2E-05**	1.2	1E-01	1.2	**9E-06**	1.0	3E-01	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase
4790	NFKB1	nuclear factor NF-kappa-B p105 subunit isoform 1	12	44	12	1.1	**4E-06**	1.0	**7E-07**	1.3	2E-01	1.1	**4E-04**	1.0	6E-01	Transcription factor activity	Nucleus	Transcription factor
10072	DPP3	dipeptidyl peptidase 3 isoform 1	18	102	18	1.1	**2E-08**	1.0	**8E-09**	1.2	**4E-04**	1.1	**2E-10**	0.9	5E-02	Aminopeptidase activity	Cytoplasm	Aminopeptidase
6389	SDHA	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial isoform 1	19	114	19	1.1	**2E-08**	1.3	**3E-07**	1.1	**7E-08**	1.0	**3E-07**	1.0	6E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
8531	CSDA; YBX3	Y-box-binding protein 3 isoform b	7	49	1	1.1	**1E-07**	1.0	**4E-05**	0.9	**2E-02**	0.9	3E-01	0.8	5E-01	#N/A	#N/A	#N/A
6902	TBCA	tubulin-specific chaperone A isoform 2	9	66	9	1.1	**1E-06**	0.9	**6E-08**	1.1	6E-01	0.7	3E-01	0.9	**3E-02**	Chaperone activity	Cytoskeleton	Chaperone
11196	SEC23IP	SEC23-interacting protein	16	85	15	1.1	**2E-05**	1.0	**2E-04**	1.1	**3E-03**	1.1	**8E-04**	0.9	9E-01	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
27020	NPTN	neuroplastin isoform b	8	43	8	1.1	**3E-03**	1.0	**9E-04**	1.1	**1E-02**	1.0	**1E-03**	1.0	3E-01	Antigen binding	Plasma membrane	Immunoglobulin
1147	CHUK	inhibitor of nuclear factor kappa-B kinase subunit alpha	9	26	8	1.1	**2E-02**	0.9	**3E-02**	1.1	1E-01	1.2	**4E-02**	1.0	4E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
8888	MCM3AP	PREDICTED: germinal-center associated nuclear protein isoform X1	1	6	1	1.1	**5E-02**	1.0	1E-01	1.2	5E-02	1.1	5E-02	1.1	5E-01	Chromatin binding	Nucleus	Cell cycle control protein
11188	NISCH	nischarin isoform 1	4	7	4	1.1	3E-01	1.2	2E-01	1.1	4E-01	1.3	3E-01	1.0	9E-01	Receptor activity	Plasma membrane	Cell surface receptor
11260	XPOT	exportin-T	19	132	19	1.1	**4E-09**	0.8	**2E-09**	1.1	**4E-10**	0.9	**1E-10**	0.9	**2E-03**	Transporter activity	Nucleus	Transport/cargo protein
8574	AKR7A2	aflatoxin B1 aldehyde reductase member 2	9	39	9	1.1	**2E-07**	1.1	**5E-07**	1.1	**2E-06**	1.1	**6E-06**	0.8	**5E-05**	Catalytic activity	Cytoplasm	Enzyme: Reductase
389	RHOC	rho-related GTP-binding protein RhoC*gi|111494251|ref|NP_001036144.1| rho-related GTP-binding protein RhoC*gi|28395033|ref|NP_786886.1| rho-related GTP-binding protein RhoC	7	72	1	1.1	**6E-07**	0.8	**1E-07**	1.0	2E-01	1.1	**7E-10**	0.9	8E-01	GTPase activity	Cytoplasm	GTPase
64423	INF2	inverted formin-2 isoform 1	16	64	16	1.1	**3E-06**	0.8	**7E-07**	1.1	**3E-02**	1.0	**3E-07**	1.2	**2E-04**	Molecular function unknown;Cytoskeletal protein binding	Nucleus;Cytoplasm	Cytoskeletal associated protein;Unclassified
57505;	AARS2	alanine--tRNA ligase, mitochondrial	9	19	9	1.1	**7E-06**	1.2	**1E-05**	1.1	**3E-04**	1.1	**1E-04**	1.1	**3E-02**	Molecular function unknown	Mitochondrion	Unclassified;Enzyme: Synthase
10466	COG5	conserved oligomeric Golgi complex subunit 5 isoform 1	12	51	12	1.1	**8E-06**	1.0	**2E-05**	1.2	**1E-02**	1.2	**1E-05**	1.0	9E-01	Transporter activity;Structural molecule activity	Golgi apparatus	Structural protein;Transport/cargo protein
5695	PSMB7	proteasome subunit beta type-7 proprotein	4	47	4	1.1	**3E-05**	1.0	**3E-05**	1.0	**2E-02**	1.1	**6E-10**	1.2	**1E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
9050	PSTPIP2	proline-serine-threonine phosphatase-interacting protein 2	10	34	10	1.1	**6E-05**	1.1	**1E-05**	1.1	**2E-03**	1.1	**5E-05**	1.0	6E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
58517	RBM25	PREDICTED: RNA-binding protein 25 isoform X1	20	93	20	1.1	**3E-03**	1.0	**1E-05**	1.1	**4E-03**	1.1	**7E-09**	1.0	4E-01	RNA binding	Nucleus	RNA binding protein
29919	C18orf8	uncharacterized protein C18orf8 isoform 1	3	12	3	1.1	**3E-02**	0.9	**5E-03**	1.2	2E-01	1.1	**2E-03**	1.0	9E-01	Molecular function unknown	Nucleus	Unclassified
10169	SERF2	small EDRK-rich factor 2 isoform c	2	12	2	1.1	**4E-02**	0.6	1E+00	0.7	**6E-03**	**0.3**	**3E-03**	0.9	**5E-02**	Nucleic acid binding	Nucleus	RNA binding protein
1729	DIAPH1	protein diaphanous homolog 1 isoform 1	37	216	36	1.1	**2E-16**	1.0	**2E-16**	1.1	**1E-02**	1.0	**2E-16**	1.0	9E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
2805	GOT1	aspartate aminotransferase, cytoplasmic	18	129	18	1.1	**2E-07**	0.9	**2E-07**	1.1	**2E-04**	1.0	**4E-07**	0.9	**3E-02**	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase
5636	PRPSAP2	PREDICTED: phosphoribosyl pyrophosphate synthase-associated protein 2 isoform X1	10	46	8	1.1	**4E-04**	0.9	**2E-04**	1.1	9E-02	1.0	**1E-03**	0.9	5E-01	Molecular function unknown	Nucleus;Cytoplasm	Regulatory/other subunit
4832	NME3	nucleoside diphosphate kinase 3	2	14	2	1.1	7E-01	1.0	**3E-02**	1.0	8E-02	1.0	8E-02	0.9	3E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
372	ARCN1	coatomer subunit delta isoform 1	25	208	25	1.1	**7E-16**	0.8	**2E-16**	1.0	**4E-07**	1.0	**2E-15**	0.9	**1E-05**	Transporter activity	Cytoplasm	Transport/cargo protein
6729	SRP54	PREDICTED: signal recognition particle 54 kDa protein isoform X1	22	119	22	1.1	**1E-08**	0.9	**4E-10**	1.1	**8E-03**	1.0	**3E-10**	0.9	**3E-02**	RNA binding	Cytoplasm	RNA binding protein
6625	SNRNP70	U1 small nuclear ribonucleoprotein 70 kDa isoform 1	15	90	15	1.1	**3E-06**	1.0	**9E-08**	1.1	**3E-03**	0.9	**4E-05**	1.0	1E+00	Ribonucleoprotein;RNA binding	Nucleus	Ribonucleoprotein;RNA binding protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
57222	ERGIC1	endoplasmic reticulum-Golgi intermediate compartment protein 1	9	66	9	1.1	**3E-06**	1.2	**1E-08**	1.1	**1E-06**	1.2	**5E-08**	1.1	7E-02	Transporter activity	Golgi apparatus	Transport/cargo protein
143	PARP4	poly [ADP-ribose] polymerase 4	15	55	15	1.1	**1E-05**	1.0	**3E-07**	1.1	**1E-02**	1.2	**4E-07**	1.0	8E-02	Catalytic activity	Nucleus	Enzyme: Ribosyltransferase
1266	CNN3	calponin-3 isoform 1	5	34	4	1.1	**1E-03**	**0.6**	**6E-04**	0.9	**4E-03**	**0.7**	**2E-02**	1.0	2E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
55471	NDUFAF7	NADH dehydrogenase [ubiquinone] complex I, assembly factor 7 isoform 1	4	14	4	1.1	**2E-03**	1.1	**1E-03**	1.2	**2E-02**	1.2	**3E-04**	1.0	9E-01	#N/A	#N/A	#N/A
9513	FXR2	fragile X mental retardation syndrome-related protein 2	11	59	8	1.1	**2E-03**	1.0	**3E-04**	1.2	**5E-02**	1.1	**1E-03**	0.9	2E-01	RNA binding	Cytoplasm	RNA binding protein
7326	UBE2G1	ubiquitin-conjugating enzyme E2 G1	4	18	4	1.1	**4E-02**	1.0	**7E-03**	1.2	8E-01	1.1	**7E-03**	0.9	1E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
594	BCKDHB	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	3	10	3	1.1	7E-02	1.4	**1E-02**	1.1	**4E-03**	1.3	**3E-03**	1.1	2E-01	Catalytic activity	Mitochondrion	Enzyme: Decarboxylase
5214	PFKP	ATP-dependent 6-phosphofructokinase, platelet type isoform 1	27	303	22	1.1	**6E-15**	0.9	**2E-16**	1.1	**3E-02**	1.2	**2E-16**	0.9	**1E-02**	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
3074	HEXB	beta-hexosaminidase subunit beta isoform 1 preproprotein	17	102	16	1.1	**4E-11**	1.1	**3E-11**	1.1	**3E-10**	1.3	**4E-11**	1.0	9E-01	Hydrolase activity	Lysosome	Enzyme: Hydrolase
1781	DYNC1I2	cytoplasmic dynein 1 intermediate chain 2 isoform 1*gi|422398885|ref|NP_001258714.1| cytoplasmic dynein 1 intermediate chain 2 isoform 1	10	70	10	1.1	**1E-08**	1.0	**3E-08**	1.0	**5E-06**	1.1	**2E-09**	0.9	6E-02	Motor activity	Cytoplasm	Motor protein
135293	PM20D2	peptidase M20 domain-containing protein 2	6	32	6	1.1	**1E-06**	0.9	**6E-07**	1.2	5E-01	1.0	**1E-04**	1.0	6E-01	Metallopeptidase activity	-	Metallo protease
2932	GSK3B	glycogen synthase kinase-3 beta isoform 1	11	56	7	1.1	**7E-06**	0.8	**2E-05**	1.0	**4E-02**	0.8	**6E-03**	0.9	1E-01	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase
154807	VKORC1L1	vitamin K epoxide reductase complex subunit 1-like protein 1 isoform 1	4	24	4	1.1	**2E-03**	1.1	**3E-03**	1.1	**7E-03**	1.3	**4E-03**	1.1	7E-02	Molecular function unknown	-	Integral membrane protein
29957	SLC25A24	calcium-binding mitochondrial carrier protein SCaMC-1 isoform 1	19	126	19	1.1	**1E-12**	1.0	**4E-13**	1.2	**4E-07**	1.4	**1E-13**	1.0	**4E-04**	Transporter activity	Mitochondrial membrane	Transport/cargo protein
22879	MON1B	vacuolar fusion protein MON1 homolog B isoform 1	3	8	3	1.1	**3E-03**	1.0	**3E-03**	1.2	2E-01	1.0	5E-02	0.9	8E-01	Molecular function unknown	Cytoplasm	Unclassified
271	AMPD2	AMP deaminase 2 isoform 1*gi|383209658|ref|NP_001244289.1| AMP deaminase 2 isoform 1	10	31	10	1.1	**4E-03**	0.9	**1E-02**	1.1	5E-01	1.2	**6E-03**	1.1	8E-01	Deaminase activity	Cytoplasm;Nucleus	Enzyme: Deaminase
11146	GLMN	PREDICTED: glomulin isoform X1	8	33	8	1.1	**1E-02**	1.0	**5E-03**	1.3	2E-01	1.2	**8E-03**	1.1	3E-01	Receptor binding;Protein domain specific binding	Cytoplasm	Unclassified;Ligand
112936	VPS26B	vacuolar protein sorting-associated protein 26B	9	30	7	1.1	6E-02	1.1	**2E-02**	1.0	2E-01	1.0	**6E-03**	1.0	2E-01	Transporter activity	Plasma membrane	Transport/cargo protein
9107	MTMR6	myotubularin-related protein 6	5	15	5	1.1	1E-01	1.0	8E-02	1.2	6E-01	0.9	**3E-02**	0.8	1E-01	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase
1738	DLD	dihydrolipoyl dehydrogenase, mitochondrial isoform 1	16	147	16	1.1	**4E-13**	1.2	**6E-13**	1.2	**5E-09**	1.4	**3E-14**	1.1	**3E-02**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
31	ACACA	acetyl-CoA carboxylase 1 isoform 1	35	140	35	1.1	**3E-07**	0.9	**9E-08**	1.0	**5E-03**	0.9	**1E-08**	1.0	2E-01	Ligase activity	Cytoplasm;Nucleus	Enzyme: Carboxylase
11164	NUDT5	ADP-sugar pyrophosphatase	6	50	6	1.1	**6E-07**	1.0	**6E-06**	1.1	**1E-03**	1.0	**7E-04**	0.9	1E-01	Hydrolase activity	-	Enzyme: Hydrolase
51260	CXorf26; PBDC1	protein PBDC1 isoform 1	10	43	10	1.1	**2E-06**	0.8	**7E-07**	1.1	**1E-02**	0.9	**3E-05**	0.9	**3E-02**	#N/A	#N/A	#N/A
10426	TUBGCP3	gamma-tubulin complex component 3 isoform 1	13	45	13	1.1	**3E-04**	1.0	**5E-05**	1.1	**5E-03**	1.1	**6E-05**	1.0	3E-01	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein
10955	SERINC3	serine incorporator 3*gi|5803193|ref|NP_006802.1| serine incorporator 3	4	16	4	1.1	**4E-04**	1.0	**2E-02**	1.0	6E-01	0.9	**8E-03**	1.1	2E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
8572	PDLIM4	PDZ and LIM domain protein 4 isoform 1	9	47	9	1.1	**5E-04**	0.9	2E-01	0.8	8E-01	0.7	3E-01	1.0	5E-01	Molecular function unknown	Cytoplasm	Unclassified
79693	YRDC	yrdC domain-containing protein, mitochondrial	5	11	5	1.1	6E-02	0.9	**1E-02**	1.4	4E-01	1.1	**4E-02**	1.0	8E-01	Molecular function unknown	-	Unclassified
5663	PSEN1	presenilin-1 isoform I-467	2	10	2	1.1	1E-01	1.0	2E-01	0.9	4E-01	0.9	1E-01	1.1	2E-01	Cell adhesion molecule activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Integral membrane protein
47	ACLY	ATP-citrate synthase isoform 3	49	484	1	1.1	**2E-16**	0.8	**2E-16**	1.3	**2E-16**	1.0	**2E-16**	0.9	**5E-04**	ATPase activity	Cytoplasm	ATPase
7170	TPM3	tropomyosin alpha-3 chain isoform Tpm3.2cy	18	284	3	1.1	**2E-16**	0.9	**2E-16**	1.3	**2E-03**	1.4	**2E-16**	1.0	4E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein;Structural protein
202	AIM1	PREDICTED: absent in melanoma 1 protein isoform X1	33	69	33	1.1	**9E-11**	1.0	**2E-12**	1.0	**4E-04**	1.2	**3E-11**	1.0	4E-01	Calcium ion binding	Cytoskeleton	Calcium binding protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3611	**ILK**	**integrin-linked protein kinase isoform 1*gi|62420873|ref|NP_001014794.1|integrin-linked protein kinase isoform 1*gi|62420875|ref|NP_001014795.1|integrin-linked protein kinase isoform 1**	13	79	13	1.1	**3E-09**	0.9	**6E-10**	1.1	1E-01	0.8	**4E-02**	0.9	**1E-02**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
10845	**CLPX**	**ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial**	14	59	14	1.1	**1E-08**	0.9	**2E-10**	1.1	1E+00	0.9	**5E-06**	0.9	3E-01	Peptidase activity	Mitochondrion	Protease
51594	**NBAS**	**neuroblastoma-amplified sequence**	17	63	17	1.1	**2E-06**	1.1	**4E-07**	1.1	**4E-06**	1.1	**2E-06**	1.0	1E-01	Molecular function unknown	Mitochondrion	Unclassified
6242	**RTKN**	**rhotekin isoform a**	11	49	11	1.1	**3E-06**	0.8	**5E-08**	1.0	**8E-04**	0.9	**1E-06**	0.9	3E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
8774	**NAPG**	**gamma-soluble NSF attachment protein**	9	35	9	1.1	**1E-04**	1.0	**4E-05**	1.2	**8E-03**	1.2	**4E-05**	0.9	2E-01	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein
390916	**NUDT19**	**nucleoside diphosphate-linked moiety X motif 19, mitochondrial**	2	20	2	1.1	**2E-04**	0.9	**1E-04**	1.1	4E-01	0.9	**2E-03**	0.9	5E-01	Hydrolase activity	-	Unclassified
11020	**IFT27**	**intraflagellar transport protein 27 homolog isoform 1**	2	10	2	1.1	**2E-02**	1.0	9E-02	1.1	3E-01	0.9	6E-02	0.9	8E-01	#N/A	#N/A	#N/A
57599	**WDR48**	**WD repeat-containing protein 48 isoform 1**	3	6	3	1.1	3E-01	1.2	3E-01	1.1	3E-01	0.9	3E-01	1.2	1E-01	Molecular function unknown	Endosome	Unclassified
5903	**RANBP2**	**E3 SUMO-protein ligase RanBP2**	56	227	54	1.1	**2E-15**	1.0	**2E-16**	1.1	**8E-07**	1.1	**1E-15**	1.0	**2E-02**	Transporter activity	Nucleus	Transport/cargo protein
23513	**SCRIB**	**protein scribble homolog isoform a**	24	100	23	1.1	**7E-09**	1.1	**1E-10**	1.2	**6E-10**	1.1	**2E-10**	1.0	6E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
81929	**SEH1L**	**nucleoporin SEH1 isoform 1**	11	53	11	1.1	**8E-05**	1.0	**3E-06**	1.1	**4E-02**	1.2	**1E-08**	1.0	4E-01	Molecular function unknown	Kinetochore	Unclassified
22878	**TRAPPC8**	**trafficking protein particle complex subunit 8**	8	26	8	1.1	**2E-04**	1.2	**6E-04**	1.2	**5E-04**	1.2	**2E-03**	1.1	1E-01	#N/A	#N/A	#N/A
3987	**LIMS1**	**LIM and senescent cell antigen-like-containing domain protein 1 isoform a**	9	41	9	1.1	**2E-04**	0.8	**7E-04**	1.0	7E-02	0.8	9E-01	0.8	**1E-02**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
445	**ASS1**	**argininosuccinate synthase**	9	50	9	1.1	**8E-04**	0.8	7E-01	0.8	**2E-02**	0.8	7E-01	1.0	2E-01	Ligase activity;Catalytic activity	Cytosol	Enzyme: Ligase
6829	**SUPT5H**	**transcription elongation factor SPT5 isoform a*gi|195546900|ref|NP_001124296.1|transcription elongation factor SPT5 isoform a*gi|20149524|ref|NP_003160.2|transcription elongation factor SPT5 isoform a**	12	40	12	1.1	**3E-03**	0.9	**1E-03**	1.2	6E-01	0.9	**2E-03**	0.9	2E-01	Transcription factor activity	Nucleus	Transcription factor
9883	**POM121**	**nuclear envelope pore membrane protein POM 121 isoform 1**	1	6	1	1.1	6E-02	1.0	**2E-02**	1.4	1E-01	1.1	6E-02	0.9	2E-01	Structural constituent of nuclear pore	Nucleus	Integral membrane protein
23352	**UBR4**	**E3 ubiquitin-protein ligase UBR4**	71	314	70	1.1	**2E-16**	1.1	**2E-16**	1.2	**5E-14**	**1.5**	**2E-16**	1.0	2E-01	Molecular function unknown	Cytoplasm	Unclassified
4139	**MARK1**	**serine/threonine-protein kinase MARK1 isoform 1**	10	40	2	1.1	**2E-06**	1.2	**2E-05**	1.1	7E-01	0.7	**2E-02**	1.0	7E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
163590	**TOR1AIP2**	**torsin-1A-interacting protein 2 isoform b**	12	49	11	1.1	**8E-06**	0.9	**9E-05**	1.0	1E-01	1.0	**1E-05**	1.1	**3E-05**	Molecular function unknown	Endoplasmic reticulum	Unclassified
4733	**DRG1**	**developmentally-regulated GTP-binding protein 1**	11	64	10	1.1	**1E-04**	1.1	**2E-06**	1.1	**4E-02**	1.1	**5E-05**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
5534	**PPP3R1**	**calcineurin subunit B type 1**	6	35	6	1.1	**3E-04**	0.9	**3E-05**	1.1	1E-01	1.0	**2E-05**	1.0	**2E-02**	Phosphatase regulator activity	Cytoplasm	Regulatory/other subunit
2319	**FLOT2**	**flotillin-2**	8	34	8	1.1	**3E-04**	1.0	**3E-05**	1.2	**4E-03**	1.4	**1E-04**	1.0	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
56901	**NDUFA4L2**	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like 2**	2	6	2	1.1	8E-02	0.6	1E-01	0.5	1E-01	0.1	1E-01	0.6	1E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
55922	**NKRF**	**NF-kappa-B-repressing factor isoform 1**	5	10	5	1.1	1E-01	1.4	**3E-02**	0.9	4E-01	0.7	5E-01	0.9	6E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
1717	**DHCR7**	**7-dehydrocholesterol reductase**	9	85	9	1.1	**1E-11**	1.1	**5E-12**	1.4	**5E-08**	1.4	**8E-12**	1.0	8E-02	Catalytic activity	Peroxisome	Enzyme: Reductase
54845	**ESRP1**	**epithelial splicing regulatory protein 1 isoform 1**	7	39	7	1.1	**3E-04**	1.0	**5E-03**	1.0	**4E-03**	1.0	**4E-03**	1.0	6E-01	RNA binding	Nucleus	RNA binding protein
348995	**NUP43**	**nucleoporin Nup43**	3	18	3	1.1	**3E-02**	0.9	**4E-02**	1.1	3E-01	1.1	**7E-03**	1.0	8E-01	Transporter activity	Nucleus	Transport/cargo protein
155435	**RBM33**	**RNA-binding protein 33**	1	6	1	1.1	1E-01	0.9	1E-01	1.2	9E-01	1.0	2E-01	1.3	9E-01	RNA binding	Nucleus	RNA binding protein
5819	**PVRL2; NECTIN2**	**nectin-2 isoform delta**	4	9	4	1.1	2E-01	1.2	**6E-03**	1.2	1E-01	1.1	**5E-03**	1.2	**5E-02**	#N/A	#N/A	#N/A
6238	**RRBP1**	**ribosome-binding protein 1**	48	306	46	1.1	**2E-16**	0.9	**2E-16**	1.1	**1E-02**	1.0	**2E-16**	1.0	**6E-04**	Transmembrane receptor activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Integral membrane protein
3069	**HDLBP**	**PREDICTED: vigilin isoform X1**	38	231	38	1.1	**3E-14**	0.9	**1E-15**	1.0	4E-01	0.7	**1E-04**	0.9	**3E-02**	Transporter activity	Cytoplasm;Plasma membrane	Transport/cargo protein;RNA binding protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
1468	**SLC25A10**	**mitochondrial dicarboxylate carrier isoform 1**	9	39	9	1.1	**1E-04**	1.1	**4E-05**	1.1	**1E-03**	1.0	**4E-04**	1.0	4E-01	Transporter activity	Mitochondrion	Transport/cargo protein
129563	**DIS3L2**	**DIS3-like exonuclease 2 isoform 1**	12	45	12	1.1	**3E-04**	0.9	**1E-04**	1.1	9E-02	1.0	**4E-02**	1.0	8E-01	Molecular function unknown	-	Unclassified
26263	**FBXO22**	**F-box only protein 22 isoform a**	5	34	5	1.1	**2E-03**	1.0	**1E-03**	1.2	**4E-02**	0.9	**1E-03**	0.9	**3E-02**	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
119559	**SFXN4**	**sideroflexin-4**	2	8	2	1.1	**1E-02**	1.2	**1E-02**	1.1	1E-01	1.4	**9E-03**	1.1	2E-01	Transporter activity	Integral to membrane	Membrane transport protein
517	**ATP5G2**	**ATP synthase F(0) complex subunit C2, mitochondrial isoform b**	1	12	1	1.1	**1E-02**	1.0	**6E-03**	1.1	2E-01	1.4	**9E-03**	1.0	8E-01	ATPase activity	Mitochondrion	ATPase
23787	**MTCH1**	**mitochondrial carrier homolog 1 PSAP-LL**	5	14	5	1.1	**2E-02**	1.3	**8E-03**	1.3	**2E-02**	**1.5**	**9E-03**	1.0	7E-01	Caspase activator activity	Mitochondrion	Unclassified
84105	**PCBD2**	**pterin-4-alpha-carbinolamine dehydratase 2**	3	14	2	1.1	**3E-02**	1.2	**1E-02**	1.1	4E-01	1.3	9E-01	1.2	3E-01	Hydro-lyase activity	-	Enzyme: Dehydratase
9562	**MINPP1**	**multiple inositol polyphosphate phosphatase 1 isoform 1**	2	8	2	1.1	6E-02	1.0	**2E-02**	1.2	4E-01	0.9	2E-01	1.0	5E-01	Lipid phosphatase activity	Endoplasmic reticulum	Lipid phosphatase
5533	**PPP3CC**	**serine/threonine-protein phosphatase 2B catalytic subunit gamma isoform isoform 1**	5	34	2	1.1	2E-01	1.2	2E-01	1.0	2E-01	1.4	8E-02	1.2	7E-01	Protein serine/threonine phosphatase activity	-	Serine/threonine phosphatase;ATPase
8021	**NUP214**	**nuclear pore complex protein Nup214**	22	83	22	1.1	**1E-10**	1.0	**2E-11**	1.1	**1E-03**	1.1	**4E-11**	1.0	6E-01	Transporter activity	Nucleus	Transport/cargo protein
2271	**FH**	**fumarate hydratase, mitochondrial**	15	115	15	1.1	**5E-10**	1.2	**2E-11**	1.2	**3E-08**	1.2	**3E-10**	1.0	**1E-02**	Catalytic activity	Mitochondrion	Enzyme: Hydratase
55717	**WDR11**	**WD repeat-containing protein 11**	15	60	15	1.1	**2E-07**	0.9	**1E-07**	1.0	4E-01	1.1	**9E-07**	1.0	7E-01	Molecular function unknown	-	Unclassified
8666	**EIF3G**	**eukaryotic translation initiation factor 3 subunit G**	10	73	10	1.1	**2E-06**	1.0	**8E-09**	1.0	8E-02	0.9	**2E-04**	0.9	**6E-03**	Translation regulator activity	Cytoplasm	Translation regulatory protein
7321	**UBE2D1**	**ubiquitin-conjugating enzyme E2 D1 isoform 1**	3	36	2	1.1	**9E-06**	0.9	**1E-07**	1.3	**6E-03**	1.1	**9E-08**	0.9	**3E-04**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
6734	**SRPR; SRPRA**	**signal recognition particle receptor subunit alpha isoform 1**	14	50	14	1.1	**2E-04**	0.9	**8E-05**	1.1	5E-01	1.1	**7E-04**	1.1	**7E-03**	#N/A	#N/A	#N/A
9183	**ZW10**	**centromere/kinetochore protein zw10 homolog**	11	47	11	1.1	**4E-03**	1.0	**9E-04**	1.1	**3E-02**	1.0	**3E-03**	1.0	9E-01	DNA binding	Cytoplasm	Cell cycle control protein
410	**ARSA**	**arylsulfatase A isoform a**	6	25	5	1.1	**2E-02**	1.1	**1E-02**	1.1	5E-02	1.2	**4E-03**	0.9	4E-01	Catalytic activity	Lysosome	Enzyme: Sulphatase
79932	**KIAA0319L**	**PREDICTED: dyslexia-associated protein KIAA0319-like protein isoform X1**	3	10	3	1.1	**2E-02**	1.2	**2E-02**	1.0	**2E-02**	1.1	**4E-02**	0.9	8E-01	Molecular function unknown	-	Integral membrane protein
1069	**CETN2**	**centrin-2**	5	16	5	1.1	1E-01	1.0	5E-02	1.0	4E-01	0.9	**3E-02**	0.9	5E-01	Calcium ion binding	Centrosome	Calcium binding protein
63891	**RNF123**	**PREDICTED: E3 ubiquitin-protein ligase RNF123 isoform X1**	2	7	2	1.1	5E-01	1.4	**3E-02**	1.6	1E-01	**2.0**	**2E-02**	1.1	6E-02	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
121457;	**IKBIP**	**inhibitor of nuclear factor kappa-B kinase-interacting protein isoform 1**	13	30	9	1.1	**1E-10**	0.8	**6E-14**	1.1	**7E-08**	0.9	**9E-11**	1.1	**4E-03**	Molecular function unknown	Endoplasmic reticulum	Unclassified
9789	**SPCS2**	**signal peptidase complex subunit 2**	11	64	11	1.1	**4E-07**	1.0	**8E-08**	1.1	**1E-03**	1.3	**1E-07**	1.0	3E-01	Peptidase activity	Microsome	Protease
521	**ATP5I**	**ATP synthase subunit e, mitochondrial**	4	33	4	1.1	**4E-06**	1.2	**9E-07**	1.1	**5E-06**	1.1	**7E-07**	1.0	**4E-02**	Transporter activity	Mitochondrion	Transport/cargo protein
253725	**FAM21C**	**WASH complex subunit FAM21C isoform 1**	13	43	13	1.1	**6E-05**	0.9	**3E-05**	1.1	1E-01	1.0	**1E-05**	1.0	2E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
5833	**PCYT2**	**ethanolamine-phosphate cytidylyltransferase isoform 1**	12	45	12	1.1	**7E-05**	0.9	**4E-05**	1.2	3E-01	0.9	**1E-04**	0.9	**3E-02**	Nucleotidyltransferase activity	Cytoplasm	Enzyme: Nucleotidyltransferase
23279	**NUP160**	**nuclear pore complex protein Nup160**	13	67	13	1.1	**8E-05**	1.0	**1E-05**	1.2	**7E-04**	1.3	**9E-07**	1.1	**2E-02**	Transporter activity	Nucleus	Transport/cargo protein
51028	**VPS36**	**vacuolar protein-sorting-associated protein 36 isoform 1**	9	36	9	1.1	**6E-04**	1.0	**2E-04**	1.0	**3E-02**	0.9	**1E-02**	0.9	5E-01	Molecular function unknown	-	Unclassified
55917	**CTTNBP2NL**	**CTTNBP2 N-terminal-like protein**	7	32	7	1.1	**2E-03**	1.0	**5E-05**	1.1	3E-01	1.0	**2E-02**	1.0	3E-01	Molecular function unknown	-	Unclassified
387082	**SUMO4**	**small ubiquitin-related modifier 4**	2	66	1	1.1	**1E-02**	1.0	**8E-03**	1.1	3E-01	0.9	**2E-03**	0.9	6E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
57404	**CYP20A1**	**cytochrome P450 20A1**	5	11	5	1.1	2E-01	1.2	1E-01	1.1	**2E-03**	1.4	**3E-03**	1.1	7E-01	Catalytic activity	-	Enzyme: Oxygenase
2597	**GAPDH**	**glyceraldehyde-3-phosphate dehydrogenase isoform 1*gi|576583524|ref|NP_001276675.1|glyceraldehyde-3-phosphate dehydrogenase isoform 1*gi|7669492|ref|NP_002037.2|glyceraldehyde-3-phosphate dehydrogenase isoform 1**	20	1256	20	1.1	**2E-16**	0.8	**2E-16**	1.0	**3E-16**	0.9	**2E-16**	1.0	8E-01	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
2820	**GPD2**	**PREDICTED: glycerol-3-phosphate dehydrogenase, mitochondrial isoform X1**	29	128	29	1.1	**2E-11**	1.0	**8E-15**	1.2	**2E-04**	1.4	**3E-14**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
54931	**TRMT10C**	**mitochondrial ribonuclease P protein 1**	18	88	18	1.1	**2E-11**	1.0	**1E-14**	1.1	**2E-03**	1.0	**9E-11**	0.9	**5E-02**	#N/A	#N/A	#N/A

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10469	**TIMM44**	**mitochondrial import inner membrane translocase subunit TIM44**	21	143	21	1.1	**1E-09**	1.0	**8E-11**	1.3	**2E-07**	**1.5**	**3E-11**	1.1	**2E-05**	Catalytic activity	Mitochondrion	Enzyme: Translocase
23155	**CLCC1**	**chloride channel CLIC-like protein 1 isoform 1**	7	12	7	1.1	**1E-05**	1.0	**4E-04**	1.0	3E-01	1.0	**1E-05**	0.9	3E-01	Ion channel activity	Endoplasmic reticulum	Ion channel
11212	**PROSC**	**proline synthase co-transcribed bacterial homolog protein**	7	23	7	1.1	**4E-05**	0.8	**5E-05**	1.1	**5E-02**	1.2	**5E-04**	0.9	3E-01	Racemase and epimerase activity	Cytoplasm	Enzyme: Racemase
5445	**PON2**	**serum paraoxonase/arylesterase 2 isoform 1**	2	16	2	1.1	**2E-03**	1.1	**9E-03**	1.1	7E-02	0.9	**5E-03**	1.0	8E-01	Hydrolase activity;Antioxidant activity	Plasma membrane	Enzyme: Esterase
157769	**FAM91A1**	**protein FAM91A1**	5	15	5	1.1	**4E-03**	1.1	**1E-03**	1.1	2E-01	1.1	**5E-04**	1.0	7E-01	Molecular function unknown	-	Unclassified
54853	**WDR55**	**WD repeat-containing protein 55**	4	15	4	1.1	7E-02	0.9	8E-02	1.0	8E-01	1.2	8E-02	1.0	2E-01	Molecular function unknown	-	Unclassified
23075	**SWAP70**	**switch-associated protein 70 isoform 1**	21	106	21	1.1	**2E-13**	1.0	**7E-14**	1.0	**1E-03**	1.0	**2E-10**	0.9	6E-02	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
2098	**ESD**	**PREDICTED: S-formylglutathione hydrolase isoform X1**	9	101	9	1.1	**4E-08**	1.0	**2E-10**	1.2	**5E-07**	1.1	**3E-11**	0.9	**2E-04**	Hydrolase activity	Cytoplasm	Enzyme: Esterase
5202	**PFDN2**	**prefoldin subunit 2**	6	62	6	1.1	**7E-08**	0.9	**2E-07**	1.2	3E-01	1.0	**1E-06**	1.0	8E-01	Chaperone activity	-	Chaperone
201595	**STT3B**	**dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B**	13	82	11	1.1	**2E-07**	1.1	**8E-08**	1.0	**5E-06**	1.0	**6E-06**	1.0	9E-02	Catalytic activity;Phosphoprotein phosphatase activity	Integral to membrane	Integral membrane protein
5289	**PIK3C3**	**phosphatidylinositol 3-kinase catalytic subunit type 3**	11	45	11	1.1	**1E-05**	0.9	**7E-07**	1.1	6E-01	1.0	**2E-06**	0.9	2E-01	Lipid kinase activity	-	Lipid Kinase
60492	**CCDC90B**	**coiled-coil domain-containing protein 90B, mitochondrial isoform 1**	5	22	1	1.1	**2E-03**	1.1	**7E-04**	1.2	**4E-03**	**1.5**	**5E-05**	1.1	6E-01	Molecular function unknown	-	Unclassified
9878	**TOX4**	**TOX high mobility group box family member 4 isoform 1**	2	12	2	1.1	1E-01	0.8	7E-02	1.0	5E-01	0.8	6E-01	0.9	4E-01	DNA binding	Nucleus	DNA binding protein
654364	**NME1-NME2**	**NME1-NME2 protein**	15	338	7	1.1	#N/A	0.8	#N/A	1.1	#N/A	0.8	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
22930	**RAB3GAP1**	**rab3 GTPase-activating protein catalytic subunit isoform 2**	19	72	19	1.1	**2E-07**	0.9	**2E-08**	1.1	2E-01	1.0	**1E-07**	1.0	9E-01	GTPase activator activity	Nucleus	GTPase activating protein
1964	**EIF1AX; LOC101060318**	**eukaryotic translation initiation factor 1A, X-chromosomal**	6	51	6	1.1	**6E-07**	0.8	**1E-06**	1.0	**4E-03**	0.8	6E-01	0.9	**5E-02**	#N/A	#N/A	#N/A
55291	**PPP6R3**	**PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform X2**	12	40	12	1.1	**3E-05**	0.9	**4E-05**	1.0	7E-01	1.0	**3E-04**	0.9	**2E-02**	#N/A	#N/A	#N/A
27347	**STK39**	**PREDICTED: STE20/SPS1-related proline-alanine-rich protein kinase isoform X2**	7	20	7	1.1	**1E-04**	1.1	**1E-04**	1.3	**2E-03**	1.4	**2E-04**	1.0	6E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
55341	**LSG1**	**large subunit GTPase 1 homolog**	7	27	6	1.1	**2E-03**	0.9	**8E-05**	1.0	4E-01	1.0	**3E-04**	0.9	9E-02	Nucleotide binding;GTPase activity	Endoplasmic reticulum	GTPase
57486	**NLN**	**neurolysin, mitochondrial**	9	46	9	1.1	**2E-02**	**1.5**	**2E-03**	1.1	**3E-02**	0.8	9E-01	1.1	**7E-03**	Metallopeptidase activity	Cytoplasm	Metallo protease
374986	**FAM73A**	**protein FAM73A isoform 2**	1	6	1	1.1	5E-02	1.1	7E-02	1.3	7E-02	1.2	8E-02	1.1	8E-02	Molecular function unknown	Integral to membrane	Integral membrane protein
11332	**ACOT7**	**cytosolic acyl coenzyme A thioester hydrolase isoform hBACHb**	20	79	13	1.1	**4E-14**	1.0	**2E-14**	1.2	**6E-03**	**1.5**	**4E-16**	1.0	5E-01	Hydrolase activity	Cytoplasm;Mitochondrion;Cytosol	Enzyme: Hydrolase
8667	**EIF3H**	**eukaryotic translation initiation factor 3 subunit H**	16	87	16	1.1	**9E-10**	0.9	**7E-11**	1.0	3E-01	0.9	**4E-08**	0.9	**2E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
6774	**STAT3**	**signal transducer and activator of transcription 3 isoform 1**	16	85	16	1.1	**2E-08**	1.0	**7E-07**	1.0	**3E-03**	0.7	5E-01	0.9	**3E-05**	Transcription factor activity	Nucleus;Extracellular matrix	Transcription factor
221092	**HNRNPUL2**	**heterogeneous nuclear ribonucleoprotein U-like protein 2**	23	131	23	1.1	**7E-08**	1.0	**2E-09**	1.3	**1E-11**	1.3	**5E-14**	0.9	2E-01	RNA binding	Nucleus	RNA binding protein
51622; 221960	**CCZ1; CCZ1B**	**vacuolar fusion protein CCZ1 homolog**	9	31	8	1.1	**5E-07**	1.0	**9E-06**	1.1	1E-01	1.1	**7E-04**	0.9	**2E-02**	#N/A	#N/A	#N/A
10241	**CALCOCO2**	**calcium-binding and coiled-coil domain-containing protein 2 isoform 1**	4	14	4	1.1	**4E-03**	0.7	6E-02	0.8	5E-02	0.6	1E-01	1.0	5E-01	Molecular function unknown	Nucleus	Unclassified
134510	**UBLCP1**	**ubiquitin-like domain-containing CTD phosphatase 1**	8	38	8	1.1	4E-01	1.0	5E-02	1.1	**4E-03**	0.9	**5E-04**	0.9	**2E-02**	Hydrolase activity	Nucleus	Enzyme: Phosphatase
9669	**EIF5B**	**eukaryotic translation initiation factor 5B**	29	184	28	1.1	**2E-16**	0.9	**2E-16**	1.0	3E-01	0.9	**6E-15**	0.9	**2E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
56851	**EMC7**	**ER membrane protein complex subunit 7**	6	32	6	1.1	**6E-06**	1.0	**5E-07**	1.2	**1E-03**	1.1	**2E-06**	1.0	3E-01	#N/A	#N/A	#N/A
5867	**RAB4A**	**ras-related protein Rab-4A isoform 1**	7	67	4	1.1	**2E-03**	0.9	**2E-03**	0.9	1E-01	0.8	3E-01	1.0	6E-01	GTPase activity	Endosome	GTPase
56850	**GRIPAP1**	**GRIP1-associated protein 1**	9	29	8	1.1	**2E-03**	1.1	**9E-03**	1.0	2E-01	1.1	**2E-03**	1.0	7E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
9894	**TELO2**	**telomere length regulation protein TEL2 homolog**	10	35	10	1.1	**9E-03**	0.9	**7E-03**	1.1	7E-01	0.9	**3E-03**	1.1	2E-01	Molecular function unknown	-	Unclassified
10078;	**TSSC4**	**protein TSSC4 isoform b**	5	11	2	1.1	8E-02	0.8	5E-02	1.1	2E-01	1.0	**2E-02**	1.0	2E-01	Molecular function unknown	Cytoplasm	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
125488	**TTC39C**	**tetratricopeptide repeat protein 39C isoform 1**	1	10	1	1.1	1E-01	1.3	**8E-04**	1.2	**3E-02**	1.0	**8E-04**	1.0	6E-01	Molecular function unknown	-	Unclassified
53938	**PPIL3**	**peptidyl-prolyl cis-trans isomerase-like 3 isoform PPIL3a**	3	12	3	1.1	1E-01	1.1	8E-02	1.3	2E-01	1.0	1E-01	0.9	**2E-02**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
28991	**COMMD5**	**COMM domain-containing protein 5**	3	7	3	1.1	1E-01	1.0	**4E-02**	1.3	1E-01	1.1	**4E-02**	0.9	9E-01	Molecular function unknown	Nucleus	Unclassified
60558	**GUF1**	**translation factor GUF1, mitochondrial**	2	8	2	1.1	2E-01	**0.6**	**2E-02**	1.3	3E-01	0.7	5E-01	1.0	9E-01	Molecular function unknown	-	Unclassified
10857	**PGRMC1**	**membrane-associated progesterone receptor component 1 isoform 1**	7	44	6	1.1	**2E-06**	1.0	**2E-06**	1.2	**3E-04**	1.4	**5E-06**	1.0	3E-01	Receptor activity	Plasma membrane	Cell surface receptor
3857	**KRT9**	**keratin, type I cytoskeletal 9**	20	926	19	1.1	**3E-05**	**1.7**	**9E-08**	1.1	**3E-07**	**1.9**	**2E-07**	**2.1**	**4E-05**	Structural molecule activity	Cytoplasm	Structural protein
51389	**RWDD1**	**RWD domain-containing protein 1 isoform a**	5	26	5	1.1	**8E-05**	0.9	**6E-05**	1.1	1E+00	0.9	**5E-05**	1.0	8E-01	Molecular function unknown	-	Unclassified
27161	**AGO2; EIF2C2**	**protein argonaute-2 isoform 1**	12	52	9	1.1	**3E-04**	0.9	**2E-04**	1.3	6E-01	1.0	**2E-03**	0.9	**8E-03**	#N/A	#N/A	#N/A
4534	**MTM1**	**PREDICTED: myotubularin isoform X1**	6	22	6	1.1	**5E-03**	1.0	**3E-03**	1.1	5E-02	1.0	**2E-03**	1.0	3E-01	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase
56888	**KCMF1**	**E3 ubiquitin-protein ligase KCMF1**	2	8	2	1.1	**2E-02**	0.8	**5E-02**	1.1	4E-01	1.4	**2E-02**	0.8	6E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
339487	**ZBTB8OS**	**protein archease**	2	10	2	1.1	**2E-02**	1.1	7E-02	1.0	2E-01	1.3	**5E-03**	1.3	6E-01	Molecular function unknown	-	Unclassified
2589	**GALNT1**	**PREDICTED: polypeptide N-acetylgalactosaminyltransferase 1 isoform X1**	3	10	3	1.1	**3E-02**	**1.5**	**1E-02**	0.9	**3E-02**	1.2	**9E-03**	1.4	1E-01	Galactosyltransferase activity	Endoplasmic reticulum	Enzyme: Galactosyltransferase
57176	**VARS2**	**valine--tRNA ligase, mitochondrial isoform 1**	3	11	3	1.1	1E-01	1.0	7E-02	1.2	8E-01	1.1	**5E-02**	1.0	4E-01	Ligase activity	Mitochondrion	Enzyme: Ligase
5817	**PVR**	**poliovirus receptor isoform alpha**	3	7	3	1.1	1E-01	0.7	6E-02	1.0	3E-01	0.8	5E-01	1.0	4E-01	Receptor activity	Plasma membrane	Cell surface receptor
9208	**LRRFIP1**	**leucine-rich repeat flightless-interacting protein 1 isoform 5**	24	108	23	1.1	**1E-09**	0.8	**4E-11**	1.0	**9E-04**	1.1	**3E-08**	0.9	**4E-02**	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
57707	**KIAA1609; TLDC1**	**PREDICTED: TLD domain-containing protein 1 isoform X1**	10	65	10	1.1	**4E-08**	0.9	**2E-08**	1.1	6E-02	1.0	**5E-08**	0.9	6E-02	#N/A	#N/A	#N/A
54862	**CC2D1A**	**coiled-coil and C2 domain-containing protein 1A**	16	63	15	1.1	**5E-07**	1.0	**6E-09**	1.2	**2E-03**	1.1	**2E-08**	1.0	6E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
2946	**GSTM2**	**glutathione S-transferase Mu 2 isoform 1**	7	33	6	1.1	**4E-06**	1.1	**6E-06**	1.3	**4E-03**	1.1	**3E-05**	0.9	8E-02	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase
5696	**PSMB8**	**proteasome subunit beta type-8 isoform E2 proprotein**	6	29	6	1.1	**1E-03**	1.1	**1E-05**	1.2	**3E-03**	1.0	**6E-04**	0.9	8E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
83475	**DOHH**	**deoxyhypusine hydroxylase**	4	24	4	1.1	**2E-03**	0.8	**3E-03**	0.9	**2E-02**	0.7	9E-01	0.9	**2E-02**	Oxidoreductase activity	-	Enzyme: Hydroxylase
3694	**ITGB6**	**integrin beta-6 isoform a**	7	26	7	1.1	**4E-03**	0.9	**1E-03**	1.0	2E-01	0.6	2E-01	1.0	4E-01	Receptor activity	Plasma membrane	Cell surface receptor
8906	**AP1G2**	**PREDICTED: AP-1 complex subunit gamma-like 2 isoform X1**	10	48	2	1.1	**1E-02**	**1.5**	**7E-03**	1.0	2E-01	0.7	9E-01	1.0	9E-01	Transporter activity	Cytosol	Transport/cargo protein
114876	**OSBPL1A**	**oxysterol-binding protein-related protein 1 isoform 2**	6	16	6	1.1	6E-02	0.9	**2E-02**	1.1	6E-01	**1.7**	**7E-03**	1.1	4E-01	Lipid binding	Cytoplasm;Nucleus	Transport/cargo protein
2874	**GPS2**	**G protein pathway suppressor 2**	1	6	1	1.1	9E-02	0.8	1E-01	1.1	8E-02	0.9	5E-02	0.8	7E-02	GTPase regulator activity	Nucleus	Growth inhibitory factor
3556	**IL1RAP**	**interleukin-1 receptor accessory protein isoform 1*gi|268840316|ref|NP_001161401.1| interleukin-1 receptor accessory protein isoform 1*gi|4504661|ref|NP_002173.1| interleukin-1 receptor accessory protein isoform 1**	4	17	4	1.1	1E-01	1.0	8E-02	0.9	8E-01	0.8	1E+00	1.0	6E-01	Receptor activity	Plasma membrane;Soluble fraction	Cell surface receptor
4670	**HNRNPM**	**PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X2**	36	145	2	1.1	**2E-16**	1.0	**2E-16**	1.1	**2E-07**	1.0	**2E-16**	0.9	**9E-03**	Ribonucleoprotein	Nucleolus;Nucleus	Ribonucleoprotein
5479	**PPIB**	**peptidyl-prolyl cis-trans isomerase B**	13	229	12	1.1	**2E-16**	0.9	**2E-16**	1.1	6E-01	0.8	**5E-06**	1.1	**2E-05**	Chaperone activity	Endoplasmic reticulum	Chaperone
10059	**DNM1L**	**dynamin-1-like protein isoform 5**	34	190	34	1.1	**2E-14**	0.8	**2E-16**	1.2	**9E-11**	1.1	**2E-16**	1.0	6E-01	GTPase activity	Cytoplasm	GTPase
160	**AP2A1**	**AP-2 complex subunit alpha-1 isoform 1**	37	235	24	1.1	**1E-12**	0.9	**1E-13**	1.1	2E-01	0.8	**9E-05**	0.9	**5E-05**	Transporter activity	Plasma membrane	Transport/cargo protein
57805	**CCAR2; KIAA1967**	**cell cycle and apoptosis regulator protein 2**	21	134	21	1.1	**4E-12**	1.0	**7E-12**	1.2	**2E-08**	1.1	**2E-11**	0.9	**1E-02**	#N/A	#N/A	#N/A
1743	**DLST**	**dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial isoform 1**	11	87	11	1.1	**1E-09**	1.2	**5E-12**	1.3	**3E-08**	**1.6**	**7E-10**	1.1	**6E-04**	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
4666	**NACA**	**nascent polypeptide-associated complex subunit alpha isoform a**	6	41	5	1.1	**2E-07**	0.9	**5E-07**	1.0	7E-02	**0.7**	**2E-02**	0.9	**3E-02**	Chaperone activity	Nucleus	Chaperone
25930	**PTPN23**	**tyrosine-protein phosphatase non-receptor type 23 isoform 1**	19	75	19	1.1	**2E-06**	1.0	**5E-07**	1.1	**3E-03**	1.0	**3E-06**	1.0	7E-01	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase
5371	**PML**	**protein PML isoform 1**	18	89	18	1.1	**4E-06**	1.0	**3E-06**	1.0	**5E-02**	0.9	**6E-07**	1.1	2E-01	Transcription regulator activity;Transporter activity	Nucleus;Cytoplasm	Transcription regulatory protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
126133	**ALDH16A1**	**aldehyde dehydrogenase family 16 member A1 isoform 1**	10	41	10	1.1	**1E-05**	1.0	**3E-06**	1.1	**4E-04**	1.0	**8E-05**	0.9	3E-01	Molecular function unknown	-	Unclassified
10011	**SRA1**	**steroid receptor RNA activator 1 isoform 1**	4	20	2	1.1	**2E-04**	0.8	**4E-05**	1.0	**4E-03**	0.6	1E-01	1.0	**1E-02**	Steroid hormone receptor activity;Molecular function unknown	Cytoplasm	Unclassified
6892	**TAPBP**	**tapasin isoform 2**	5	23	5	1.1	**5E-04**	1.0	**1E-03**	1.0	**2E-02**	0.8	**2E-02**	1.0	6E-01	Chaperone activity	Endoplasmic reticulum	Chaperone
51076	**CUTC**	**copper homeostasis protein cutC homolog**	3	14	3	1.1	**3E-03**	1.0	**2E-02**	1.4	6E-02	**1.5**	**2E-02**	0.9	4E-01	Molecular function unknown	Nucleolus	Unclassified
84058	**WDR54**	**WD repeat-containing protein 54**	2	8	2	1.1	**6E-03**	1.1	**2E-02**	1.0	1E-01	1.0	9E-02	0.9	4E-01	Molecular function unknown	-	Unclassified
79643	**CHMP6**	**charged multivesicular body protein 6**	1	6	1	1.1	**6E-03**	1.0	**4E-03**	1.1	5E-01	0.9	5E-02	1.1	5E-01	Molecular function unknown	-	Unclassified
1523	**CUX1**	**protein CASP isoform d**	10	30	10	1.1	**2E-02**	1.1	**1E-02**	1.0	**6E-04**	0.9	5E-02	1.0	1E+00	Transcription regulator activity	Nucleus	Transcription regulatory protein
5423	**POLB**	**DNA polymerase beta**	5	30	4	1.1	**2E-02**	1.4	**2E-02**	1.5	**5E-02**	1.4	**4E-02**	1.1	1E-01	DNA-directed DNA polymerase activity	Nucleus	DNA polymerase
26509	**MYOF**	**myoferlin isoform a**	66	368	65	1.1	**2E-16**	1.0	**2E-16**	0.9	**2E-04**	**0.7**	**6E-11**	1.0	**1E-05**	Molecular function unknown	Plasma membrane;Nucleus	Integral membrane protein
23165	**NUP205**	**nuclear pore complex protein Nup205**	38	190	38	1.1	**2E-10**	0.9	**2E-12**	1.2	1E-01	1.1	**5E-13**	1.0	6E-01	Molecular function unknown	Nucleus	Unclassified
6284	**S100A13**	**protein S100-A13**	6	65	6	1.1	**4E-10**	0.8	**6E-12**	1.3	**5E-05**	1.2	**1E-11**	1.0	3E-01	Calcium ion binding	Nucleus	Calcium binding protein
928	**CD9**	**CD9 antigen**	4	42	4	1.1	**3E-08**	0.9	**5E-09**	1.2	2E-01	0.9	**3E-07**	0.9	6E-02	Molecular function unknown	Cell surface	Unclassified
26520	**TIMM9**	**mitochondrial import inner membrane translocase subunit Tim9 isoform a**	5	28	5	1.1	**5E-04**	1.1	**3E-05**	1.1	**4E-04**	1.2	**2E-06**	1.1	4E-01	Transporter activity	Mitochondrial membrane	Transport/cargo protein
57511	**COG6**	**conserved oligomeric Golgi complex subunit 6 isoform 1**	5	15	4	1.1	**8E-03**	1.0	**1E-02**	1.1	2E-01	1.2	**1E-02**	1.0	4E-01	Structural molecule activity	Golgi apparatus	Structural protein
11135	**CDC42EP1**	**cdc42 effector protein 1**	4	14	4	1.1	**9E-03**	0.9	**3E-03**	1.1	9E-01	0.9	9E-02	1.1	8E-01	Structural constituent of cytoskeleton	Extracellular	Cytoskeletal protein
23186	**RCOR1**	**REST corepressor 1**	4	13	4	1.1	**1E-02**	0.9	**5E-03**	1.1	8E-01	1.0	**4E-03**	1.0	7E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
23210	**JMJD6**	**bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 isoform 1**	3	7	3	1.1	3E-01	1.1	2E-01	1.4	6E-01	1.0	2E-01	1.1	8E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
10644	**IGF2BP2**	**insulin-like growth factor 2 mRNA-binding protein 2 isoform c**	17	84	14	1.1	**7E-13**	0.9	**6E-14**	1.2	6E-01	1.3	**2E-14**	1.0	1E-01	RNA binding;Translation regulator activity	Cytoplasm	RNA binding protein
10981	**RAB32**	**ras-related protein Rab-32**	8	51	6	1.1	**4E-07**	0.7	**1E-07**	0.9	**5E-04**	0.7	3E-01	1.0	3E-01	GTPase activity	Mitochondrion	GTPase
5036	**PA2G4**	**proliferation-associated protein 2G4**	23	229	23	1.1	**2E-06**	1.0	**2E-06**	1.1	5E-01	1.0	**9E-04**	1.0	3E-01	Transcription regulator activity;DNA binding	Nucleus	Transcription regulatory protein
58490	**RPRD1B**	**regulation of nuclear pre-mRNA domain-containing protein 1B**	6	29	5	1.1	**1E-05**	1.2	**6E-06**	1.2	**9E-03**	1.1	**8E-05**	0.9	7E-01	Molecular function unknown	Nucleus	Unclassified
51020	**HDDC2**	**HD domain-containing protein 2**	4	17	4	1.1	**2E-05**	1.1	**2E-03**	1.3	9E-02	1.2	**2E-04**	1.0	4E-01	Molecular function unknown	-	Unclassified
2275	**FHL3**	**four and a half LIM domains protein 3 isoform 1**	5	26	5	1.1	**3E-04**	0.9	**1E-03**	0.9	8E-01	0.7	2E-01	0.9	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9474	**ATG5**	**autophagy protein 5 isoform a**	6	28	6	1.1	**2E-03**	1.0	**2E-03**	1.3	**3E-02**	1.3	**2E-02**	1.0	2E-01	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein
813	**CALU**	**calumenin isoform c**	13	111	4	1.1	**1E-09**	0.8	**2E-11**	1.2	**5E-03**	0.9	**5E-10**	1.1	**2E-04**	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein
10672	**GNA13**	**guanine nucleotide-binding protein subunit alpha-13 isoform 1**	11	70	8	1.1	**4E-05**	1.0	**3E-05**	1.2	**2E-03**	1.1	**2E-04**	0.9	9E-01	GTPase activity	Plasma membrane	G protein
51566	**ARMCX3**	**armadillo repeat-containing X-linked protein 3*gi|29540566|ref|NP_808817.1|armadillo repeat-containing X-linked protein 3*gi|7705274|ref|NP_057691.1|armadillo repeat-containing X-linked protein 3**	2	10	2	1.1	6E-02	0.7	1E-01	1.0	1E-01	0.8	5E-01	1.0	1E+00	Molecular function unknown	Plasma membrane	Unclassified
84617	**TUBB6**	**tubulin beta-6 chain isoform 1**	21	502	2	1.1	**2E-16**	0.8	**2E-16**	1.0	**3E-05**	1.0	**2E-16**	1.0	4E-01	Structural constituent of cytoskeleton	-	Cytoskeletal protein
3842	**TNPO1**	**transportin-1 isoform 1**	17	136	13	1.1	**6E-12**	0.8	**3E-12**	1.1	**2E-04**	1.1	**3E-13**	0.9	**2E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
56886	**UGGT1**	**UDP-glucose:glycoprotein glucosyltransferase 1**	25	131	25	1.1	**3E-09**	1.0	**1E-10**	1.1	**9E-07**	1.0	**5E-13**	1.0	5E-01	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase
5872	**RAB13**	**ras-related protein Rab-13 isoform 1**	10	71	7	1.1	**2E-03**	1.0	**2E-03**	1.0	**7E-03**	0.8	**2E-02**	0.9	**1E-02**	GTPase activity	Cytoplasmic vesicle	GTPase
79666	**PLEKHF2**	**pleckstrin homology domain-containing family F member 2**	3	14	3	1.1	**3E-03**	0.7	**2E-04**	1.0	3E-01	0.8	1E-01	0.9	7E-02	Molecular function unknown	Cytoplasm	Unclassified
6885	**MAP3K7**	**mitogen-activated protein kinase kinase kinase 7 isoform B**	4	7	4	1.1	1E-01	0.9	8E-02	1.0	7E-01	0.9	**2E-02**	0.8	2E-01	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase
3066	**HDAC2**	**histone deacetylase 2**	8	41	4	1.1	2E-01	0.9	2E-01	1.1	8E-01	0.9	9E-02	0.9	2E-01	Transcription regulator activity;DNA binding	Nucleus	Transcription regulatory protein
2316	**FLNA**	**filamin-A isoform 2**	118	1259	106	1.1	**2E-16**	0.8	**2E-16**	1.0	**7E-13**	0.9	**2E-16**	1.0	8E-02	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein;Structural protein
30846	**EHD2**	**EH domain-containing protein 2**	27	182	23	1.1	**3E-14**	1.0	**7E-11**	0.9	**9E-06**	**0.6**	**2E-05**	0.9	**3E-02**	Molecular function unknown	Cytoplasm	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9733	SART3	squamous cell carcinoma antigen recognized by T-cells 3	13	48	13	1.1	**3E-05**	1.0	**4E-07**	1.2	1E-01	1.1	**8E-07**	1.0	5E-01	RNA binding	Nucleus	RNA binding protein
23184	MESDC2	LDLR chaperone MESD	8	53	8	1.1	**2E-04**	0.9	**2E-04**	1.1	2E-01	0.9	**4E-05**	1.0	**1E-03**	Chaperone activity	Endoplasmic reticulum	Chaperone
9391	CIAO1	probable cytosolic iron-sulfur protein assembly protein CIAO1	1	10	1	1.1	**5E-04**	0.9	**8E-03**	1.2	5E-01	1.1	7E-02	1.0	6E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
5476	CTSA	lysosomal protective protein isoform a	3	16	3	1.1	**1E-03**	1.2	**2E-03**	1.2	**5E-03**	1.4	**2E-03**	1.0	1E-01	Serine-type peptidase activity	Lysosome	Serine protease
6197	RPS6KA3	ribosomal protein S6 kinase alpha-3	21	111	12	1.1	**2E-03**	1.0	**1E-03**	1.2	**6E-03**	1.2	**8E-04**	0.9	**5E-03**	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
23080	AVL9	late secretory pathway protein AVL9 homolog	3	14	3	1.1	**1E-02**	0.9	**2E-02**	1.1	8E-01	1.1	**1E-02**	1.0	5E-01	Molecular function unknown	-	Unclassified
858	CAV2	caveolin-2 isoform a	3	12	3	1.1	**1E-02**	0.7	**5E-02**	0.9	2E-01	0.6	3E-01	1.0	9E-01	Protein binding	Plasma membrane	Integral membrane protein
23180	RFTN1	PREDICTED: raftlin isoform X1	4	14	4	1.1	**2E-02**	0.8	6E-02	0.9	6E-01	0.4	8E-02	0.9	6E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
10142	AKAP9	A-kinase anchor protein 9 isoform 2	6	9	5	1.1	7E-02	1.0	2E-01	1.2	2E-01	1.0	3E-01	1.0	4E-01	Receptor signaling complex scaffold activity	Centrosome	Adapter molecule
8661	EIF3A	eukaryotic translation initiation factor 3 subunit A	56	408	56	1.1	**2E-16**	0.9	**2E-16**	1.0	4E-01	0.9	**2E-16**	1.0	2E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
10989	IMMT	MICOS complex subunit MIC60 isoform 2	31	192	1	1.1	**2E-16**	1.3	**2E-16**	1.3	**2E-16**	**1.5**	**2E-16**	1.0	**8E-03**	Motor activity	Mitochondrion	Motor protein
121457	IKBIP	inhibitor of nuclear factor kappa-B kinase-interacting protein isoform 2	11	54	7	1.1	**1E-10**	0.8	**6E-14**	1.1	**7E-08**	1.0	**9E-11**	1.0	**4E-03**	Molecular function unknown	Endoplasmic reticulum	Unclassified
23420	NOMO1	nodal modulator 1	26	120	26	1.1	**3E-07**	1.0	**9E-10**	1.0	**5E-03**	1.2	**4E-10**	1.0	2E-01	Molecular function unknown	Endoplasmic reticulum	Growth inhibitory factor
159	ADSS	adenylosuccinate synthetase isozyme 2	9	51	9	1.1	**1E-05**	0.9	**2E-05**	1.0	1E-01	0.7	**2E-02**	1.0	4E-01	Ligase activity	Cytoplasm	Enzyme: Synthase
7458	EIF4H	eukaryotic translation initiation factor 4H isoform 1	9	63	9	1.1	**4E-05**	0.9	**3E-05**	1.1	2E-01	1.0	**3E-05**	0.9	**5E-02**	Translation regulator activity	Cytoplasm	Translation regulatory protein
79568	C2orf47	uncharacterized protein C2orf47, mitochondrial	6	31	6	1.1	**7E-05**	1.3	**3E-05**	1.2	**3E-04**	1.3	**1E-04**	1.1	**3E-02**	Molecular function unknown	-	Unclassified
7295	TXN	thioredoxin isoform 1	5	88	5	1.1	**8E-03**	0.8	**1E-03**	1.4	2E-01	1.0	**4E-05**	0.9	**3E-02**	Catalytic activity	Cytoplasm	Enzyme: Reductase
3312	HSPA8	PREDICTED: heat shock cognate 71 kDa protein isoform X1	38	1052	24	1.1	**2E-16**	0.8	**2E-16**	1.0	**2E-10**	0.7	7E-01	0.9	**4E-04**	Heat shock protein activity	Nucleolus;Cytoplasm	Heat shock protein
26135	SERBP1	plasminogen activator inhibitor 1 RNA-binding protein isoform 1	21	183	21	1.1	**8E-13**	1.0	**4E-13**	1.0	**2E-04**	**0.6**	**9E-06**	0.9	**2E-03**	RNA binding	Cytoplasm;Nucleus	RNA binding protein
5430	POLR2A	DNA-directed RNA polymerase II subunit RPB1	19	54	19	1.1	**2E-04**	0.9	**5E-05**	1.1	2E-01	0.9	**3E-05**	1.0	6E-02	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
6093	ROCK1	rho-associated protein kinase 1	20	69	15	1.1	**5E-04**	0.9	**1E-04**	1.1	3E-01	1.0	**8E-07**	1.1	3E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
10427;	SEC24B	protein transport protein Sec24B isoform a	8	22	7	1.1	**9E-04**	0.9	**7E-04**	1.1	**2E-02**	1.0	**9E-04**	0.9	**6E-03**	Transporter activity	Cytoplasm	Transport/cargo protein
79876	UBA5	ubiquitin-like modifier-activating enzyme 5 isoform 1	5	21	5	1.1	**1E-03**	1.0	**1E-03**	1.1	**9E-03**	1.2	**1E-03**	1.0	4E-01	Protein binding	Integral to membrane	Ubiquitin proteasome system protein
54968	TMEM70	transmembrane protein 70, mitochondrial isoform a	3	14	3	1.1	**4E-03**	1.0	**7E-04**	1.2	**1E-02**	1.3	**9E-04**	1.1	**6E-03**	Molecular function unknown	Mitochondrion	Unclassified
51204	TACO1	translational activator of cytochrome c oxidase 1	5	20	5	1.1	**2E-02**	1.1	**1E-02**	1.2	1E-01	1.4	**7E-03**	1.1	3E-01	Molecular function unknown	-	Unclassified
124540	MSI2	RNA-binding protein Musashi homolog 2 isoform a	3	20	3	1.1	**2E-02**	1.4	**4E-02**	1.1	1E-01	0.8	3E-01	1.1	6E-01	RNA binding	Cytoplasm	RNA binding protein
9689	BZW1	basic leucine zipper and W2 domain-containing protein 1 isoform 2	23	160	20	1.1	**1E-10**	0.9	**3E-13**	1.1	1E-01	1.3	**1E-10**	0.9	**4E-03**	Transcription factor activity	Nucleus	Transcription factor
7174	TPP2	tripeptidyl-peptidase 2	28	138	28	1.1	**4E-10**	0.9	**4E-11**	1.1	8E-01	1.1	**1E-10**	1.0	1E-01	Aminopeptidase activity	Cytoplasm	Aminopeptidase
987	LRBA	lipopolysaccharide-responsive and beige-like anchor protein isoform 2	29	111	29	1.1	**6E-10**	1.1	**3E-09**	1.1	**6E-07**	1.1	**3E-10**	1.0	4E-01	Cytoskeletal anchoring activity	Golgi apparatus	Anchor protein
55210	ATAD3A	ATPase family AAA domain-containing protein 3A isoform 2	21	131	7	1.1	**2E-09**	1.2	**3E-11**	1.3	**6E-09**	**1.5**	**3E-12**	1.1	**2E-03**	ATPase activity	-	ATPase
10480	EIF3M	eukaryotic translation initiation factor 3 subunit M	11	65	11	1.1	**2E-07**	0.9	**1E-06**	1.0	8E-01	0.9	**4E-07**	0.9	**2E-03**	Molecular function unknown	-	Unclassified
7266	DNAJC7	dnaJ homolog subfamily C member 7 isoform 1	16	83	16	1.1	**3E-06**	0.9	**2E-07**	1.0	9E-01	0.7	1E-01	0.9	**2E-03**	Chaperone activity	Cytoplasm	Chaperone
11273	ATXN2L	ataxin-2-like protein isoform A	17	85	16	1.1	**9E-06**	0.9	**1E-06**	1.1	1E-01	0.8	**4E-04**	0.9	2E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
201626	PDE12	2',5'-phosphodiesterase 12	7	31	7	1.1	**3E-04**	0.9	**3E-04**	1.2	4E-01	1.0	**4E-03**	0.9	5E-02	Phosphoric diester hydrolase activity	-	Enzyme: Phosphodiesterase
284106	CISD3	CDGSH iron-sulfur domain-containing protein 3, mitochondrial	2	12	2	1.1	**2E-03**	0.8	**1E-02**	0.9	**3E-02**	0.8	3E-01	1.0	1E+00	Metal ion binding	-	Unclassified
6856	SYPL1	synaptophysin-like protein 1 isoform a	3	24	3	1.1	**3E-03**	1.2	**2E-04**	1.2	**5E-03**	**1.5**	**1E-03**	1.0	2E-01	Transporter activity	Cytoplasmic vesicle	Integral membrane protein
9570	GOSR2	Golgi SNAP receptor complex member 2 isoform B	4	16	4	1.1	**6E-03**	0.9	**3E-03**	1.1	9E-01	0.9	3E-01	1.0	8E-01	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9997	**SCO2**	**protein SCO2 homolog, mitochondrial**	2	12	2	1.1	**2E-02**	1.1	**7E-03**	1.4	**5E-03**	1.2	**1E-03**	0.9	8E-01	Chaperone activity	Mitochondrion	Chaperone
2939	**GSTA2**	**PREDICTED: glutathione S-transferase A2 isoform X1**	1	6	1	1.1	**2E-02**	1.2	**1E-02**	1.1	**4E-02**	1.2	9E-02	1.2	**2E-02**	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase
28972	**SPCS1**	**signal peptidase complex subunit 1**	2	10	2	1.1	**2E-02**	1.0	**1E-02**	1.2	5E-01	1.3	1E-01	1.0	8E-01	Signal peptidase activity	Endoplasmic reticulum membrane	Unclassified
338382	**RAB7B**	**ras-related protein Rab-7b isoform a**	3	16	3	1.1	**4E-02**	1.2	4E-01	0.7	5E-02	**0.5**	**2E-02**	0.9	9E-02	RNA binding	Lysosome	RNA binding protein
3703	**STT3A**	**dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A isoform a**	18	130	16	1.1	**4E-11**	1.0	**4E-12**	1.1	**1E-07**	1.2	**2E-14**	1.1	**1E-07**	Molecular function unknown	Plasma membrane	Integral membrane protein
55749	**CCAR1**	**cell division cycle and apoptosis regulator protein 1 isoform a**	16	86	16	1.1	**1E-08**	1.0	**4E-10**	1.2	**2E-06**	0.9	**2E-07**	1.0	9E-01	Molecular function unknown	Cytoplasm	Cell cycle control protein
10539	**GLRX3**	**glutaredoxin-3**	12	99	12	1.1	**2E-07**	0.8	**3E-09**	1.1	**1E-04**	0.8	**2E-02**	0.9	**1E-03**	Molecular function unknown	Cytoplasm	Unclassified
60678	**EEFSEC**	**selenocysteine-specific elongation factor**	8	26	8	1.1	**3E-05**	1.0	**4E-04**	1.2	**4E-03**	1.2	**8E-04**	1.0	9E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
8834	**TMEM11**	**transmembrane protein 11, mitochondrial**	4	20	4	1.1	**4E-05**	1.2	**3E-07**	1.3	**1E-05**	1.4	**5E-07**	1.1	**3E-02**	Molecular function unknown	Plasma membrane	Integral membrane protein
55161	**TMEM33**	**PREDICTED: transmembrane protein 33 isoform X1**	6	51	6	1.1	**1E-04**	0.9	**8E-05**	1.1	8E-01	1.3	**2E-04**	1.1	**3E-04**	Molecular function unknown	Membrane fraction	Unclassified
5531	**PPP4C**	**serine/threonine-protein phosphatase 4 catalytic subunit isoform 1*gi|746816144|ref|NP_001290432.1| serine/threonine-protein phosphatase 4 catalytic subunit isoform 1**	5	31	4	1.1	**2E-03**	0.9	**1E-03**	1.3	3E-01	1.0	**4E-03**	0.9	2E-01	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase
133686	**NADK2; NADKD1**	**NAD kinase 2, mitochondrial isoform 1**	4	17	4	1.1	**7E-03**	0.9	**5E-03**	1.0	6E-01	1.0	**1E-04**	1.0	7E-01	#N/A	#N/A	#N/A
115207	**KCTD12**	**BTB/POZ domain-containing protein KCTD12**	4	14	4	1.1	**1E-02**	**0.7**	**2E-02**	1.0	2E-01	0.8	7E-01	1.0	4E-01	Ion channel activity	-	Ion channel
7324	**UBE2E1**	**ubiquitin-conjugating enzyme E2 E1 isoform 1**	3	22	1	1.1	**2E-02**	**0.7**	**2E-02**	1.2	**1E-02**	0.8	2E-01	0.9	**4E-02**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
10856	**RUVBL2**	**ruvB-like 2**	21	152	21	1.1	**1E-13**	1.0	**6E-14**	1.1	**2E-03**	1.0	**4E-12**	0.9	**9E-03**	Transcription regulator activity	Nucleus	Transcription regulatory protein
54927	**CHCHD3**	**MICOS complex subunit MIC19**	9	56	9	1.1	**2E-07**	1.1	**1E-08**	1.2	**3E-06**	1.2	**2E-07**	1.0	8E-01	Molecular function unknown	-	Unclassified
9512	**PMPCB**	**mitochondrial-processing peptidase subunit beta**	14	81	13	1.1	**2E-06**	1.1	**2E-07**	1.0	**4E-04**	1.0	**4E-07**	1.0	4E-01	Peptidase activity	Mitochondrion	Protease
5586	**PKN2**	**serine/threonine-protein kinase N2**	10	41	9	1.1	**1E-05**	1.0	**1E-06**	1.0	**1E-02**	1.0	**5E-06**	1.0	4E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
9406	**ZRANB2**	**zinc finger Ran-binding domain-containing protein 2 isoform 1**	7	38	7	1.1	**3E-04**	0.9	**1E-04**	1.1	7E-01	1.0	**8E-03**	1.0	8E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
961	**CD47**	**leukocyte surface antigen CD47 isoform 1**	3	18	3	1.1	**9E-04**	0.9	**7E-04**	1.1	6E-01	0.9	**2E-03**	1.1	**1E-02**	Molecular function unknown	Plasma membrane;Cell surface	Unclassified
10979	**FERMT2**	**fermitin family homolog 2 isoform 2**	8	29	5	1.1	**1E-03**	1.1	**4E-03**	1.1	9E-01	1.1	**5E-03**	1.2	2E-01	Structural constituent of cytoskeleton	Plasma membrane;Nucleus;Cytoplasm	Cytoskeletal protein
64841	**GNPNAT1**	**PREDICTED: glucosamine 6-phosphate N-acetyltransferase isoform X1**	7	25	7	1.1	**2E-03**	0.8	**1E-03**	1.2	2E-01	1.1	**1E-03**	0.9	8E-02	Acyltransferase activity	-	Enzyme: Acyltransferase
54815	**GATAD2A**	**transcriptional repressor p66-alpha isoform 2**	6	13	4	1.1	**2E-02**	0.9	**9E-03**	1.1	4E-01	1.0	**3E-02**	1.0	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
57700	**FAM160B1**	**protein FAM160B1 isoform a**	8	23	6	1.1	**4E-02**	0.9	**5E-03**	1.0	5E-01	1.0	**6E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
26986	**PABPC1**	**polyadenylate-binding protein 1**	26	293	21	1.1	**5E-14**	0.9	**2E-16**	1.0	**2E-03**	0.9	**6E-15**	0.9	**2E-07**	RNA binding	Cytoplasm	RNA binding protein
9097	**USP14**	**ubiquitin carboxyl-terminal hydrolase 14 isoform a**	24	139	24	1.1	**4E-11**	1.0	**1E-12**	1.1	**6E-03**	1.0	**2E-13**	1.0	6E-01	Ubiquitin-specific protease activity	Cytosol	Ubiquitin proteasome system protein
8504	**PEX3**	**peroxisomal biogenesis factor 3**	6	27	6	1.1	**3E-05**	1.1	**3E-03**	1.1	**6E-04**	1.2	8E-02	1.0	5E-01	Protein binding	Peroxisome	Integral membrane protein
2130	**EWSR1**	**RNA-binding protein EWS isoform 1**	3	24	3	1.1	**5E-04**	0.9	**1E-04**	1.1	8E-01	0.8	8E-01	0.9	2E-01	RNA binding	Nucleus	RNA binding protein
55293	**UEVLD**	**ubiquitin-conjugating enzyme E2 variant 3 isoform a**	6	23	6	1.1	**3E-03**	0.9	**6E-03**	1.1	4E-01	1.1	**2E-03**	1.0	8E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
653519;	**GPR89A**	**Golgi pH regulator A isoform 2**	3	7	3	1.1	**9E-03**	1.0	**4E-03**	1.2	3E-01	1.1	**8E-04**	1.1	5E-01	G-protein coupled receptor activity	-	G protein coupled receptor
23243	**ANKRD28**	**serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A isoform a**	4	15	4	1.1	**2E-02**	0.9	**1E-03**	1.1	5E-01	1.0	**4E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
79877	**DCAKD**	**dephospho-CoA kinase domain-containing protein**	2	10	2	1.1	**5E-02**	1.0	**2E-02**	1.4	6E-02	1.0	1E-01	1.0	5E-01	Kinase activity	-	Enzyme: Phosphorylase
1933	**EEF1B2**	**elongation factor 1-beta**	10	132	7	1.1	**3E-15**	0.9	**7E-15**	1.0	**1E-02**	0.9	**2E-12**	0.9	**3E-04**	Translation regulator activity	Cytoplasm	Translation regulatory protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
5160	**PDHA1**	**pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform 2**	13	75	13	1.1	**1E-10**	1.2	**3E-12**	1.2	**1E-10**	1.4	**7E-12**	1.1	**4E-03**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
9475	**ROCK2**	**rho-associated protein kinase 2**	21	79	16	1.1	**2E-10**	1.0	**2E-11**	1.2	**7E-03**	1.1	**2E-11**	1.0	1E+00	Protein serine/threonine kinase activity	Nucleus;Cytoplasm	Serine/threonine kinase
5062	**PAK2**	**serine/threonine-protein kinase PAK 2**	14	100	10	1.1	**4E-06**	0.7	**1E-06**	1.0	**6E-05**	0.7	**4E-02**	0.9	**2E-03**	Protein serine/threonine kinase activity	Endoplasmic reticulum	Serine/threonine kinase
5886	**RAD23A**	**UV excision repair protein RAD23 homolog A isoform 1**	6	44	4	1.1	**1E-05**	1.0	**3E-08**	1.3	**2E-03**	1.0	**1E-05**	0.8	**2E-03**	DNA binding	Nucleus	DNA repair protein
26003	**GORASP2**	**Golgi reassembly-stacking protein 2 isoform 1**	7	25	6	1.1	**1E-04**	1.1	**1E-04**	1.2	**2E-03**	1.3	**8E-04**	1.0	3E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
6832	**SUPV3L1**	**ATP-dependent RNA helicase SUPV3L1, mitochondrial isoform 1**	10	46	10	1.1	**4E-04**	1.0	**7E-04**	1.2	**4E-03**	1.1	**4E-04**	1.0	4E-01	RNA binding	Mitochondrion	RNA binding protein
24144	**TFIP11**	**tuftelin-interacting protein 11**	10	37	10	1.1	**5E-04**	0.8	**1E-05**	1.2	8E-02	1.0	**2E-03**	0.9	9E-02	Extracellular matrix structural constituent	Nucleus	Extracellular matrix protein
348	**APOE**	**apolipoprotein E isoform a**	7	20	7	1.1	**7E-04**	0.9	2E-01	0.8	1E+00	1.1	**1E-02**	1.2	9E-02	Transporter activity	Extracellular	Transport/cargo protein
10928	**RALBP1**	**ralA-binding protein 1**	6	16	6	1.1	**6E-03**	0.9	**3E-02**	1.2	3E-01	1.2	**2E-02**	1.0	8E-01	GTPase activator activity	Plasma membrane	GTPase activating protein
90231	**KIAA2013**	**uncharacterized protein KIAA2013**	2	8	2	1.1	**2E-02**	0.9	8E-02	0.8	5E-01	0.9	8E-02	1.0	5E-01	Molecular function unknown	Integral to membrane	Unclassified
10591	**C6orf108; DNPH1**	**2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 1**	4	19	4	1.1	**3E-02**	0.9	**1E-02**	1.2	6E-01	1.1	**4E-02**	0.9	**3E-02**	#N/A	#N/A	#N/A
11194	**ABCB8**	**ATP-binding cassette sub-family B member 8, mitochondrial isoform a**	4	15	4	1.1	**4E-02**	1.2	**1E-02**	1.3	**2E-02**	**1.5**	**3E-02**	1.1	3E-01	Transporter activity	Mitochondrion	Transport/cargo protein
10855	**HPSE**	**heparanase isoform 1 preproprotein**	2	8	2	1.1	7E-02	0.8	7E-02	1.3	2E-01	1.2	**2E-02**	1.1	**2E-02**	Catalytic activity	Lysosome	Enzyme: Glycosidase
84134	**TOMM40L**	**PREDICTED: mitochondrial import receptor subunit TOM40B isoform X1**	1	8	1	1.1	2E-01	1.3	**8E-03**	1.2	**4E-02**	**1.6**	**7E-04**	1.2	2E-01	Molecular function unknown	-	Unclassified
6136	**RPL12**	**60S ribosomal protein L12**	10	105	10	1.1	**6E-12**	1.0	**2E-08**	0.9	**3E-04**	0.8	1E-01	1.0	2E-01	Structural constituent of ribosome	Nucleus	Ribosomal subunit
5714	**PSMD8**	**26S proteasome non-ATPase regulatory subunit 8**	12	107	12	1.1	**1E-10**	1.0	**7E-12**	1.2	**2E-06**	1.3	**2E-13**	1.0	1E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
27069	**GHITM**	**growth hormone-inducible transmembrane protein**	5	35	5	1.1	**7E-08**	1.2	**4E-08**	1.2	**1E-07**	1.2	**1E-07**	0.9	**3E-02**	Molecular function unknown	Integral to membrane	Integral membrane protein
153443	**SRFBP1**	**serum response factor-binding protein 1**	5	15	5	1.1	**4E-03**	0.7	**6E-03**	1.1	**2E-02**	**0.6**	**4E-02**	0.8	**2E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
996	**CDC27**	**cell division cycle protein 27 homolog isoform 1**	6	19	6	1.1	**4E-03**	1.0	**3E-02**	1.0	**1E-02**	**1.5**	**3E-02**	1.0	5E-01	Protein binding	Nucleus	Cell cycle control protein
6002	**RGS12**	**PREDICTED: regulator of G-protein signaling 12 isoform X1**	3	11	3	1.1	**5E-03**	1.0	**2E-02**	1.1	8E-02	1.1	2E-01	1.0	6E-01	GTPase activator activity	Nucleus	GTPase activating protein
23382	**AHCYL2**	**putative adenosylhomocysteinase 3 isoform b**	15	90	6	1.1	**2E-02**	0.9	8E-02	0.8	5E-01	0.7	8E-02	0.9	3E-01	Molecular function unknown	-	Enzyme: Lyase;Unclassified
51029	**DESI2**	**desumoylating isopeptidase 2 isoform 1**	1	5	1	1.1	**5E-02**	1.1	**4E-02**	1.2	2E-01	**1.5**	**4E-03**	1.0	5E-01	#N/A	#N/A	#N/A
4140	**MARK3**	**MAP/microtubule affinity-regulating kinase 3 isoform a**	16	54	7	1.1	**5E-02**	1.0	6E-02	1.2	4E-01	1.2	**4E-02**	1.1	2E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
54861	**SNRK**	**SNF-related serine/threonine-protein kinase**	1	3	1	1.1	1E-01	0.9	1E-01	1.1	3E-01	1.2	2E-01	1.0	4E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
23019	**CNOT1**	**CCR4-NOT transcription complex subunit 1 isoform a**	39	152	39	1.1	**2E-16**	1.0	**2E-16**	1.1	**2E-04**	1.1	**4E-15**	1.0	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
7791	**ZYX**	**zyxin*gi|58530845|ref|NP_001010972.1| zyxin**	8	62	8	1.1	**1E-08**	0.7	**4E-09**	0.9	**4E-06**	0.7	**5E-04**	0.9	6E-02	Cell adhesion molecule activity	Plasma membrane;Cytoplasm	Adhesion molecule
65985	**AACS**	**acetoacetyl-CoA synthetase**	14	67	14	1.1	**5E-07**	0.8	**6E-08**	1.0	6E-02	**0.6**	**1E-05**	0.9	**6E-03**	Ligase activity	Cytoplasm	Enzyme: Ligase
1265	**CNN2**	**calponin-2 isoform d**	8	75	7	1.1	**1E-05**	0.8	**6E-05**	0.9	**2E-02**	0.8	1E+00	0.9	7E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
2585	**GALK2**	**N-acetylgalactosamine kinase isoform 1**	5	30	5	1.1	**3E-03**	1.0	**3E-03**	1.3	**7E-03**	1.1	**4E-04**	1.0	4E-01	Galactosyltransferase activity	Cytoplasm	Enzyme: Sugar phosphotransferase
79879	**CCDC134**	**coiled-coil domain-containing protein 134 isoform 1**	3	12	3	1.1	**1E-02**	0.9	**1E-02**	1.2	1E+00	1.1	**4E-02**	0.9	6E-01	Molecular function unknown	-	Unclassified
51330	**TNFRSF12A**	**tumor necrosis factor receptor superfamily member 12A**	1	6	1	1.1	**2E-02**	1.1	1E-01	0.9	2E-01	**0.6**	**2E-03**	1.4	**3E-02**	Receptor activity	Plasma membrane	Cell surface receptor
7402	**UTRN**	**utrophin**	8	18	7	1.1	6E-02	0.9	2E-01	1.0	8E-01	0.9	8E-01	1.0	9E-01	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein
9946	**CRYZL1**	**quinone oxidoreductase-like protein 1**	4	12	4	1.1	1E-01	1.0	1E-01	1.0	2E-01	0.9	1E-01	1.0	9E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
3099	**HK2**	**hexokinase-2**	25	178	20	1.1	**1E-13**	0.9	**8E-14**	1.0	7E-02	0.9	**3E-07**	1.0	**9E-04**	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
51292	**GMPR2**	**GMP reductase 2 isoform 4**	11	45	11	1.1	**8E-06**	1.0	**2E-05**	1.2	**1E-05**	1.1	**3E-07**	1.0	7E-01	Catalytic activity	Cytoplasm	Enzyme: Reductase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6742	**SSBP1**	**single-stranded DNA-binding protein, mitochondrial*gi|374671785|ref|NP_001243440.1| single-stranded DNA-binding protein, mitochondrial*gi|374671787|ref|NP_001243441.1| single-stranded DNA-binding protein, mitochondrial*gi|374671789|ref|NP_001243442.1| single-stranded DNA-binding protein, mitochondrial*gi|4507231|ref|NP_003134.1| single-stranded DNA-binding protein, mitochondrial**	6	87	6	1.1	**2E-05**	1.1	**8E-06**	1.2	**5E-07**	1.2	**1E-10**	1.0	6E-02	DNA binding	Mitochondrion	DNA binding protein
123803;	**NTAN1**	**protein N-terminal asparagine amidohydrolase isoform 1**	10	22	3	1.1	**4E-04**	0.8	**8E-05**	0.9	8E-01	0.7	3E-01	0.9	**4E-03**	Hydrolase activity	-	Enzyme: Hydrolase
1613	**DAPK3**	**PREDICTED: death-associated protein kinase 3 isoform X1**	8	31	7	1.1	**1E-02**	0.9	**8E-03**	1.1	7E-01	0.8	**2E-02**	1.0	7E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
54704	**PDP1**	**pyruvate dehyrogenase phosphatase catalytic subunit 1 isoform 2**	5	17	5	1.1	**2E-02**	1.1	**1E-02**	1.3	**3E-02**	1.0	**1E-02**	1.2	6E-02	Protein serine/threonine phosphatase activity	Mitochondrion	Serine/threonine phosphatase
10939	**AFG3L2**	**AFG3-like protein 2**	22	125	22	1.1	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	1.1	**2E-16**	1.0	**3E-02**	ATPase activity	Mitochondrion	ATPase
3030	**HADHA**	**trifunctional enzyme subunit alpha, mitochondrial**	31	257	31	1.1	**2E-16**	1.3	**2E-16**	1.2	**2E-16**	**1.5**	**2E-16**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
6499	**SKIV2L**	**helicase SKI2W**	18	77	18	1.1	**3E-06**	1.2	**9E-07**	1.2	**1E-05**	1.2	**4E-07**	1.0	4E-01	RNA binding	Nucleolus	RNA binding protein
27000	**DNAJC2**	**dnaJ homolog subfamily C member 2 isoform 1**	12	36	12	1.1	**3E-04**	0.9	**1E-04**	1.1	6E-02	1.0	**3E-05**	1.0	8E-01	Chaperone activity	Nucleus	Chaperone
23327	**NEDD4L**	**E3 ubiquitin-protein ligase NEDD4-like isoform 1**	9	43	5	1.1	**1E-03**	0.8	**7E-06**	0.9	2E-01	0.9	**2E-05**	1.0	1E-01	Ubiquitin-specific protease activity	Plasma membrane;Perinuclear region	Ubiquitin proteasome system protein
84916	**CIRH1A; UTP4**	**cirhin**	5	19	5	1.1	**3E-03**	0.9	**3E-03**	1.3	1E-01	0.9	8E-02	0.9	9E-01	#N/A	#N/A	#N/A
10533	**ATG7**	**ubiquitin-like modifier-activating enzyme ATG7 isoform a**	4	14	4	1.1	**4E-03**	0.9	**4E-03**	1.1	6E-01	1.0	**3E-03**	0.9	7E-02	Molecular function unknown	Cytoplasm	Unclassified
329	**BIRC2**	**baculoviral IAP repeat-containing protein 2 isoform 1**	2	8	2	1.1	**9E-03**	1.0	9E-02	0.9	2E-01	0.9	1E-01	1.0	8E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
64146	**PDF**	**peptide deformylase, mitochondrial**	2	8	2	1.1	**1E-02**	0.9	**2E-02**	1.3	6E-01	1.3	**2E-02**	1.0	6E-01	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase
3909	**LAMA3**	**laminin subunit alpha-3 isoform 1**	66	617	65	1.1	**2E-16**	0.8	**2E-16**	1.2	**2E-08**	1.3	**2E-16**	1.4	**2E-16**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
6184	**RPN1**	**dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1**	32	273	32	1.1	**2E-16**	1.0	**2E-16**	1.1	**2E-10**	1.2	**2E-16**	1.1	**1E-07**	Ubiquitin-specific protease activity	Endoplasmic reticulum;Nucleus;Cytosol	Ubiquitin proteasome system protein
79709	**COLGALT1; GLT25D1**	**procollagen galactosyltransferase 1**	18	111	18	1.1	**5E-09**	0.9	**2E-09**	1.2	6E-01	1.0	**4E-10**	0.9	**5E-02**	#N/A	#N/A	#N/A
23788	**MTCH2**	**mitochondrial carrier homolog 2**	12	74	12	1.1	**7E-07**	1.2	**8E-07**	1.2	**7E-06**	1.2	**1E-06**	1.0	3E-01	Molecular function unknown	Mitochondrion	Unclassified
10471	**PFDN6**	**prefoldin subunit 6*gi|388240786|ref|NP_001252525.1| prefoldin subunit 6*gi|388240788|ref|NP_001252524.1| prefoldin subunit 6*gi|7657162|ref|NP_055075.1| prefoldin subunit 6**	7	47	7	1.1	**2E-05**	0.9	**4E-06**	1.2	8E-01	1.0	**1E-06**	1.0	2E-01	Chaperone activity	-	Chaperone
58485	**TRAPPC1**	**trafficking protein particle complex subunit 1*gi|262263327|ref|NP_001160093.1| trafficking protein particle complex subunit 1**	3	14	3	1.1	**1E-03**	1.1	**9E-04**	1.1	**3E-02**	1.2	**6E-05**	1.1	8E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
8379	**MAD1L1**	**mitotic spindle assembly checkpoint protein MAD1 isoform a**	8	22	8	1.1	**6E-03**	1.0	**5E-05**	1.3	3E-01	1.1	**9E-04**	1.0	5E-01	Molecular function unknown;Transcription regulator activity	Nucleus	Transcription regulatory protein;Unclassified
57171	**DOLPP1**	**dolichyldiphosphatase 1 isoform a**	1	5	1	1.1	8E-02	1.2	8E-02	1.3	**5E-02**	1.6	7E-02	1.2	1E-01	Acid phosphatase activity	Endoplasmic reticulum	Enzyme: Acid phosphatase
57169	**ZNFX1**	**NFX1-type zinc finger-containing protein 1**	3	6	3	1.1	3E-01	0.8	4E-01	1.0	2E-01	0.8	6E-01	0.9	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
10283	**CWC27**	**peptidyl-prolyl cis-trans isomerase CWC27 homolog isoform 1**	3	11	3	1.1	4E-01	1.1	3E-01	1.0	**3E-02**	0.9	2E-01	1.0	2E-01	Isomerase activity	-	Enzyme: Isomerase
10776	**ARPP19**	**PREDICTED: cAMP-regulated phosphoprotein 19 isoform X2**	4	20	3	1.1	#N/A	0.9	#N/A	1.2	#N/A	0.9	#N/A	1.0	#N/A	Molecular function unknown	Cytoplasm	Unclassified
7407	**VARS**	**valine--tRNA ligase**	42	277	42	1.1	**5E-15**	1.0	**2E-15**	1.2	**1E-11**	1.1	**2E-16**	1.0	2E-01	Ligase activity	-	Enzyme: Ligase
79180	**EFHD2**	**EF-hand domain-containing protein D2**	12	83	11	1.1	**2E-08**	0.9	**1E-10**	1.2	**1E-03**	1.0	**3E-12**	1.1	**1E-02**	Molecular function unknown	Nucleus;Cytoplasm	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
25813	SAMM50	sorting and assembly machinery component 50 homolog	13	72	13	1.1	**4E-07**	1.1	**4E-07**	1.2	**1E-05**	1.3	**3E-07**	1.0	**2E-02**	Molecular function unknown	Mitochondrion	Unclassified
26019	UPF2	regulator of nonsense transcripts 2	11	50	11	1.1	**8E-06**	0.9	**1E-06**	1.0	9E-01	0.9	**5E-03**	1.0	4E-01	RNA binding;MRNA binding	Cytoplasm	RNA binding protein
4594	MUT	PREDICTED: methylmalonyl-CoA mutase, mitochondrial isoform X1	11	44	11	1.1	**4E-05**	1.2	**4E-05**	1.5	**5E-05**	**1.6**	**5E-05**	1.0	**1E-02**	Catalytic activity	Mitochondrion	Enzyme: Mutase
5050	PAFAH1B3	platelet-activating factor acetylhydrolase IB subunit gamma	6	37	6	1.1	**3E-04**	0.9	**1E-04**	1.4	8E-01	1.2	**9E-05**	1.1	1E-01	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
22929	SEPHS1	selenide, water dikinase 1 isoform 1	6	22	5	1.1	**2E-03**	0.8	**1E-03**	1.2	2E-01	1.1	**3E-03**	0.9	3E-01	ATP binding	-	Enzyme: Synthase
83594	NUDT12	peroxisomal NADH pyrophosphatase NUDT12 isoform 1	4	12	4	1.1	**3E-03**	1.2	**2E-02**	1.2	5E-02	1.3	**2E-03**	0.8	7E-02	Hydrolase activity	Peroxisome	Enzyme: Hydrolase
65059;	RAPH1	ras-associated and pleckstrin homology domains-containing protein 1 isoform 1	3	7	3	1.1	**5E-03**	0.8	**2E-02**	1.2	2E-01	1.3	**8E-03**	1.0	9E-01	Cytoskeletal protein binding	Cell projection	Cytoskeletal associated protein
8650	NUMB	protein numb homolog isoform 4	9	32	9	1.1	**6E-03**	1.0	**6E-03**	1.2	**7E-03**	1.1	**2E-03**	1.0	9E-01	Molecular function unknown	Plasma membrane;Nucleus;Cytoplasm	Unclassified
1739	DLG1	disks large homolog 1 isoform 1	11	44	11	1.1	**9E-03**	1.3	**4E-04**	1.2	**7E-06**	1.0	**2E-02**	1.0	2E-01	Cell adhesion molecule activity	Plasma membrane;Nucleus;Cytoplasm;Membrane fraction;Cell junction	Cell junction protein
125228;	FAM210A	protein FAM210A*gi|149408153|ref|NP_001092271.1| protein FAM210A	2	4	2	1.1	7E-02	0.9	**1E-02**	1.0	3E-01	1.1	5E-02	1.1	**5E-02**	#N/A	#N/A	#N/A
1195	CLK1	dual specificity protein kinase CLK1 isoform 2	2	7	2	1.1	1E-01	1.1	**4E-02**	1.1	5E-01	1.8	8E-02	1.1	3E-01	Protein threonine/tyrosine kinase activity	Nucleus	Dual specificity kinase
5929	RBBP5	retinoblastoma-binding protein 5 isoform 1	3	14	3	1.1	**3E-04**	0.8	**7E-04**	1.2	**1E-02**	0.7	4E-01	0.8	**4E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
55706	NDC1; TMEM48	nucleoporin NDC1 isoform 1	5	19	5	1.1	**8E-04**	1.0	**6E-05**	1.2	1E-01	1.1	**6E-04**	1.1	**2E-02**	#N/A	#N/A	#N/A
25963	TMEM87A	transmembrane protein 87A isoform 1	6	24	6	1.1	**7E-03**	1.1	**3E-02**	1.0	**2E-02**	0.9	7E-02	1.0	9E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
23365	ARHGEF12	rho guanine nucleotide exchange factor 12 isoform 1	7	20	6	1.1	7E-02	1.0	**4E-02**	1.0	2E-01	0.9	1E-01	0.9	2E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
79901	CYBRD1	cytochrome b reductase 1 isoform 1	3	12	3	1.1	7E-02	1.3	2E-01	0.8	**5E-02**	0.7	4E-01	0.9	3E-01	Oxidoreductase activity	Plasma membrane	Enzyme: Oxidoreductase
6175	RPLP0	60S acidic ribosomal protein P0	12	178	12	1.1	**2E-16**	1.0	**2E-16**	1.0	**7E-06**	0.8	**1E-04**	1.0	8E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
3094	HINT1	histidine triad nucleotide-binding protein 1	5	57	5	1.1	**3E-10**	0.8	**2E-08**	1.1	1E-01	0.9	**9E-06**	0.9	**2E-07**	ATPase activity	Cytoplasm	ATPase
847	CAT	catalase	12	62	12	1.1	**6E-07**	1.3	**2E-07**	1.1	**2E-06**	**1.5**	**3E-08**	0.9	8E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
2010	EMD	emerin	8	50	8	1.1	**2E-05**	1.2	**4E-06**	1.3	**3E-05**	1.4	**3E-06**	1.0	2E-01	Structural molecule activity	Nucleus	Structural protein
26528	DAZAP1	DAZ-associated protein 1 isoform b	4	14	4	1.1	**3E-04**	0.9	**5E-03**	1.1	3E-01	0.7	4E-01	0.8	**2E-02**	RNA binding	Nucleus	RNA binding protein
593	BCKDHA	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial isoform 1	6	22	6	1.1	**3E-03**	1.2	**2E-03**	1.1	**3E-03**	1.1	**2E-04**	1.0	8E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
54664	TMEM106B	transmembrane protein 106B*gi|40254893|ref|NP_060844.2| transmembrane protein 106B	4	12	4	1.1	**6E-03**	0.9	**8E-03**	1.0	7E-01	1.3	**2E-03**	0.9	2E-01	Molecular function unknown	Integral to membrane	Unclassified
79594	MUL1	mitochondrial ubiquitin ligase activator of NFKB 1	1	6	1	1.1	**7E-03**	1.0	**4E-03**	1.0	4E-01	1.2	2E-01	1.2	3E-01	Molecular function unknown	-	Unclassified
10682	EBP	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	2	11	2	1.1	**9E-03**	**1.9**	**4E-03**	1.3	**8E-04**	**2.3**	**1E-03**	1.4	**2E-03**	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase
1525	CXADR	coxsackievirus and adenovirus receptor isoform 1	3	12	3	1.1	**1E-02**	1.0	3E-01	0.7	2E-01	**0.5**	**1E-02**	1.0	2E-01	Receptor activity	Plasma membrane	Cell surface receptor
114884	OSBPL10	oxysterol-binding protein-related protein 10 isoform 1	7	33	6	1.1	5E-02	0.8	9E-02	1.1	2E-01	1.0	**3E-02**	1.0	4E-01	Transporter activity	Cytoplasm	Transport/cargo protein
293	SLC25A6	ADP/ATP translocase 3	18	286	2	1.1	**2E-16**	1.0	**2E-16**	1.0	**2E-16**	1.2	**2E-16**	1.0	**2E-02**	Transporter activity	Mitochondrion	Transport/cargo protein
9775	EIF4A3	eukaryotic initiation factor 4A-III	19	166	16	1.1	**7E-12**	0.9	**1E-13**	1.2	1E-01	0.9	**6E-08**	1.0	3E-01	Molecular function unknown	Nucleus	Unclassified
10960	LMAN2	vesicular integral-membrane protein VIP36	11	83	11	1.1	**9E-11**	1.0	**3E-11**	1.2	**3E-05**	1.0	**5E-10**	1.0	8E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
4939	OAS2	2'-5'-oligoadenylate synthase 2 isoform 1	12	52	12	1.1	**3E-04**	0.8	**7E-03**	0.6	3E-01	0.9	7E-01	1.0	7E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
80346	REEP4	receptor expression-enhancing protein 4	4	18	4	1.1	**8E-04**	1.0	**8E-03**	1.1	**1E-03**	1.2	**2E-04**	1.0	8E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
22911	WDR47	WD repeat-containing protein 47 isoform 1	8	28	8	1.1	**1E-03**	0.8	**4E-04**	1.0	1E-01	0.8	4E-01	0.9	2E-01	Molecular function unknown	-	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
116985	**ARAP1**	**arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform c**	5	20	5	1.1	**3E-03**	1.0	**1E-03**	1.5	2E-01	1.2	**2E-03**	1.0	6E-01	GTPase activator activity	Golgi apparatus	GTPase activating protein
956	**ENTPD3**	**ectonucleoside triphosphate diphosphohydrolase 3 isoform 1*gi|634743275|ref|NP_001278889.1| ectonucleoside triphosphate diphosphohydrolase 3 isoform 1**	1	6	1	1.1	**3E-02**	0.8	**4E-02**	1.3	3E-01	1.1	**4E-03**	1.1	**1E-02**	Hydrolase activity	Plasma membrane	Enzyme: Hydrolase
23410	**SIRT3**	**NAD-dependent protein deacetylase sirtuin-3, mitochondrial isoform a**	2	6	2	1.1	1E-01	1.1	8E-02	1.2	**4E-02**	1.4	**2E-02**	1.0	9E-01	Deacetylase activity	Mitochondrion	Enzyme: Deacetylase
7094	**TLN1**	**talin-1**	79	407	79	1.1	**2E-16**	1.0	**2E-16**	1.1	**9E-07**	1.1	**2E-16**	1.0	6E-02	Cytoskeletal protein binding	Extracellular	Cytoskeletal associated protein
3921	**RPSA**	**40S ribosomal protein SA isoform 2**	13	140	13	1.1	**3E-10**	0.9	**2E-09**	0.9	**4E-02**	0.8	**2E-02**	1.0	6E-01	Structural constituent of ribosome;Cell adhesion molecule activity	Cytoplasm	Cell surface receptor;Ribosomal subunit
6451	**SH3BGRL**	**SH3 domain-binding glutamic acid-rich-like protein**	8	49	8	1.1	**2E-05**	1.1	**2E-05**	1.1	**4E-05**	**0.7**	**3E-03**	1.0	5E-01	Molecular function unknown	-	Unclassified
10273	**STUB1**	**E3 ubiquitin-protein ligase CHIP isoform a**	11	65	11	1.1	**1E-04**	1.0	**3E-05**	1.0	**9E-03**	0.8	**2E-02**	0.9	6E-02	Ligase activity	Cytoplasm	Enzyme: Ligase
51428	**DDX41**	**probable ATP-dependent RNA helicase DDX41**	7	23	7	1.1	**2E-03**	1.0	**2E-03**	1.4	**3E-02**	1.2	**2E-03**	1.1	**1E-02**	Helicase activity	Nucleolus	RNA helicase
30968	**STOML2**	**stomatin-like protein 2, mitochondrial isoform a**	11	90	11	1.1	**3E-07**	1.1	**1E-09**	1.3	**4E-07**	1.3	**7E-10**	1.0	**1E-02**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
1841	**DTYMK**	**thymidylate kinase isoform 1**	10	64	10	1.1	**9E-06**	0.8	**7E-07**	1.1	**8E-03**	0.9	**3E-07**	1.0	7E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
2776	**GNAQ**	**guanine nucleotide-binding protein G(q) subunit alpha**	9	38	4	1.1	**4E-05**	1.1	**6E-05**	1.1	3E-01	1.2	**4E-05**	1.1	2E-01	GTPase activity	Plasma membrane	G protein
1176	**AP3S1**	**AP-3 complex subunit sigma-1**	4	25	4	1.1	**3E-03**	1.0	**3E-03**	1.0	**3E-02**	0.9	**4E-02**	1.0	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
8440	**NCK2**	**cytoplasmic protein NCK2 isoform A*gi|52630425|ref|NP_001004720.1| cytoplasmic protein NCK2 isoform A**	7	24	6	1.1	**7E-03**	0.8	**1E-02**	1.0	2E-01	0.9	**9E-03**	0.9	1E-01	Signal transducer activity	Cytoplasm	Adapter molecule
26061	**HACL1**	**2-hydroxyacyl-CoA lyase 1 isoform a**	6	17	6	1.1	**3E-02**	1.1	**3E-03**	1.2	**2E-02**	**1.5**	**7E-03**	1.1	2E-01	Lyase activity	Peroxisome	Enzyme: Lyase
653583	**PHLDB3**	**pleckstrin homology-like domain family B member 3**	3	8	3	1.1	8E-02	1.2	9E-02	1.2	1E-01	1.3	**4E-02**	1.4	3E-01	Molecular function unknown	-	Unclassified
6191	**RPS4X**	**40S ribosomal protein S4, X isoform X isoform**	17	194	17	1.1	**1E-10**	1.0	**4E-09**	0.9	**4E-05**	0.8	**1E-03**	1.0	8E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
55705	**IPO9**	**importin-9**	18	98	18	1.1	**6E-10**	0.9	**2E-12**	1.1	**2E-02**	0.9	**6E-10**	1.0	4E-01	Transporter activity	Cytoplasm	Transport/cargo protein
10452	**TOMM40**	**mitochondrial import receptor subunit TOM40 homolog**	6	40	6	1.1	**8E-06**	1.0	**1E-05**	1.1	**9E-06**	1.2	**1E-05**	1.0	1E+00	Transporter activity	Mitochondrion	Transport/cargo protein
80349	**WDR61**	**WD repeat-containing protein 61 isoform a**	7	33	7	1.1	**2E-05**	1.1	**4E-06**	1.1	**9E-04**	1.0	**1E-06**	1.0	2E-01	Molecular function unknown	-	Unclassified
116540	**MRPL53**	**39S ribosomal protein L53, mitochondrial**	4	20	4	1.1	**5E-05**	1.3	**2E-04**	1.1	**3E-02**	1.0	**2E-02**	1.2	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
54543	**TOMM7**	**mitochondrial import receptor subunit TOM7 homolog**	2	10	2	1.1	**2E-03**	1.0	**3E-03**	1.2	**2E-03**	1.2	**6E-03**	1.0	2E-01	Transporter activity	Mitochondrion	Transport/cargo protein
9648	**GCC2**	**GRIP and coiled-coil domain-containing protein 2**	8	38	6	1.1	**2E-03**	1.0	**1E-02**	1.1	2E-01	1.2	**4E-03**	1.0	2E-01	Structural molecule activity	Golgi apparatus	Structural protein
10162	**LPCAT3**	**lysophospholipid acyltransferase 5**	3	10	3	1.1	**6E-03**	1.4	**6E-04**	1.2	**8E-04**	1.3	**2E-04**	1.0	7E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
10892	**MALT1**	**mucosa-associated lymphoid tissue lymphoma translocation protein 1 isoform a**	6	19	6	1.1	**7E-03**	1.0	**1E-02**	1.1	1E-01	1.0	1E-01	0.9	9E-01	Endopeptidase activity	Cytoplasm	Enzyme: Hydrolase
11230	**PRAF2**	**PRA1 family protein 2**	2	15	2	1.1	**2E-02**	1.1	**2E-02**	1.2	**9E-03**	1.3	**7E-03**	1.1	8E-02	Molecular function unknown	-	Integral membrane protein
23078	**VWA8**	**von Willebrand factor A domain-containing protein 8 isoform a**	16	51	16	1.1	**8E-05**	1.0	**8E-05**	1.0	**2E-03**	0.9	**1E-04**	1.0	9E-01	#N/A	#N/A	#N/A
29926	**GMPPA**	**mannose-1-phosphate guanyltransferase alpha**	7	44	7	1.1	**3E-04**	0.9	**8E-05**	1.2	9E-01	1.3	**1E-04**	1.0	4E-01	Phosphorylase activity	-	Enzyme: Phosphorylase
9491	**PSMF1**	**proteasome inhibitor PI31 subunit*gi|145611430|ref|NP_848693.2| proteasome inhibitor PI31 subunit**	4	11	4	1.1	**1E-03**	0.8	**2E-03**	0.9	7E-02	0.7	2E-01	1.0	4E-01	Protease inhibitor activity	Nuclear membrane	Protease inhibitor
10300	**KATNB1**	**katanin p80 WD40 repeat-containing subunit B1**	4	20	4	1.1	**2E-02**	0.9	**4E-04**	1.2	3E-01	0.9	9E-02	1.1	9E-01	Transporter activity	Centrosome	Transport/cargo protein
1.01E+08	**RPL36A-HNRNPH2**	**RPL36A-HNRNPH2 protein isoform a**	6	52	2	1.1	#N/A	1.0	#N/A	1.0	#N/A	0.7	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
10525	**HYOU1**	**hypoxia up-regulated protein 1**	36	247	36	1.1	**2E-16**	0.9	**2E-16**	1.2	7E-02	1.1	**2E-16**	1.0	**7E-05**	Chaperone activity	Endoplasmic reticulum	Chaperone
3614	**IMPDH1**	**inosine-5'-monophosphate dehydrogenase 1 isoform a**	13	54	11	1.1	**3E-05**	0.8	**3E-06**	1.2	2E-01	0.9	**1E-04**	1.1	2E-01	Catalytic activity	Cytosol	Enzyme: Dehydrogenase

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10322	**SMYD5**	**SET and MYND domain-containing protein 5**	4	26	4	1.1	**4E-05**	0.9	**4E-05**	1.2	1E+00	1.1	**2E-03**	1.0	2E-01	Methyltransferase activity	-	Enzyme: Methyltransferase
25801	**GCA**	**grancalcin**	3	13	3	1.1	**4E-03**	0.9	**1E-03**	1.2	8E-01	1.0	**2E-02**	1.0	6E-01	Calcium ion binding	Cytoplasm	Calcium binding protein
84936	**ZFYVE19**	**abscission/NoCut checkpoint regulator isoform 1**	2	8	1	1.1	**7E-03**	0.9	**5E-04**	1.2	5E-01	1.1	6E-02	1.0	4E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
7263	**TST**	**thiosulfate sulfurtransferase*gi|395394071|ref|NP_001257412.1| thiosulfate sulfurtransferase**	2	9	2	1.1	**1E-02**	1.0	**1E-02**	0.9	5E-02	0.8	3E-01	0.9	3E-01	Sulfotransferase activity	Mitochondrion	Enzyme: Sulphotransferase
9927	**MFN2**	**mitofusin-2*gi|7662004|ref|NP_055689.1| mitofusin-2**	7	30	6	1.1	**2E-02**	1.0	**2E-02**	1.2	2E-01	1.2	**1E-02**	1.0	4E-01	Molecular function unknown	Mitochondrion	Unclassified
84958	**SYTL1**	**synaptotagmin-like protein 1 isoform 1**	4	18	4	1.1	**2E-02**	**1.6**	**1E-02**	1.0	**3E-03**	1.0	**2E-03**	1.0	9E-01	Molecular function unknown	Plasma membrane	Unclassified
104	**ADARB1**	**double-stranded RNA-specific editase 1 isoform 3**	2	4	2	1.1	4E-01	1.2	2E-01	1.4	3E-01	1.2	1E-01	1.1	7E-01	Deaminase activity	Nucleus	Enzyme: Deaminase
7073	**TIAL1**	**nucleolysin TIAR isoform 2**	11	55	7	1.1	**2E-06**	0.9	**3E-06**	1.2	7E-02	1.0	**4E-04**	1.0	8E-01	RNA binding	Nucleus	RNA binding protein
22	**ABCB7**	**ATP-binding cassette sub-family B member 7, mitochondrial isoform 1**	4	12	4	1.1	**2E-02**	1.0	**2E-02**	1.1	**3E-02**	1.3	**5E-02**	1.1	6E-02	Transporter activity	Mitochondrion	Transport/cargo protein
55015	**PRPF39**	**pre-mRNA-processing factor 39**	3	13	3	1.1	**3E-02**	0.7	**2E-02**	1.2	3E-01	0.8	9E-02	0.9	1E-01	Molecular function unknown	-	Unclassified
84062	**DTNBP1**	**dysbindin isoform a**	3	10	3	1.1	3E-01	0.9	**2E-02**	1.2	6E-01	1.1	2E-01	0.9	3E-01	Protein binding	Cytoplasm	Unclassified
55379	**LRRC59**	**leucine-rich repeat-containing protein 59**	14	167	14	1.1	**7E-13**	0.8	**2E-13**	1.1	**3E-05**	1.0	**3E-16**	1.0	**1E-03**	Molecular function unknown	Integral to membrane	Unclassified
27436	**EML4**	**echinoderm microtubule-associated protein-like 4 isoform a**	16	70	16	1.1	**4E-08**	0.9	**2E-10**	1.2	8E-02	1.1	**1E-10**	0.9	1E-01	Structural molecule activity	Cytoplasm	Structural protein
4144	**MAT2A**	**S-adenosylmethionine synthase isoform type-2**	18	99	18	1.1	**1E-06**	0.7	**4E-07**	1.1	**4E-03**	0.7	1E-01	0.9	**9E-05**	Catalytic activity	Cytoplasm	Enzyme: Adenosyltransferase
2937	**GSS**	**PREDICTED: glutathione synthetase isoform X1**	18	96	18	1.1	**3E-06**	1.0	**3E-07**	1.1	**1E-05**	1.0	**1E-07**	1.0	3E-01	Ligase activity	-	Enzyme: Ligase
10498	**CARM1**	**histone-arginine methyltransferase CARM1**	9	48	9	1.1	**4E-05**	0.8	**2E-05**	1.0	**1E-02**	0.9	**8E-06**	0.9	**2E-02**	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase
79714	**CCDC51**	**coiled-coil domain-containing protein 51 isoform 1*gi|94536784|ref|NP_078937.3| coiled-coil domain-containing protein 51 isoform 1**	10	29	10	1.1	**2E-03**	0.9	**1E-03**	1.2	2E-01	1.2	**4E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
51478	**HSD17B7**	**3-keto-steroid reductase isoform 1**	5	23	4	1.1	**7E-03**	1.1	**5E-03**	1.2	**4E-03**	1.3	**1E-03**	1.1	8E-02	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
25816	**TNFAIP8**	**tumor necrosis factor alpha-induced protein 8 isoform c**	3	22	3	1.1	**1E-02**	0.9	**8E-03**	1.2	3E-01	1.0	**1E-02**	0.9	**1E-02**	Molecular function unknown	Cytoplasm	Unclassified
84172	**POLR1B**	**DNA-directed RNA polymerase I subunit RPA2 isoform 3**	5	15	5	1.1	5E-02	0.8	**5E-02**	1.2	2E-01	0.9	4E-01	1.0	5E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
1434	**CSE1L**	**exportin-2 isoform 1**	32	286	32	1.1	**2E-16**	0.9	**2E-16**	1.1	5E-01	1.0	**2E-16**	0.9	**7E-04**	Transporter activity	Nucleus	Transport/cargo protein
5910	**RAP1GDS1**	**rap1 GTPase-GDP dissociation stimulator 1 isoform 1**	16	113	3	1.1	**2E-16**	0.9	**1E-13**	1.0	**5E-03**	0.9	**4E-10**	1.0	3E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
1508	**CTSB**	**cathepsin B preproprotein**	8	75	8	1.1	**5E-09**	1.1	**3E-09**	1.2	**2E-07**	1.1	**4E-09**	0.9	7E-02	Cysteine-type peptidase activity	Lysosome	Cysteine protease
3866	**KRT15**	**keratin, type I cytoskeletal 15**	34	3546	15	1.1	**1E-08**	1.2	**5E-07**	0.9	**1E-14**	**1.6**	**9E-13**	1.1	**2E-05**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
7064	**THOP1**	**thimet oligopeptidase**	17	88	17	1.1	**7E-07**	0.9	**8E-08**	1.1	3E-01	1.0	**9E-09**	1.0	9E-01	Metallopeptidase activity	Cytoplasm	Metallo protease
1457	**CSNK2A1**	**casein kinase II subunit alpha isoform a*gi|4503095|ref|NP_001886.1| casein kinase II subunit alpha isoform a**	9	50	8	1.1	**2E-06**	1.0	**2E-06**	1.1	2E-01	1.2	**2E-06**	1.1	2E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
56052	**ALG1**	**chitobiosyldiphosphodolichol beta-mannosyltransferase**	6	24	6	1.1	**6E-04**	1.1	**2E-04**	1.1	**4E-03**	1.0	**2E-03**	1.0	8E-01	Mannosyltransferase activity	Endoplasmic reticulum	Enzyme: Mannosyltransferase
5499	**PPP1CA**	**serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 1**	15	136	3	1.1	**5E-08**	0.9	**2E-10**	1.2	8E-02	1.0	**4E-09**	0.9	**2E-05**	Protein serine/threonine phosphatase activity	Cytoskeleton	Serine/threonine phosphatase
1017	**CDK2**	**cyclin-dependent kinase 2 isoform 1**	7	36	6	1.1	**6E-07**	0.8	**2E-06**	1.2	2E-01	1.1	**3E-04**	1.2	6E-02	Kinase activity	Nucleus	Cell cycle control protein
51603	**METTL13**	**methyltransferase-like protein 13 isoform 1**	5	22	5	1.1	**2E-03**	0.9	**6E-04**	1.1	5E-01	0.9	1E-01	1.0	7E-01	Molecular function unknown	-	Unclassified
10280	**SIGMAR1**	**sigma non-opioid intracellular receptor 1 isoform 1**	5	26	5	1.1	**5E-03**	1.0	**1E-03**	1.3	2E-01	1.3	**4E-03**	1.0	6E-01	Transmembrane receptor activity	Plasma membrane	Integral membrane protein
6560	**SLC12A4**	**solute carrier family 12 member 4 isoform c**	6	21	6	1.1	**8E-03**	1.1	**4E-03**	1.0	4E-01	1.3	**3E-03**	1.2	**3E-02**	Ion transporter activity	Plasma membrane	Integral membrane protein
9986; 79703	**RCE1; C11orf80**	**CAAX prenyl protease 2 isoform 1**	1	5	1	1.1	**2E-02**	1.1	5E-02	1.5	5E-01	**1.6**	**2E-02**	1.2	9E-02	#N/A	#N/A	#N/A

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
613	BCR	breakpoint cluster region protein isoform 1	8	42	6	1.1	**3E-02**	0.9	**2E-02**	1.1	4E-01	1.0	**1E-02**	1.0	2E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
1984	EIF5A	eukaryotic translation initiation factor 5A-1 isoform A	11	235	11	1.1	**2E-16**	0.9	**2E-16**	1.1	1E-01	0.9	**8E-16**	1.0	5E-01	Translation factor activity, nucleic acid binding	Cytoplasm	Translation Factor
5836	PYGL	glycogen phosphorylase, liver form isoform 1	46	481	39	1.1	**2E-16**	0.9	**2E-16**	1.1	7E-02	0.9	**2E-16**	0.9	**6E-05**	Phosphorylase activity	-	Enzyme: Phosphorylase
3704	ITPA	inosine triphosphate pyrophosphatase isoform a	6	35	6	1.1	**4E-07**	1.1	**4E-08**	1.2	**9E-04**	1.0	**4E-06**	0.9	**7E-03**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
4864	NPC1	PREDICTED: Niemann-Pick C1 protein isoform X1	12	34	12	1.1	**2E-06**	1.1	**2E-07**	1.4	**9E-07**	**1.6**	**2E-07**	1.1	**7E-03**	Receptor activity	Cytoplasm	Cell surface receptor
26608	TBL2	transducin beta-like protein 2	14	66	14	1.1	**5E-06**	0.9	**2E-07**	1.1	4E-01	1.1	**4E-05**	1.0	1E+00	Molecular function unknown	Nucleus	Unclassified
8428	STK24	serine/threonine-protein kinase 24 isoform a	15	102	7	1.1	**1E-05**	0.9	**2E-06**	1.1	3E-01	1.2	**9E-05**	1.0	4E-01	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase
90861	HN1L	hematological and neurological expressed 1-like protein	6	44	6	1.1	**1E-04**	0.8	**4E-05**	1.0	**2E-04**	**0.6**	**7E-05**	0.9	**3E-04**	Transcription regulator activity	Nucleus	Transcription regulatory protein
9416	DDX23	probable ATP-dependent RNA helicase DDX23	19	82	19	1.1	**3E-04**	1.0	**4E-05**	1.2	**4E-02**	1.0	**9E-07**	1.0	2E-01	RNA binding	Nucleus	RNA binding protein
57122	NUP107	nuclear pore complex protein Nup107	9	35	9	1.1	**2E-03**	1.0	**1E-03**	1.1	**2E-03**	1.2	**2E-03**	1.1	9E-02	Transporter activity	Nucleus	Transport/cargo protein
2027	ENO3	beta-enolase isoform 1*gi|301897477|ref|NP_443739.3| beta-enolase isoform 1	5	112	1	1.1	5E-02	1.1	2E-01	1.1	1E-01	0.8	5E-01	1.2	4E-01	Catalytic activity	Extracellular	Enzyme: Hydratase
23016	EXOSC7	exosome complex component RRP42	3	8	3	1.1	1E-01	0.9	6E-02	1.3	1E+00	1.0	7E-02	0.9	8E-01	Ribonuclease activity	Nucleolus	Ribonuclease
6204	RPS10	40S ribosomal protein S10*gi|323276700|ref|NP_001191020.1| 40S ribosomal protein S10*gi|4506679|ref|NP_001005.1| 40S ribosomal protein S10	10	233	9	1.1	**2E-16**	0.9	**2E-16**	1.0	**4E-04**	0.7	**6E-03**	1.0	3E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
142	PARP1	poly [ADP-ribose] polymerase 1	30	123	30	1.1	**5E-16**	0.8	**3E-15**	1.0	**1E-04**	0.7	1E-01	0.9	3E-01	Catalytic activity	Nucleus	Enzyme: Ribosyltransferase
8125	ANP32A	acidic leucine-rich nuclear phosphoprotein 32 family member A	10	94	5	1.1	**2E-09**	1.0	**5E-11**	1.2	1E-01	1.0	**2E-06**	0.9	8E-01	MHC class I receptor activity;MHC class II receptor activity	Nucleus	MHC complex protein
56829	ZC3HAV1	zinc finger CCCH-type antiviral protein 1 isoform 1	15	47	15	1.1	**3E-05**	0.8	**1E-06**	1.0	1E+00	1.0	**3E-02**	1.1	3E-01	Defense/immunity protein activity	Cytoplasm;Nucleus	-
6788	STK3	PREDICTED: serine/threonine-protein kinase 3 isoform X1	10	41	7	1.1	**2E-04**	0.9	**2E-04**	1.2	3E-01	1.2	**2E-04**	1.1	1E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
22796	COG2	conserved oligomeric Golgi complex subunit 2 isoform 1	5	20	5	1.1	**8E-04**	0.9	**4E-05**	1.1	3E-01	1.1	**2E-04**	0.9	4E-01	Structural molecule activity	Golgi apparatus	Structural protein
285282;	RABL3	rab-like protein 3	3	8	3	1.1	**1E-02**	1.2	**4E-03**	1.1	**9E-03**	**1.6**	**7E-03**	1.0	1E-01	GTPase activity	-	GTPase
6311	ATXN2	ataxin-2	8	31	7	1.1	**2E-02**	1.0	**2E-03**	1.2	8E-02	1.0	**9E-04**	0.9	4E-01	RNA binding	Cytoplasm	RNA binding protein
79763	ISOC2	isochorismatase domain-containing protein 2, mitochondrial isoform 2	2	8	2	1.1	8E-02	1.0	6E-02	1.2	2E-01	1.1	8E-02	0.9	5E-01	Molecular function unknown	-	Unclassified
219402	MTIF3	PREDICTED: translation initiation factor IF-3, mitochondrial isoform X1	2	8	2	1.1	1E-01	1.2	1E-01	1.2	1E-01	1.1	9E-02	1.1	3E-01	Translation regulator activity	Mitochondrion	Translation regulatory protein
3735	KARS	lysine--tRNA ligase isoform 2	23	208	23	1.1	**6E-13**	0.8	**7E-14**	1.1	8E-02	1.0	**1E-09**	1.0	7E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
1650	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	9	93	9	1.1	**1E-09**	1.0	**5E-11**	1.1	**4E-03**	1.1	**2E-09**	1.0	9E-02	Galactosyltransferase activity	Endoplasmic reticulum	Enzyme: Galactosyltransferase
9646	CTR9	RNA polymerase-associated protein CTR9 homolog	8	28	8	1.1	**2E-04**	1.0	**1E-03**	1.1	2E-01	0.9	**4E-02**	1.3	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
57572	DOCK6	dedicator of cytokinesis protein 6	11	26	8	1.1	**6E-04**	1.2	**3E-05**	1.1	**4E-03**	1.3	**2E-03**	1.1	3E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
57521	RPTOR	regulatory-associated protein of mTOR isoform 1	8	25	8	1.1	**8E-04**	1.0	**2E-03**	1.1	**1E-02**	1.0	**1E-03**	1.0	2E-01	Molecular function unknown	Cytoplasm	Unclassified
8812	CCNK	PREDICTED: cyclin-K isoform X1	3	17	3	1.1	**6E-03**	0.9	**2E-03**	1.1	5E-01	0.9	**9E-04**	1.1	5E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
113251;	LARP4	la-related protein 4 isoform f	6	10	6	1.1	**7E-03**	1.0	**2E-05**	1.1	1E-01	1.1	**9E-03**	1.0	2E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
5074	PAWR	PRKC apoptosis WT1 regulator protein	5	22	5	1.1	**1E-02**	1.0	**3E-03**	1.0	3E-01	0.9	**1E-02**	1.0	1E+00	Transcription regulator activity	Nucleus	Transcription regulatory protein
56984	PSMG2	proteasome assembly chaperone 2 isoform 1	5	16	5	1.1	**2E-02**	0.9	**1E-02**	1.4	1E-01	1.0	**7E-03**	0.9	6E-01	Molecular function unknown	Nucleus	Cell cycle control protein
51074	APIP	methylthioribulose-1-phosphate dehydratase	3	14	3	1.1	**4E-02**	0.9	**2E-02**	1.5	5E-01	0.8	4E-01	1.1	6E-01	Molecular function unknown	Cytoplasm	Unclassified
191	AHCY	adenosylhomocysteinase isoform 1	22	261	21	1.1	**2E-16**	0.9	**2E-16**	1.1	4E-01	1.0	**2E-16**	1.0	3E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
6202	RPS8	40S ribosomal protein S8	8	130	8	1.1	**3E-12**	1.0	**2E-11**	0.9	**5E-03**	0.8	**1E-04**	0.9	**2E-06**	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
84955	NUDCD1	nudC domain-containing protein 1 isoform 1	13	71	13	1.1	**4E-10**	0.8	**3E-12**	1.1	**1E-05**	1.1	**4E-11**	1.0	9E-02	Molecular function unknown	-	Unclassified

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8882	ZNF259; ZPR1	zinc finger protein ZPR1	9	58	9	1.1	**1E-03**	0.8	**4E-04**	1.1	**2E-02**	0.8	**1E-03**	0.9	**1E-02**	#N/A	#N/A	#N/A
10157	AASS	alpha-aminoadipic semialdehyde synthase, mitochondrial	7	22	7	1.1	**3E-03**	1.0	**7E-04**	1.0	**3E-02**	0.9	**3E-02**	1.1	5E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase;Enzyme: Synthase
9882	TBC1D4	TBC1 domain family member 4 isoform 1	6	15	6	1.1	**1E-02**	0.9	**7E-03**	1.1	2E-01	0.9	1E-01	1.0	7E-01	GTPase activator activity	Nucleus;Cytoplasm	GTPase activating protein
9361	LONP1	lon protease homolog, mitochondrial isoform 1	25	134	25	1.1	**8E-13**	1.1	**5E-13**	1.1	**2E-09**	1.2	**2E-12**	1.0	**2E-02**	Serine-type peptidase activity	Mitochondrion	Serine protease
8450	CUL4B	cullin-4B isoform 1	21	122	11	1.1	**1E-07**	1.0	**1E-08**	1.0	**1E-02**	1.0	**2E-06**	0.9	7E-02	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
6224	RPS20	40S ribosomal protein S20 isoform 1	4	54	4	1.1	**2E-07**	0.9	**4E-08**	1.0	**4E-02**	0.8	2E-01	0.9	1E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
85441	HELZ2	helicase with zinc finger domain 2 isoform 1	7	13	7	1.1	**3E-03**	0.8	**2E-02**	0.9	1E-01	0.8	1E-01	1.0	4E-01	#N/A	#N/A	#N/A
51586	MED15	mediator of RNA polymerase II transcription subunit 15 isoform a	4	12	4	1.1	8E-02	0.9	**6E-03**	1.1	6E-01	1.0	7E-02	0.9	2E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
7453	WARS	tryptophan--tRNA ligase, cytoplasmic isoform a*gi|47419916|ref|NP_776049.1| tryptophan--tRNA ligase, cytoplasmic isoform a	13	109	13	1.1	**2E-12**	0.8	**3E-11**	1.2	**2E-03**	0.9	**6E-12**	0.9	**7E-07**	Ligase activity	Cytoplasm	Enzyme: Ligase
10432	RBM14	RNA-binding protein 14 isoform 1	18	105	18	1.1	**5E-11**	0.9	**7E-12**	1.2	7E-01	0.9	**5E-10**	1.0	7E-02	RNA binding	Nucleus	RNA binding protein
6675	UAP1	PREDICTED: UDP-N-acetylhexosamine pyrophosphorylase isoform X1	19	61	18	1.1	**6E-11**	**0.5**	**2E-06**	0.8	**4E-11**	**0.5**	**3E-08**	1.0	7E-01	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase
10558	SPTLC1	serine palmitoyltransferase 1 isoform a	11	66	11	1.1	**9E-10**	1.0	**5E-09**	1.0	**2E-04**	1.0	**8E-09**	1.0	8E-01	Palmitoyltransferase activity	Endoplasmic reticulum	Enzyme: Palmitoyltransferase
64210	MMS19	MMS19 nucleotide excision repair protein homolog isoform 1	18	74	18	1.1	**7E-07**	0.9	**7E-09**	1.1	6E-01	1.1	**1E-08**	1.1	**2E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
23196	FAM120A	constitutive coactivator of PPAR-gamma-like protein 1 isoform a	23	85	23	1.1	**9E-07**	0.9	**2E-06**	1.1	4E-01	0.8	**2E-04**	1.0	1E-01	Molecular function unknown	Nucleus	Unclassified
51372	TMA7	translation machinery-associated protein 7	2	18	2	1.1	**1E-02**	0.8	**2E-02**	1.0	2E-01	**0.6**	**3E-03**	0.7	**3E-04**	#N/A	#N/A	#N/A
84272	YIPF4	protein YIPF4	2	12	2	1.1	**2E-02**	1.0	**1E-02**	1.1	7E-02	1.0	**1E-02**	0.9	5E-01	Molecular function unknown	-	Unclassified
9277	WDR46	WD repeat-containing protein 46 isoform 1	1	8	1	1.1	**3E-02**	0.7	**6E-03**	1.1	5E-01	1.0	3E-01	1.2	4E-01	Molecular function unknown	Nucleolus	Unclassified
23677	SH3BP4	PREDICTED: SH3 domain-binding protein 4 isoform X1	4	9	4	1.1	6E-02	1.1	**2E-02**	0.8	7E-01	0.7	7E-01	1.0	5E-01	Receptor signaling complex scaffold activity	-	Adapter molecule
57698	KIAA1598; SHTN1	shootin-1 isoform a	21	92	21	1.1	**3E-11**	0.9	**1E-13**	1.0	3E-01	0.9	**4E-03**	1.0	2E-01	#N/A	#N/A	#N/A
6772	STAT1	PREDICTED: signal transducer and activator of transcription 1-alpha/beta isoform X1	31	86	31	1.1	**2E-09**	0.9	**1E-06**	0.6	2E-01	**0.4**	**1E-08**	0.8	**1E-06**	Transcription factor activity	Cytoplasm	Transcription factor
11331	PHB2	prohibitin-2 isoform 1	21	169	21	1.1	**2E-08**	1.1	**6E-10**	1.2	**4E-09**	1.4	**4E-10**	1.0	**7E-05**	Transcription regulator activity	Nucleus	Transcription regulatory protein
55854	ZC3H15	zinc finger CCCH domain-containing protein 15	11	47	11	1.1	**3E-07**	1.0	**5E-06**	1.2	**8E-03**	1.0	**3E-06**	1.0	2E-01	DNA binding	Nucleus;Cytoplasm	DNA binding protein
55735	DNAJC11	dnaJ homolog subfamily C member 11	12	68	12	1.1	**4E-06**	1.2	**6E-08**	1.2	**2E-06**	1.2	**3E-08**	1.1	6E-02	Molecular function unknown	-	Unclassified
8883	NAE1	NEDD8-activating enzyme E1 regulatory subunit isoform d	12	47	12	1.1	**2E-04**	1.0	**1E-05**	1.3	**1E-03**	1.3	**5E-05**	1.0	7E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
126003	TRAPPC5	trafficking protein particle complex subunit 5	7	31	7	1.1	**4E-04**	1.0	**2E-04**	1.0	7E-01	0.9	**3E-02**	1.0	4E-01	Molecular function unknown	-	Unclassified
347734	SLC35B2	adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform a	5	26	5	1.1	**4E-04**	0.7	**1E-04**	1.0	**9E-04**	0.7	2E-01	0.9	**3E-02**	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein
116143	WDR92	WD repeat-containing protein 92 isoform 1	4	18	4	1.1	**2E-03**	0.9	**2E-03**	1.2	7E-01	0.8	2E-01	0.9	6E-02	Calcium ion binding;Caspase activator activity	Nucleus	Calcium binding protein
27237	ARHGEF16	rho guanine nucleotide exchange factor 16	7	31	7	1.1	**2E-03**	1.1	**5E-03**	1.3	**4E-04**	1.4	**1E-02**	1.0	2E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
9135	RABEP1	rab GTPase-binding effector protein 1 isoform 1	5	18	5	1.1	6E-02	0.9	**2E-02**	1.1	3E-01	1.1	**5E-03**	0.9	8E-02	GTPase activator activity	Cytoplasm;Nucleus	GTPase activating protein
84632	AFAP1L2	actin filament-associated protein 1-like 2 isoform 3	7	18	7	1.1	6E-02	0.8	5E-02	1.1	2E-01	1.0	**7E-03**	1.0	7E-01	Transcription regulator activity	Cytoplasm	Adapter molecule
158219	TTC39B	tetratricopeptide repeat protein 39B isoform 1	2	8	2	1.1	7E-02	1.4	**5E-02**	1.3	**5E-02**	**1.6**	**3E-02**	1.0	3E-01	Molecular function unknown	-	Unclassified
605	BCL7A	B-cell CLL/lymphoma 7 protein family member A isoform a	2	9	2	1.1	2E-01	0.8	1E-01	1.2	3E-01	0.7	3E-01	0.9	2E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
204	AK2	adenylate kinase 2, mitochondrial isoform a	13	113	13	1.1	**9E-10**	1.1	**1E-10**	1.2	**4E-11**	1.1	**1E-10**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase
7378	UPP1	uridine phosphorylase 1 isoform a	13	95	13	1.1	**2E-08**	**0.5**	**4E-09**	1.2	**1E-11**	1.3	**7E-12**	1.0	**3E-02**	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
23521	**RPL13A**	**60S ribosomal protein L13a isoform 1**	8	96	8	1.1	**2E-08**	0.9	**9E-11**	0.9	3E-01	0.7	6E-01	1.0	3E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
51008	**ASCC1**	**activating signal cointegrator 1 complex subunit 1 isoform b*gi|311771712|ref|NP_001185729.1| activating signal cointegrator 1 complex subunit 1 isoform b**	5	31	5	1.1	**2E-06**	1.0	**8E-06**	1.1	**9E-04**	0.9	**7E-03**	1.0	9E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
23173	**METAP1**	**methionine aminopeptidase 1**	8	38	8	1.1	**3E-05**	1.0	**2E-05**	1.1	**3E-02**	1.0	**3E-05**	0.9	2E-01	Aminopeptidase activity	Nucleolus	Aminopeptidase
7247	**TSN**	**translin isoform 1**	10	60	10	1.1	**5E-05**	0.9	**4E-05**	1.1	7E-02	1.0	**1E-05**	0.9	**3E-02**	DNA binding	Nucleus	DNA binding protein
84324	**SARNP**	**SAP domain-containing ribonucleoprotein**	6	42	6	1.1	**2E-04**	1.0	**4E-05**	1.1	**1E-02**	0.7	1E-01	1.0	5E-01	Molecular function unknown	Nucleus	Unclassified
6830	**SUPT6H**	**transcription elongation factor SPT6**	6	31	5	1.1	**3E-03**	0.9	**2E-05**	1.4	3E-01	1.3	**2E-03**	0.9	2E-01	Transcription factor activity	Nucleus	Transcription factor
29101	**SSU72**	**RNA polymerase II subunit A C-terminal domain phosphatase SSU72**	5	19	5	1.1	**6E-03**	0.8	**2E-03**	1.0	1E-01	0.9	2E-01	0.8	**8E-04**	Molecular function unknown	-	Unclassified
57510	**XPO5**	**exportin-5**	10	41	10	1.1	**7E-03**	1.0	**9E-03**	1.0	9E-02	0.8	4E-01	1.0	5E-01	Transporter activity	Nucleus	Transport/cargo protein
9556	**C14orf2**	**6.8 kDa mitochondrial proteolipid isoform 1**	2	7	2	1.1	**1E-02**	1.1	**1E-02**	1.1	**2E-02**	0.8	1E-01	0.9	2E-01	Molecular function unknown	-	Unclassified
1859	**DYRK1A**	**PREDICTED: dual specificity tyrosine-phosphorylation-regulated kinase 1A isoform X2**	3	8	3	1.1	**1E-02**	0.8	**4E-02**	1.2	2E-01	1.1	**4E-02**	1.0	5E-01	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase
3835	**KIF22**	**kinesin-like protein KIF22 isoform 1**	1	6	1	1.1	**5E-02**	1.0	1E-01	1.1	3E-01	0.9	**9E-04**	1.1	5E-02	DNA binding	Nucleus	DNA binding protein
200014	**CC2D1B**	**coiled-coil and C2 domain-containing protein 1B**	11	15	10	1.1	1E-01	0.9	6E-02	1.1	1E-01	0.9	5E-01	0.9	2E-01	Molecular function unknown	-	Unclassified
1969	**EPHA2**	**ephrin type-A receptor 2**	21	104	18	1.1	**3E-13**	0.8	**2E-13**	1.2	**1E-06**	1.2	**8E-12**	1.1	**4E-05**	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase
8879	**SGPL1**	**PREDICTED: sphingosine-1-phosphate lyase 1 isoform X1**	13	74	13	1.1	**4E-08**	1.1	**8E-09**	1.1	**7E-04**	1.3	**2E-07**	1.0	7E-01	Lyase activity	Endoplasmic reticulum	Enzyme: Lyase
23586	**DDX58**	**probable ATP-dependent RNA helicase DDX58**	7	25	7	1.1	**3E-04**	0.8	1E+00	0.7	8E-02	0.6	2E-01	1.0	4E-01	Molecular function unknown	Cytoplasm	RNA helicase
79033	**ERI3**	**ERI1 exoribonuclease 3 isoform 1**	3	11	3	1.1	**5E-04**	1.0	**1E-03**	1.3	1E-01	1.1	**3E-02**	0.9	9E-01	Molecular function unknown	-	Unclassified
60526	**C2orf43; LDAH**	**UPF0554 protein C2orf43 isoform a**	3	9	3	1.1	**2E-03**	1.0	**3E-03**	1.0	3E-01	1.1	**3E-03**	1.0	9E-01	#N/A	#N/A	#N/A
8480	**RAE1**	**mRNA export factor**	7	28	7	1.1	**2E-03**	1.0	**5E-04**	1.2	5E-02	1.1	**2E-04**	1.0	8E-01	RNA binding	Nucleus	RNA binding protein
10717	**AP4B1**	**AP-4 complex subunit beta-1 isoform 1**	3	9	3	1.1	**3E-03**	0.8	**1E-02**	1.0	2E-01	1.1	**6E-03**	0.9	8E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
201965	**RWDD4**	**RWD domain-containing protein 4**	2	11	2	1.1	5E-02	0.8	**3E-02**	1.2	5E-01	0.9	**5E-02**	1.1	6E-01	#N/A	#N/A	#N/A
4047	**LSS**	**lanosterol synthase isoform 1**	19	119	19	1.1	**7E-16**	1.0	**2E-15**	1.2	**7E-08**	1.1	**6E-16**	1.1	**6E-03**	Catalytic activity	Endoplasmic reticulum	Enzyme: Mutase
3796	**KIF2A**	**kinesin-like protein KIF2A isoform 2**	11	36	11	1.1	**1E-05**	1.0	**1E-06**	1.1	**2E-02**	1.1	**7E-06**	1.1	**2E-02**	Motor activity	Cytoplasm	Motor protein
4124	**MAN2A1**	**alpha-mannosidase 2**	7	25	7	1.1	**5E-04**	1.0	**5E-05**	1.0	2E-01	0.9	**2E-02**	1.0	2E-01	Catalytic activity	Golgi apparatus	Enzyme: Glycosidase
90678	**LRSAM1**	**E3 ubiquitin-protein ligase LRSAM1 isoform 1*gi|53729361|ref|NP_001005373.1| E3 ubiquitin-protein ligase LRSAM1 isoform 1*gi|53729363|ref|NP_001005374.1| E3 ubiquitin-protein ligase LRSAM1 isoform 1**	6	18	5	1.1	**1E-03**	1.0	**3E-03**	1.0	**4E-02**	0.9	**3E-02**	0.9	8E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
94134	**ARHGAP12**	**rho GTPase-activating protein 12 isoform 1**	5	14	5	1.1	**8E-03**	0.8	**1E-02**	1.1	**3E-02**	1.3	**2E-02**	0.9	6E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
51125	**GOLGA7**	**Golgin subfamily A member 7 isoform a**	4	20	4	1.1	**1E-02**	1.1	**4E-04**	1.0	**6E-03**	1.4	**1E-03**	1.0	1E-01	Transporter activity	Golgi apparatus	Integral membrane protein
1.01E+08	**C15orf38-AP3S2**	**C15orf38-AP3S2 fusion protein**	2	8	2	1.1	#N/A	1.2	#N/A	1.2	#N/A	0.9	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
57136	**APMAP**	**adipocyte plasma membrane-associated protein**	14	98	14	1.1	**3E-16**	1.1	**2E-16**	1.2	**2E-08**	1.2	**2E-16**	1.0	**3E-02**	#N/A	#N/A	#N/A
8607	**RUVBL1**	**ruvB-like 1**	19	139	19	1.1	**2E-15**	0.9	**4E-14**	1.2	**5E-03**	1.0	**1E-14**	1.0	2E-01	DNA binding	Nucleus	DNA binding protein
55623	**THUMPD1**	**THUMP domain-containing protein 1**	11	54	11	1.1	**2E-09**	0.9	**5E-11**	1.2	7E-01	0.8	**3E-02**	0.9	**7E-03**	Molecular function unknown	Cytoplasm	Unclassified
34	**ACADM**	**medium-chain specific acyl-CoA dehydrogenase, mitochondrial isoform d**	10	58	10	1.1	**2E-07**	1.1	**2E-08**	1.2	**2E-07**	1.1	**8E-09**	1.1	**2E-02**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
178	**AGL**	**glycogen debranching enzyme isoform 1**	21	72	21	1.1	**4E-07**	1.1	**7E-07**	1.0	**8E-03**	1.1	**2E-05**	1.1	7E-02	Glucosidase activity	Cytoplasm	Enzyme: Glucosidase
54884	**RETSAT**	**all-trans-retinol 13,14-reductase**	14	73	14	1.1	**2E-04**	1.0	**4E-06**	1.2	**1E-02**	1.1	**5E-07**	0.9	**2E-05**	Catalytic activity	Endoplasmic reticulum membrane	Enzyme: Reductase
51690	**LSM7**	**U6 snRNA-associated Sm-like protein LSm7**	4	30	3	1.1	**3E-04**	0.9	**4E-05**	1.3	8E-01	0.9	**5E-03**	1.0	1E+00	RNA binding	Cytoplasm	RNA binding protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8226	**HDHD1; PUDP**	**pseudouridine-5'-monophosphatase isoform a**	3	14	3	1.1	**4E-04**	1.0	**1E-03**	1.2	1E-01	1.1	**6E-04**	1.0	1E+00	#N/A	#N/A	#N/A
83787	**ARMC10**	**armadillo repeat-containing protein 10 isoform a**	5	22	5	1.1	**4E-04**	1.1	**3E-04**	1.2	**1E-03**	1.1	**9E-04**	1.0	6E-01	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein
2767	**GNA11**	**guanine nucleotide-binding protein subunit alpha-11**	11	62	6	1.1	**8E-04**	0.9	**1E-03**	1.1	1E-01	1.0	**2E-03**	1.0	7E-02	GTPase activity	Plasma membrane	G protein
6009	**RHEB**	**GTP-binding protein Rheb**	6	34	6	1.1	**1E-03**	0.8	**4E-04**	1.0	**2E-03**	**0.7**	**2E-02**	0.9	2E-01	GTPase activity	Plasma membrane	GTPase
91754	**NEK9**	**serine/threonine-protein kinase Nek9**	8	26	8	1.1	**2E-03**	1.1	**2E-03**	1.1	**2E-02**	0.9	**1E-02**	0.9	8E-01	Kinase activity	Cytoplasm	Serine/threonine kinase;Cell cycle control protein
25979	**DHRS7B**	**dehydrogenase/reductase SDR family member 7B**	6	23	6	1.1	**7E-03**	1.1	**1E-02**	1.2	**6E-03**	1.3	**4E-03**	1.0	8E-01	Oxidoreductase activity	Cytosol	Enzyme: Oxidoreductase
384	**ARG2**	**arginase-2, mitochondrial**	4	10	4	1.1	**2E-02**	0.9	**3E-02**	1.3	1E+00	1.3	**2E-02**	1.0	1E-01	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase
4793	**NFKBIB**	**NF-kappa-B inhibitor beta isoform 1**	2	6	2	1.1	2E-01	0.9	3E-01	0.9	7E-01	1.0	7E-02	0.9	5E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
2746	**GLUD1**	**glutamate dehydrogenase 1, mitochondrial**	19	174	19	1.1	**2E-16**	1.2	**2E-16**	1.3	**2E-16**	**1.5**	**2E-16**	1.0	**5E-03**	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
6185	**RPN2**	**dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 isoform 1**	14	146	14	1.1	**2E-13**	1.0	**2E-14**	1.1	**8E-05**	1.1	**3E-15**	1.0	**2E-04**	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase
95	**ACY1**	**aminoacylase-1 isoform a**	11	61	11	1.1	**4E-08**	1.2	**3E-08**	1.4	**1E-07**	1.3	**1E-08**	1.0	4E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
57120	**GOPC**	**Golgi-associated PDZ and coiled-coil motif-containing protein isoform a**	8	33	8	1.1	**8E-05**	0.9	**2E-05**	1.1	6E-01	0.9	2E-01	1.0	8E-01	Receptor signaling complex scaffold activity	Golgi apparatus	Unclassified
1355	**COX15**	**cytochrome c oxidase assembly protein COX15 homolog isoform 1**	5	26	5	1.1	**2E-04**	**1.6**	**5E-06**	1.2	**1E-04**	1.2	**4E-05**	1.1	**5E-02**	Molecular function unknown	Mitochondrion	Unclassified
490	**ATP2B1**	**plasma membrane calcium-transporting ATPase 1 isoform 1b**	19	77	9	1.1	**9E-04**	0.9	**8E-09**	1.1	**2E-05**	0.9	**9E-07**	1.0	**2E-03**	ATPase activity	Plasma membrane	ATPase
51573	**GDE1**	**glycerophosphodiester phosphodiesterase 1**	2	10	2	1.1	**1E-03**	1.1	**3E-02**	1.0	2E-01	1.7	5E-02	1.0	3E-01	Cytoskeletal anchoring activity	Plasma membrane	Anchor protein
1020	**CDK5**	**cyclin-dependent-like kinase 5 isoform 1**	3	32	2	1.1	**2E-03**	1.0	**1E-02**	1.2	**1E-02**	1.1	**3E-02**	1.2	**5E-02**	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
6341	**SCO1**	**protein SCO1 homolog, mitochondrial**	4	17	4	1.1	**2E-03**	1.1	**7E-05**	1.3	**6E-03**	1.2	**7E-05**	1.1	**4E-02**	Molecular function unknown	Mitochondrion	Unclassified
11160	**ERLIN2**	**PREDICTED: erlin-2 isoform X1**	9	30	7	1.1	**3E-03**	1.2	**4E-03**	1.2	**5E-03**	1.1	**1E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
60684	**TRAPPC11**	**trafficking protein particle complex subunit 11 isoform a**	3	9	3	1.1	6E-02	1.1	**2E-02**	1.1	1E-01	1.2	**2E-02**	1.0	4E-01	#N/A	#N/A	#N/A
10606	**PAICS**	**multifunctional protein ADE2 isoform 1**	18	136	18	1.1	**7E-15**	0.8	**3E-14**	1.2	**1E-03**	0.9	**3E-11**	1.0	2E-01	Ligase activity	Nucleus	Enzyme: Carboxylase
5536	**PPP5C**	**serine/threonine-protein phosphatase 5 isoform 1**	12	67	12	1.1	**2E-08**	0.9	**3E-09**	1.3	4E-01	1.1	**2E-08**	1.0	5E-01	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase
64359	**NXN**	**nucleoredoxin isoform 1**	13	66	13	1.1	**7E-08**	0.9	**3E-07**	1.1	2E-01	0.8	2E-01	1.0	1E-01	Oxidoreductase activity	Nucleus	Enzyme: Oxidoreductase
587	**BCAT2**	**branched-chain-amino-acid aminotransferase, mitochondrial isoform a**	7	39	7	1.1	**2E-05**	1.2	**1E-06**	1.3	**2E-04**	1.3	**3E-06**	0.9	1E-01	Transaminase activity	Mitochondrion	Enzyme: Aminotransferase
6606; 6607	**SMN1; SMN2**	**survival motor neuron protein isoform a**	4	12	4	1.1	**3E-03**	1.1	**4E-03**	1.2	**3E-02**	1.2	**2E-03**	1.1	2E-01	#N/A	#N/A	#N/A
51056	**LAP3**	**cytosol aminopeptidase**	22	143	22	1.1	**9E-09**	0.9	**3E-11**	1.0	**3E-02**	0.8	**3E-02**	0.9	5E-02	Aminopeptidase activity	Cytoplasm	Aminopeptidase
85440	**DOCK7**	**dedicator of cytokinesis protein 7 isoform 1**	13	37	10	1.1	**1E-02**	1.0	**2E-02**	1.0	7E-01	0.9	7E-02	0.9	6E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor
9805	**SCRN1**	**secernin-1 isoform b**	9	43	9	1.1	**6E-06**	0.9	**1E-05**	1.2	9E-01	1.2	**4E-05**	1.0	7E-01	Peptidase activity	Cytoplasm	Protease
84263	**HSDL2**	**hydroxysteroid dehydrogenase-like protein 2 isoform 1**	7	33	7	1.1	**2E-05**	1.4	**1E-05**	1.2	**9E-06**	1.2	**4E-05**	1.1	**1E-02**	Molecular function unknown	-	Unclassified
5286	**PIK3C2A**	**phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha**	11	43	11	1.1	**3E-05**	1.0	**2E-05**	1.3	**2E-02**	1.3	**1E-05**	1.1	**1E-02**	Lipid kinase activity	Cytosol	Lipid Kinase
23644	**EDC4**	**enhancer of mRNA-decapping protein 4**	14	48	14	1.1	**2E-04**	0.9	**2E-05**	1.2	9E-01	1.1	**4E-06**	0.9	1E-01	Molecular function unknown	Nucleus	Unclassified
11047	**ADRM1**	**proteasomal ubiquitin receptor ADRM1 isoform 1**	7	56	7	1.1	**9E-04**	1.0	**5E-04**	1.2	2E-01	1.1	**6E-05**	0.9	7E-02	Receptor activity;Molecular function unknown	Cytoplasm;Microsome	Adhesion molecule;Cell surface receptor
9328	**GTF3C5**	**general transcription factor 3C polypeptide 5 isoform 1**	3	11	3	1.1	**4E-02**	1.1	**2E-02**	1.2	2E-01	1.0	1E-01	1.2	2E-01	Transcription factor activity	Nucleus	Transcription factor
549	**AUH**	**methylglutaconyl-CoA hydratase, mitochondrial**	2	6	2	1.1	2E-01	1.3	1E-01	1.0	**1E-02**	1.3	**2E-02**	1.1	3E-01	RNA binding	Mitochondrion	RNA binding protein
23317	**DNAJC13**	**dnaJ homolog subfamily C member 13**	16	55	16	1.1	**7E-05**	1.0	**1E-06**	1.0	1E-01	1.0	**1E-08**	1.1	1E-01	Chaperone activity;Molecular function unknown	Endosome	Unclassified;Chaperone
841	**CASP8**	**caspase-8 isoform G**	8	27	8	1.1	**3E-04**	0.8	**7E-05**	1.1	**1E-02**	0.9	**1E-05**	0.9	**4E-02**	Cysteine-type peptidase activity	Cytosol;Cytoplasm	Cysteine protease
56650	**CLDND1**	**claudin domain-containing protein 1 isoform b**	3	18	3	1.1	**1E-03**	1.0	**2E-04**	1.0	1E-01	1.0	**2E-04**	1.0	8E-01	Molecular function unknown	-	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
56103;	**PCDHGB2**	**protocadherin gamma-B2 isoform 2**	2	4	2	1.1	**2E-03**	1.1	**2E-02**	1.5	3E-01	0.9	4E-01	0.9	5E-01	Cell adhesion molecule activity	Integral to membrane	Adhesion molecule
79068	**FTO**	**alpha-ketoglutarate-dependent dioxygenase FTO**	10	30	10	1.1	**3E-03**	0.9	**5E-05**	1.2	8E-01	0.8	8E-02	1.0	1E+00	Molecular function unknown	-	Unclassified
28964	**GIT1**	**ARF GTPase-activating protein GIT1 isoform 1**	6	23	5	1.1	**1E-02**	1.0	**7E-03**	1.1	2E-01	1.0	**4E-02**	0.9	4E-01	GTPase activator activity	Cytoplasm	GTPase activating protein
26517	**TIMM13**	**mitochondrial import inner membrane translocase subunit Tim13**	4	39	4	1.1	**2E-04**	1.1	**2E-04**	1.3	**2E-03**	1.2	**2E-04**	0.9	**5E-02**	Transporter activity	Mitochondrion	Transport/cargo protein
55308	**DDX19A**	**ATP-dependent RNA helicase DDX19A**	16	91	2	1.1	**6E-04**	0.9	**5E-04**	1.1	4E-01	0.9	**3E-02**	0.9	**9E-03**	Molecular function unknown	-	Unclassified
1399	**CRKL**	**crk-like protein**	10	43	10	1.1	**2E-03**	0.8	**2E-03**	1.3	2E-01	1.0	**7E-05**	0.9	**2E-02**	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
56993	**TOMM22**	**mitochondrial import receptor subunit TOM22 homolog**	1	18	1	1.1	**3E-03**	1.0	**2E-04**	1.1	**1E-02**	1.2	**7E-04**	0.9	8E-02	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
54707	**GPN2**	**GPN-loop GTPase 2**	1	6	1	1.1	**2E-02**	0.8	**1E-02**	1.1	6E-01	0.9	9E-02	0.9	2E-01	Molecular function unknown	-	Unclassified
3631	**INPP4A**	**type I inositol 3,4-bisphosphate 4-phosphatase isoform d**	1	5	1	1.1	5E-01	0.9	6E-01	1.2	6E-01	1.1	2E-01	1.1	5E-01	Hydrolase activity	Cytoplasm	Enzyme: Phosphatase
149373	**LOC149373**	**uncharacterized protein LOC149373**	10	22	10	1.1	**2E-08**	1.1	**9E-05**	1.2	**4E-05**	1.1	**1E-03**	1.1	**2E-02**	#N/A	#N/A	#N/A
26092	**TOR1AIP1**	**torsin-1A-interacting protein 1 isoform 2**	16	106	15	1.1	**9E-07**	0.9	**1E-07**	1.2	1E-01	1.3	**7E-08**	1.0	1E-01	Molecular function unknown	Nucleus	Unclassified
7020	**TFAP2A**	**transcription factor AP-2-alpha isoform a**	5	34	5	1.1	**5E-06**	1.1	**4E-07**	1.2	**9E-03**	1.0	**1E-07**	0.9	3E-01	Transcription factor activity	Nucleus	Transcription factor
4706	**NDUFAB1**	**acyl carrier protein, mitochondrial**	2	44	2	1.1	**1E-04**	1.1	**7E-05**	1.4	**9E-04**	1.3	**2E-05**	0.9	**2E-02**	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
435;	**ASL**	**argininosuccinate lyase isoform 3**	10	27	8	1.1	**6E-04**	1.0	**2E-04**	1.2	**2E-02**	1.3	**2E-04**	0.9	**5E-02**	Lyase activity	-	Enzyme: Lyase
29922	**NME7**	**nucleoside diphosphate kinase 7 isoform a**	3	10	3	1.1	**1E-03**	0.7	**9E-03**	0.9	**4E-02**	0.7	7E-01	1.0	9E-01	Catalytic activity	-	Enzyme: Phosphotransferase
55324	**ABCF3**	**ATP-binding cassette sub-family F member 3**	7	20	7	1.1	**4E-03**	0.9	**3E-03**	1.0	9E-01	0.8	4E-01	0.9	**2E-02**	Transporter activity	-	Transport/cargo protein
63875	**MRPL17**	**39S ribosomal protein L17, mitochondrial**	3	10	3	1.1	**1E-02**	1.3	**6E-03**	1.3	**6E-03**	1.2	8E-02	1.1	3E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
79065	**ATG9A**	**autophagy-related protein 9A*gi|116089287|ref|NP_076990.4| autophagy-related protein 9A**	4	10	4	1.1	**4E-02**	1.1	9E-02	1.1	2E-01	1.0	1E-01	1.1	2E-01	Molecular function unknown	Cytosol;Nucleus	Integral membrane protein
48	**ACO1**	**PREDICTED: cytoplasmic aconitate hydratase isoform X1**	18	96	18	1.1	**3E-11**	1.1	**2E-15**	1.3	**3E-07**	1.1	**2E-12**	1.0	9E-01	Isomerase activity	Cytoplasm	Enzyme: Isomerase
51060	**TXNDC12**	**thioredoxin domain-containing protein 12**	5	51	5	1.1	**1E-06**	0.9	**4E-08**	1.3	7E-01	1.0	**9E-07**	1.0	9E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase
64786	**TBC1D15**	**TBC1 domain family member 15 isoform 1**	8	38	8	1.1	**2E-06**	0.9	**4E-05**	1.1	6E-01	1.0	**5E-04**	0.9	8E-01	GTPase activator activity	-	GTPase activating protein
1478	**CSTF2**	**cleavage stimulation factor subunit 2**	7	24	7	1.1	**1E-05**	0.8	**4E-07**	1.1	5E-02	0.8	6E-01	0.9	1E-01	RNA binding	Nucleus	RNA binding protein
25957	**PNISR**	**arginine/serine-rich protein PNISR**	1	6	1	1.1	8E-02	1.0	**3E-02**	1.2	1E-01	1.1	8E-02	1.0	4E-01	#N/A	#N/A	#N/A
10801	**SEPT9**	**septin-9 isoform a**	24	202	24	1.1	**5E-10**	0.9	**3E-11**	1.2	7E-01	0.9	**1E-06**	1.0	8E-01	#N/A	#N/A	#N/A
5356	**PLRG1**	**pleiotropic regulator 1 isoform 1**	9	34	9	1.2	**4E-04**	1.1	**7E-05**	1.2	**4E-02**	0.8	4E-01	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
5351	**PLOD1**	**procollagen-lysine,2-oxoglutarate 5-dioxygenase 1**	11	38	10	1.2	**9E-04**	0.8	**2E-03**	1.0	**2E-02**	0.9	**2E-02**	1.0	4E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase
9777	**TM9SF4**	**transmembrane 9 superfamily member 4**	5	26	5	1.2	7E-02	1.1	7E-02	1.1	6E-02	1.3	**4E-02**	1.2	2E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
10521	**DDX17**	**probable ATP-dependent RNA helicase DDX17 isoform 3**	28	217	19	1.2	**2E-16**	0.9	**2E-16**	1.1	2E-01	0.9	**2E-03**	1.0	2E-01	ATPase activity	Nucleus	RNA helicase;ATPase
6181	**RPLP2**	**60S acidic ribosomal protein P2**	7	136	7	1.2	**2E-16**	1.0	**2E-16**	1.0	**1E-04**	0.8	**1E-03**	1.0	8E-01	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
1983	**EIF5**	**eukaryotic translation initiation factor 5**	16	106	16	1.2	**8E-10**	0.8	**7E-12**	1.2	**2E-06**	1.0	**6E-10**	0.8	**2E-05**	Translation regulator activity;GTPase activator activity	Cytoplasm	Translation regulatory protein;GTPase activating protein
81542	**TMX1**	**thioredoxin-related transmembrane protein 1**	10	97	10	1.2	**7E-09**	1.0	**2E-08**	1.1	**2E-04**	1.2	**2E-09**	1.1	**2E-03**	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase
9631	**NUP155**	**nuclear pore complex protein Nup155 isoform 1**	18	86	18	1.2	**8E-08**	1.0	**7E-09**	1.2	**1E-03**	1.3	**5E-10**	1.0	9E-01	Transporter activity	Nucleus	Transport/cargo protein
23353	**SUN1**	**SUN domain-containing protein 1 isoform a**	14	61	14	1.2	**1E-07**	1.1	**1E-07**	1.1	**5E-06**	1.2	**8E-10**	1.0	6E-01	Intracellular transporter activity	Nucleus	Integral membrane protein
222068	**TMED4**	**transmembrane emp24 domain-containing protein 4 isoform 1**	8	38	5	1.2	**8E-06**	1.2	**1E-06**	1.3	**4E-06**	**1.5**	**7E-06**	1.0	4E-01	Molecular function unknown	-	Integral membrane protein
55269	**PSPC1**	**PREDICTED: paraspeckle component 1 isoform X1**	12	48	11	1.2	**3E-05**	1.0	**9E-06**	1.6	**2E-03**	**1.5**	**8E-06**	1.0	7E-01	RNA binding	Nucleus	RNA binding protein
79731	**NARS2**	**probable asparagine--tRNA ligase, mitochondrial isoform 1**	7	19	7	1.2	**9E-04**	1.0	**3E-03**	1.2	**5E-02**	1.2	**4E-03**	1.0	1E-01	Ligase activity	-	Enzyme: Ligase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
25978	CHMP2B	charged multivesicular body protein 2b isoform 1	7	42	6	1.2	**9E-04**	0.9	**5E-04**	1.1	1E-01	1.2	**3E-04**	0.9	**3E-02**	Transporter activity	-	Transport/cargo protein
6157	RPL27A	60S ribosomal protein L27a	5	42	5	1.2	**2E-03**	0.9	**5E-03**	0.9	6E-01	**0.7**	**1E-02**	0.9	**3E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6187	RPS2	40S ribosomal protein S2	18	188	18	1.2	**2E-16**	1.0	**2E-16**	0.9	**8E-05**	0.8	**5E-05**	1.0	8E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
9141	PDCD5	programmed cell death protein 5	7	70	7	1.2	**3E-08**	0.8	**4E-10**	1.2	**4E-03**	0.7	2E-01	1.0	5E-01	Molecular function unknown	Cytoplasm	Unclassified
5201	PFDN1	prefoldin subunit 1	6	37	6	1.2	**2E-06**	0.9	**4E-07**	1.2	9E-01	1.0	**2E-07**	0.9	**4E-02**	Chaperone activity	Cytoplasm	Chaperone
9610	RIN1	ras and Rab interactor 1	11	26	12	1.2	**6E-05**	1.0	**3E-07**	1.2	**4E-03**	1.0	**1E-04**	1.0	1E+00	Molecular function unknown	Plasma membrane	Unclassified
9126	SMC3	structural maintenance of chromosomes protein 3	21	67	21	1.2	**3E-04**	1.3	**4E-05**	1.1	**9E-03**	1.0	**2E-04**	1.1	**4E-02**	Molecular function unknown	Nucleus	Unclassified
84300	MNF1; UQCC2	ubiquinol-cytochrome-c reductase complex assembly factor 2	3	14	3	1.2	**1E-02**	1.1	**5E-03**	1.3	**4E-03**	1.2	**3E-03**	1.0	2E-01	#N/A	#N/A	#N/A
29074	MRPL18	39S ribosomal protein L18, mitochondrial	3	14	3	1.2	8E-02	1.1	6E-02	1.2	**2E-02**	1.1	6E-02	1.1	7E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
9130	FAM50A	protein FAM50A	3	11	3	1.2	1E-01	0.8	**2E-02**	1.3	4E-01	0.8	5E-01	0.9	3E-01	DNA binding	Nucleus	DNA binding protein
7812	CSDE1	cold shock domain-containing protein E1 isoform 4	29	130	29	1.2	**1E-11**	0.9	**3E-08**	1.0	3E-01	0.8	3E-01	0.9	**7E-04**	RNA binding	Cytoplasm	RNA binding protein
5213	PFKM	PREDICTED: ATP-dependent 6-phosphofructokinase, muscle type isoform X1	20	132	18	1.2	**5E-07**	1.1	**3E-09**	1.3	**1E-06**	1.3	**6E-10**	1.0	6E-01	Catalytic activity	-	Enzyme: Phosphotransferase
23122	CLASP2	CLIP-associating protein 2 isoform 1	13	59	9	1.2	**3E-06**	1.0	**2E-05**	1.1	8E-02	1.1	**2E-06**	1.0	9E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
51154	MRTO4	mRNA turnover protein 4 homolog	9	48	9	1.2	**4E-04**	0.8	**8E-05**	1.1	6E-02	0.7	4E-01	0.8	2E-01	Molecular function unknown	Nucleolus	Unclassified
84823	LMNB2	lamin-B2	35	238	32	1.2	**4E-16**	1.1	**2E-16**	1.2	**2E-10**	1.4	**2E-16**	1.1	**6E-05**	Structural molecule activity	Nucleus	Structural protein
6156	RPL30	60S ribosomal protein L30	8	107	7	1.2	**7E-12**	1.0	**1E-09**	1.0	**4E-02**	**0.7**	**2E-03**	0.9	**5E-03**	Structural constituent of ribosome	-	Ribosomal subunit
6228	RPS23	40S ribosomal protein S23	8	75	8	1.2	**2E-06**	1.0	**1E-07**	1.0	**3E-04**	0.8	**6E-03**	1.0	9E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
55327	LIN7C	protein lin-7 homolog C	5	41	5	1.2	**2E-06**	1.0	**9E-06**	1.1	**2E-03**	0.8	**2E-02**	0.9	4E-01	Molecular function unknown	Extracellular	Unclassified
9818	NUPL1; NUP58	nucleoporin p58/p45 isoform a	7	31	7	1.2	**8E-05**	0.9	**7E-05**	1.2	5E-01	1.2	**1E-04**	1.1	3E-01	#N/A	#N/A	#N/A
23381	SMG5	protein SMG5	3	6	3	1.2	**5E-02**	1.1	**6E-03**	1.3	2E-01	1.3	9E-02	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
6169	RPL38	60S ribosomal protein L38	4	52	4	1.2	**8E-07**	0.9	**5E-07**	1.0	**2E-02**	**0.6**	**3E-03**	0.9	**4E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
84313	VPS25	vacuolar protein-sorting-associated protein 25	4	24	4	1.2	**7E-03**	1.0	**1E-02**	1.1	9E-02	0.9	**4E-02**	0.9	5E-02	Transporter activity	Endosome	Transport/cargo protein
80018	NAA25	N-alpha-acetyltransferase 25, NatB auxiliary subunit	11	39	11	1.2	**1E-02**	1.0	**9E-03**	1.2	**3E-02**	1.0	**1E-02**	1.0	9E-01	Molecular function unknown	-	Unclassified
337867	UBAC2	ubiquitin-associated domain-containing protein 2 isoform 1	4	14	4	1.2	**2E-02**	0.9	**3E-02**	0.9	3E-01	1.1	5E-02	1.0	5E-01	Molecular function unknown	-	Unclassified
1397	CRIP2	cysteine-rich protein 2 isoform 1	1	6	1	1.2	9E-01	0.8	4E-01	1.5	4E-01	0.7	8E-01	0.9	3E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
151011	SEPT10	septin-10 isoform 1	7	42	7	1.2	**4E-03**	1.0	**7E-04**	1.0	1E-01	0.9	**1E-02**	0.9	1E-01	#N/A	#N/A	#N/A
1646	AKR1C2	aldo-keto reductase family 1 member C2 isoform 1	13	165	1	1.2	**3E-13**	1.3	**4E-14**	3.6	**2E-13**	**2.2**	**2E-14**	0.7	**7E-10**	Oxidoreductase activity;Transporter activity	Cytosol	Enzyme: Dehydrogenase
2582	GALE	UDP-glucose 4-epimerase	10	70	10	1.2	**1E-10**	1.0	**1E-11**	1.4	**1E-04**	**1.6**	**3E-10**	1.0	8E-01	Racemase and epimerase activity	-	Enzyme: Epimerase
4200	ME2	NAD-dependent malic enzyme, mitochondrial isoform 1	16	68	16	1.2	**1E-06**	1.2	**5E-07**	1.2	**1E-05**	1.3	**3E-08**	1.1	**9E-03**	Carboxy-lyase activity	Mitochondrion	Enzyme: Decarboxylase
10458	BAIAP2	brain-specific angiogenesis inhibitor 1-associated protein 2 isoform 3	22	147	21	1.2	**6E-14**	0.8	**3E-14**	1.1	**1E-02**	0.9	**2E-09**	0.9	1E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6418	SET	PREDICTED: protein SET isoform X1	9	81	1	1.2	**2E-12**	0.8	**5E-14**	1.0	1E-01	1.0	**3E-12**	1.0	6E-01	MHC class I receptor activity;MHC class II receptor activity	Nucleus	MHC complex protein
7798	LUZP1	PREDICTED: leucine zipper protein 1 isoform X1	28	119	27	1.2	**7E-08**	0.9	**5E-08**	1.1	3E-01	0.9	**5E-08**	1.0	9E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
6193	RPS5	40S ribosomal protein S5	8	134	8	1.2	**4E-07**	0.9	**1E-09**	1.0	3E-01	0.7	3E-01	0.9	**8E-07**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
4482	MSRA	mitochondrial peptide methionine sulfoxide reductase isoform a	4	18	4	1.2	**2E-04**	1.0	**6E-04**	1.0	**7E-03**	0.9	**4E-03**	1.0	1E+00	Catalytic activity	Mitochondrion	Enzyme: Reductase
125988	C19orf70	protein QIL1	2	10	2	1.2	**1E-02**	1.1	**7E-03**	1.2	**1E-02**	1.1	**3E-04**	1.1	3E-01	Molecular function unknown	-	Unclassified
6924	TCEB3	transcription elongation factor B polypeptide 3	6	18	6	1.2	**2E-02**	1.0	**2E-02**	1.2	**7E-03**	0.8	1E+00	0.9	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
57449	PLEKHG5	pleckstrin homology domain-containing family G member 5 isoform d	3	10	3	1.2	**3E-02**	1.1	**3E-02**	1.2	1E-01	1.2	8E-02	1.0	2E-01	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
390	**RND3**	**rho-related GTP-binding protein RhoE*gi|4885069|ref|NP_005159.1| rho-related GTP-binding protein RhoE**	2	8	2	1.2	1E-01	0.8	7E-02	1.0	2E-01	0.9	8E-02	1.4	1E-01	GTPase activity	Plasma membrane	G protein
16	**AARS**	**alanine--tRNA ligase, cytoplasmic**	35	251	35	1.2	**2E-16**	0.8	**2E-16**	1.0	**2E-07**	0.8	5E-01	1.0	7E-02	Ligase activity	Cytoplasm	Enzyme: Ligase
51377	**UCHL5**	**ubiquitin carboxyl-terminal hydrolase isozyme L5 isoform 1**	8	46	8	1.2	**3E-08**	1.1	**3E-08**	1.2	**2E-04**	1.1	**7E-07**	0.9	8E-02	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
2873	**GPS1**	**COP9 signalosome complex subunit 1 isoform 1**	10	61	1	1.2	**9E-08**	0.9	**9E-09**	1.3	7E-01	1.1	**8E-08**	0.8	**2E-03**	Signal transducer activity	Nucleus	Unclassified
11124	**FAF1**	**FAS-associated factor 1**	4	13	4	1.2	**3E-04**	0.9	**5E-04**	1.3	1E+00	0.8	**3E-02**	1.0	6E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
7498	**XDH**	**xanthine dehydrogenase/oxidase**	9	30	9	1.2	**4E-04**	1.0	**6E-05**	**1.6**	**2E-02**	**1.9**	**7E-05**	1.1	**2E-02**	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase
10741	**RBBP9**	**putative hydrolase RBBP9**	3	14	3	1.2	**5E-04**	1.3	**1E-03**	**1.5**	**4E-03**	1.3	**7E-04**	1.0	6E-01	Molecular function unknown	Nucleus	Cell cycle control protein;Unclassified
4245	**MGAT1**	**PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X1**	5	19	5	1.2	**3E-03**	1.0	**2E-02**	0.9	5E-01	0.7	5E-01	1.0	4E-01	Transferase activity	Golgi apparatus	Enzyme: Glucosaminyltransferase
494115	**RBMXL1**	**RNA binding motif protein, X-linked-like-1**	15	104	4	1.2	**6E-03**	1.0	**9E-04**	1.3	3E-01	1.0	**2E-03**	1.0	6E-01	-	-	-
4154	**MBNL1**	**PREDICTED: muscleblind-like protein 1 isoform X1**	7	33	7	1.2	**6E-03**	0.9	**4E-03**	1.0	4E-01	0.8	6E-01	0.9	1E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
79567	**FAM65A**	**protein FAM65A isoform 3**	3	9	3	1.2	**1E-02**	1.2	**1E-02**	**1.9**	**2E-02**	**1.5**	**7E-03**	1.5	5E-02	Molecular function unknown	-	Unclassified
25917	**THUMPD3**	**PREDICTED: THUMP domain-containing protein 3 isoform X1**	5	14	5	1.2	**2E-02**	0.8	5E-02	1.0	2E-01	0.8	5E-01	0.8	7E-01	Molecular function unknown	-	Unclassified
80305;	**TRABD**	**traB domain-containing protein**	2	7	2	1.2	**3E-02**	0.9	**1E-02**	1.3	2E-01	0.9	3E-01	1.1	2E-01	Molecular function unknown	-	Unclassified
8148	**TAF15**	**TATA-binding protein-associated factor 2N isoform 1**	6	36	3	1.2	9E-02	1.0	2E-01	1.0	2E-01	0.5	6E-02	1.0	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9045	**RPL14**	**60S ribosomal protein L14**	8	127	8	1.2	**5E-15**	0.9	**1E-11**	1.0	9E-01	0.8	4E-01	0.9	**3E-04**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
1173	**AP2M1**	**AP-2 complex subunit mu isoform a**	20	124	20	1.2	**6E-09**	1.0	**6E-10**	1.1	**2E-03**	0.9	**6E-06**	1.0	1E-01	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule
6400	**SEL1L**	**protein sel-1 homolog 1 isoform 1**	4	10	4	1.2	**2E-02**	0.9	**2E-02**	1.1	2E-01	1.2	**1E-02**	0.9	6E-01	Binding	Cytoplasmic vesicle	Integral membrane protein
9462	**RASAL2**	**ras GTPase-activating protein nGAP isoform 2**	3	12	2	1.2	9E-02	0.8	7E-02	1.2	5E-01	1.0	1E-01	1.0	5E-01	GTPase activity	Nucleus	GTPase
51520	**LARS**	**leucine--tRNA ligase, cytoplasmic**	40	238	40	1.2	**2E-16**	0.9	**2E-16**	1.1	**4E-03**	1.1	**2E-16**	1.0	3E-01	Ligase activity	Mitochondrion	Enzyme: Ligase
6432	**SRSF7**	**serine/arginine-rich splicing factor 7 isoform 1**	7	67	6	1.2	**5E-08**	0.9	**4E-08**	1.2	1E-01	1.1	**6E-09**	1.0	8E-01	#N/A	#N/A	#N/A
51495	**PTPLAD1; HACD3**	**very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3**	6	50	6	1.2	**9E-05**	0.9	**4E-05**	1.3	3E-01	**1.5**	**7E-07**	1.0	6E-02	#N/A	#N/A	#N/A
334	**APLP2**	**amyloid-like protein 2 isoform 1**	9	40	8	1.2	**4E-04**	0.8	9E-02	0.8	2E-01	0.9	**9E-04**	1.2	**4E-03**	Protein binding	Plasma membrane	Integral membrane protein
9968	**MED12**	**PREDICTED: mediator of RNA polymerase II transcription subunit 12 isoform X1**	4	8	3	1.2	**3E-02**	1.0	**2E-02**	1.3	7E-01	1.1	**1E-02**	1.1	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
203547	**VMA21**	**vacuolar ATPase assembly integral membrane protein VMA21**	1	8	1	1.2	1E-01	1.1	9E-02	1.0	**4E-02**	1.1	6E-02	1.2	5E-02	Molecular function unknown	-	Unclassified
9604	**RNF14**	**E3 ubiquitin-protein ligase RNF14 isoform 1**	3	7	3	1.2	3E-01	0.8	6E-02	1.1	5E-01	0.9	**1E-02**	1.7	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
1665;	**DHX15**	**putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15**	35	133	34	1.2	**2E-16**	0.9	**2E-16**	1.3	8E-02	1.2	**2E-16**	1.0	**6E-03**	RNA binding	Nucleus	RNA binding protein
55862	**ECHDC1**	**ethylmalonyl-CoA decarboxylase isoform 3**	8	33	8	1.2	**2E-05**	0.9	**2E-06**	1.1	4E-01	0.8	2E-01	1.0	1E-01	Molecular function unknown	-	Unclassified
5908;	**RAP1B**	**ras-related protein Rap-1b isoform 1*gi|7661678|ref|NP_056461.1| ras-related protein Rap-1b isoform 1**	7	46	3	1.2	**8E-05**	1.0	**1E-04**	1.2	**7E-03**	1.2	**5E-05**	1.1	**5E-03**	GTPase activity	Nucleus	GTPase
81608	**FIP1L1**	**pre-mRNA 3'-end-processing factor FIP1 isoform 1**	4	24	4	1.2	**7E-03**	1.1	**6E-03**	1.1	**1E-02**	1.0	**2E-04**	0.9	**2E-02**	Molecular function unknown	Nucleus	Unclassified
23408	**SIRT5**	**NAD-dependent protein deacylase sirtuin-5, mitochondrial isoform 2**	2	7	2	1.2	**8E-03**	1.0	**5E-02**	1.1	1E-01	1.2	**3E-03**	1.0	4E-01	Deacetylase activity;Translation regulator activity	Nucleus	Enzyme: Deacetylase;Enzyme: Ribosyltransferase
7009	**TMBIM6**	**PREDICTED: bax inhibitor 1 isoform X1**	1	6	1	1.2	**1E-02**	0.7	**3E-02**	1.0	1E-01	0.7	9E-01	0.9	2E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
400745	**SH2D5**	**SH2 domain-containing protein 5 isoform 1**	3	10	3	1.2	**2E-02**	0.9	**3E-02**	1.1	7E-01	1.0	**2E-02**	1.1	**4E-02**	Protein binding	-	Unclassified
51101	**ZC2HC1A**	**zinc finger C2HC domain-containing protein 1A**	1	6	1	1.2	7E-02	1.1	**3E-02**	1.3	3E-01	0.8	4E-01	0.8	8E-01	#N/A	#N/A	#N/A
5216	**PFN1**	**profilin-1**	13	319	13	1.2	**2E-16**	0.7	**2E-16**	1.1	**2E-09**	0.7	**4E-02**	1.1	**2E-03**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6210	RPS15A	40S ribosomal protein S15a*gi|71772415|ref|NP_001025180.1|40S ribosomal protein S15a	8	160	8	1.2	**2E-16**	0.9	**7E-15**	1.0	**2E-02**	0.9	**6E-07**	1.1	5E-02	Structural constituent of ribosome	Ribosome	Ribosomal subunit
8531	CSDA; YBX3	Y-box-binding protein 3 isoform a	7	51	1	1.2	**1E-07**	0.8	**4E-05**	0.9	**2E-02**	0.5	3E-01	0.7	5E-01	#N/A	#N/A	#N/A
114882	OSBPL8	oxysterol-binding protein-related protein 8 isoform a	9	27	9	1.2	**9E-04**	1.0	**1E-03**	1.3	**5E-03**	1.3	**7E-04**	1.0	6E-02	Transporter activity	Mitochondrion	Transport/cargo protein
1486	CTBS	di-N-acetylchitobiase	5	16	5	1.2	**7E-03**	1.3	**2E-03**	1.3	**5E-04**	1.4	**7E-04**	1.0	3E-01	Catalytic activity	Lysosome	Enzyme: Glycosidase
28974	C19orf53	leydig cell tumor 10 kDa protein homolog	3	7	2	1.2	**1E-02**	0.8	**1E-03**	1.2	3E-01	0.9	2E-01	1.1	9E-02	Molecular function unknown	Nucleolus	Unclassified
8986	RPS6KA4	ribosomal protein S6 kinase alpha-4 isoform a	5	23	3	1.2	**2E-02**	0.7	**8E-04**	1.4	2E-01	0.8	2E-01	1.0	4E-01	Protein serine/threonine kinase activity;Transcription regulator activity	Nucleus	Translation regulatory protein;Serine/threonine kinase
64215	DNAJC1	dnaJ homolog subfamily C member 1	3	8	3	1.2	8E-02	1.0	**3E-03**	0.9	6E-01	0.7	9E-01	1.1	9E-02	Chaperone activity	Endoplasmic reticulum	Chaperone
23367	LARP1	PREDICTED: la-related protein 1 isoform X1	23	53	23	1.2	**3E-11**	0.9	**9E-13**	1.1	1E+00	0.8	**9E-03**	0.9	**5E-04**	Molecular function unknown;Ribonucleoprotein	Nucleus;Cytoplasm	Unclassified;Ribonucleoprotein
23592	LEMD3	inner nuclear membrane protein Man1 isoform 1	9	46	9	1.2	**1E-04**	0.9	**3E-05**	1.1	3E-01	1.1	**4E-05**	0.9	6E-02	Nucleotide binding	Nucleus	Integral membrane protein
11165	NUDT3	diphosphoinositol polyphosphate phosphohydrolase 1	4	20	3	1.2	**3E-03**	0.9	**3E-03**	1.2	1E-01	0.9	**2E-03**	1.0	5E-01	Hydrolase activity	-	Enzyme: Hydrolase
121441	NEDD1	PREDICTED: protein NEDD1 isoform X1	4	14	4	1.2	**2E-02**	0.8	**1E-03**	1.1	3E-01	0.8	7E-02	0.9	1E-01	Molecular function unknown	-	Unclassified
661	POLR3D	DNA-directed RNA polymerase III subunit RPC4	3	13	3	1.2	**2E-02**	1.0	**9E-03**	1.2	**3E-02**	0.9	**4E-03**	1.0	3E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
653784	MZT2A	mitotic-spindle organizing protein 2A	1	8	1	1.2	8E-02	0.9	**3E-02**	1.2	7E-01	0.9	7E-02	0.9	2E-01	#N/A	#N/A	#N/A
7514	XPO1	PREDICTED: exportin-1 isoform X1	32	242	31	1.2	**2E-16**	0.9	**2E-16**	1.2	6E-01	1.1	**2E-16**	1.0	2E-01	Transporter activity	Nucleus	Transport/cargo protein
57019	CIAPIN1	anamorsin	13	68	13	1.2	**1E-06**	0.9	**3E-07**	1.1	9E-01	0.9	**2E-03**	0.9	**1E-02**	Molecular function unknown	Cytoplasm	Unclassified
53981	CPSF2	cleavage and polyadenylation specificity factor subunit 2	9	36	9	1.2	**1E-05**	0.9	**3E-08**	1.1	9E-01	0.9	**4E-03**	1.0	7E-01	RNA binding	Nucleus	RNA binding protein
8731	RNMT	PREDICTED: mRNA cap guanine-N7 methyltransferase isoform X1	12	46	11	1.2	**1E-04**	1.0	**9E-05**	1.1	**4E-02**	1.0	**1E-05**	1.0	1E-01	RNA methyltransferase activity	Cytoplasm	RNA methyltransferase
27350	APOBEC3C	DNA dC-_dU-editing enzyme APOBEC-3C	3	11	3	1.2	**6E-03**	1.0	**4E-03**	1.1	**4E-02**	0.9	**5E-03**	1.1	4E-01	Deaminase activity	-	Enzyme: Deaminase
1209	CLPTM1	cleft lip and palate transmembrane protein 1 isoform 2	4	16	4	1.2	**2E-02**	0.9	**2E-02**	1.1	8E-01	1.1	**1E-02**	0.9	3E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
23480	SEC61G	protein transport protein Sec61 subunit gamma	1	8	1	1.2	**3E-02**	1.2	**2E-02**	1.2	8E-02	1.0	**4E-02**	1.4	**4E-02**	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
79002	C19orf43	uncharacterized protein C19orf43	3	9	3	1.2	**4E-02**	0.7	**3E-02**	1.2	6E-02	0.7	2E-01	0.9	1E-01	Molecular function unknown	-	Unclassified
124995	MRPL10	39S ribosomal protein L10, mitochondrial isoform a	3	10	3	1.2	6E-02	1.0	**5E-02**	1.2	**2E-02**	1.1	**2E-02**	1.0	8E-01	Structural constituent of ribosome	Mitochondrion	RNA binding protein
10399	GNB2L1; RACK1	guanine nucleotide-binding protein subunit beta-2-like 1	18	242	18	1.2	**2E-16**	1.0	**1E-14**	1.0	**3E-04**	0.9	**2E-05**	1.0	6E-01	#N/A	#N/A	#N/A
1982	EIF4G2	eukaryotic translation initiation factor 4 gamma 2 isoform 1*gi|289577116|ref|NP_001166176.1|eukaryotic translation initiation factor 4 gamma 2 isoform 1	33	205	33	1.2	**6E-16**	0.8	**2E-16**	1.2	**4E-04**	1.1	**3E-16**	0.9	**8E-05**	Translation regulator activity	Cytoplasm	Translation regulatory protein
5901	RAN	GTP-binding nuclear protein Ran isoform 1	11	135	11	1.2	**4E-12**	0.8	**2E-14**	1.2	**8E-04**	1.0	**4E-09**	0.9	**2E-03**	GTPase activity	Nucleus	GTPase
55746	NUP133	nuclear pore complex protein Nup133	16	61	16	1.2	**3E-09**	0.9	**2E-09**	1.2	9E-02	1.2	**3E-09**	1.0	**1E-02**	Transporter activity	Nucleus	Transport/cargo protein
6143	RPL19	60S ribosomal protein L19	7	57	7	1.2	**1E-05**	0.9	**2E-05**	0.9	9E-01	**0.6**	**4E-04**	0.8	**7E-05**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
55148;	UBR7	putative E3 ubiquitin-protein ligase UBR7	9	20	9	1.2	**7E-05**	1.0	**8E-04**	1.2	**1E-02**	1.4	**4E-05**	1.0	8E-01	Molecular function unknown	-	Unclassified
55110	MAGOHB	protein mago nashi homolog 2 isoform 1	11	65	11	1.2	**3E-03**	0.9	**1E-03**	1.2	4E-01	0.8	**4E-03**	1.0	3E-01	Molecular function unknown	Nucleus	Unclassified
91445	RNF185	PREDICTED: E3 ubiquitin-protein ligase RNF185 isoform X1	4	12	4	1.2	**2E-02**	0.9	**2E-02**	0.9	8E-01	0.7	3E-01	0.9	9E-02	Molecular function unknown	-	Unclassified
274	BIN1	myc box-dependent-interacting protein 1 isoform 1	3	8	3	1.2	**4E-02**	0.8	**3E-02**	1.2	3E-01	0.9	5E-01	1.0	8E-01	Receptor signaling complex scaffold activity	Cytoplasm;Nucleus	Adapter molecule
10061	ABCF2	PREDICTED: ATP-binding cassette sub-family F member 2 isoform X1	18	87	18	1.2	**2E-11**	0.9	**1E-12**	1.0	8E-01	0.7	**2E-02**	0.9	**3E-03**	Molecular function unknown	Mitochondrion	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
28989;	**NTMT1**	**N-terminal Xaa-Pro-Lys N-methyltransferase 1 isoform a*gi|557948039|ref|NP_001273727.1| N-terminal Xaa-Pro-Lys N-methyltransferase 1 isoform a*gi|557948057|ref|NP_001273725.1| N-terminal Xaa-Pro-Lys N-methyltransferase 1 isoform a*gi|557948069|ref|NP_001273728.1| N-terminal Xaa-Pro-Lys N-methyltransferase 1 isoform a*gi|56676399|ref|NP_054783.2| N-terminal Xaa-Pro-Lys N-methyltransferase 1 isoform a**	7	17	6	1.2	**1E-06**	0.9	**4E-06**	1.5	8E-01	1.3	**8E-06**	1.1	3E-01	#N/A	#N/A	#N/A
23041	**MON2**	**protein MON2 homolog isoform 1**	11	41	11	1.2	**6E-05**	1.1	**7E-05**	1.1	**2E-03**	1.0	**4E-06**	1.0	3E-01	Molecular function unknown	-	Unclassified
51645	**PPIL1**	**peptidyl-prolyl cis-trans isomerase-like 1**	7	34	7	1.2	**1E-04**	1.0	**5E-04**	1.2	6E-02	1.1	**2E-04**	1.0	1E-01	Isomerase activity	Cytoplasm	Enzyme: Isomerase
5217	**PFN2**	**profilin-2 isoform b**	4	28	2	1.2	**3E-04**	0.9	**3E-04**	1.3	3E-01	1.0	**8E-05**	1.0	5E-01	Structural molecule activity	Cytoplasm	Structural protein
29777	**ABT1**	**activator of basal transcription 1**	3	11	3	1.2	**2E-03**	0.9	**9E-03**	1.2	8E-01	0.9	3E-01	1.0	8E-01	Transcription factor activity	Nucleus	Transcription factor
24148	**PRPF6**	**pre-mRNA-processing factor 6**	19	79	19	1.2	**9E-03**	0.9	**1E-10**	1.2	2E-01	1.0	**8E-04**	0.9	3E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
2548	**GAA**	**lysosomal alpha-glucosidase preproprotein**	5	12	5	1.2	**2E-02**	**1.8**	**2E-02**	1.2	**4E-02**	1.2	**2E-02**	1.0	3E-01	Glucosidase activity	Lysosome	Enzyme: Glucosidase
64328;	**XPO4**	**exportin-4**	7	21	6	1.2	7E-02	0.9	**5E-03**	1.2	8E-01	1.0	6E-02	1.0	4E-01	Transporter activity	Nucleus	Transport/cargo protein
9675	**TTI1**	**TELO2-interacting protein 1 homolog**	1	6	1	1.2	8E-02	0.7	8E-02	1.1	7E-02	0.8	6E-01	1.0	4E-01	#N/A	#N/A	#N/A
55033	**FKBP14**	**peptidyl-prolyl cis-trans isomerase FKBP14**	3	6	3	1.2	3E-01	0.8	2E-01	1.3	3E-01	1.2	1E-01	1.1	6E-01	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase
79657	**RPAP3**	**RNA polymerase II-associated protein 3 isoform 1**	7	30	7	1.2	**1E-07**	1.0	**1E-06**	1.2	1E-01	0.9	**8E-03**	0.9	4E-01	Molecular function unknown	Cytoplasm	Unclassified
8451	**CUL4A**	**cullin-4A isoform 1**	28	143	18	1.2	**9E-06**	1.0	**2E-05**	1.1	**1E-02**	0.8	**6E-04**	0.9	**2E-02**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
9477	**MED20**	**mediator of RNA polymerase II transcription subunit 20**	3	14	3	1.2	**1E-03**	0.8	**4E-03**	1.2	7E-02	0.9	7E-02	0.8	1E-01	Transcription regulator activity	-	Transcription regulatory protein
8635	**RNASET2**	**ribonuclease T2**	2	12	2	1.2	**2E-02**	1.1	**1E-02**	1.3	1E-01	1.2	**2E-03**	1.0	6E-01	Ribonuclease activity	Cytoplasm	Ribonuclease
23511	**NUP188**	**nucleoporin NUP188 homolog**	17	71	17	1.2	**5E-07**	1.0	**2E-06**	1.2	**6E-04**	1.2	**2E-07**	1.1	**1E-02**	Molecular function unknown	Nuclear membrane	Unclassified
401505	**TOMM5**	**mitochondrial import receptor subunit TOM5 homolog isoform 3**	3	20	3	1.2	**6E-05**	1.0	**4E-05**	1.1	**8E-03**	1.2	**4E-05**	1.0	6E-01	Molecular function unknown	-	Unclassified
27351	**DESI1**	**desumoylating isopeptidase 1**	2	12	2	1.2	**4E-04**	0.9	**1E-04**	1.0	4E-01	0.7	4E-01	0.9	**2E-02**	#N/A	#N/A	#N/A
128	**ADH5**	**alcohol dehydrogenase class-3**	11	121	11	1.2	**1E-11**	1.0	**2E-11**	1.2	**7E-04**	1.2	**6E-15**	0.9	**3E-02**	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
8540	**AGPS**	**alkyldihydroxyacetonephosphate synthase, peroxisomal**	12	54	12	1.2	**3E-07**	1.1	**4E-09**	1.2	**1E-04**	1.3	**1E-07**	1.1	8E-02	Transferase activity	Peroxisome	Enzyme: Synthase
65080	**MRPL44**	**39S ribosomal protein L44, mitochondrial**	4	16	4	1.2	**2E-05**	0.9	**4E-05**	1.1	6E-01	1.0	**3E-03**	0.9	**1E-02**	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
6176	**RPLP1**	**60S acidic ribosomal protein P1 isoform 1**	2	36	2	1.2	**3E-05**	1.0	**2E-05**	1.1	**3E-02**	0.8	**4E-02**	1.0	3E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
3321	**IGSF3**	**immunoglobulin superfamily member 3 isoform 2**	7	21	7	1.2	**2E-02**	0.8	**3E-02**	0.9	4E-01	0.6	2E-01	1.0	3E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
10455	**ECI2**	**enoyl-CoA delta isomerase 2, mitochondrial isoform 2**	7	30	7	1.2	**7E-08**	1.1	**5E-08**	**1.5**	**3E-05**	**1.7**	**4E-08**	1.0	9E-01	#N/A	#N/A	#N/A
10137	**RBM12**	**RNA-binding protein 12**	12	72	12	1.2	**5E-07**	0.8	**3E-07**	1.2	**8E-03**	0.9	**5E-05**	0.9	**2E-04**	RNA binding	Mitochondrion	RNA binding protein
84661	**DPY30**	**protein dpy-30 homolog**	2	29	2	1.2	**2E-05**	0.8	**3E-05**	1.5	2E-01	1.0	**4E-07**	1.0	6E-01	Molecular function unknown	-	Unclassified
25764	**HYPK**	**huntingtin-interacting protein K isoform 1**	3	18	3	1.2	**2E-04**	0.8	**6E-04**	1.2	4E-01	0.8	1E-01	0.8	**5E-02**	#N/A	#N/A	#N/A
8289	**ARID1A**	**AT-rich interactive domain-containing protein 1A isoform a**	4	18	4	1.2	**3E-04**	1.0	**3E-03**	1.1	5E-01	1.0	**8E-04**	1.0	7E-01	RNA binding	Cytoplasm	RNA binding protein
8394	**PIP5K1A**	**phosphatidylinositol 4-phosphate 5-kinase type-1 alpha isoform 1**	5	16	5	1.2	**8E-03**	0.9	**2E-04**	1.1	7E-01	1.2	**7E-04**	1.1	3E-01	Lipid kinase activity	Plasma membrane	Lipid Kinase
9978	**RBX1**	**E3 ubiquitin-protein ligase RBX1**	1	6	1	1.2	**1E-02**	1.0	1E-01	1.1	5E-01	1.0	**3E-03**	0.9	5E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
55695	**NSUN5**	**probable 28S rRNA (cytosine-C(5))-methyltransferase isoform 1**	3	12	3	1.2	**1E-02**	0.9	**1E-02**	1.1	2E-01	1.0	**4E-02**	1.0	9E-01	Molecular function unknown	-	Cell cycle control protein
387338	**NSUN4**	**5-methylcytosine rRNA methyltransferase NSUN4 isoform a**	2	7	2	1.2	8E-02	0.9	7E-02	1.1	8E-01	0.9	2E-01	1.0	1E+00	Molecular function unknown	-	Unclassified
6207	**RPS13**	**40S ribosomal protein S13**	9	128	9	1.2	**3E-16**	1.0	**3E-15**	1.0	**6E-03**	0.7	6E-01	1.0	1E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
3998	**LMAN1**	**protein ERGIC-53**	16	107	15	1.2	**5E-09**	1.0	**6E-09**	1.2	**1E-05**	**1.5**	**1E-09**	1.0	**6E-03**	Chaperone activity	Endoplasmic reticulum	Chaperone
10284	**SAP18**	**histone deacetylase complex subunit SAP18**	6	27	6	1.2	**7E-06**	0.9	**3E-06**	1.2	3E-01	0.9	**3E-02**	0.9	7E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10011;	**SRA1**	**steroid receptor RNA activator 1 isoform 2**	4	12	2	1.2	**2E-04**	0.8	**4E-05**	1.2	**4E-03**	0.7	1E-01	0.8	**1E-02**	Steroid hormone receptor activity;Molecular function unknown	Cytoplasm	Unclassified
55347	**ABHD10**	**mycophenolic acid acyl-glucuronide esterase, mitochondrial isoform 1**	4	16	4	1.2	**1E-02**	1.1	**7E-03**	1.3	**2E-02**	**1.5**	**2E-02**	0.9	1E+00	Hydrolase activity	-	Enzyme: Hydrolase
23659	**PLA2G15**	**group XV phospholipase A2**	1	6	1	1.2	**2E-02**	1.3	**7E-03**	1.5	7E-02	1.4	**2E-02**	1.0	4E-01	Phospholipase activity	Extracellular	Enzyme: Phospholipase
23351	**KHNYN**	**protein KHNYN isoform 2**	5	12	5	1.2	**4E-02**	1.1	**2E-02**	1.4	**3E-02**	1.1	**1E-02**	1.0	5E-01	Molecular function unknown	Nucleus	Unclassified
548644	**POLR2J**	**PREDICTED: DNA-directed RNA polymerase II subunit RPB11-b2 isoform X1**	3	9	3	1.2	#N/A	0.9	#N/A	1.2	#N/A	0.7	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
7874	**USP7**	**ubiquitin carboxyl-terminal hydrolase 7 isoform 1**	24	114	24	1.2	**2E-10**	1.0	**2E-16**	1.2	**3E-04**	1.0	**5E-15**	1.0	7E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
8721	**EDF1**	**endothelial differentiation-related factor 1 isoform alpha**	10	52	10	1.2	**7E-07**	0.9	**1E-06**	1.0	7E-01	0.7	1E-01	0.9	**3E-02**	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein
57446	**NDRG3**	**protein NDRG3 isoform a**	3	16	3	1.2	**6E-04**	0.8	**6E-04**	1.0	**3E-02**	0.7	**2E-02**	1.0	2E-01	Molecular function unknown	Cytoplasm	Unclassified;Cell cycle control protein
157638	**FAM84B**	**protein FAM84B**	6	12	6	1.2	**2E-03**	0.9	**4E-03**	1.7	1E+00	**1.7**	**4E-03**	1.0	5E-02	Molecular function unknown	Plasma membrane	Unclassified
161424	**NOP9**	**nucleolar protein 9 isoform 1**	3	19	3	1.2	**3E-03**	0.8	**2E-03**	1.2	3E-01	0.9	2E-01	1.0	1E+00	#N/A	#N/A	#N/A
63933	**CCDC90A; MCUR1**	**mitochondrial calcium uniporter regulator 1**	3	10	3	1.2	**3E-03**	1.1	**3E-04**	1.2	**2E-03**	1.4	**1E-03**	1.0	5E-01	#N/A	#N/A	#N/A
5955	**RCN2**	**reticulocalbin-2 isoform b**	5	23	5	1.2	**3E-02**	0.8	**3E-02**	1.1	8E-02	0.8	1E+00	1.0	9E-02	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein
2876	**GPX1**	**glutathione peroxidase 1 isoform 1**	9	74	9	1.2	**4E-09**	0.8	**1E-11**	1.3	**3E-02**	**1.5**	**6E-10**	1.0	2E-01	Peroxidase activity	Cytosol	Enzyme: Peroxidase
6144	**RPL21**	**60S ribosomal protein L21**	9	86	9	1.2	**8E-08**	1.0	**4E-06**	1.0	**2E-03**	0.8	3E-01	1.0	3E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
9061	**PAPSS1**	**bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1**	11	46	11	1.2	**3E-07**	0.7	**1E-06**	1.2	**3E-05**	**0.7**	**2E-03**	0.9	**2E-03**	Nucleotidyltransferase activity	Nucleus	Enzyme: Synthase
10713	**USP39**	**U4/U6.U5 tri-snRNP-associated protein 2 isoform 1**	6	29	6	1.2	**8E-05**	0.9	**1E-04**	1.2	9E-01	0.9	6E-02	0.9	**7E-03**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
25962	**KIAA1429**	**protein virilizer homolog isoform 1**	6	28	6	1.2	**2E-04**	0.9	**8E-04**	1.2	9E-01	0.9	6E-02	1.0	3E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
8455	**ATRN**	**attractin isoform 1 preproprotein**	2	12	2	1.2	**8E-03**	1.1	**4E-04**	1.1	3E-01	0.8	8E-02	1.1	3E-01	Defense/immunity protein activity	Extracellular;Plasma membrane	Defensin
10548	**TM9SF1**	**transmembrane 9 superfamily member 1 isoform a**	5	17	5	1.2	**4E-02**	1.2	6E-02	0.9	**4E-03**	0.9	**2E-02**	0.9	6E-01	Receptor activity	Plasma membrane	Integral membrane protein
27257	**LSM1**	**U6 snRNA-associated Sm-like protein LSm1**	2	10	2	1.2	1E-01	1.0	**4E-02**	1.3	2E-01	1.3	**5E-02**	1.0	1E+00	RNA binding	Cytoplasm	RNA binding protein
85313	**PPIL4**	**peptidyl-prolyl cis-trans isomerase-like 4**	1	6	1	1.2	1E-01	1.0	2E-01	1.2	3E-01	0.9	2E-01	1.1	1E-01	Chaperone activity	Nucleus	Chaperone
54935	**DUSP23**	**dual specificity protein phosphatase 23**	5	12	5	1.2	#N/A	1.2	#N/A	1.2	#N/A	3.3	#N/A	1.5	#N/A	Protein tyrosine/serine/threonine phosphatase activity	Cytoplasm	Dual specificity phosphatase
9397	**NMT2**	**glycylpeptide N-tetradecanoyltransferase 2**	10	68	6	1.2	**2E-05**	1.1	**6E-06**	1.4	7E-02	**2.1**	**3E-06**	1.0	7E-02	Transferase activity	Cytoplasm	Enzyme: Transferase
10040	**TOM1L1**	**TOM1-like protein 1**	4	17	4	1.2	**2E-04**	0.9	**6E-04**	1.1	8E-01	0.8	7E-02	0.9	5E-02	Receptor signaling complex scaffold activity	Endosome	Adapter molecule
79716	**NPEPL1**	**probable aminopeptidase NPEPL1 isoform 1**	3	10	3	1.2	**1E-03**	1.4	**8E-04**	1.2	**3E-03**	**1.5**	**2E-04**	1.1	2E-01	Aminopeptidase activity	-	Aminopeptidase
55201	**MAP1S**	**microtubule-associated protein 1S**	4	15	4	1.2	**1E-02**	0.8	**9E-03**	1.4	3E-01	1.2	**5E-03**	1.0	2E-01	Structural constituent of cytoskeleton	Microtubule	Cytoskeletal protein
6161	**RPL32**	**60S ribosomal protein L32**	9	90	9	1.2	**2E-02**	0.9	4E-01	0.9	3E-01	0.6	1E-01	0.9	**3E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6170; 285785	**RPL39; RPL39P3**	**60S ribosomal protein L39**	1	10	1	1.2	1E-01	1.1	1E-01	0.9	2E-01	0.7	2E-01	0.8	2E-01	#N/A	#N/A	#N/A
214	**ALCAM**	**CD166 antigen isoform 1**	9	48	9	1.2	**4E-04**	0.9	**1E-03**	1.0	3E-01	1.2	**6E-05**	1.0	5E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
9939	**RBM8A; LOC101060541**	**RNA-binding protein 8A**	5	30	5	1.2	**2E-02**	0.8	**2E-02**	1.2	9E-02	0.8	9E-01	1.0	2E-01	#N/A	#N/A	#N/A
51434	**ANAPC7**	**anaphase-promoting complex subunit 7 isoform a**	3	11	3	1.2	**3E-02**	0.8	**9E-03**	1.1	4E-01	0.9	5E-01	0.9	2E-01	Protein binding	Cytoplasm	Cell cycle control protein
84081	**NSRP1**	**nuclear speckle splicing regulatory protein 1 isoform 1**	3	8	3	1.2	**4E-02**	0.8	2E-01	0.9	9E-01	0.8	6E-01	0.8	**2E-02**	#N/A	#N/A	#N/A
64172	**OSGEPL1**	**PREDICTED: probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial isoform X1**	3	7	3	1.2	1E-01	1.3	1E-01	1.2	2E-01	1.0	1E-01	0.9	7E-01	Peptidase activity	-	Protease
9688	**NUP93**	**PREDICTED: nuclear pore complex protein Nup93 isoform X1**	32	166	32	1.2	**2E-16**	1.0	**2E-16**	1.2	**5E-08**	1.2	**2E-16**	1.0	4E-01	Auxiliary transport protein activity	Nucleus	Membrane transport protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6152	**RPL24**	**60S ribosomal protein L24**	10	153	10	1.2	**3E-14**	0.9	**4E-14**	1.0	1E-01	0.7	4E-01	1.0	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
64866	**CDCP1**	**CUB domain-containing protein 1 isoform 1**	8	39	8	1.2	**4E-07**	0.9	**8E-07**	1.1	7E-01	0.9	**4E-05**	1.1	9E-01	Molecular function unknown;Cell adhesion molecule activity	Plasma membrane	Adhesion molecule;Unclassified
689	**BTF3**	**transcription factor BTF3 isoform A**	7	45	5	1.2	**3E-05**	0.8	**2E-07**	1.0	**4E-02**	0.6	2E-01	0.9	**1E-02**	Transcription factor activity	Nucleus	Transcription factor
55262	**C7orf43**	**uncharacterized protein C7orf43 isoform 1**	2	7	2	1.2	**9E-04**	1.1	**2E-02**	1.1	1E-01	1.1	**1E-02**	1.0	**2E-02**	Molecular function unknown	-	Unclassified
28992	**MACROD1**	**O-acetyl-ADP-ribose deacetylase MACROD1**	3	13	3	1.2	6E-02	1.4	1E-01	1.5	2E-01	1.8	1E-01	1.1	5E-01	Molecular function unknown	Mitochondrion	Unclassified
6133	**RPL9**	**60S ribosomal protein L9*gi|67944630|ref|NP_001020092.1|60S ribosomal protein L9**	10	121	10	1.2	**4E-15**	1.0	**2E-15**	1.0	7E-02	0.8	5E-01	0.9	5E-02	Structural constituent of ribosome	Ribosome	Ribosomal subunit
80155	**NAA15**	**N-alpha-acetyltransferase 15, NatA auxiliary subunit**	34	208	4	1.2	**2E-11**	0.8	**2E-11**	1.0	6E-02	0.9	**3E-15**	0.8	**3E-05**	Transferase activity	Cytoplasm;Nucleus	Enzyme: Transferase
5270	**SERPINE2**	**glia-derived nexin isoform c**	4	17	4	1.2	**2E-03**	**0.6**	**2E-02**	0.8	**1E-03**	0.6	5E-02	1.1	**1E-02**	Protease inhibitor activity	Extracellular	Protease inhibitor
253943	**YTHDF3**	**YTH domain-containing family protein 3 isoform b*gi|481026557|ref|NP_001264743.1|YTH domain-containing family protein 3 isoform b**	7	37	4	1.2	**2E-03**	0.7	**2E-04**	1.1	**3E-03**	0.8	2E-01	1.0	**4E-02**	Molecular function unknown	-	Unclassified
4508	**ATP6**	**ATP synthase F0 subunit 6 (mitochondrion)**	2	6	2	1.2	**1E-02**	1.3	**1E-02**	0.9	**6E-03**	1.0	**4E-03**	1.1	**4E-02**	#N/A	#N/A	#N/A
79736	**TEFM**	**transcription elongation factor, mitochondrial**	3	9	3	1.2	**2E-02**	0.9	**2E-02**	1.1	6E-01	1.0	9E-02	1.0	5E-01	#N/A	#N/A	#N/A
199731	**CADM4**	**cell adhesion molecule 4**	1	5	1	1.2	**2E-02**	**0.7**	**4E-02**	1.1	5E-01	1.4	**2E-02**	0.9	3E-01	Molecular function unknown	Integral to membrane	Unclassified
66005	**CHID1**	**chitinase domain-containing protein 1 isoform a*gi|218083182|ref|NP_001136146.1|chitinase domain-containing protein 1 isoform a*gi|218083215|ref|NP_001136147.1|chitinase domain-containing protein 1 isoform a**	3	8	3	1.2	6E-02	1.1	**2E-02**	1.1	**3E-02**	0.7	8E-01	0.9	2E-01	Transporter activity	Lysosome	Transport/cargo protein
79078	**C1orf50**	**uncharacterized protein C1orf50**	1	8	1	1.2	1E-01	1.0	**8E-03**	1.2	8E-01	1.1	**4E-02**	1.1	9E-01	Molecular function unknown	-	Unclassified
5094	**PCBP2**	**poly(rC)-binding protein 2 isoform b**	11	132	6	1.2	**1E-12**	0.8	**4E-13**	1.0	**3E-08**	0.8	**2E-06**	0.9	**2E-04**	RNA binding;DNA binding	Nucleus	RNA binding protein
53407	**STX18**	**syntaxin-18**	6	26	6	1.2	**3E-03**	1.1	**6E-03**	1.1	**8E-03**	1.0	**2E-03**	1.0	5E-01	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein
29115	**SAP30BP**	**SAP30-binding protein isoform 1**	3	16	3	1.2	**4E-03**	1.0	**1E-02**	1.2	5E-01	1.0	**2E-02**	0.9	6E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
54994	**GID8**	**glucose-induced degradation protein 8 homolog**	1	6	1	1.2	6E-02	1.0	6E-02	1.2	5E-01	1.3	**3E-02**	0.9	8E-01	#N/A	#N/A	#N/A
163	**AP2B1**	**AP-2 complex subunit beta isoform b**	32	210	16	1.2	**8E-14**	0.9	**1E-15**	1.1	2E-01	0.9	**2E-09**	1.0	5E-01	Molecular function unknown;Transporter activity	Plasma membrane	Unclassified;Transport/cargo protein
10605	**PAIP1**	**polyadenylate-binding protein-interacting protein 1 isoform 1**	9	60	9	1.2	**2E-07**	0.8	**3E-07**	1.1	**8E-04**	0.8	**3E-02**	0.9	**2E-03**	Translation regulator activity;Protein binding	Cytoplasm	Translation regulatory protein
22800	**RRAS2**	**ras-related protein R-Ras2 isoform a**	9	48	7	1.2	**2E-07**	0.8	**4E-06**	0.9	**3E-03**	0.9	**9E-07**	1.0	9E-01	GTPase activity	Plasma membrane	GTPase
4928	**NUP98**	**nuclear pore complex protein Nup98-Nup96 isoform 1**	22	102	22	1.2	**1E-05**	1.0	**5E-07**	1.2	**2E-03**	1.2	**5E-08**	1.0	1E-01	Transporter activity	Nucleus;Nuclear membrane;Cytoplasm	Transport/cargo protein
56267	**CCBL2; KYAT3**	**kynurenine--oxoglutarate transaminase 3 isoform 1**	11	74	10	1.2	**2E-05**	1.3	**3E-07**	1.3	**6E-05**	1.4	**9E-07**	1.0	3E-01	#N/A	#N/A	#N/A
54870	**QRICH1**	**glutamine-rich protein 1*gi|38570099|ref|NP_942581.1|glutamine-rich protein 1**	7	26	7	1.2	**2E-03**	0.8	**1E-03**	1.3	1E-01	1.1	**3E-03**	1.0	3E-01	Molecular function unknown	-	Unclassified
58505	**OSTC**	**oligosaccharyltransferase complex subunit OSTC isoform 3**	1	12	1	1.2	**5E-03**	0.9	**5E-03**	1.1	8E-01	1.0	**2E-03**	0.9	2E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
117246	**FTSJ3**	**pre-rRNA processing protein FTSJ3**	11	46	11	1.2	**2E-04**	0.9	**3E-04**	1.2	1E-01	0.7	9E-01	1.0	1E-01	Molecular function unknown	Nucleolus	Unclassified
51065	**RPS27L**	**40S ribosomal protein S27-like**	4	42	2	1.2	**7E-04**	1.2	**6E-04**	1.1	5E-02	1.1	**3E-03**	1.0	9E-02	Molecular function unknown	Ribosome	Unclassified
56339	**METTL3**	**N6-adenosine-methyltransferase 70 kDa subunit**	4	16	4	1.2	**1E-02**	1.0	**2E-02**	1.1	2E-01	0.9	6E-02	1.0	8E-01	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase
84888	**SPPL2A**	**signal peptide peptidase-like 2A**	2	8	2	1.2	**5E-02**	0.8	7E-02	1.1	2E-01	0.8	2E-01	1.0	9E-01	#N/A	#N/A	#N/A
84833	**USMG5**	**up-regulated during skeletal muscle growth protein 5**	1	14	1	1.2	1E-01	1.1	**2E-02**	1.0	6E-01	1.1	**2E-02**	1.0	8E-01	Molecular function unknown	Integral to membrane	Integral membrane protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
2782	**GNB1**	**guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 isoform 1*gi|543173169|ref|NP_001269468.1| guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 isoform 1**	8	77	4	1.2	**2E-09**	0.9	**2E-10**	1.1	**1E-03**	0.9	**4E-06**	0.9	8E-02	GTPase activity	Plasma membrane	G protein
865	**CBFB**	**core-binding factor subunit beta isoform 2**	5	35	5	1.2	**3E-04**	0.8	**2E-04**	1.3	**4E-02**	1.1	**2E-04**	1.0	6E-01	Transcription factor activity	Cytoplasm	Transcription factor
2653	**GCSH**	**glycine cleavage system H protein, mitochondrial**	2	10	2	1.2	**3E-03**	1.2	**5E-03**	1.2	**3E-04**	1.4	**2E-03**	0.9	3E-01	Transferase activity	Mitochondrion	Enzyme: Transferase
1E+08	**TMED7-TICAM2**	**TRAM adaptor with GOLD domain isoform 1**	7	49	7	1.2	#N/A	1.0	#N/A	1.1	#N/A	1.2	#N/A	1.1	#N/A	#N/A	#N/A	#N/A
6203	**RPS9**	**PREDICTED: 40S ribosomal protein S9 isoform X1**	13	178	13	1.2	**2E-16**	0.9	**4E-15**	1.0	**4E-03**	0.9	**3E-07**	1.0	4E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
3843	**IPO5**	**PREDICTED: importin-5 isoform X1**	30	186	30	1.2	**2E-13**	0.7	**3E-16**	1.0	**2E-06**	**0.6**	**5E-05**	0.9	**4E-06**	Transporter activity	Cytoplasm	Transport/cargo protein
23534	**TNPO3**	**transportin-3 isoform 1**	19	79	19	1.2	**2E-09**	0.9	**4E-10**	1.3	2E-01	1.2	**8E-10**	1.0	9E-01	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor
10549	**PRDX4**	**peroxiredoxin-4**	10	157	8	1.2	**3E-08**	1.0	**3E-14**	1.1	2E-01	1.0	**4E-14**	1.0	4E-01	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase
4082	**MARCKS**	**myristoylated alanine-rich C-kinase substrate**	9	72	8	1.2	**3E-06**	0.9	**6E-06**	1.1	5E-01	**0.6**	**2E-02**	1.1	**3E-02**	Structural constituent of cytoskeleton	Plasma membrane	Cytoskeletal protein
90850	**ZNF598**	**zinc finger protein 598**	8	30	8	1.2	**2E-03**	1.0	**2E-03**	1.2	4E-01	0.9	**4E-02**	0.9	**1E-02**	DNA binding	Nucleus	DNA binding protein
60682	**SMAP1**	**stromal membrane-associated protein 1 isoform B**	6	20	6	1.2	**2E-03**	1.0	**4E-03**	1.1	7E-01	1.4	6E-02	1.1	8E-02	Binding	Integral to membrane	Integral membrane protein
84164	**ASCC2**	**PREDICTED: activating signal cointegrator 1 complex subunit 2 isoform X2**	8	12	4	1.2	**4E-03**	1.1	**1E-05**	1.1	**6E-03**	0.9	**3E-04**	1.0	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
158747	**MOSPD2**	**motile sperm domain-containing protein 2 isoform 1**	5	14	5	1.2	**2E-02**	1.2	**2E-03**	1.3	1E-01	1.3	**2E-03**	1.0	4E-01	Molecular function unknown	Nucleus;Cytoplasm	Integral membrane protein
1660	**DHX9**	**ATP-dependent RNA helicase A**	35	262	35	1.2	**2E-16**	0.9	**2E-16**	1.2	**7E-04**	0.9	**2E-16**	1.0	7E-01	Transcription factor activity	Nucleus	Transcription factor
22870	**PPP6R1**	**serine/threonine-protein phosphatase 6 regulatory subunit 1**	3	14	3	1.2	**3E-04**	0.9	**1E-03**	1.4	1E-01	**1.5**	**2E-03**	1.1	4E-01	#N/A	#N/A	#N/A
7328	**UBE2H**	**ubiquitin-conjugating enzyme E2 H isoform 1**	3	16	3	1.2	**3E-03**	0.7	**1E-03**	0.9	**2E-02**	1.0	**7E-03**	0.9	**3E-02**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
5578	**PRKCA**	**protein kinase C alpha type**	3	10	2	1.2	**4E-02**	1.3	**5E-02**	1.4	8E-02	1.1	**3E-02**	1.0	1E+00	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
6622	**SNCA**	**PREDICTED: alpha-synuclein isoform X2**	6	20	6	1.2	6E-02	0.9	6E-02	1.0	9E-02	0.5	1E+00	1.1	8E-02	Chaperone activity	Cytoplasm	Chaperone
6188	**RPS3**	**40S ribosomal protein S3 isoform 1**	19	271	19	1.2	**2E-16**	1.0	**2E-16**	1.0	**7E-08**	0.9	**2E-11**	1.0	6E-01	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
6059	**ABCE1**	**ATP-binding cassette sub-family E member 1*gi|108773784|ref|NP_001035809.1| ATP-binding cassette sub-family E member 1**	19	110	19	1.2	**4E-15**	0.8	**2E-15**	1.1	**1E-08**	0.8	6E-01	0.9	**7E-06**	Transporter activity	Cytoplasm	Transport/cargo protein
1595	**CYP51A1**	**lanosterol 14-alpha demethylase isoform 1**	6	27	6	1.2	**1E-04**	0.8	**1E-05**	1.2	**4E-02**	**0.6**	**2E-02**	1.0	2E-01	Molecular function unknown	Endoplasmic reticulum	Unclassified
6904	**TBCD**	**tubulin-specific chaperone D**	12	57	12	1.2	**1E-04**	0.8	**1E-05**	1.2	9E-01	0.8	**8E-03**	0.9	3E-01	Chaperone activity	Microtubule	Chaperone
10055	**SAE1**	**SUMO-activating enzyme subunit 1 isoform a**	14	57	14	1.2	**6E-04**	1.0	**7E-07**	1.2	**2E-02**	0.9	**1E-06**	0.9	**2E-02**	Ligase activity	Nucleus	Enzyme: Ligase
23392	**KIAA0368**	**proteasome-associated protein ECM29 homolog**	25	106	25	1.2	**1E-11**	1.0	**3E-10**	1.1	**8E-06**	1.0	**2E-11**	1.0	**1E-02**	Translation regulator activity	Centrosome	Translation regulatory protein
9039	**UBA3**	**NEDD8-activating enzyme E1 catalytic subunit isoform 1**	10	45	10	1.2	**5E-06**	1.0	**9E-06**	1.4	**6E-04**	1.2	**3E-08**	0.9	**9E-03**	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
6208	**RPS14**	**40S ribosomal protein S14**	5	66	5	1.2	**4E-05**	0.9	**4E-06**	1.0	**3E-02**	0.8	8E-01	0.9	**3E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
50628	**GEMIN4**	**gem-associated protein 4**	10	46	10	1.2	**3E-04**	1.0	**2E-04**	1.2	1E-01	1.0	**4E-05**	1.0	9E-01	Molecular function unknown	Nucleus	Unclassified
23609	**MKRN2**	**probable E3 ubiquitin-protein ligase makorin-2 isoform 1**	5	17	5	1.2	**2E-03**	0.9	**2E-04**	1.1	7E-01	0.9	6E-02	0.9	5E-01	Ribonucleoprotein	-	Unclassified
23509	**POFUT1**	**GDP-fucose protein O-fucosyltransferase 1 isoform 1**	5	23	5	1.2	**1E-02**	0.9	**8E-03**	1.1	3E-01	1.0	**2E-03**	1.0	5E-01	Transferase activity	Golgi membrane	Enzyme: Transferase
6687	**SPG7**	**paraplegin isoform 1**	3	12	3	1.2	**2E-02**	1.2	**8E-03**	1.1	**5E-04**	1.1	**6E-03**	1.0	4E-01	Metallopeptidase activity	Mitochondrion	Metallo protease
147407	**SLC25A52**	**solute carrier family 25 member 52**	1	5	1	1.2	**3E-02**	0.9	**3E-03**	1.3	4E-01	1.2	**4E-03**	1.1	1E-01	#N/A	#N/A	#N/A
4841	**NONO**	**non-POU domain-containing octamer-binding protein isoform 1**	17	105	15	1.2	**7E-08**	0.9	**5E-07**	1.1	1E-01	0.8	4E-01	1.1	8E-02	RNA binding	Nucleus	RNA binding protein
23385	**NCSTN**	**nicastrin isoform 1**	9	48	9	1.2	**7E-07**	0.8	**9E-06**	1.1	**9E-05**	1.0	**1E-06**	1.0	6E-01	Protein binding	Plasma membrane	Integral membrane protein
7388	**UQCRH**	**cytochrome b-c1 complex subunit 6, mitochondrial isoform 1**	4	23	4	1.2	**2E-04**	1.3	**9E-04**	**1.5**	**8E-03**	1.3	**9E-03**	1.0	3E-01	Catalytic activity	Mitochondrion	Enzyme: Reductase

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health

Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
56254	**RNF20**	**PREDICTED: E3 ubiquitin-protein ligase BRE1A isoform X1**	5	11	5	1.2	**7E-03**	1.0	**1E-03**	1.3	2E-01	1.0	4E-01	0.9	8E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
23063	**WAPAL; WAPL**	**wings apart-like protein homolog**	4	12	4	1.2	**3E-02**	1.0	**1E-02**	1.2	**2E-02**	0.9	**4E-03**	0.9	2E-01	#N/A	#N/A	#N/A
27229	**TUBGCP4**	**gamma-tubulin complex component 4 isoform a**	3	10	3	1.2	7E-02	0.9	**3E-02**	1.2	9E-01	1.2	5E-02	1.2	7E-02	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein
7520	**XRCC5**	**X-ray repair cross-complementing protein 5**	28	228	28	1.2	**2E-16**	1.1	**2E-16**	1.2	**9E-09**	0.9	**4E-08**	1.0	3E-01	DNA repair protein	Nucleus	DNA binding protein
87178	**PNPT1**	**polyribonucleotide nucleotidyltransferase 1, mitochondrial**	18	90	18	1.2	**1E-10**	1.0	**4E-10**	1.1	**9E-05**	0.9	**1E-08**	1.1	1E-01	Exonuclease activity	Mitochondrion	RNA exonuclease
10946	**SF3A3**	**splicing factor 3A subunit 3**	13	67	13	1.2	**8E-10**	0.9	**2E-11**	1.3	9E-01	1.0	**4E-06**	1.0	4E-01	RNA binding	Nucleus	RNA binding protein
81567	**TXNDC5**	**thioredoxin domain-containing protein 5 isoform 1**	16	96	16	1.2	**1E-09**	0.9	**7E-11**	1.2	3E-01	0.9	**2E-09**	1.0	6E-02	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase
23022	**PALLD**	**PREDICTED: palladin isoform X1**	20	54	20	1.2	**7E-09**	0.7	**1E-06**	0.9	**3E-09**	**0.5**	**1E-08**	0.9	**1E-03**	Molecular function unknown	Cytoplasm	Unclassified
8836	**GGH**	**gamma-glutamyl hydrolase**	9	45	9	1.2	**5E-08**	1.4	**3E-08**	1.7	**4E-08**	**1.6**	**1E-07**	1.1	**6E-03**	Hydrolase activity	Lysosome	Enzyme: Hydrolase
10844	**TUBGCP2**	**gamma-tubulin complex component 2 isoform 1**	15	45	15	1.2	**9E-04**	1.0	**4E-05**	1.2	**3E-02**	1.0	**9E-05**	1.0	5E-01	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein
131474	**CHCHD4**	**mitochondrial intermembrane space import and assembly protein 40 isoform 2**	3	14	3	1.2	**2E-02**	1.3	**1E-02**	1.5	**2E-02**	1.3	**4E-03**	1.1	4E-01	Molecular function unknown	-	Unclassified
92017	**SNX29**	**sorting nexin-29**	2	8	2	1.2	1E-01	1.1	1E-01	1.2	2E-01	1.1	1E-01	1.1	8E-01	Molecular function unknown	Integral to membrane	Unclassified
28969	**BZW2**	**PREDICTED: basic leucine zipper and W2 domain-containing protein 2 isoform X1**	18	106	15	1.2	**9E-11**	1.0	**2E-11**	1.2	3E-01	0.8	**2E-04**	1.0	8E-01	Translation regulator activity	Nucleolus	Translation regulatory protein
11052	**CPSF6**	**cleavage and polyadenylation specificity factor subunit 6 isoform 2**	10	56	10	1.2	**1E-07**	0.9	**2E-07**	1.2	8E-01	0.9	**2E-08**	0.9	**3E-02**	RNA binding	Nucleus	RNA binding protein
6229	**RPS24**	**40S ribosomal protein S24 isoform d**	5	51	5	1.2	**7E-07**	1.0	**6E-08**	1.0	**4E-02**	0.9	**3E-06**	0.9	7E-02	Structural constituent of ribosome	Ribosome	Ribosomal subunit
92667	**C20orf72; MGME1**	**mitochondrial genome maintenance exonuclease 1**	6	24	6	1.2	**1E-05**	1.0	**4E-05**	1.3	**3E-04**	1.1	**1E-05**	1.1	1E-01	#N/A	#N/A	#N/A
57418	**WDR18**	**WD repeat-containing protein 18**	8	43	8	1.2	**1E-03**	0.9	**9E-05**	1.2	2E-01	1.1	**8E-05**	1.0	7E-01	Molecular function unknown	Nucleolus	Unclassified
8260	**NAA10**	**N-alpha-acetyltransferase 10 isoform 1**	6	21	6	1.2	**4E-03**	0.9	**3E-03**	1.2	1E+00	1.1	**4E-03**	1.0	4E-01	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
5880	**RAC2**	**ras-related C3 botulinum toxin substrate 2**	7	48	3	1.2	**3E-02**	0.7	**4E-02**	1.5	9E-02	1.4	**2E-02**	1.1	**1E-02**	GTPase activity	Plasma membrane	GTPase
5966	**REL**	**proto-oncogene c-Rel isoform 1**	3	10	3	1.2	**4E-02**	0.8	**2E-02**	1.1	8E-01	0.9	6E-02	0.8	**1E-02**	Transcription factor activity	Nucleus	Transcription factor
23244	**PDS5A**	**PREDICTED: sister chromatid cohesion protein PDS5 homolog A isoform X1**	18	70	16	1.2	**9E-06**	1.0	**2E-07**	1.1	**4E-02**	1.0	**3E-07**	1.0	1E+00	Molecular function unknown	Nucleus	Unclassified
54938	**SARS2**	**serine--tRNA ligase, mitochondrial isoform a**	5	32	5	1.2	**8E-05**	1.4	**2E-04**	1.5	**1E-02**	1.3	**3E-03**	1.0	**3E-02**	Ligase activity	Mitochondrion	Enzyme: Ligase
113174	**SAAL1**	**protein SAAL1**	3	17	3	1.2	**2E-04**	0.9	**5E-05**	1.2	7E-01	1.0	**1E-03**	1.1	2E-01	Molecular function unknown	-	Unclassified
3911	**LAMA5**	**laminin subunit alpha-5**	3	9	3	1.2	**4E-03**	0.9	**2E-03**	0.9	4E-01	0.8	1E+00	0.9	3E-01	Cell adhesion molecule activity	Extracellular	Adhesion molecule
64073	**C19orf33**	**immortalization up-regulated protein**	3	16	3	1.2	**7E-03**	1.0	**4E-03**	1.3	2E-01	1.1	**8E-03**	0.9	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
140838	**NANP**	**N-acylneuraminate-9-phosphatase**	2	9	2	1.2	**1E-02**	0.8	**1E-02**	1.3	5E-01	1.1	**2E-02**	1.1	1E-01	Hydrolase activity	-	Enzyme: Hydrolase
5442	**POLRMT**	**DNA-directed RNA polymerase, mitochondrial**	1	5	1	1.2	**3E-02**	1.2	1E-01	1.3	**1E-02**	1.2	**5E-02**	1.0	5E-01	DNA-directed RNA polymerase activity	Mitochondrion	RNA polymerase
10944	**C11orf58**	**small acidic protein**	2	14	2	1.2	**3E-02**	0.9	**3E-02**	1.2	1E+00	0.9	**1E-02**	0.9	**5E-02**	Molecular function unknown	-	Unclassified
84985	**FAM83A**	**protein FAM83A isoform a**	3	7	3	1.2	6E-02	1.0	8E-02	1.6	1E-01	1.7	1E-01	1.0	4E-01	Molecular function unknown	-	Unclassified
4521	**NUDT1**	**7,8-dihydro-8-oxoguanine triphosphatase isoform p22**	4	17	4	1.2	8E-02	0.8	8E-02	1.2	**5E-02**	0.8	1E+00	1.0	4E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
374659	**HDDC3**	**guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase MESH1 isoform 1**	1	6	1	1.2	1E-01	1.1	1E-01	1.4	1E-01	1.2	1E-01	0.9	2E-01	Catalytic activity	-	Enzyme: Phosphohydrolase
10131	**TRAP1**	**heat shock protein 75 kDa, mitochondrial isoform 1**	23	208	22	1.2	**2E-16**	1.1	**2E-16**	1.3	**2E-11**	1.1	**2E-16**	1.0	**4E-02**	Heat shock protein activity	Mitochondrion	Heat shock protein
217	**ALDH2**	**aldehyde dehydrogenase, mitochondrial isoform 1**	13	94	11	1.2	**3E-07**	**1.5**	**2E-07**	1.0	**5E-08**	**0.6**	**2E-05**	0.9	8E-02	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
51504	**TRMT112**	**multifunctional methyltransferase subunit TRM112-like protein isoform 1**	4	20	4	1.2	**4E-05**	**0.6**	**7E-05**	1.1	**1E-03**	**0.6**	**3E-02**	0.8	**8E-03**	Molecular function unknown	-	Unclassified
79029	**SPATA5L1**	**spermatogenesis-associated protein 5-like protein 1**	6	18	6	1.2	**1E-03**	0.8	**3E-05**	1.1	2E-01	1.1	**3E-04**	1.0	4E-01	Molecular function unknown	-	Unclassified
9167	**COX7A2L**	**PREDICTED: cytochrome c oxidase subunit 7A-related protein, mitochondrial isoform X1**	2	10	2	1.2	**1E-02**	0.9	**4E-02**	1.1	8E-01	0.8	6E-01	0.9	4E-01	Catalytic activity	Mitochondrion	Enzyme: Oxidase
64853	**AIDA**	**axin interactor, dorsalization-associated protein**	5	14	5	1.2	7E-02	1.1	7E-02	1.2	1E-01	0.9	**3E-02**	1.1	2E-01	Molecular function unknown	-	Unclassified

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
197322	**ACSF3**	**acyl-CoA synthetase family member 3, mitochondrial isoform 1*gi|187761345|ref|NP_001120686.1| acyl-CoA synthetase family member 3, mitochondrial isoform 1*gi|343168767|ref|NP_001230208.1| acyl-CoA synthetase family member 3, mitochondrial isoform 1**	4	8	4	1.2	2E-01	1.2	3E-01	1.1	2E-01	1.3	2E-01	1.1	2E-01	Molecular function unknown	-	Unclassified
9219	**MTA2**	**metastasis-associated protein MTA2**	15	66	12	1.2	**2E-06**	1.0	**1E-07**	1.1	1E-01	0.9	**9E-05**	1.0	5E-01	DNA binding	Nucleus	Regulatory/other subunit
51043	**ZBTB7B**	**PREDICTED: zinc finger and BTB domain-containing protein 7B isoform X1**	3	14	3	1.2	**6E-03**	1.2	**3E-03**	1.1	**9E-03**	0.8	2E-01	0.9	**1E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
9101	**USP8**	**ubiquitin carboxyl-terminal hydrolase 8 isoform a**	5	11	5	1.2	**1E-02**	1.0	**1E-02**	1.3	1E-01	0.9	2E-01	1.0	6E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
153339	**TMEM167A**	**protein kish-A**	2	12	2	1.2	**3E-02**	**1.6**	**4E-02**	1.0	**5E-03**	**1.6**	**4E-02**	2.3	6E-02	Molecular function unknown	-	Integral membrane protein
51507	**RTFDC1**	**protein RTF2 homolog isoform a**	3	8	3	1.2	1E-01	0.8	9E-02	1.1	5E-01	0.8	7E-01	1.0	3E-01	#N/A	#N/A	#N/A
3376	**IARS**	**isoleucine--tRNA ligase, cytoplasmic**	40	288	40	1.2	**2E-16**	0.9	**2E-16**	1.1	**2E-02**	1.1	**2E-16**	1.0	9E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
1656	**DDX6**	**probable ATP-dependent RNA helicase DDX6**	12	68	12	1.2	**8E-09**	0.9	**8E-10**	1.1	7E-01	0.7	**2E-02**	0.9	**2E-04**	RNA binding	Cytoplasm	RNA binding protein
8971	**H1FX**	**histone H1x**	8	46	8	1.2	**2E-07**	0.9	**2E-08**	1.6	7E-02	1.3	**6E-06**	1.1	**2E-05**	DNA binding	Nucleus	DNA binding protein
26958	**COPG2**	**coatomer subunit gamma-2 isoform 1**	13	64	10	1.2	**1E-05**	1.2	**6E-04**	1.1	**5E-02**	1.1	**8E-03**	1.0	6E-01	Transporter activity	Cytoplasm	Transport/cargo protein
10952	**SEC61B**	**protein transport protein Sec61 subunit beta**	4	26	4	1.2	**2E-03**	1.0	**2E-03**	1.1	**2E-02**	0.9	**2E-03**	1.0	1E-01	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein
11171	**STRAP**	**serine-threonine kinase receptor-associated protein**	16	105	16	1.2	**1E-12**	0.9	**1E-13**	1.1	2E-01	0.8	**3E-04**	0.9	**5E-05**	Receptor binding	Cytoplasm	Cell cycle control protein
6428	**SRSF3**	**serine/arginine-rich splicing factor 3**	8	114	7	1.2	**1E-09**	0.9	**6E-10**	1.1	1E+00	0.9	**6E-08**	0.9	**5E-03**	#N/A	#N/A	#N/A
6426	**SRSF1**	**serine/arginine-rich splicing factor 1 isoform 1**	13	126	13	1.2	**1E-09**	1.0	**7E-11**	1.2	**8E-03**	1.1	**1E-10**	1.0	7E-02	#N/A	#N/A	#N/A
7410	**VAV2**	**guanine nucleotide exchange factor VAV2 isoform 1**	10	36	10	1.2	**5E-05**	0.9	**1E-04**	1.2	7E-01	0.9	**3E-03**	1.0	2E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
11224	**RPL35**	**60S ribosomal protein L35**	6	61	6	1.2	**1E-04**	1.0	**2E-04**	1.0	9E-02	**0.7**	**4E-02**	0.9	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6470	**SHMT1**	**serine hydroxymethyltransferase, cytosolic isoform 1**	9	47	8	1.2	**4E-04**	1.2	**2E-04**	1.2	**9E-04**	0.9	**1E-02**	1.1	2E-01	Methyltransferase activity;RNA binding	Cytoplasm	Enzyme: Methyltransferase;RNA binding protein
197131	**UBR1**	**E3 ubiquitin-protein ligase UBR1**	6	25	6	1.2	**4E-04**	0.9	**9E-05**	1.1	1E-01	1.0	**2E-04**	1.0	8E-02	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
25870	**SUMF2**	**sulfatase-modifying factor 2 isoform b**	6	27	6	1.2	**4E-04**	1.0	**7E-04**	1.0	6E-01	0.8	3E-01	1.0	6E-01	Molecular function unknown	Endoplasmic reticulum	Unclassified
5715	**PSMD9**	**26S proteasome non-ATPase regulatory subunit 9 isoform 1**	7	38	7	1.2	**7E-04**	1.0	**7E-06**	1.2	2E-01	1.1	**2E-05**	0.9	5E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
9698	**PUM1**	**pumilio homolog 1 isoform 1**	5	28	3	1.2	**2E-03**	0.8	**3E-03**	1.1	1E-01	1.0	**7E-03**	0.9	2E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
55742	**PARVA**	**alpha-parvin**	7	36	5	1.2	**4E-03**	0.8	**2E-03**	1.1	**9E-03**	0.9	**2E-02**	1.0	4E-01	Cytoskeletal protein binding	Plasma membrane;Nucleus	Cytoskeletal associated protein
27429	**HTRA2**	**serine protease HTRA2, mitochondrial isoform 1 preproprotein**	3	5	3	1.2	1E-01	1.3	1E-01	1.3	2E-01	1.5	1E-01	1.1	2E-01	Serine-type peptidase activity	Mitochondrion	Serine protease
402;	**ARL2**	**ADP-ribosylation factor-like protein 2 isoform 2**	6	14	4	1.2	2E-01	0.7	8E-02	1.2	4E-01	0.8	2E-01	0.8	1E+00	GTPase activity	Cytoplasm	GTPase
7307; 102724594	**U2AF1; LOC102724594; U2AF1L5**	**PREDICTED: splicing factor U2AF 35 kDa subunit isoform X1**	7	33	7	1.2	#N/A	0.9	#N/A	1.1	#N/A	1.0	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
6189	**RPS3A**	**40S ribosomal protein S3a isoform 1**	22	286	22	1.2	**2E-16**	0.9	**2E-16**	1.0	**1E-02**	0.8	**2E-05**	0.9	4E-01	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
22826	**DNAJC8**	**dnaJ homolog subfamily C member 8**	9	55	9	1.2	**3E-09**	0.8	**5E-09**	1.3	**2E-04**	0.7	**9E-03**	0.9	**1E-04**	Chaperone activity	Nucleolus	Chaperone
6222	**RPS18**	**40S ribosomal protein S18**	9	119	9	1.2	**6E-09**	1.0	**4E-05**	1.1	**2E-03**	0.8	2E-01	1.1	**1E-03**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
10291	**SF3A1**	**splicing factor 3A subunit 1**	21	103	21	1.2	**2E-07**	0.9	**1E-09**	1.2	1E-01	1.0	**8E-05**	0.9	3E-01	RNA binding	Nucleus	RNA binding protein
51109	**RDH11**	**retinol dehydrogenase 11 isoform 1**	7	62	5	1.2	**5E-07**	1.0	**3E-06**	1.3	**1E-03**	1.4	**6E-06**	1.1	**3E-02**	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase
57062	**DDX24**	**ATP-dependent RNA helicase DDX24**	11	40	11	1.2	**1E-04**	0.8	**4E-05**	1.1	**3E-02**	0.7	6E-02	1.0	8E-01	Transporter activity	Nucleus	Transport/cargo protein
9371	**KIF3B**	**kinesin-like protein KIF3B**	4	14	3	1.2	**3E-02**	1.1	**9E-03**	1.2	**1E-02**	1.0	**7E-03**	1.2	4E-01	Motor activity	Cytoplasm	Motor protein

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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
26090	ABHD12	monoacylglycerol lipase ABHD12 isoform b	3	10	3	1.2	5E-02	1.2	**5E-02**	1.2	6E-02	1.3	6E-02	1.0	7E-02	Molecular function unknown	-	Integral membrane protein
1855	DVL1	segment polarity protein dishevelled homolog DVL-1	3	12	1	1.2	1E-01	**0.6**	**2E-04**	1.1	2E-01	0.9	7E-02	1.0	8E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
1655	DDX5	PREDICTED: probable ATP-dependent RNA helicase DDX5 isoform X1	31	274	22	1.2	**2E-16**	0.7	**2E-16**	1.1	**1E-11**	**0.6**	**5E-10**	0.8	**6E-13**	RNA binding	Nucleus	RNA binding protein
7175	TPR	nucleoprotein TPR	67	304	66	1.2	**2E-16**	1.0	**2E-16**	1.2	**4E-08**	1.2	**2E-16**	1.0	**2E-03**	Molecular function unknown	Cytoplasm	Unclassified
9349	RPL23	60S ribosomal protein L23	8	146	8	1.2	**2E-11**	0.9	**2E-12**	1.0	4E-01	**0.7**	**2E-03**	0.9	**7E-03**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
23277	CLUH; KIAA0664	clustered mitochondria protein homolog	24	111	24	1.2	**4E-11**	0.9	**2E-09**	1.0	1E+00	**0.7**	**3E-03**	0.9	**8E-04**	#N/A	#N/A	#N/A
8570	KHSRP	far upstream element-binding protein 2	26	175	22	1.2	**2E-09**	0.9	**9E-10**	1.2	4E-01	0.7	3E-01	0.9	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
6301	SARS	serine--tRNA ligase, cytoplasmic	17	128	17	1.2	**2E-09**	1.0	**3E-09**	1.4	**3E-06**	**1.5**	**7E-09**	1.0	1E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
5931	RBBP7	histone-binding protein RBBP7 isoform 2	6	37	3	1.2	**4E-08**	0.9	**2E-10**	1.0	2E-01	0.8	7E-01	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
8473	OGT	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit isoform 1	8	36	8	1.2	**7E-07**	0.9	**6E-07**	1.1	2E-01	1.0	**1E-06**	0.9	3E-01	Transferase activity	Nucleus	Enzyme: Glucosaminyltransferase
10907	TXNL4A	thioredoxin-like protein 4A isoform 1	3	14	3	1.2	**9E-05**	0.9	**3E-04**	1.2	4E-01	0.7	7E-01	0.9	7E-01	Spliceosomal catalysis	Nucleus	Unclassified
440275	EIF2AK4	eukaryotic translation initiation factor 2-alpha kinase 4	4	19	4	1.2	**4E-03**	0.9	**2E-03**	1.1	1E+00	0.9	7E-02	1.1	7E-02	Transmembrane receptor protein tyrosine kinase activity	Cytoplasm	Receptor tyrosine kinase
57106	NAT14	N-acetyltransferase 14	1	8	1	1.2	**7E-03**	1.1	**4E-02**	1.4	2E-01	**1.7**	**1E-02**	1.1	5E-01	Transcription factor activity	Nucleus	Transcription factor
4331	MNAT1	PREDICTED: CDK-activating kinase assembly factor MAT1 isoform X1	3	7	3	1.2	**3E-02**	0.8	**2E-02**	1.2	7E-01	1.0	5E-01	1.0	8E-01	Kinase binding	Nucleus	Cell cycle control protein
9238	TBRG4	protein TBRG4 isoform 3	8	28	8	1.2	**4E-02**	1.2	**2E-02**	1.4	**1E-02**	1.0	**3E-02**	1.0	5E-01	Molecular function unknown	Mitochondrion;Nucleus	Cell cycle control protein
3912	LAMB1	laminin subunit beta-1	2	8	2	1.2	6E-02	0.8	**2E-02**	1.1	4E-01	0.8	3E-01	1.2	3E-01	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
8761	PABPC4	polyadenylate-binding protein 4 isoform 1	20	175	14	1.2	**2E-16**	0.9	**2E-16**	1.1	1E+00	1.0	**2E-14**	0.9	**8E-03**	RNA binding	Cytoplasm	RNA binding protein
6223	RPS19	40S ribosomal protein S19	10	136	10	1.2	**2E-14**	0.9	**2E-16**	1.0	**4E-02**	**0.6**	**1E-08**	0.9	**2E-05**	Structural constituent of ribosome	Nucleolus	Ribosomal subunit
6201	RPS7	40S ribosomal protein S7	9	113	9	1.2	**4E-14**	1.0	**7E-13**	1.0	**3E-05**	0.8	**2E-02**	1.0	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
55246	CCDC25	coiled-coil domain-containing protein 25 isoform 1	9	43	9	1.2	**1E-06**	1.0	**6E-08**	1.2	**2E-03**	0.9	**2E-03**	0.8	**4E-03**	Molecular function unknown	-	Unclassified
114793	FMNL2	formin-like protein 2	9	28	9	1.2	**3E-03**	0.9	**1E-04**	1.2	9E-01	1.1	**1E-06**	1.0	7E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
10436	EMG1	ribosomal RNA small subunit methyltransferase NEP1	4	16	4	1.2	**1E-02**	0.8	**7E-03**	1.1	3E-01	0.8	3E-01	1.0	3E-01	Translation regulator activity	Nucleus	Translation regulatory protein
1994	ELAVL1	ELAV-like protein 1	11	57	11	1.2	**2E-07**	0.9	**9E-07**	1.2	5E-01	0.9	**2E-06**	1.0	8E-01	RNA binding	Nucleus	RNA binding protein
7916	PRRC2A	protein PRRC2A	18	71	17	1.2	**4E-05**	1.0	**1E-04**	1.2	**4E-02**	1.1	**7E-05**	1.0	8E-01	#N/A	#N/A	#N/A
6227	RPS21	40S ribosomal protein S21	4	73	4	1.2	**5E-05**	0.9	**2E-05**	0.9	1E+00	**0.6**	**3E-06**	1.1	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
5361	PLXNA1	plexin-A1	6	24	3	1.2	**1E-04**	0.8	**2E-04**	1.1	7E-01	1.0	**1E-02**	1.2	**4E-03**	Receptor activity	Plasma membrane	Cell surface receptor
81892	SLIRP	SRA stem-loop-interacting RNA-binding protein, mitochondrial isoform 1	7	35	7	1.2	**7E-04**	1.0	**1E-04**	1.2	**1E-02**	0.7	2E-01	1.0	7E-01	#N/A	#N/A	#N/A
4363	ABCC1	multidrug resistance-associated protein 1	8	29	7	1.2	**1E-03**	1.1	**6E-03**	1.3	**1E-03**	1.1	**2E-02**	1.1	2E-01	Transporter activity	Plasma membrane	Transport/cargo protein
23360	FNBP4	formin-binding protein 4	2	12	2	1.2	**2E-03**	1.2	**1E-02**	1.5	5E-02	1.3	**4E-02**	1.1	**2E-02**	Molecular function unknown	Nucleus	Unclassified
55671	SMEK1; PPP4R3A	serine/threonine-protein phosphatase 4 regulatory subunit 3A isoform 1	9	35	5	1.2	**6E-03**	1.0	**4E-03**	1.4	3E-01	1.0	**5E-03**	1.0	4E-01	#N/A	#N/A	#N/A
347862	PDDC1	Parkinson disease 7 domain-containing protein 1	3	16	3	1.2	**1E-02**	1.1	**1E-03**	1.1	**3E-02**	1.2	**2E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
28971	AAMDC	PREDICTED: mth938 domain-containing protein isoform X1	4	20	4	1.2	**1E-02**	1.0	**2E-02**	1.0	**3E-02**	0.8	2E-01	1.0	1E-01	#N/A	#N/A	#N/A
123169	LEO1	RNA polymerase-associated protein LEO1 isoform 1	2	10	2	1.2	**2E-02**	0.7	**4E-02**	1.1	**3E-02**	0.9	4E-01	0.8	5E-02	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
129285	PPP1R21	protein phosphatase 1 regulatory subunit 21 isoform 1	7	23	7	1.2	**3E-02**	1.0	**1E-02**	1.1	**5E-02**	1.0	**2E-04**	1.0	1E+00	#N/A	#N/A	#N/A
4720	NDUFS2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial isoform 1	10	42	10	1.2	**1E-05**	0.9	**1E-03**	1.1	5E-01	1.1	**5E-02**	1.0	6E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
6182	MRPL12	39S ribosomal protein L12, mitochondrial	4	27	4	1.2	**1E-04**	1.1	**4E-05**	1.3	**3E-04**	1.2	**2E-05**	1.0	5E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
55621	TRMT1	tRNA (guanine(26)-N(2))-dimethyltransferase isoform 1	6	26	6	1.2	**2E-04**	1.0	**4E-04**	1.3	2E-01	1.0	**2E-03**	1.0	5E-01	RNA methyltransferase activity	-	RNA methyltransferase
988	CDC5L	cell division cycle 5-like protein	14	57	14	1.2	**4E-04**	0.9	**5E-04**	1.3	9E-01	1.0	**5E-03**	1.0	4E-01	Protein binding	Nucleus	Cell cycle control protein
23612	PHLDA3	pleckstrin homology-like domain family A member 3	3	14	3	1.2	**1E-03**	**0.7**	**2E-05**	1.2	**1E-02**	0.7	8E-01	1.1	1E-01	Molecular function unknown	-	Unclassified
51324	SPG21	maspardin isoform a	5	23	5	1.2	**9E-03**	0.9	**4E-03**	1.2	9E-01	0.9	**1E-02**	0.9	8E-01	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
57038	RARS2	probable arginine--tRNA ligase, mitochondrial	5	17	5	1.2	**2E-02**	1.1	**2E-02**	1.1	**2E-02**	0.9	2E-01	1.0	8E-01	Catalytic activity	-	Enzyme: Synthase
6421	SFPQ	PREDICTED: splicing factor, proline- and glutamine-rich isoform X1	24	216	23	1.2	**2E-16**	0.8	**2E-16**	1.1	**3E-08**	0.9	**1E-06**	0.9	**1E-04**	RNA binding	Nucleus	RNA binding protein
27044	SND1	staphylococcal nuclease domain-containing protein 1	37	242	37	1.2	**2E-16**	0.9	**2E-16**	1.0	7E-01	0.7	**1E-02**	1.0	6E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
2289	FKBP5	peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1*gi|224809329|ref|NP_001139248.1| peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1*gi|4758384|ref|NP_004108.1| peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1	23	156	23	1.2	**1E-14**	1.0	**8E-14**	1.1	**6E-09**	0.8	7E-02	0.9	**2E-09**	Isomerase activity	Cytoplasm	Enzyme: Isomerase
10286	BCAS2	pre-mRNA-splicing factor SPF27	7	33	7	1.2	**8E-05**	1.0	**7E-05**	1.3	**1E-03**	0.9	**2E-03**	1.0	3E-01	Pre-mRNA splicing factor activity	Nucleus	Cell cycle control protein
27042	DIEXF	digestive organ expansion factor homolog	2	7	2	1.2	**1E-03**	0.7	**7E-03**	1.2	1E-01	0.8	5E-01	1.1	4E-01	#N/A	#N/A	#N/A
27247	NFU1	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial isoform 2	5	27	5	1.2	**3E-03**	1.0	**6E-04**	1.2	**5E-03**	1.0	**7E-05**	1.0	3E-01	Molecular function unknown	Mitochondrion;Cytosol	Unclassified
84890	ADO	2-aminoethanethiol dioxygenase	5	21	5	1.2	**4E-03**	0.9	**3E-03**	1.2	3E-01	0.9	**3E-02**	0.9	9E-02	Molecular function unknown	-	Unclassified
6217	RPS16	40S ribosomal protein S16	12	147	12	1.2	**1E-14**	0.9	**2E-14**	1.0	4E-01	0.8	**1E-04**	1.0	1E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
2729	GCLC	glutamate--cysteine ligase catalytic subunit isoform a	17	119	16	1.2	**5E-10**	1.1	**6E-11**	1.3	**1E-06**	1.2	**4E-11**	0.9	**3E-02**	Ligase activity	-	Enzyme: Ligase
9352	TXNL1	thioredoxin-like protein 1	9	49	9	1.2	**7E-05**	0.9	**8E-05**	1.4	1E-01	1.4	**1E-04**	0.9	2E-01	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase
23479	ISCU	iron-sulfur cluster assembly enzyme ISCU, mitochondrial isoform ISCU2	4	16	4	1.2	**2E-03**	1.1	**2E-03**	1.3	**5E-03**	1.0	**1E-02**	1.0	7E-01	Molecular function unknown	Cytosol;Mitochondrion	Unclassified
145482	PTGR2	prostaglandin reductase 2	3	12	3	1.2	**4E-03**	1.2	**9E-03**	1.2	**4E-02**	1.4	**2E-02**	0.9	3E-01	Catalytic activity	-	Enzyme: Dehydrogenase
4077	NBR1	next to BRCA1 gene 1 protein isoform a	1	6	1	1.2	**5E-03**	0.7	6E-01	0.8	2E-01	1.2	7E-02	1.2	5E-01	Molecular function unknown	Cytoplasm	Unclassified
84259	DCUN1D5	DCN1-like protein 5	3	10	3	1.2	**8E-03**	0.7	**3E-03**	1.0	1E-01	0.8	5E-02	0.9	1E-01	Molecular function unknown	-	Unclassified
80011	FAM192A	protein FAM192A	6	22	6	1.2	**1E-02**	1.0	**1E-02**	1.2	3E-01	0.8	5E-01	1.1	2E-01	Molecular function unknown	Nucleus	Unclassified
6124	RPL4	60S ribosomal protein L4	21	340	21	1.2	**2E-16**	0.9	**2E-16**	1.0	2E-01	0.8	7E-01	0.9	**7E-04**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6130	RPL7A	60S ribosomal protein L7a	13	165	13	1.2	**2E-16**	1.0	**2E-16**	1.0	**8E-08**	0.8	**3E-02**	1.0	**4E-04**	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
6472	SHMT2	serine hydroxymethyltransferase, mitochondrial isoform 1	22	190	21	1.2	**2E-16**	1.0	**2E-16**	1.3	**6E-13**	1.2	**2E-16**	1.1	**2E-02**	Methyltransferase activity	Mitochondrion	Enzyme: Methyltransferase
5660	PSAP	prosaposin isoform b preproprotein	18	145	18	1.2	**6E-13**	0.7	**7E-10**	1.1	**2E-06**	0.9	**3E-04**	0.9	**3E-02**	Lipid binding	Lysosome	Integral membrane protein
375056	MIA3	melanoma inhibitory activity protein 3 isoform 1	17	59	16	1.2	**7E-09**	1.0	**2E-09**	1.1	**5E-04**	1.1	**2E-07**	1.0	3E-01	Molecular function unknown	-	Unclassified
9410	SNRNP40	U5 small nuclear ribonucleoprotein 40 kDa protein	6	33	6	1.2	**3E-07**	1.0	**2E-07**	1.2	6E-02	0.8	1E-01	1.0	2E-01	Ribonucleoprotein	Nucleus	RNA binding protein
7158	TP53BP1	tumor suppressor p53-binding protein 1 isoform 1	7	20	7	1.2	**7E-03**	1.0	**5E-03**	1.3	**4E-02**	1.0	**8E-03**	1.1	7E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
92140	MTDH	protein LYRIC	18	101	18	1.2	**1E-10**	1.0	**1E-12**	1.2	**8E-07**	0.9	**1E-11**	1.0	7E-02	Molecular function unknown	Endoplasmic reticulum	Unclassified
27043	PELP1	proline-, glutamic acid- and leucine-rich protein 1 isoform 1	12	65	12	1.2	**4E-07**	1.0	**4E-08**	1.3	**7E-03**	1.1	**2E-07**	1.0	9E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
51663	ZFR	zinc finger RNA-binding protein	9	39	9	1.2	**9E-07**	0.8	**3E-07**	1.2	**1E-02**	0.8	3E-01	0.9	**3E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
23549	DNPEP	aspartyl aminopeptidase	9	39	9	1.2	**5E-06**	1.0	**4E-07**	1.3	**1E-02**	1.4	**5E-07**	1.0	5E-01	Aminopeptidase activity	Cytoplasm	Aminopeptidase
4898	NRD1; NRDC	nardilysin isoform a	15	65	15	1.2	**4E-04**	1.0	**7E-05**	1.1	**4E-06**	1.1	**2E-05**	1.1	5E-02	#N/A	#N/A	#N/A
22916	NCBP2	nuclear cap-binding protein subunit 2 isoform 1	5	20	5	1.2	**8E-04**	0.8	**4E-04**	1.2	2E-01	0.8	8E-01	0.9	2E-01	RNA binding	Nucleus	RNA binding protein
9263	STK17A	serine/threonine-protein kinase 17A	2	10	2	1.2	**5E-02**	0.7	**4E-02**	1.0	1E-01	0.9	8E-02	0.9	7E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
160418	TMTC3	transmembrane and TPR repeat-containing protein 3	14	63	13	1.2	**6E-09**	1.0	**2E-07**	1.1	**4E-06**	1.0	**4E-04**	1.0	1E-01	Molecular function unknown	-	Unclassified
8915	BCL10	B-cell lymphoma/leukemia 10	5	25	5	1.2	**1E-03**	1.0	**8E-04**	1.2	2E-01	0.9	3E-01	0.9	9E-02	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
65109	**UPF3B**	**regulator of nonsense transcripts 3B isoform 1**	2	10	2	1.2	1E-01	1.1	**4E-02**	1.2	2E-01	0.9	3E-01	0.9	6E-01	RNA binding	Nucleus	RNA binding protein
5245	**PHB**	**prohibitin isoform 1**	16	160	16	1.2	**1E-12**	1.1	**8E-13**	1.3	**7E-11**	**1.5**	**2E-12**	1.0	**4E-02**	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule
960	**CD44**	**CD44 antigen isoform 1**	10	142	10	1.2	**6E-12**	0.8	**9E-12**	1.0	1E-01	**0.5**	**4E-04**	0.9	4E-01	Receptor activity	Plasma membrane	Cell surface receptor
26007	**DAK; TKFC**	**bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)**	10	46	10	1.2	**2E-08**	1.3	**9E-10**	1.2	**8E-06**	1.0	**4E-05**	1.0	2E-01	#N/A	#N/A	#N/A
221294	**NT5DC1**	**5'-nucleotidase domain-containing protein 1**	9	48	9	1.2	**5E-07**	1.0	**3E-06**	1.1	**4E-04**	0.8	**3E-02**	0.9	6E-02	Molecular function unknown	Cytoplasm	Unclassified
25915	**NDUFAF3**	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 isoform a**	3	16	3	1.2	**1E-04**	0.9	**2E-04**	1.4	4E-01	1.1	**9E-05**	1.1	**2E-03**	Molecular function unknown	-	Unclassified
7919	**DDX39B**	**spliceosome RNA helicase DDX39B*gi|4758112|ref|NP_004631.1| spliceosome RNA helicase DDX39B**	16	120	6	1.2	**2E-03**	0.8	**2E-03**	1.2	**3E-02**	0.8	**1E-02**	0.9	**3E-03**	#N/A	#N/A	#N/A
166785	**MMAA**	**PREDICTED: methylmalonic aciduria type A protein, mitochondrial isoform X1**	5	14	5	1.2	**7E-03**	1.1	**1E-02**	1.3	7E-02	1.2	**5E-02**	1.2	7E-02	ATPase activity	Mitochondrion	ATPase
56163	**RNF17**	**RING finger protein 17 isoform 1**	1	6	1	1.2	**4E-02**	0.8	6E-02	1.1	5E-01	1.0	**4E-02**	1.1	4E-01	Molecular function unknown	-	Unclassified
23413	**NCS1**	**neuronal calcium sensor 1 isoform 1**	2	7	2	1.2	6E-02	0.9	**4E-02**	1.1	9E-01	0.9	2E-01	1.0	6E-01	Calcium ion binding	Golgi apparatus	Calcium binding protein
51510	**CHMP5**	**charged multivesicular body protein 5 isoform 1**	4	14	4	1.2	8E-02	1.1	5E-02	1.5	3E-01	1.3	6E-02	0.9	**9E-03**	Transporter activity	-	Transport/cargo protein
10884	**MRPS30**	**28S ribosomal protein S30, mitochondrial**	2	7	2	1.2	9E-02	1.0	**4E-02**	1.1	4E-01	0.9	4E-01	1.0	1E+00	Structural molecule activity	Mitochondrion	Structural protein
54507	**ADAMTSL4**	**PREDICTED: ADAMTS-like protein 4 isoform X1**	2	5	2	1.2	#N/A	2.7	#N/A	0.9	#N/A	2.0	#N/A	1.1	#N/A	Molecular function unknown	Lysosome	Unclassified
1.01E+08	**ISY1-RAB43**	**ISY1-RAB43 protein**	4	8	4	1.2	#N/A	0.9	#N/A	1.3	#N/A	0.7	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
10492	**SYNCRIP**	**heterogeneous nuclear ribonucleoprotein Q isoform 1**	26	257	18	1.2	**5E-12**	0.9	**7E-12**	1.2	4E-01	1.0	**2E-11**	1.0	1E-01	RNA binding	Cytoplasm	RNA binding protein
9100	**USP10**	**ubiquitin carboxyl-terminal hydrolase 10 isoform 1**	12	64	12	1.2	**1E-08**	0.9	**1E-07**	1.1	9E-02	0.7	6E-01	0.9	**3E-03**	Ubiquitin-specific protease activity	Nucleus;Cytoplasm	Ubiquitin proteasome system protein
2773	**GNAI3**	**guanine nucleotide-binding protein G(k) subunit alpha**	11	100	5	1.2	**2E-04**	0.9	**3E-04**	1.3	**2E-02**	0.8	2E-01	0.9	4E-01	GTPase activity	Plasma membrane	G protein
6748	**SSR4**	**translocon-associated protein subunit delta isoform 1**	5	34	5	1.2	**3E-03**	1.0	**2E-03**	1.2	**8E-03**	1.2	**5E-03**	1.1	**1E-02**	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein
5434	**POLR2E**	**DNA-directed RNA polymerases I, II, and III subunit RPABC1**	5	21	5	1.2	**3E-03**	1.1	**6E-04**	1.3	**2E-02**	1.0	**4E-02**	1.0	7E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
5226	**PGD**	**6-phosphogluconate dehydrogenase, decarboxylating isoform 1**	24	227	24	1.2	**3E-16**	1.0	**3E-16**	1.7	**2E-06**	**1.5**	**2E-16**	0.9	**2E-03**	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
11100	**HNRNPUL1**	**heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform a**	17	82	17	1.2	**2E-11**	0.9	**8E-12**	1.3	8E-02	1.0	**2E-11**	0.9	6E-02	Ribonucleoprotein;RNA binding	Nucleus	RNA binding protein
5902	**RANBP1**	**ran-specific GTPase-activating protein isoform 1**	6	63	6	1.2	**3E-06**	0.9	**3E-07**	1.2	3E-01	0.9	**2E-05**	0.9	4E-01	Transporter activity	Cytoplasm	Transport/cargo protein
158	**ADSL**	**adenylosuccinate lyase isoform a**	7	48	7	1.2	**2E-05**	0.8	**4E-05**	1.1	**2E-02**	0.9	**4E-04**	0.9	**1E-02**	Lyase activity	Cytoplasm	Enzyme: Lyase
9049	**AIP**	**AH receptor-interacting protein isoform 1**	6	27	6	1.2	**1E-04**	0.9	**3E-05**	1.4	2E-01	1.1	**2E-04**	0.9	**8E-03**	Transcription regulator activity	Nucleus	Transcription regulatory protein
79767	**ELMO3**	**engulfment and cell motility protein 3**	6	29	6	1.2	**1E-04**	0.9	**1E-04**	1.2	8E-01	0.9	**4E-03**	0.9	8E-02	Motor activity	-	Motor protein
4074	**M6PR**	**cation-dependent mannose-6-phosphate receptor isoform 1**	7	36	7	1.2	**3E-04**	1.0	**2E-04**	1.1	6E-02	1.0	**9E-04**	1.0	7E-01	Receptor activity	Plasma membrane	Integral membrane protein
79896	**THNSL1**	**PREDICTED: threonine synthase-like 1 isoform X1**	5	18	5	1.2	**2E-03**	1.0	**9E-04**	1.2	**5E-03**	1.0	**4E-03**	1.0	7E-01	Molecular function unknown	-	Unclassified
8732	**RNGTT**	**mRNA-capping enzyme isoform a**	1	6	1	1.2	1E-01	0.8	1E-01	1.1	**3E-02**	**0.6**	**1E-02**	0.8	**1E-02**	Catalytic activity	Nucleus	Enzyme: Adenosyltransferase
4430	**MYO1B**	**PREDICTED: unconventional myosin-Ib isoform X1**	42	302	42	1.2	**2E-16**	0.9	**2E-16**	1.1	6E-01	1.1	**2E-16**	1.0	**3E-03**	Motor activity	Plasma membrane	Motor protein
55236	**UBA6**	**ubiquitin-like modifier-activating enzyme 6**	33	193	33	1.2	**2E-16**	0.8	**2E-16**	1.1	**6E-04**	1.2	**3E-16**	1.0	1E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
23344	**ESYT1**	**extended synaptotagmin-1 isoform 2**	28	159	27	1.2	**6E-13**	0.9	**3E-14**	1.1	5E-02	1.0	**3E-15**	1.1	**3E-07**	Calcium ion binding	Plasma membrane	Calcium binding protein
5204	**PFDN5**	**prefoldin subunit 5 isoform alpha**	6	43	6	1.2	**1E-05**	1.0	**7E-06**	1.3	**3E-02**	1.1	**2E-05**	1.0	8E-01	Chaperone activity	Nucleus	Chaperone
29920	**PYCR2**	**pyrroline-5-carboxylate reductase 2 isoform 1**	7	31	7	1.2	**2E-05**	1.0	**8E-06**	1.4	9E-02	1.3	**8E-07**	1.0	2E-01	Molecular function unknown	Mitochondrion	Unclassified
64755	**C16orf58**	**RUS1 family protein C16orf58**	4	15	4	1.2	**2E-03**	1.3	**1E-03**	1.3	**2E-02**	**1.7**	**4E-04**	1.0	8E-01	Molecular function unknown	-	Integral membrane protein
81887	**LAS1L**	**ribosomal biogenesis protein LAS1L isoform 1**	8	27	8	1.2	**2E-02**	1.0	**4E-03**	1.2	7E-02	1.1	**3E-03**	1.2	9E-02	Molecular function unknown	Nucleus	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7936	NELFE; RDBP	negative elongation factor E	3	10	3	1.2	**3E-02**	1.0	8E-02	1.2	4E-01	0.9	2E-01	1.0	1E-01	#N/A	#N/A	#N/A
11321	GPN1	GPN-loop GTPase 1 isoform a	3	8	3	1.2	4E-01	0.8	2E-01	1.3	2E-01	1.1	3E-01	0.9	7E-01	GTPase activity	Cytoplasm	GTPase
23451	SF3B1	splicing factor 3B subunit 1 isoform 1	32	165	32	1.2	**2E-16**	1.0	**2E-16**	1.2	**3E-04**	0.9	**9E-16**	1.0	1E+00	Ribonucleoprotein	Nucleus	RNA binding protein
3428	IFI16	gamma-interferon-inducible protein 16 isoform 2	26	156	26	1.2	**2E-06**	0.9	2E-01	0.9	1E-01	**0.6**	**3E-02**	0.9	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
210	ALAD	delta-aminolevulinic acid dehydratase	3	9	3	1.2	9E-02	1.4	3E-01	1.2	1E-01	1.1	3E-01	0.9	9E-01	Hydro-lyase activity	Cytoplasm	Enzyme: Dehydratase
283871	PGP	phosphoglycolate phosphatase	2	8	2	1.2	1E-01	0.9	1E-01	1.1	5E-01	1.0	1E-01	0.9	7E-02	Molecular function unknown	-	Unclassified
166378	SPATA5	spermatogenesis-associated protein 5	11	60	10	1.2	**1E-08**	1.0	**7E-09**	1.3	2E-01	1.2	**1E-08**	1.1	3E-01	ATPase activity	Mitochondrion	ATPase
79711	IPO4	importin-4	15	67	15	1.2	**2E-06**	0.9	**5E-08**	1.2	6E-01	0.8	**4E-03**	1.0	7E-01	Transporter activity	Cytoplasm	Transport/cargo protein
6160	RPL31	60S ribosomal protein L31 isoform 2	6	67	6	1.2	**4E-06**	1.0	**2E-07**	1.1	**2E-05**	0.7	**6E-03**	1.0	7E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
4842	NOS1	nitric oxide synthase, brain isoform 2	10	25	10	1.2	**1E-04**	0.9	**8E-05**	1.2	9E-01	0.9	**3E-04**	1.0	7E-01	Oxidoreductase activity	Plasma membrane	Enzyme: Synthase
6294	SAFB	scaffold attachment factor B1 isoform 1	14	74	10	1.2	**9E-08**	1.0	**3E-08**	1.2	**8E-05**	0.9	**3E-07**	1.0	5E-01	Transcription factor activity	Nucleus	Transcription factor
1051	CEBPB	CCAAT/enhancer-binding protein beta isoform a	3	14	3	1.2	**1E-02**	**1.5**	**1E-03**	1.6	**3E-04**	1.3	**2E-03**	1.2	2E-01	Transcription factor activity	Nucleus	Transcription factor
29785	CYP2S1	cytochrome P450 2S1	3	12	3	1.2	**2E-02**	1.1	**8E-03**	1.2	**4E-02**	1.0	**1E-02**	1.1	4E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase
1509	CTSD	cathepsin D preproprotein	12	190	12	1.2	**5E-11**	1.0	**8E-11**	1.3	**5E-11**	0.8	6E-01	0.8	**1E-07**	Aspartic-type signal peptidase activity	Lysosome	Aspartic protease
6626	SNRPA	U1 small nuclear ribonucleoprotein A	9	67	7	1.2	**1E-08**	0.8	**4E-10**	1.2	1E-01	0.8	9E-02	1.0	4E-01	RNA binding	Nucleus	RNA binding protein
8939	FUBP3	far upstream element-binding protein 3	16	100	12	1.2	**2E-08**	1.0	**1E-07**	1.2	**4E-03**	1.0	**1E-06**	1.0	4E-01	Transcription factor activity	Nucleus	Transcription factor
2963	GTF2F2	general transcription factor IIF subunit 2	9	44	9	1.2	**3E-04**	0.8	**2E-04**	1.3	**8E-03**	0.8	4E-01	0.9	**4E-03**	Transcription factor activity	Nucleus	Transcription factor
57092	PCNP	PEST proteolytic signal-containing nuclear protein	6	13	6	1.2	**7E-03**	0.9	**4E-03**	1.2	8E-01	0.8	9E-01	0.9	1E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
6167	RPL37	60S ribosomal protein L37	4	17	4	1.2	**2E-02**	1.0	**4E-03**	1.0	9E-01	0.6	3E-01	0.9	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
23264	ZC3H7B	zinc finger CCCH domain-containing protein 7B	3	10	3	1.2	9E-02	1.0	**4E-02**	1.3	8E-01	0.9	2E-01	0.9	6E-01	Translation regulator activity	Nucleus	Translation regulatory protein
471	ATIC	bifunctional purine biosynthesis protein PURH	27	207	27	1.2	**2E-16**	0.9	**2E-16**	1.2	1E-01	1.1	**2E-16**	1.0	2E-01	Hydrolase activity	-	Enzyme: Hydrolase
6390	SDHB	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	11	82	11	1.2	**2E-09**	1.2	**2E-09**	1.1	**1E-10**	0.9	**1E-06**	1.0	4E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
5318	PKP2	plakophilin-2 isoform 2b	17	69	16	1.2	**3E-05**	**0.7**	**4E-05**	1.0	**3E-04**	1.1	**5E-06**	1.1	**5E-06**	Molecular function unknown	Nucleus	Unclassified
60314	C12orf10	UPF0160 protein MYG1, mitochondrial	5	27	5	1.2	**3E-05**	0.9	**9E-06**	1.2	5E-01	1.0	**6E-03**	0.9	9E-01	Molecular function unknown	Cytosol	Unclassified
55795	PCID2	PCI domain-containing protein 2 isoform 2	5	28	5	1.2	**3E-05**	1.0	**5E-06**	1.2	3E-01	0.8	7E-02	0.9	3E-01	Molecular function unknown	-	Unclassified
23185	LARP4B	la-related protein 4B	9	42	9	1.2	**5E-04**	1.0	**3E-07**	1.1	8E-01	1.0	3E-01	1.0	1E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
221937	FOXK1	forkhead box protein K1	6	26	6	1.2	**1E-03**	0.9	**1E-03**	1.2	6E-02	0.8	8E-02	0.9	**1E-02**	Transcription factor activity	Nucleus	Transcription factor
4686	NCBP1	PREDICTED: nuclear cap-binding protein subunit 1 isoform X1	11	50	11	1.2	**2E-03**	0.9	**2E-03**	1.2	1E-01	0.9	**1E-03**	0.9	5E-02	RNA binding	Nucleus	RNA binding protein
11054	OGFR	opioid growth factor receptor	4	16	4	1.2	**1E-02**	0.8	**5E-03**	1.1	1E-01	1.0	**5E-03**	1.0	3E-01	Ligand-dependent nuclear receptor activity	Nucleus;Cytoplasm	Nuclear receptor
388650	FAM69A	protein FAM69A isoform 1	2	6	2	1.2	**2E-02**	1.2	**2E-02**	1.2	5E-02	1.1	**3E-02**	0.9	8E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
23530	NNT	NAD(P) transhydrogenase, mitochondrial*gi|122939155|ref|NP_036475.3| NAD(P) transhydrogenase, mitochondrial	25	115	25	1.2	**2E-12**	1.3	**1E-13**	1.2	**8E-15**	1.2	**5E-14**	1.0	1E-01	Oxidoreductase activity	Mitochondrial membrane	Enzyme: Oxidoreductase
80142	PTGES2	prostaglandin E synthase 2 isoform 1	10	55	10	1.2	**4E-09**	1.3	**3E-09**	1.1	**2E-09**	1.2	**3E-09**	1.1	**3E-03**	Isomerase activity	Nucleus	Enzyme: Isomerase
64848	YTHDC2	probable ATP-dependent RNA helicase YTHDC2	10	38	9	1.2	**1E-06**	1.1	**3E-05**	1.1	**3E-02**	1.0	**1E-02**	1.1	**8E-03**	Molecular function unknown	Nucleus	Unclassified
64175	LEPRE1; P3H1	prolyl 3-hydroxylase 1 isoform 3	9	53	9	1.2	**6E-06**	0.9	**7E-07**	1.2	6E-01	1.0	**3E-05**	1.0	1E+00	#N/A	#N/A	#N/A
83440	ADPGK	ADP-dependent glucokinase	3	34	3	1.2	**2E-04**	0.9	**8E-05**	1.2	7E-01	1.0	**2E-05**	0.9	4E-01	Phosphorylase activity	-	Enzyme: Phosphorylase
55256	ADI1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	5	18	5	1.2	**2E-02**	1.2	**2E-02**	1.2	**4E-02**	1.0	**1E-02**	0.8	**8E-03**	Oxidoreductase activity	Plasma membrane	Growth inhibitory factor
9910	RABGAP1L	PREDICTED: rab GTPase-activating protein 1-like isoform X1	5	10	3	1.2	**3E-02**	0.8	**2E-02**	1.2	5E-01	0.9	3E-01	0.9	1E-01	GTPase activator activity	-	GTPase activating protein
23435	TARDBP	TAR DNA-binding protein 43	9	52	9	1.2	**2E-07**	1.0	**1E-07**	1.2	**5E-05**	1.1	**7E-08**	1.0	7E-01	DNA binding	Nucleus	DNA binding protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
51768	**TM7SF3**	**transmembrane 7 superfamily member 3**	5	29	5	1.2	**3E-05**	**0.6**	**4E-06**	1.2	**4E-03**	0.7	5E-01	0.8	**6E-04**	Molecular function unknown	Plasma membrane	Integral membrane protein
4170	**MCL1**	**induced myeloid leukemia cell differentiation protein Mcl-1 isoform 1**	1	10	1	1.2	**1E-03**	1.0	**2E-03**	1.1	2E-01	0.9	3E-01	1.2	**9E-03**	Protein binding;Chaperone activity	Mitochondrial membrane	Chaperone
328	**APEX1**	**DNA-(apurinic or apyrimidinic site) lyase*gi|18375503|ref|NP_542379.1| DNA-(apurinic or apyrimidinic site) lyase*gi|18375505|ref|NP_542380.1| DNA-(apurinic or apyrimidinic site) lyase*gi|346644849|ref|NP_001231178.1| DNA-(apurinic or apyrimidinic site) lyase**	9	40	9	1.2	**2E-03**	1.0	**1E-03**	1.2	**4E-02**	0.9	**4E-03**	1.1	5E-01	DNA repair protein;Transcription regulator activity	Cytoplasm	DNA repair protein
51258	**MRPL51**	**39S ribosomal protein L51, mitochondrial**	2	7	2	1.2	**4E-02**	1.1	**4E-02**	1.1	**1E-03**	0.9	**1E-02**	0.9	9E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
84248	**FYTTD1**	**UAP56-interacting factor isoform 1**	4	19	4	1.2	6E-02	1.0	**2E-02**	1.1	7E-01	0.8	5E-01	1.0	4E-01	Molecular function unknown	-	Unclassified
8568	**RRP1**	**ribosomal RNA processing protein 1 homolog A**	2	12	2	1.2	6E-02	1.1	2E-01	0.9	4E-01	0.6	6E-01	1.1	5E-01	Molecular function unknown	Nucleolus	Unclassified
282991	**BLOC1S2**	**biogenesis of lysosome-related organelles complex 1 subunit 2 isoform 1**	2	12	2	1.2	2E-01	1.0	8E-02	1.1	2E-01	0.8	4E-01	0.9	3E-01	Molecular function unknown	-	Unclassified
116228	**COX20**	**cytochrome c oxidase protein 20 homolog**	7	16	2	1.2	1E-01	0.9	1E-01	1.1	**8E-03**	1.2	1E-01	0.8	5E-01	#N/A	#N/A	#N/A
6129	**RPL7**	**60S ribosomal protein L7**	16	247	15	1.2	**2E-16**	1.0	**5E-15**	1.0	**2E-06**	0.8	**9E-04**	1.0	9E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6147	**RPL23A**	**60S ribosomal protein L23a**	9	143	9	1.2	**5E-12**	1.0	**1E-12**	1.0	1E-01	0.8	5E-01	0.9	5E-01	RNA binding	Cytoplasm	RNA binding protein
23111	**SPG20**	**PREDICTED: spartin isoform X1**	11	43	11	1.2	**1E-05**	0.9	**1E-05**	1.2	5E-01	0.9	**4E-02**	1.1	8E-02	Molecular function unknown	Cytoplasm	Unclassified
8683	**SRSF9**	**serine/arginine-rich splicing factor 9**	8	49	8	1.2	**4E-05**	1.0	**1E-05**	1.2	**4E-02**	1.0	**4E-04**	1.0	4E-01	#N/A	#N/A	#N/A
10994	**ILVBL**	**acetolactate synthase-like protein**	5	20	5	1.2	**4E-04**	1.1	**8E-05**	1.0	**4E-02**	1.2	**4E-04**	1.0	8E-01	Coenzyme binding	-	Enzyme: Synthase
80218	**NAA50**	**N-alpha-acetyltransferase 50**	7	44	7	1.2	**1E-05**	0.9	**5E-06**	1.1	6E-01	0.9	**2E-04**	0.9	7E-02	Acyltransferase activity	-	Enzyme: Acyltransferase
4927	**NUP88**	**nuclear pore complex protein Nup88**	11	45	11	1.2	**7E-05**	0.9	**6E-05**	1.1	7E-01	1.2	**4E-06**	1.1	9E-01	Transporter activity	Nucleus	Transport/cargo protein
81619	**TSPAN14**	**PREDICTED: tetraspanin-14 isoform X1**	3	8	3	1.2	1E-01	0.9	**3E-02**	0.9	2E-01	0.9	**5E-02**	1.0	4E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
6165	**RPL35A**	**PREDICTED: 60S ribosomal protein L35a isoform X1**	8	78	8	1.2	**8E-09**	0.9	**1E-07**	1.0	7E-01	**0.7**	**4E-03**	0.9	**3E-03**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6638; 8926	**SNRPN; SNURF**	**small nuclear ribonucleoprotein-associated protein N**	7	50	7	1.2	**1E-06**	1.0	**2E-07**	1.3	7E-02	0.9	**8E-06**	1.1	**4E-02**	#N/A	#N/A	#N/A
3915	**LAMC1**	**laminin subunit gamma-1**	8	30	8	1.2	**3E-05**	0.9	**2E-04**	1.2	3E-01	0.9	5E-02	1.1	**2E-02**	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
3685	**ITGAV**	**integrin alpha-V isoform 1**	20	73	4	1.2	**6E-04**	1.0	**2E-05**	1.1	2E-01	0.8	**1E-02**	1.0	6E-01	Receptor activity	Plasma membrane	Cell surface receptor
23431	**AP4E1**	**AP-4 complex subunit epsilon-1 isoform 1**	6	20	6	1.2	**3E-03**	0.9	**6E-04**	1.2	4E-01	1.0	**2E-02**	1.2	3E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
64975	**MRPL41**	**39S ribosomal protein L41, mitochondrial**	1	6	1	1.2	**1E-02**	0.9	**4E-02**	1.3	7E-01	1.0	**2E-02**	1.0	5E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
51497	**NELFCD; TH1L**	**negative elongation factor C/D**	2	9	2	1.2	**3E-02**	1.1	**2E-02**	1.1	1E-01	0.8	2E-01	0.9	5E-01	#N/A	#N/A	#N/A
22902	**RUFY3**	**protein RUFY3 isoform 1**	5	23	4	1.2	**3E-02**	1.0	**2E-03**	1.0	1E-01	0.8	**5E-02**	0.9	9E-01	Molecular function unknown	-	Unclassified
5019	**OXCT1**	**succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial**	5	32	5	1.2	**3E-05**	1.2	**3E-04**	1.2	**6E-05**	1.1	**5E-04**	1.0	9E-01	CoA-transferase activity	Mitochondrion	Enzyme: CoA transferase
4361	**MRE11A**	**PREDICTED: double-strand break repair protein MRE11A isoform X1**	9	32	9	1.2	**2E-04**	0.9	**3E-05**	1.1	9E-01	0.8	**8E-03**	1.0	8E-01	Exonuclease activity	Nucleus;Cytoplasm	DNA repair protein
57451	**TENM2**	**teneurin-2**	7	24	6	1.2	**1E-03**	1.0	**2E-05**	**1.6**	**5E-02**	0.8	2E-01	0.9	8E-01	#N/A	#N/A	#N/A
1856	**DVL2**	**segment polarity protein dishevelled homolog DVL-2**	6	22	3	1.2	**1E-03**	0.9	**2E-04**	1.4	4E-01	1.3	**3E-04**	0.9	5E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
4830	**NME1**	**nucleoside diphosphate kinase A isoform a**	9	225	1	1.2	**3E-03**	0.9	**2E-03**	1.1	2E-01	0.9	**2E-03**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase
51517	**NCKIPSD**	**NCK-interacting protein with SH3 domain isoform 1**	2	12	2	1.2	**7E-03**	1.2	**7E-04**	1.0	**5E-02**	1.0	**2E-02**	1.2	5E-02	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
26049	**FAM169A**	**soluble lamin-associated protein of 75 kDa**	2	8	2	1.2	**1E-02**	1.1	**3E-03**	1.3	**1E-02**	**1.5**	**1E-02**	1.1	**4E-03**	Molecular function unknown	-	Unclassified
26519	**TIMM10**	**mitochondrial import inner membrane translocase subunit Tim10**	3	14	3	1.2	**4E-02**	1.1	**3E-02**	**1.5**	**4E-02**	**1.6**	**2E-02**	0.9	3E-01	Chaperone activity	Mitochondrial membrane	Chaperone
5315	**PKM**	**pyruvate kinase PKM isoform c**	40	1120	4	1.2	**2E-16**	1.1	**2E-16**	1.4	**7E-07**	1.2	**3E-07**	1.0	**4E-02**	#N/A	#N/A	#N/A

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	**p-value**	**Median Fold change**	**p-value**	**Median Fold change**	**p-value**	**Median Fold change**	**p-value**	**Median Fold change**	**p-value**			
2590	**GALNT2**	**polypeptide N-acetylgalactosaminyltransferase 2**	13	54	12	1.2	**7E-07**	0.9	**8E-04**	0.8	5E-01	**0.7**	**5E-02**	0.9	1E-01	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase
28960	**DCPS**	**m7GpppX diphosphatase**	10	57	10	1.2	**1E-04**	1.0	**7E-08**	1.2	**3E-05**	0.8	**5E-03**	0.9	**4E-02**	Hydrolase activity	Nucleus	Enzyme: Hydrolase
54885	**TBC1D8B**	**TBC1 domain family member 8B isoform a**	4	12	3	1.2	**1E-02**	1.1	1E-01	1.0	2E-01	1.2	8E-02	1.0	8E-01	Molecular function unknown	-	Unclassified
6598	**SMARCB1**	**SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 isoform a**	3	9	3	1.2	1E-01	1.1	2E-01	1.3	7E-01	1.0	9E-02	0.9	3E-01	DNA binding	Nucleus	Unclassified
10956	**OS9**	**protein OS-9 isoform 1**	4	9	4	1.2	2E-01	1.1	3E-01	1.0	4E-01	1.1	2E-01	1.2	6E-01	Molecular function unknown	Cytoplasm;Endoplasmic reticulum	Unclassified
23524	**SRRM2**	**serine/arginine repetitive matrix protein 2**	26	112	26	1.2	**7E-14**	1.0	**4E-16**	1.2	**3E-04**	1.2	**2E-10**	1.1	**8E-04**	RNA binding	Nucleus	RNA binding protein
6141	**RPL18**	**60S ribosomal protein L18 isoform 1**	6	78	6	1.2	**1E-06**	1.0	**2E-06**	1.0	**2E-04**	0.8	6E-01	0.9	**2E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
9128	**PRPF4**	**U4/U6 small nuclear ribonucleoprotein Prp4 isoform 1**	7	25	7	1.2	**4E-04**	0.9	**1E-04**	1.2	8E-01	1.0	**2E-02**	0.9	7E-01	Ribonucleoprotein	Nucleus	RNA binding protein
27430	**MAT2B**	**methionine adenosyltransferase 2 subunit beta isoform 1**	9	45	9	1.2	**5E-04**	0.8	**4E-05**	1.2	**3E-02**	0.9	**7E-04**	0.9	**1E-02**	Catalytic activity	Cytoplasm	Enzyme: Adenosyltransferase
4718	**NDUFC2**	**NADH dehydrogenase [ubiquinone] 1 subunit C2 isoform 1**	4	15	4	1.2	**6E-04**	1.0	**3E-04**	1.1	2E-01	0.9	**2E-02**	1.1	3E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
55149	**MTPAP**	**poly(A) RNA polymerase, mitochondrial**	4	17	4	1.2	**6E-04**	1.0	**2E-03**	1.2	2E-01	0.8	6E-01	1.1	8E-01	DNA-directed RNA polymerase activity	Mitochondrion	RNA polymerase
4716	**NDUFB10**	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	4	18	4	1.2	**2E-03**	1.0	**2E-03**	1.1	7E-01	1.1	**4E-02**	1.1	9E-02	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
7389	**UROD**	**uroporphyrinogen decarboxylase**	6	25	6	1.2	**4E-03**	0.9	**6E-04**	1.1	7E-01	0.7	9E-01	0.9	2E-01	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase
3313	**HSPA9**	**stress-70 protein, mitochondrial**	34	460	33	1.2	**2E-16**	1.0	**2E-16**	1.1	**2E-07**	1.0	**2E-16**	1.0	**2E-03**	Chaperone activity	Mitochondrion	Chaperone
10915	**TCERG1**	**transcription elongation regulator 1 isoform 1**	21	89	21	1.2	**2E-08**	1.0	**1E-08**	1.2	**1E-04**	1.0	**4E-09**	1.0	5E-01	Transcription factor activity	Nucleus	Transcription factor
3065	**HDAC1**	**histone deacetylase 1**	10	50	6	1.2	**2E-08**	0.9	**6E-08**	1.2	5E-02	0.9	**2E-04**	0.9	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
25804	**LSM4**	**U6 snRNA-associated Sm-like protein LSm4 isoform 1**	6	46	6	1.2	**4E-07**	0.9	**1E-08**	1.4	1E-01	1.0	**2E-07**	0.9	**2E-04**	RNA binding	Cytoplasm	RNA binding protein
2230	**FDX1**	**adrenodoxin, mitochondrial**	4	9	4	1.2	**1E-02**	1.1	**2E-02**	1.1	**4E-02**	0.8	3E-01	1.0	3E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
2717	**GLA**	**alpha-galactosidase A**	3	9	3	1.2	**3E-02**	1.4	**2E-02**	1.4	**3E-02**	1.1	**5E-03**	1.0	1E+00	Galactosidase activity	Endoplasmic reticulum	Enzyme: Galactosidase
2975	**GTF3C1**	**general transcription factor 3C polypeptide 1 isoform 1**	6	16	6	1.2	1E-01	1.3	**3E-02**	1.2	7E-02	1.6	8E-02	1.0	8E-01	Transcription factor activity	Nucleus	Transcription factor
50640	**PNPLA8**	**calcium-independent phospholipase A2-gamma isoform 1**	4	13	4	1.2	2E-01	1.1	**2E-02**	1.1	**3E-02**	**1.7**	**5E-02**	1.2	2E-01	Phospholipase activity	Plasma membrane	Enzyme: Phospholipase
10250	**SRRM1**	**serine/arginine repetitive matrix protein 1 isoform 1**	4	26	4	1.2	**1E-06**	0.9	**3E-06**	1.2	1E-01	1.0	**2E-02**	0.9	1E-01	Ribonuclease activity	Nucleus	Ribonuclease
55787	**TXLNG**	**gamma-taxilin isoform 1**	7	33	7	1.2	**3E-03**	0.8	**2E-04**	1.1	**1E-02**	**0.7**	**5E-02**	1.0	4E-01	#N/A	#N/A	#N/A
6868	**ADAM17**	**disintegrin and metalloproteinase domain-containing protein 17 preproprotein**	4	13	4	1.2	**2E-02**	0.9	**2E-02**	1.2	7E-01	0.9	1E-01	1.0	6E-01	Metallopeptidase activity	Plasma membrane	Metallo protease
5725	**PTBP1**	**polypyrimidine tract-binding protein 1 isoform a**	14	203	11	1.2	**2E-16**	0.9	**2E-16**	1.3	**1E-02**	0.9	**2E-15**	1.0	3E-01	Ribonucleoprotein	Nucleus	Ribonucleoprotein
86	**ACTL6A**	**actin-like protein 6A isoform 1**	11	53	11	1.2	**6E-06**	0.9	**3E-06**	1.3	2E-01	0.9	**8E-07**	1.0	6E-01	Chromatin binding	Cytoplasm;Nucleus	DNA binding protein
404636	**FAM45A**	**protein FAM45A isoform 1**	5	23	5	1.2	**2E-03**	1.0	**2E-03**	1.2	1E-01	1.1	**2E-02**	1.0	5E-01	Molecular function unknown	-	Unclassified
129401	**NUP35**	**nucleoporin NUP53 isoform a**	6	11	6	1.2	**2E-02**	1.0	**3E-02**	1.4	8E-01	1.2	**3E-02**	1.1	2E-01	Transporter activity	Nuclear membrane	Transport/cargo protein
64708	**COPS7B**	**COP9 signalosome complex subunit 7b isoform b**	2	9	2	1.2	**4E-02**	1.0	**6E-03**	1.3	4E-01	1.2	**2E-02**	1.1	3E-01	Molecular function unknown	Cytoplasm	Unclassified
84640	**USP38**	**ubiquitin carboxyl-terminal hydrolase 38 isoform 2**	2	7	2	1.2	1E-01	0.9	1E-01	1.2	9E-01	0.9	**5E-02**	1.0	3E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
10095	**ARPC1B**	**PREDICTED: actin-related protein 2/3 complex subunit 1B isoform X1**	13	93	13	1.2	**4E-14**	0.9	**1E-12**	1.2	8E-01	1.2	**2E-14**	1.0	5E-01	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
2802	**GOLGA3**	**PREDICTED: golgin subfamily A member 3 isoform X1**	20	75	20	1.2	**2E-04**	0.9	**9E-06**	1.2	9E-02	1.0	**7E-07**	1.0	6E-01	Structural molecule activity	Golgi apparatus;Nucleus	Structural protein
4026	**LPP**	**PREDICTED: lipoma-preferred partner isoform X1**	7	27	7	1.2	**6E-04**	1.0	**1E-04**	1.2	**9E-03**	0.9	**1E-04**	1.0	4E-01	Molecular function unknown	Cytoplasm	Unclassified
5763	**PTMS**	**parathymosin**	3	28	3	1.2	**2E-03**	1.0	**3E-03**	1.2	1E-01	0.7	9E-01	1.0	4E-01	DNA binding	Nucleus	DNA binding protein
56259	**CTNNBL1**	**beta-catenin-like protein 1 isoform 1**	8	42	8	1.2	**4E-03**	0.9	**3E-03**	1.3	3E-01	1.0	**1E-02**	0.9	3E-01	Molecular function unknown	Nucleus	Unclassified
677	**ZFP36L1**	**zinc finger protein 36, C3H1 type-like 1 isoform 2**	1	6	1	1.2	2E-01	0.9	1E-01	1.1	9E-01	1.0	2E-01	1.0	4E-01	Transcription factor activity	Nucleus	Transcription factor
1.01E+08	**RPL17-C18ORF32**	**RPL17-C18orf32 protein isoform 1**	11	134	10	1.2	#N/A	1.0	#N/A	1.1	#N/A	0.8	#N/A	0.9	#N/A	#N/A	#N/A	#N/A

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9898	UBAP2L	PREDICTED: ubiquitin-associated protein 2-like isoform X1	16	105	1	1.2	**6E-10**	0.9	**7E-10**	1.2	**5E-02**	**0.7**	**1E-02**	0.9	**2E-05**	Molecular function unknown	Nucleus	Unclassified
1632	ECI1	enoyl-CoA delta isomerase 1, mitochondrial isoform 1	8	50	8	1.2	**1E-03**	1.1	**3E-04**	1.2	**2E-03**	**1.5**	**5E-05**	1.0	5E-01	#N/A	#N/A	#N/A
56983	POGLUT1	protein O-glucosyltransferase 1	2	8	2	1.2	1E-01	1.1	2E-01	1.1	3E-01	0.7	8E-01	1.0	3E-01	#N/A	#N/A	#N/A
118881	COMTD1	catechol O-methyltransferase domain-containing protein 1	1	6	1	1.2	**2E-02**	**1.6**	**8E-03**	1.1	7E-02	1.4	**3E-02**	1.3	**7E-03**	Molecular function unknown	-	Unclassified
1642	DDB1	DNA damage-binding protein 1	32	213	32	1.2	**2E-13**	1.1	**4E-16**	1.2	**5E-12**	0.8	**4E-09**	0.9	**1E-03**	DNA repair protein	Cytoplasm	DNA binding protein
83940	TATDN1	putative deoxyribonuclease TATDN1 isoform a	7	35	7	1.2	**6E-05**	1.0	**5E-06**	1.3	**2E-02**	1.2	**6E-07**	1.0	9E-01	Molecular function unknown	-	Unclassified
51115	FAM82B; RMDN1	regulator of microtubule dynamics protein 1 isoform 1	11	58	10	1.2	**1E-04**	1.3	**3E-06**	1.4	**8E-06**	1.3	**8E-06**	1.0	**1E-02**	#N/A	#N/A	#N/A
55250	ELP2	elongator complex protein 2 isoform 1	5	17	5	1.2	**2E-04**	0.8	**2E-04**	1.2	**2E-02**	0.8	**3E-02**	0.9	1E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule
6890	TAP1	antigen peptide transporter 1 isoform 1	7	25	7	1.2	**2E-03**	1.2	**2E-04**	1.2	**7E-03**	1.0	**4E-03**	1.1	1E-01	Transporter activity	Plasma membrane	Transport/cargo protein
10953	TOMM34	mitochondrial import receptor subunit TOM34	6	24	6	1.2	**3E-03**	0.9	**5E-05**	1.3	3E-01	0.8	5E-01	1.0	6E-01	Transporter activity	Cytoplasm	Transport/cargo protein
55119	PRPF38B	pre-mRNA-splicing factor 38B	5	17	5	1.2	**2E-02**	1.0	**4E-03**	1.3	5E-02	1.4	**6E-03**	1.1	**3E-02**	RNA binding	-	RNA binding protein
1186	CLCN7	H(+)/Cl(-) exchange transporter 7 isoform a	6	21	6	1.2	**4E-02**	1.1	**2E-02**	1.2	**4E-02**	1.3	**4E-02**	1.1	2E-01	Voltage-gated ion channel activity	Plasma membrane	Voltage gated channel
148223	C19orf25	PREDICTED: UPF0449 protein C19orf25 isoform X1	3	10	3	1.2	1E-01	0.9	1E-01	1.1	1E+00	0.9	2E-01	0.9	4E-01	Molecular function unknown	-	Unclassified
5339	PLEC	plectin isoform 1	284	3379	3	1.2	**2E-16**	0.9	**2E-16**	1.2	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	#N/A	#N/A	#N/A
51602	NOP58	nucleolar protein 58	13	83	13	1.2	**1E-08**	1.0	**2E-07**	1.2	**8E-05**	1.1	**1E-06**	1.0	5E-01	Ribonucleoprotein	Nucleolus	RNA binding protein
9368	SLC9A3R1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	12	50	12	1.2	**2E-07**	0.9	**4E-07**	1.2	1E+00	0.9	**4E-05**	0.9	**2E-03**	Receptor binding	Cytoplasm;Membrane fraction	Membrane bound ligand
126308	MOB3A	PREDICTED: MOB kinase activator 3A isoform X1	2	12	2	1.2	**6E-04**	0.7	**8E-04**	1.3	4E-01	0.9	3E-01	1.0	9E-01	#N/A	#N/A	#N/A
6605	SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	4	16	3	1.2	**3E-03**	1.0	**2E-03**	1.1	9E-02	0.8	**4E-02**	0.9	**1E-02**	DNA binding	Nucleus	DNA binding protein
10240	MRPS31	28S ribosomal protein S31, mitochondrial	6	23	6	1.2	**1E-02**	1.1	**8E-03**	1.2	**2E-02**	1.0	**3E-03**	0.9	8E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
54814	QPCTL	glutaminyl-peptide cyclotransferase-like protein isoform 1	3	14	3	1.2	**1E-02**	0.9	**5E-04**	1.2	7E-01	1.0	**1E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
11186	RASSF1	ras association domain-containing protein 1 isoform D	2	7	2	1.2	9E-02	0.8	9E-02	1.1	8E-01	0.9	5E-02	1.0	4E-01	Cytoskeletal protein binding	Microtubule	Cytoskeletal associated protein
10594	PRPF8	pre-mRNA-processing-splicing factor 8	65	295	64	1.2	**2E-16**	1.0	**2E-16**	1.3	**5E-09**	1.0	**2E-16**	1.0	5E-01	RNA binding	Nucleus	RNA binding protein
7358	UGDH	UDP-glucose 6-dehydrogenase isoform 1	13	60	13	1.2	**9E-10**	0.7	**1E-11**	1.2	**3E-06**	0.8	2E-01	0.9	**9E-05**	Catalytic activity	-	Enzyme: Dehydrogenase
80335	WDR82	WD repeat-containing protein 82	9	49	9	1.2	**1E-04**	0.8	**5E-05**	1.1	**4E-04**	0.7	1E-01	0.9	**5E-04**	Molecular function unknown	Nucleus	Integral membrane protein
6789	STK4	serine/threonine-protein kinase 4	7	35	4	1.2	**1E-03**	0.9	**2E-03**	1.1	1E-01	1.0	**5E-04**	1.1	5E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
25904	CNOT10	CCR4-NOT transcription complex subunit 10 isoform 3	5	18	5	1.2	**2E-03**	0.8	**5E-03**	1.2	2E-01	1.0	**9E-03**	0.9	5E-01	Molecular function unknown	-	Unclassified
11266	DUSP12	dual specificity protein phosphatase 12	5	12	5	1.2	**4E-03**	0.7	**1E-03**	1.1	8E-01	0.9	**5E-03**	1.0	6E-01	Protein tyrosine/serine/threonine phosphatase activity	Nucleus	Dual specificity phosphatase
131566	DCBLD2	discoidin, CUB and LCCL domain-containing protein 2	2	8	2	1.2	**3E-02**	0.6	8E-02	0.9	8E-02	0.6	5E-01	1.1	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
4709	NDUFB3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3*gi|4505361|ref|NP_002482.1| NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	3	10	3	1.2	8E-02	1.1	**4E-02**	1.0	4E-01	0.9	3E-01	1.0	9E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
3020; 440926; 3021	H3F3A; H3F3AP4; H3F3B	histone H3.3	6	277	1	1.2	**1E-15**	0.9	**2E-13**	1.3	**4E-05**	0.9	**1E-11**	1.1	**6E-06**	#N/A	#N/A	#N/A
1891;	ECH1	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	10	39	10	1.2	**1E-14**	1.4	**2E-16**	1.7	**5E-13**	**1.7**	**1E-15**	1.0	1E-01	Catalytic activity	Peroxisome	Enzyme: Hydratase
8189	SYMPK	symplekin	14	64	14	1.2	**3E-10**	0.9	**1E-11**	1.2	5E-01	1.0	**1E-07**	1.0	6E-01	Cell adhesion molecule activity	Plasma membrane	Cell junction protein
57003	CCDC47	coiled-coil domain-containing protein 47	15	82	15	1.2	**8E-10**	0.9	**5E-09**	1.2	2E-01	1.0	**4E-11**	1.0	4E-01	Molecular function unknown	Mitochondrion	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
9093	DNAJA3	dnaJ homolog subfamily A member 3, mitochondrial isoform 1	5	24	5	1.2	**3E-06**	1.0	**2E-06**	1.2	7E-02	1.3	**2E-05**	1.1	**2E-02**	Chaperone activity	Mitochondrion	Chaperone
345778	MTX3	metaxin-3 isoform 2	4	14	4	1.2	**4E-02**	1.0	**4E-02**	1.4	1E-01	1.2	**5E-02**	0.9	2E-01	Molecular function unknown	-	Unclassified
2547	XRCC6	X-ray repair cross-complementing protein 6 isoform 1	31	326	31	1.2	**2E-16**	1.0	**2E-16**	1.3	**3E-12**	0.9	**6E-09**	1.0	5E-02	DNA binding	Nucleus	DNA binding protein
1108	CHD4	chromodomain-helicase-DNA-binding protein 4 isoform 1	34	122	34	1.2	**3E-13**	1.0	**7E-16**	1.2	**4E-03**	1.0	**5E-11**	1.0	6E-01	DNA binding	Nucleus;Cytoplasm	DNA binding protein
22985	ACIN1	apoptotic chromatin condensation inducer in the nucleus isoform 1	25	126	1	1.2	**6E-13**	1.0	**5E-14**	1.2	**2E-03**	0.9	**2E-12**	1.0	3E-01	DNA binding	Nucleus;Cytoplasm	DNA binding protein
1371	CPOX	oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	10	69	10	1.2	**5E-05**	1.0	**4E-05**	1.4	**6E-04**	1.3	**4E-05**	1.0	6E-01	Catalytic activity	Mitochondrion	Enzyme: Oxidase
389677	RBM12B	PREDICTED: RNA-binding protein 12B isoform X1	7	25	7	1.2	**3E-04**	0.8	**3E-03**	1.3	4E-01	1.0	**2E-03**	1.0	3E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
113828	FAM83F	protein FAM83F	7	23	7	1.2	**1E-03**	1.2	**2E-04**	1.1	**2E-02**	0.7	8E-01	1.0	5E-01	Molecular function unknown	-	Unclassified
7803	PTP4A1	PREDICTED: protein tyrosine phosphatase type IVA 1 isoform X1	4	12	4	1.2	**8E-03**	0.9	**8E-04**	1.2	9E-02	0.7	9E-01	1.1	1E-01	Protein tyrosine phosphatase activity	Nucleus	Tyrosine phosphatase
56474	CTPS2	PREDICTED: CTP synthase 2 isoform X1	12	62	10	1.2	**7E-03**	1.0	**8E-03**	1.2	4E-01	1.2	**4E-04**	1.0	5E-01	Ligase activity	-	Enzyme: Synthase;Enzyme: Ligase
51747	LUC7L3	luc7-like protein 3	4	26	4	1.2	**2E-02**	0.9	**2E-02**	1.1	1E-01	1.0	**1E-02**	0.9	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
64744	SMAP2	stromal membrane-associated protein 2 isoform 1	3	11	3	1.2	**3E-02**	0.8	**2E-02**	1.0	2E-01	0.9	8E-02	1.0	6E-01	GTPase activator activity	-	GTPase activating protein
79016	DDA1	DET1- and DDB1-associated protein 1	3	14	3	1.2	**3E-02**	0.8	**2E-02**	1.2	4E-01	0.8	4E-01	0.9	3E-01	Molecular function unknown	-	Unclassified
11232	POLG2	DNA polymerase subunit gamma-2, mitochondrial	2	9	2	1.2	**4E-02**	1.3	7E-02	1.3	1E-01	1.5	9E-02	1.2	7E-02	DNA-directed DNA polymerase activity	Mitochondrion	DNA polymerase
51347	TAOK3	PREDICTED: serine/threonine-protein kinase TAO3 isoform X1	12	41	10	1.2	**6E-08**	1.0	**3E-08**	1.4	2E-01	1.2	**2E-06**	1.0	6E-01	Protein serine/threonine kinase activity	-	Serine/threonine kinase
26499	PLEK2	pleckstrin-2	6	29	6	1.2	**7E-06**	0.8	**2E-06**	1.3	**6E-03**	0.9	**1E-02**	1.2	**1E-03**	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
79009	DDX50	ATP-dependent RNA helicase DDX50	10	21	8	1.2	**2E-04**	1.0	**3E-05**	1.2	7E-02	0.8	4E-01	1.0	2E-01	RNA binding	Nucleolus	RNA binding protein
115704	EVI5L	PREDICTED: EVI5-like protein isoform X1	2	5	2	1.2	1E-01	1.6	1E-01	1.2	1E-01	0.9	8E-01	1.2	9E-01	Transporter activity	-	Transport/cargo protein
3609	ILF3	interleukin enhancer-binding factor 3 isoform d	30	262	30	1.2	**2E-16**	1.0	**2E-16**	1.2	**5E-08**	0.8	**2E-12**	1.0	1E+00	Transcription factor activity;Transcription regulator activity	Nucleus	Transcription factor;RNA binding protein
6142	RPL18A	60S ribosomal protein L18a	9	108	9	1.2	**6E-10**	0.9	**3E-10**	1.0	2E-01	0.7	6E-01	1.0	7E-01	RNA binding	Cytoplasm	RNA binding protein
58477	SRPRB	signal recognition particle receptor subunit beta	11	55	11	1.2	**3E-06**	0.8	**2E-06**	1.2	**1E-02**	1.1	**4E-08**	1.0	7E-02	GTPase activity	Endoplasmic reticulum	GTPase
57532	NUFIP2	nuclear fragile X mental retardation-interacting protein 2	9	30	9	1.2	**1E-03**	0.8	**3E-04**	1.2	9E-02	0.9	**8E-03**	1.0	2E-01	RNA binding	Nucleus	RNA binding protein
280636	C11orf31	selenoprotein H	5	24	5	1.2	**1E-02**	1.0	**2E-03**	1.6	7E-02	0.9	**7E-03**	1.0	4E-01	Molecular function unknown	-	Unclassified
9443;	MED7	mediator of RNA polymerase II transcription subunit 7*gi|4758064|ref|NP_004261.1| mediator of RNA polymerase II transcription subunit 7	1	3	1	1.2	**4E-02**	0.9	1E-01	1.2	8E-01	1.0	2E-01	0.8	3E-01	Transcription factor activity	Nucleus	Transcription factor
65979	PHACTR4	phosphatase and actin regulator 4 isoform 2	2	6	2	1.2	**4E-02**	**1.7**	**4E-02**	1.2	2E-01	1.6	6E-02	1.3	1E-01	Phosphatase regulator activity	Perinuclear region	Regulatory/other subunit
2483	FRG1	protein FRG1	2	8	2	1.2	1E-01	0.7	1E-01	1.2	2E-01	0.6	2E-01	0.9	6E-01	Molecular function unknown	Nucleolus	Unclassified
23076	RRP1B	ribosomal RNA processing protein 1 homolog B	8	39	8	1.2	**8E-06**	0.9	**8E-06**	1.3	3E-01	0.8	**4E-02**	0.9	8E-01	Molecular function unknown	Nucleolus	Unclassified
9317	PTER	phosphotriesterase-related protein isoform 1	3	12	3	1.2	**1E-02**	0.9	**4E-03**	1.4	6E-01	**1.5**	**4E-03**	0.9	7E-01	Molecular function unknown	-	Unclassified
81609	SNX27	sorting nexin-27	8	26	8	1.2	**1E-02**	0.9	**3E-03**	1.1	4E-01	0.8	8E-02	1.0	4E-01	Transporter activity	Cytosol	Transport/cargo protein
3064	HTT	huntingtin	4	9	4	1.2	**2E-02**	1.0	**2E-02**	1.0	**5E-02**	1.0	**3E-02**	1.2	2E-01	DNA binding	-	DNA binding protein
81605;	URM1	ubiquitin-related modifier 1 isoform a	3	8	3	1.2	**5E-02**	0.8	**9E-03**	1.1	8E-02	0.7	5E-01	0.9	**5E-03**	Molecular function unknown	-	Unclassified
25873	RPL36	60S ribosomal protein L36	5	90	4	1.2	**5E-11**	0.9	**2E-09**	1.1	2E-01	0.7	2E-01	1.0	7E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
7555	CNBP	cellular nucleic acid-binding protein isoform 1	6	32	6	1.2	**2E-06**	1.1	**1E-05**	1.1	**7E-03**	0.7	**2E-02**	1.0	1E+00	RNA binding	Cytoplasm	RNA binding protein
1503	CTPS1	PREDICTED: CTP synthase 1 isoform X1	19	115	17	1.2	**2E-06**	0.8	**1E-06**	1.2	**1E-04**	0.9	**7E-07**	0.9	**2E-03**	#N/A	#N/A	#N/A
80895	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	8	31	8	1.2	**1E-05**	0.8	**4E-05**	1.2	1E-01	0.9	**1E-02**	1.0	2E-01	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
55601	DDX60	probable ATP-dependent RNA helicase DDX60	12	33	12	1.2	**2E-04**	1.1	7E-02	0.9	**1E-02**	0.7	1E+00	1.0	3E-01	DNA binding	-	DNA binding protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6119	**RPA3**	**replication protein A 14 kDa subunit**	3	20	3	1.2	**1E-03**	1.0	**1E-04**	1.4	7E-02	0.8	3E-01	0.9	3E-01	DNA binding	Nucleolus	DNA binding protein
54477	**PLEKHA5**	**pleckstrin homology domain-containing family A member 5 isoform 4**	5	14	5	1.2	**1E-02**	0.9	**8E-03**	1.2	3E-01	1.0	**1E-03**	1.2	**9E-03**	Receptor signaling complex scaffold activity	Nucleus;Cytoplasm	Adapter molecule
1659	**DHX8**	**ATP-dependent RNA helicase DHX8 isoform 1**	3	18	2	1.2	5E-02	1.1	**2E-02**	1.4	4E-01	1.1	**4E-02**	1.2	3E-01	RNA binding	Nucleus	RNA binding protein
118	**ADD1**	**alpha-adducin isoform b**	1	6	1	1.2	1E-01	0.7	1E-01	1.0	3E-01	0.7	9E-01	0.9	2E-01	Structural molecule activity	Nucleus;Cytoplasm	Structural protein
6194	**RPS6**	**40S ribosomal protein S6**	12	103	12	1.2	**4E-12**	1.0	**8E-10**	1.1	**2E-02**	0.9	**9E-04**	0.9	**4E-03**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
8899	**PRPF4B**	**serine/threonine-protein kinase PRP4 homolog**	7	27	7	1.2	**5E-05**	0.9	**4E-06**	1.1	1E-01	1.0	**5E-04**	1.0	5E-01	Transcription regulator activity;Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
23767	**FLRT3**	**PREDICTED: leucine-rich repeat transmembrane protein FLRT3 isoform X1**	8	33	8	1.2	**1E-04**	0.9	**2E-05**	1.3	1E-01	0.8	8E-02	0.9	2E-01	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
25844	**YIPF3**	**protein YIPF3**	2	18	2	1.2	**8E-03**	1.0	**2E-03**	1.0	**3E-02**	1.0	**1E-03**	1.0	1E-01	Molecular function unknown	-	Integral membrane protein
25920	**COBRA1; NELFB**	**negative elongation factor B**	4	17	4	1.2	**1E-02**	1.0	**3E-03**	1.3	3E-01	1.0	**1E-02**	1.0	9E-01	#N/A	#N/A	#N/A
1808	**DPYSL2**	**dihydropyrimidinase-related protein 2 isoform 1**	17	112	16	1.2	**6E-12**	0.8	**1E-13**	1.2	**1E-05**	1.0	**5E-09**	1.0	**2E-02**	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
51005	**AMDHD2**	**putative N-acetylglucosamine-6-phosphate deacetylase isoform 2**	2	7	2	1.2	**3E-02**	1.2	**2E-02**	1.3	8E-02	1.1	**2E-02**	1.0	7E-01	Molecular function unknown	-	Unclassified
51691	**NAA38; LSM8**	**LSM8 homolog, U6 small nuclear RNA associated**	4	30	4	1.2	**2E-05**	1.0	**2E-05**	1.3	**4E-02**	1.0	**2E-05**	1.0	3E-01	#N/A	#N/A	#N/A
4849	**CNOT3**	**CCR4-NOT transcription complex subunit 3**	5	21	5	1.2	**3E-04**	1.1	**4E-04**	1.2	6E-02	1.0	**3E-03**	1.2	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
51604	**PIGT**	**GPI transamidase component PIG-T isoform 1**	5	24	5	1.2	**9E-04**	1.0	**3E-04**	1.2	**1E-04**	1.3	**4E-04**	1.0	7E-01	Transaminase activity	Endoplasmic reticulum	Enzyme: Aminotransferase
9667	**SAFB2**	**scaffold attachment factor B2**	9	37	5	1.2	**2E-03**	0.9	**2E-03**	1.3	4E-01	0.9	1E-01	1.0	6E-01	Molecular function unknown	Cytoplasm	Unclassified
5440	**POLR2K**	**DNA-directed RNA polymerases I, II, and III subunit RPABC4**	1	6	1	1.2	**8E-03**	0.7	**2E-02**	1.2	2E-01	0.6	9E-02	0.8	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
8738	**CRADD**	**death domain-containing protein CRADD**	1	6	1	1.2	**1E-02**	1.2	3E-01	0.9	3E-01	0.8	4E-01	0.9	2E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
56288	**PARD3**	**partitioning defective 3 homolog isoform 1**	5	13	4	1.2	7E-02	1.1	**3E-02**	1.1	**2E-02**	1.0	**2E-02**	1.1	4E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
6624	**FSCN1**	**fascin**	24	421	24	1.2	**2E-16**	0.8	**2E-16**	**1.5**	**1E-03**	1.3	**2E-16**	0.9	**2E-04**	Structural molecule activity	Cytoplasm	Structural protein
3054	**HCFC1**	**host cell factor 1**	14	62	14	1.2	**8E-09**	0.9	**6E-10**	1.3	2E-01	1.0	**1E-07**	0.9	**1E-02**	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor
3608	**ILF2**	**interleukin enhancer-binding factor 2 isoform 1**	13	96	13	1.2	**2E-08**	1.0	**6E-10**	1.2	**2E-06**	0.8	**8E-08**	1.0	2E-01	Transcription factor activity	Nucleus	Transcription factor
7381	**UQCRB**	**cytochrome b-c1 complex subunit 7 isoform 3**	6	32	6	1.2	**3E-05**	1.0	**4E-04**	0.9	**2E-02**	0.7	**3E-02**	0.9	8E-02	Catalytic activity	Mitochondrion	Enzyme: Reductase
9536	**PTGES**	**prostaglandin E synthase**	1	6	1	1.2	**2E-02**	1.0	**2E-02**	1.2	7E-01	**2.2**	**3E-02**	0.9	9E-01	Molecular function unknown	Microsome	Enzyme: Synthase
402	**ARL2**	**ADP-ribosylation factor-like protein 2 isoform 1**	4	21	2	1.2	2E-01	1.0	8E-02	1.0	4E-01	0.9	2E-01	1.0	1E+00	GTPase activity	Cytoplasm	GTPase
9791	**PTDSS1**	**phosphatidylserine synthase 1 isoform 1**	6	34	6	1.2	**1E-04**	1.1	**3E-04**	1.1	**7E-03**	1.1	**4E-03**	1.1	**8E-03**	Transferase activity	Mitochondrion	Enzyme: Synthase
6135	**RPL11**	**60S ribosomal protein L11 isoform 1**	6	67	6	1.2	**2E-04**	0.8	**3E-04**	1.1	4E-01	0.8	2E-01	0.9	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
1728	**NQO1**	**NAD(P)H dehydrogenase [quinone] 1 isoform a**	9	89	9	1.2	**4E-08**	1.0	**3E-08**	**3.4**	**2E-04**	**3.9**	**1E-08**	0.9	**2E-02**	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
53371	**NUP54**	**nucleoporin p54 isoform 1**	13	58	13	1.2	**7E-05**	0.9	**3E-04**	1.2	**4E-02**	1.1	**6E-06**	1.0	5E-01	Transporter activity	Nucleus	Transport/cargo protein
84321	**THOC3**	**THO complex subunit 3**	7	40	7	1.2	**4E-03**	0.8	**1E-03**	1.1	**2E-02**	0.8	7E-01	0.8	**4E-03**	RNA binding	Nucleus	RNA binding protein
9904	**RBM19**	**probable RNA-binding protein 19**	5	20	5	1.2	**4E-03**	1.8	1E+00	0.7	8E-02	0.7	9E-01	1.8	9E-02	RNA binding	Nucleolus	RNA binding protein
5432	**POLR2C**	**DNA-directed RNA polymerase II subunit RPB3**	1	6	1	1.2	7E-02	0.8	8E-02	1.2	3E-01	0.8	3E-01	0.8	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
5965	**RECQL**	**ATP-dependent DNA helicase Q1*gi|14591904|ref|NP_002898.2| ATP-dependent DNA helicase Q1**	20	119	20	1.2	**4E-09**	0.9	**1E-09**	1.3	1E-01	0.9	**2E-04**	1.0	3E-01	DNA repair protein	Nucleus	DNA helicase
2631	**GBAS**	**protein NipSnap homolog 2 isoform 1**	5	37	3	1.2	**2E-08**	1.4	**5E-08**	1.4	**2E-06**	1.4	**2E-07**	1.0	7E-01	Molecular function unknown	Plasma membrane	Unclassified
23262	**PPIP5K2**	**inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 isoform 3**	6	25	6	1.2	**2E-05**	1.0	**4E-06**	1.1	**2E-03**	1.0	**2E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
11231	**SEC63**	**translocation protein SEC63 homolog**	12	78	12	1.2	**5E-04**	1.0	**4E-04**	1.3	**8E-04**	1.3	**1E-05**	1.1	**3E-02**	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
3996	**LLGL1**	**lethal(2) giant larvae protein homolog 1**	5	18	5	1.2	**2E-02**	1.0	**4E-03**	1.3	9E-02	1.1	**2E-02**	1.0	4E-01	Structural constituent of cytoskeleton	Cytoplasm;Plasma membrane;Cell junction	Cytoskeletal protein
6122	**RPL3**	**60S ribosomal protein L3 isoform a**	24	227	24	1.2	**2E-16**	1.0	**2E-16**	1.0	**1E-07**	0.8	**6E-04**	1.1	7E-02	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3655	ITGA6	integrin alpha-6 isoform b	29	235	3	1.2	**1E-15**	1.1	**1E-04**	**0.7**	**2E-16**	**0.5**	**2E-04**	1.3	**7E-06**	Receptor activity	Plasma membrane	Cell surface receptor
5411	PNN	pinin	14	64	14	1.2	**7E-09**	1.0	**8E-09**	1.2	**6E-05**	1.1	**3E-09**	1.1	8E-02	Cell adhesion molecule activity	Plasma membrane;Nucleus	Adhesion molecule
4925	NUCB2	nucleobindin-2	10	52	9	1.2	**1E-08**	1.1	**9E-07**	1.1	**5E-05**	1.0	**3E-06**	1.1	**4E-04**	Calcium ion binding	Golgi apparatus;Nucleus	Calcium binding protein
7329	UBE2I	SUMO-conjugating enzyme UBC9	6	47	6	1.2	**2E-07**	0.9	**4E-08**	1.4	4E-01	0.9	**3E-02**	0.9	**3E-04**	Ubiquitin-specific protease activity;Protein binding	Nucleus	Ubiquitin proteasome system protein
55082	ARGLU1	arginine and glutamate-rich protein 1	9	49	8	1.2	**4E-06**	0.9	**5E-06**	1.1	5E-01	0.8	**3E-04**	1.0	3E-01	Molecular function unknown	-	Unclassified
283742	FAM98B	protein FAM98B	4	24	2	1.2	**2E-04**	1.4	**5E-03**	1.2	**2E-02**	1.2	**2E-03**	1.2	3E-01	Molecular function unknown	-	Unclassified
10482	NXF1	nuclear RNA export factor 1 isoform 1	5	24	5	1.2	**8E-04**	1.1	**2E-04**	1.2	1E-01	1.1	**4E-03**	1.1	3E-01	RNA binding	Nucleus	RNA binding protein
6385	SDC4	syndecan-4	2	9	2	1.2	**2E-03**	**0.7**	**3E-02**	1.2	**2E-02**	0.9	8E-02	0.9	4E-01	Receptor activity	Plasma membrane	Cell surface receptor
440574	MINOS1	MICOS complex subunit MIC10 isoform c	1	7	1	1.2	**6E-03**	1.1	**7E-05**	1.2	**1E-02**	**1.5**	**3E-03**	1.1	8E-01	#N/A	#N/A	#N/A
79038	ZFYVE21	zinc finger FYVE domain-containing protein 21 isoform 1	3	9	3	1.2	**6E-03**	0.7	**1E-02**	1.0	2E-01	0.7	3E-01	1.0	4E-01	Transporter activity	-	Transport/cargo protein
6637	SNRPG	small nuclear ribonucleoprotein G	3	30	3	1.2	**1E-02**	1.0	**1E-02**	1.3	5E-02	0.9	**2E-03**	1.0	8E-01	RNA binding	Nucleus	Ribonucleoprotein
27258	LSM3	U6 snRNA-associated Sm-like protein LSm3	2	18	2	1.2	**1E-02**	0.8	**2E-02**	1.5	6E-02	0.9	**3E-02**	1.0	5E-01	RNA binding	Cytoplasm	RNA binding protein
1384	CRAT	carnitine O-acetyltransferase isoform 1	4	15	4	1.2	**2E-02**	**1.5**	**4E-03**	**1.5**	**3E-02**	**1.7**	**7E-04**	1.1	5E-01	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase
6205	RPS11	40S ribosomal protein S11	11	127	11	1.2	**6E-12**	0.9	**8E-15**	1.0	2E-01	0.7	**5E-02**	0.9	**2E-03**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6230	RPS25	40S ribosomal protein S25	7	152	7	1.2	**9E-12**	1.0	**1E-12**	1.0	**2E-02**	0.8	8E-02	1.0	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
51011	FAHD2A	PREDICTED: fumarylacetoacetate hydrolase domain-containing protein 2A isoform X1	8	44	8	1.2	**5E-05**	1.1	**1E-05**	1.2	**1E-02**	1.2	**7E-05**	1.3	2E-01	Molecular function unknown	-	Unclassified
5001	ORC5	origin recognition complex subunit 5 isoform 1	3	13	3	1.2	**2E-03**	0.8	**4E-03**	1.1	1E+00	0.8	4E-01	1.0	4E-01	#N/A	#N/A	#N/A
91746	YTHDC1	YTH domain-containing protein 1 isoform 1	4	14	4	1.2	**5E-03**	1.1	**4E-03**	1.2	1E-01	1.1	**1E-02**	1.1	1E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
60487	TRMT11	tRNA (guanine(10)-N2)-methyltransferase homolog	4	12	4	1.2	**2E-02**	1.0	**1E-02**	1.2	5E-01	1.2	**8E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
11253	MAN1B1	endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	7	19	6	1.2	**2E-02**	1.0	**3E-02**	1.2	**2E-02**	0.9	3E-01	1.2	2E-01	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase
29886	SNX8	sorting nexin-8	2	6	2	1.2	8E-02	0.8	2E-01	1.1	1E+00	1.3	1E-01	0.7	3E-01	Transporter activity	-	Transport/cargo protein
9354	UBE4A	ubiquitin conjugation factor E4 A isoform 1	4	12	4	1.2	9E-02	1.0	9E-02	1.1	4E-01	0.9	**5E-02**	0.9	3E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
23020	SNRNP200	U5 small nuclear ribonucleoprotein 200 kDa helicase	52	275	52	1.2	**2E-16**	1.0	**2E-16**	1.3	**8E-10**	1.0	**2E-16**	1.0	8E-01	Ribonucleoprotein	Nucleus	Ribonucleoprotein
5721	PSME2	proteasome activator complex subunit 2	10	59	10	1.2	**5E-08**	1.0	**1E-08**	1.3	**5E-05**	1.0	**2E-07**	0.9	2E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
5610	EIF2AK2	interferon-induced, double-stranded RNA-activated protein kinase isoform a	13	79	13	1.2	**2E-06**	0.8	**3E-03**	0.8	**1E-06**	**0.6**	**6E-06**	0.9	7E-02	Protein serine/threonine kinase activity	Ribosome	Serine/threonine kinase
9521	EEF1E1	eukaryotic translation elongation factor 1 epsilon-1 isoform 1	7	41	7	1.2	**8E-05**	1.0	**2E-04**	1.4	**8E-03**	**1.6**	**1E-04**	1.0	1E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
51102	MECR	trans-2-enoyl-CoA reductase, mitochondrial isoform a	5	19	5	1.2	**1E-04**	1.4	**3E-04**	1.3	**2E-06**	1.4	**6E-05**	1.0	7E-02	Catalytic activity	Mitochondrion	Enzyme: Reductase
55658	RNF126	E3 ubiquitin-protein ligase RNF126	2	8	2	1.2	**8E-04**	0.9	**1E-02**	1.3	3E-01	1.3	**2E-02**	1.1	2E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
1104	RCC1	regulator of chromosome condensation isoform a	3	20	3	1.2	**1E-03**	1.0	**3E-03**	1.2	1E-01	1.3	**2E-03**	1.0	3E-01	Guanyl-nucleotide exchange factor activity	Nucleus	Guanine nucleotide exchange factor
6464	SHC1	SHC-transforming protein 1 isoform 3	9	24	9	1.2	5E-02	1.1	**2E-02**	1.2	**2E-02**	1.0	**3E-02**	1.1	4E-01	Protein binding	Cytoplasm	Adapter molecule
257364	SNX33	sorting nexin-33	6	19	5	1.2	7E-02	0.8	6E-02	1.0	6E-01	0.9	2E-01	1.0	4E-01	Molecular function unknown	-	Unclassified
6277	S100A6	protein S100-A6	8	642	8	1.2	**2E-16**	1.2	**2E-16**	**1.5**	**1E-12**	**1.7**	**2E-16**	1.3	**2E-16**	Calcium ion binding	Cytoplasm	Calcium binding protein
3189	HNRNPH3	PREDICTED: heterogeneous nuclear ribonucleoprotein H3 isoform X2	7	88	6	1.2	**1E-05**	0.9	**7E-07**	1.3	2E-01	1.2	**9E-07**	1.0	5E-01	Ribonucleoprotein	Nucleus	Ribonucleoprotein
79902	NUP85	nuclear pore complex protein Nup85 isoform 1	10	31	10	1.2	**1E-04**	1.1	**5E-05**	1.3	**4E-03**	1.4	**1E-05**	1.0	2E-01	Cytoskeletal anchoring activity	Centrosome	Anchor protein
23211	ZC3H4	zinc finger CCCH domain-containing protein 4	2	8	2	1.2	**2E-02**	0.9	**4E-03**	1.2	2E-01	1.0	1E-01	1.0	5E-01	Molecular function unknown	-	Unclassified
9810	RNF40	E3 ubiquitin-protein ligase BRE1B isoform 1	5	16	4	1.2	**3E-02**	1.0	**4E-02**	1.2	3E-01	0.8	2E-01	1.0	8E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
56262	LRRC8A	volume-regulated anion channel subunit LRRC8A	15	63	14	1.2	**1E-07**	0.7	**3E-06**	0.9	**1E-05**	0.8	9E-01	1.0	**3E-02**	Molecular function unknown	Integral to membrane	Unclassified;Integral membrane protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
29078	NDUFAF4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	7	31	7	1.2	**3E-04**	1.0	**8E-05**	1.4	**8E-03**	1.2	**3E-05**	1.0	**3E-02**	Molecular function unknown	-	Cell cycle control protein
10951	CBX1	chromobox protein homolog 1	5	14	4	1.2	**5E-04**	1.0	**1E-04**	1.3	1E-01	0.9	1E-01	0.9	3E-01	DNA binding	Nucleus	DNA binding protein
10802	SEC24A	protein transport protein Sec24A isoform 1	6	23	4	1.2	**6E-03**	0.9	**1E-02**	1.3	4E-01	1.1	**3E-02**	1.2	1E-01	Transporter activity	Endoplasmic reticulum	Transport/cargo protein
84612	PARD6B	partitioning defective 6 homolog beta	2	7	2	1.2	**3E-02**	1.2	1E-01	1.1	**3E-02**	0.9	8E-02	0.9	4E-01	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule
9780	PIEZO1	piezo-type mechanosensitive ion channel component 1	2	5	2	1.2	1E-01	1.8	3E-01	0.9	3E-01	0.9	4E-01	1.9	3E-01	#N/A	#N/A	#N/A
4012	LNPEP	leucyl-cystinyl aminopeptidase isoform 1	19	85	19	1.3	**1E-11**	1.0	**9E-12**	1.2	**1E-03**	0.9	**4E-06**	1.0	**2E-02**	Aminopeptidase activity	Plasma membrane	Aminopeptidase
11163;	NUDT4	diphosphoinositol polyphosphate phosphohydrolase 2 isoform 3	11	23	10	1.3	**1E-04**	1.0	**3E-05**	1.2	**3E-04**	1.1	**2E-04**	1.0	8E-01	Molecular function unknown	-	Unclassified
11128	POLR3A	DNA-directed RNA polymerase III subunit RPC1	5	17	5	1.3	**4E-04**	1.0	**1E-04**	1.4	7E-02	0.9	**6E-03**	1.0	9E-01	DNA-directed RNA polymerase activity	-	RNA polymerase
79612	NAA16	N-alpha-acetyltransferase 16, NatA auxiliary subunit isoform 1	10	50	4	1.3	**1E-03**	1.2	**1E-03**	1.3	**9E-04**	**1.5**	**6E-04**	1.2	**3E-02**	Molecular function unknown	-	Unclassified
1022	CDK7	cyclin-dependent kinase 7	3	18	3	1.3	**7E-03**	0.8	**1E-02**	1.2	2E-01	0.7	9E-01	0.9	**2E-02**	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
3191	HNRNPL	heterogeneous nuclear ribonucleoprotein L isoform a	17	239	16	1.3	**2E-16**	0.9	**2E-16**	1.3	9E-01	1.0	**2E-16**	0.9	1E-01	RNA binding	Nucleus	Ribonucleoprotein
3183	HNRNPC	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b*gi|117190254|ref|NP_001070911.1| heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	20	281	20	1.3	**3E-15**	0.9	**2E-16**	1.2	5E-01	0.7	5E-01	0.9	**3E-03**	RNA binding	Nucleus	RNA binding protein
64167	ERAP2	endoplasmic reticulum aminopeptidase 2	12	49	12	1.3	**1E-07**	0.8	**4E-08**	1.1	7E-02	**0.7**	**3E-03**	1.0	**3E-02**	Aminopeptidase activity	Endoplasmic reticulum	Aminopeptidase
84267	C9orf64	UPF0553 protein C9orf64	13	57	13	1.3	**2E-07**	0.9	**1E-07**	1.5	5E-01	1.3	**9E-08**	1.0	7E-01	Molecular function unknown	-	Unclassified
51182	HSPA14	heat shock 70 kDa protein 14 isoform 1	6	28	6	1.3	**4E-04**	1.0	**4E-05**	1.2	**3E-02**	1.1	**6E-05**	1.1	1E-01	Chaperone activity	-	Chaperone
10147	SUGP2	SURP and G-patch domain-containing protein 2	4	10	4	1.3	**2E-02**	0.8	**2E-02**	1.2	4E-01	0.7	4E-01	1.2	7E-01	#N/A	#N/A	#N/A
9804	TOMM20	mitochondrial import receptor subunit TOM20 homolog	2	8	2	1.3	**3E-02**	1.0	**1E-02**	1.2	2E-01	1.1	**2E-02**	1.1	2E-01	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
3945	LDHB	L-lactate dehydrogenase B chain	15	358	14	1.3	**2E-16**	0.9	**2E-16**	1.3	**1E-04**	0.9	**1E-15**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
55920	RCC2	protein RCC2*gi|29789090|ref|NP_061185.1| protein RCC2	16	103	16	1.3	**3E-11**	1.0	**3E-11**	1.3	**3E-03**	0.8	**3E-02**	1.0	3E-01	Protein binding	Nucleus	Cell cycle control protein
9782	MATR3	matrin-3 isoform a*gi|303227924|ref|NP_001181883.1| matrin-3 isoform a*gi|303227926|ref|NP_001181884.1| matrin-3 isoform a*gi|62750354|ref|NP_954659.1| matrin-3 isoform a	26	176	26	1.3	**2E-10**	0.9	**2E-10**	1.2	2E-01	0.8	6E-01	0.9	**3E-04**	RNA binding	Nucleus	RNA binding protein
6138	RPL15	60S ribosomal protein L15 isoform 1	10	76	10	1.3	**5E-06**	0.9	**4E-06**	1.1	4E-01	0.8	**4E-03**	0.9	1E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
57570	TRMT5	tRNA (guanine(37)-N1)-methyltransferase	12	44	12	1.3	**1E-04**	1.0	**3E-05**	1.3	**4E-02**	1.0	**1E-06**	1.0	2E-01	Methyltransferase activity	-	Enzyme: Methyltransferase
2037	EPB41L2	band 4.1-like protein 2 isoform a	16	52	16	1.3	**3E-04**	0.9	**8E-05**	1.1	7E-01	1.1	**2E-05**	1.1	**7E-03**	Structural constituent of cytoskeleton	Plasma membrane	Cytoskeletal protein
2762	GMDS	GDP-mannose 4,6 dehydratase isoform 1	5	17	5	1.3	**1E-03**	1.1	**2E-04**	1.3	**1E-02**	1.2	**7E-04**	1.0	8E-01	Hydro-lyase activity	Cytoplasm	Enzyme: Dehydratase
9147	NEMF	nuclear export mediator factor NEMF isoform 1	9	29	9	1.3	**1E-02**	1.1	**6E-03**	1.1	**2E-02**	1.0	**6E-03**	1.2	9E-02	#N/A	#N/A	#N/A
23557	SNAPIN	SNARE-associated protein Snapin	1	6	1	1.3	6E-02	1.0	2E-01	1.2	4E-01	1.0	**2E-02**	0.8	3E-01	Auxiliary transport protein activity	Cytoplasm	Membrane transport protein
445815	PALM2-AKAP2	PALM2-AKAP2 protein isoform 2	10	43	10	1.3	#N/A	0.8	#N/A	0.9	#N/A	0.6	#N/A	1.1	#N/A	Molecular function unknown	Plasma membrane	Unclassified
6195	RPS6KA1	ribosomal protein S6 kinase alpha-1 isoform b	23	147	14	1.3	**5E-11**	1.0	**7E-13**	1.3	**6E-06**	1.2	**2E-12**	1.0	7E-02	Protein serine/threonine kinase activity	Cytosol	Serine/threonine kinase
4723	NDUFV1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial isoform 1	5	22	5	1.3	**2E-03**	1.1	**1E-03**	0.9	**2E-02**	0.9	**7E-03**	1.0	1E+00	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
23190	UBXN4	UBX domain-containing protein 4	4	15	4	1.3	**5E-03**	1.2	**5E-03**	1.2	1E+00	1.0	8E-01	0.9	3E-01	Molecular function unknown	-	Unclassified
90411	MCFD2	multiple coagulation factor deficiency protein 2 isoform A	1	7	1	1.3	**5E-03**	0.9	**3E-02**	1.3	4E-01	**0.6**	**2E-02**	0.9	**4E-02**	Molecular function unknown	Extracellular	Unclassified
2079	ERH	enhancer of rudimentary homolog	4	35	4	1.3	**9E-03**	0.9	**5E-03**	1.2	9E-01	0.7	4E-01	0.9	**4E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7205	**TRIP6**	**PREDICTED: thyroid receptor-interacting protein 6 isoform X1**	8	14	8	1.3	#N/A	1.0	#N/A	1.0	#N/A	0.7	#N/A	1.0	#N/A	Transcription regulator activity	Nucleus	Transcription regulatory protein
29763	**PACSIN3**	**protein kinase C and casein kinase substrate in neurons protein 3**	11	53	11	1.3	**4E-05**	1.0	**5E-05**	1.3	**1E-02**	0.9	**5E-02**	1.0	3E-01	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
54495	**TMX3**	**protein disulfide-isomerase TMX3**	7	31	7	1.3	**4E-04**	1.1	**2E-03**	1.1	**5E-02**	1.0	**4E-02**	1.0	3E-01	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase
51808	**PHAX**	**phosphorylated adapter RNA export protein**	3	9	3	1.3	**8E-03**	1.0	**2E-02**	1.1	7E-01	0.8	2E-01	0.8	1E-01	RNA binding	Nucleus	RNA binding protein
780	**DDR1**	**epithelial discoidin domain-containing receptor 1 isoform 2**	4	8	4	1.3	1E-01	0.9	2E-01	1.1	6E-01	0.8	3E-01	1.1	9E-01	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase
83871	**RAB34**	**ras-related protein Rab-34 isoform 5**	3	7	3	1.3	5E-01	0.8	3E-01	1.3	6E-01	1.2	**5E-02**	1.1	5E-01	GTPase activity	Golgi apparatus	GTPase
6741	**SSB**	**lupus La protein**	27	189	27	1.3	**2E-16**	1.0	**2E-16**	1.3	**9E-05**	0.8	**2E-10**	1.0	2E-01	RNA binding	Nucleus	RNA binding protein
65123	**INTS3**	**integrator complex subunit 3**	3	12	3	1.3	**1E-02**	1.0	**4E-03**	1.1	**4E-02**	1.0	2E-01	1.0	1E-01	Molecular function unknown	-	Unclassified
9343	**EFTUD2**	**116 kDa U5 small nuclear ribonucleoprotein component isoform a**	26	146	25	1.3	**7E-12**	1.0	**2E-15**	1.2	**4E-05**	1.0	**4E-12**	1.0	3E-01	GTPase activity	Nucleus	Unclassified
85476	**GFM1**	**elongation factor G, mitochondrial**	11	52	11	1.3	**2E-08**	1.0	**1E-08**	1.2	**9E-04**	1.0	**8E-05**	1.0	3E-01	Translation regulator activity	Mitochondrion	Translation regulatory protein
8932;	**MBD2**	**methyl-CpG-binding domain protein 2 isoform 1**	11	18	5	1.3	**5E-07**	1.0	**1E-06**	1.2	3E-01	0.9	**6E-05**	1.0	6E-02	DNA binding	Nucleus;Cytoplasm	Transcription regulatory protein
10189	**ALYREF**	**THO complex subunit 4**	4	39	4	1.3	**3E-06**	1.0	**3E-07**	1.3	**2E-02**	0.8	2E-01	1.0	9E-01	#N/A	#N/A	#N/A
151987	**PPP4R2**	**serine/threonine-protein phosphatase 4 regulatory subunit 2**	3	8	3	1.3	**3E-03**	0.8	**5E-03**	1.3	8E-01	0.9	**2E-02**	0.9	2E-01	Protein serine/threonine phosphatase activity	Centrosome	Serine/threonine phosphatase
29945	**ANAPC4**	**anaphase-promoting complex subunit 4 isoform 1**	3	10	3	1.3	**3E-03**	1.0	**9E-03**	1.4	6E-01	0.9	6E-02	1.2	1E+00	Molecular function unknown	Nucleus	Cell cycle control protein
170506	**DHX36**	**ATP-dependent RNA helicase DHX36 isoform 1**	6	19	5	1.3	**1E-02**	0.9	**2E-02**	1.1	3E-01	0.8	8E-01	1.0	1E+00	RNA binding	Plasma membrane	RNA binding protein
9823	**ARMCX2**	**armadillo repeat-containing X-linked protein 2**	1	6	1	1.3	3E-01	1.0	8E-02	1.2	7E-02	1.2	9E-02	0.8	8E-01	Molecular function unknown	Plasma membrane	Unclassified
6209	**RPS15**	**40S ribosomal protein S15**	4	74	4	1.3	**9E-07**	0.9	**2E-06**	1.1	**1E-02**	0.7	8E-02	0.9	2E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
51599	**LSR**	**lipolysis-stimulated lipoprotein receptor isoform 2**	6	30	6	1.3	**1E-05**	0.9	**2E-04**	1.1	8E-01	0.8	2E-01	1.1	2E-01	Receptor activity	Plasma membrane	Integral membrane protein
55234	**SMU1**	**WD40 repeat-containing protein SMU1**	10	52	10	1.3	**4E-05**	0.9	**3E-05**	1.3	5E-01	1.0	**8E-03**	0.9	5E-02	Molecular function unknown	Nucleus	Unclassified
10285	**SMNDC1**	**survival of motor neuron-related-splicing factor 30**	4	20	4	1.3	**9E-05**	0.7	**2E-05**	1.3	**4E-02**	0.8	7E-01	1.1	7E-01	Structural molecule activity	Nucleus	Structural protein
7030	**TFE3**	**transcription factor E3 isoform 1**	1	6	1	1.3	6E-02	1.0	9E-02	1.0	**3E-02**	1.0	9E-02	0.9	4E-01	Transcription factor activity	Nucleus	Transcription factor
51340	**CRNKL1**	**crooked neck-like protein 1 isoform a**	4	14	4	1.3	7E-02	0.8	6E-02	1.2	6E-02	0.8	3E-01	0.9	1E-01	RNA binding	Nucleus	RNA binding protein
124944	**C17orf49**	**chromatin complexes subunit BAP18 isoform 1**	1	6	1	1.3	#N/A	1.3	#N/A	1.6	#N/A	0.8	#N/A	1.1	#N/A	Molecular function unknown	Nucleus	Unclassified
29927	**SEC61A1**	**protein transport protein Sec61 subunit alpha isoform 1**	7	45	7	1.3	**2E-05**	1.1	**3E-06**	1.1	**4E-03**	1.1	**1E-04**	1.1	**3E-02**	Protein translocase activity;Intracellular transporter activity	Endoplasmic reticulum	Integral membrane protein
64949	**MRPS26**	**28S ribosomal protein S26, mitochondrial**	7	20	7	1.3	**4E-04**	1.1	**4E-04**	1.3	**6E-03**	1.0	**1E-03**	1.1	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
79023	**NUP37**	**nucleoporin Nup37**	7	25	7	1.3	**4E-04**	0.9	**3E-04**	1.2	4E-01	1.0	**3E-04**	0.9	**1E-02**	Transporter activity	Nucleus	Transport/cargo protein
5514	**PPP1R10**	**PREDICTED: serine/threonine-protein phosphatase 1 regulatory subunit 10 isoform X1**	8	20	8	1.3	**1E-03**	1.0	**2E-04**	1.2	2E-01	0.9	1E-01	1.0	1E-01	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase
9991	**PTBP3**	**polypyrimidine tract-binding protein 3 isoform 6**	6	89	3	1.3	**2E-08**	0.9	**5E-13**	1.3	6E-02	1.1	**3E-08**	1.0	6E-02	#N/A	#N/A	#N/A
8087	**FXR1**	**fragile X mental retardation syndrome-related protein 1 isoform a**	16	99	14	1.3	**2E-07**	0.9	**7E-10**	1.1	5E-01	0.9	3E-01	1.0	9E-01	RNA binding	Nucleolus	RNA binding protein
64062	**RBM26**	**RNA-binding protein 26 isoform 1**	12	52	12	1.3	**6E-07**	0.9	**2E-07**	1.3	2E-01	1.1	**2E-05**	1.0	7E-01	RNA binding	Nucleus	RNA binding protein
9972	**NUP153**	**nuclear pore complex protein Nup153 isoform 1**	8	32	8	1.3	**3E-04**	1.0	**7E-05**	1.4	4E-01	1.2	**4E-04**	1.0	4E-01	Transporter activity	Nucleus	Transport/cargo protein
54974	**THG1L**	**probable tRNA(His) guanylyltransferase**	4	14	4	1.3	**5E-03**	0.9	**6E-03**	1.1	9E-01	1.1	**1E-02**	1.1	**5E-02**	Molecular function unknown	Cytoplasm	Cell cycle control protein
90701	**SEC11C**	**signal peptidase complex catalytic subunit SEC11C**	3	10	3	1.3	**7E-03**	1.1	**2E-02**	1.0	1E-01	1.1	7E-02	1.1	1E-01	Aminopeptidase activity	Microsome	Aminopeptidase
7307	**U2AF1**	**splicing factor U2AF 65 kDa subunit isoform a**	26	122	7	1.3	#N/A	0.9	#N/A	1.2	#N/A	0.9	#N/A	1.0	#N/A	RNA binding	Nucleus	Ribonucleoprotein
7408	**VASP**	**PREDICTED: vasodilator-stimulated phosphoprotein isoform X1**	17	72	1	1.3	**1E-10**	1.2	**2E-11**	1.5	3E-01	**2.0**	**7E-11**	1.0	5E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10768	**AHCYL1**	**putative adenosylhomocysteinase 2 isoform a**	12	91	3	1.3	**8E-10**	0.8	**3E-09**	1.2	8E-01	0.9	**2E-08**	1.1	7E-01	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
10923	**SUB1**	**PREDICTED: activated RNA polymerase II transcriptional coactivator p15 isoform X1**	9	73	9	1.3	**2E-09**	0.8	**9E-10**	1.4	6E-02	0.8	**1E-02**	1.0	6E-01	Transcription factor activity	Nucleus	Transcription factor
6134	**RPL10**	**60S ribosomal protein L10 isoform a**	9	84	9	1.3	**2E-07**	0.9	**5E-06**	1.2	9E-01	0.8	1E-01	0.9	**1E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
682	**BSG**	**basigin isoform 1**	9	66	9	1.3	**1E-06**	0.8	**7E-07**	1.2	**6E-03**	0.8	5E-01	0.9	**1E-02**	Receptor activity	Plasma membrane;Nucleus;Cytoplasm	Cell surface receptor
8498	**RANBP3**	**ran-binding protein 3 isoform RANBP3-d**	12	49	11	1.3	**2E-06**	0.9	**7E-08**	1.3	4E-01	1.0	**9E-07**	0.9	**4E-03**	Transporter activity	Nucleus	Transport/cargo protein
112858	**TP53RK**	**TP53-regulating kinase**	2	14	2	1.3	**7E-04**	1.0	**6E-04**	1.2	7E-02	1.1	**9E-03**	0.9	**2E-02**	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
25921	**ZDHHC5**	**PREDICTED: palmitoyltransferase ZDHHC5 isoform X1**	5	15	5	1.3	3E-01	0.9	7E-02	1.0	6E-01	0.7	6E-01	1.1	3E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
10613	**ERLIN1**	**erlin-1*gi|154800489|ref|NP_001094096.1|erlin-1**	8	52	6	1.3	**6E-06**	1.2	**3E-05**	1.3	**9E-04**	0.9	**2E-04**	1.1	**1E-02**	Molecular function unknown	Plasma membrane	Unclassified
84245	**MRI1**	**methylthioribose-1-phosphate isomerase isoform 1**	7	29	7	1.3	**9E-06**	1.1	**2E-06**	1.4	**4E-02**	1.3	**9E-05**	1.0	1E+00	Translation regulator activity;Molecular function unknown	-	Translation regulatory protein;Unclassified
79039	**DDX54**	**ATP-dependent RNA helicase DDX54 isoform 2**	12	37	11	1.3	**5E-04**	0.8	**7E-03**	1.1	7E-01	0.7	6E-01	1.0	9E-01	RNA binding	Nucleolus	RNA helicase
29937	**NENF**	**neudesin**	5	29	5	1.3	**8E-04**	0.8	**1E-03**	1.1	**1E-02**	0.7	4E-01	1.0	4E-01	Kinase regulator activity	Extracellular	Secreted polypeptide
25777	**SUN2**	**SUN domain-containing protein 2 isoform a**	7	24	7	1.3	**1E-03**	1.0	**2E-04**	1.2	**4E-02**	1.1	**7E-04**	1.0	6E-01	Molecular function unknown	Integral to membrane	Unclassified
56897	**WRNIP1**	**ATPase WRNIP1 isoform 1**	2	11	2	1.3	**2E-02**	1.0	**2E-02**	1.3	7E-02	0.9	1E-01	0.9	4E-01	DNA repair protein	Nucleus;Cytoplasm	ATPase
59285	**CACNG6**	**voltage-dependent calcium channel gamma-6 subunit isoform a**	1	3	1	1.3	**5E-02**	0.9	**2E-02**	1.2	6E-01	1.0	**3E-02**	1.0	5E-01	Voltage-gated ion channel activity	Plasma membrane	Voltage gated channel
54888	**NSUN2**	**tRNA (cytosine(34)-C(5))-methyltransferase isoform 1**	22	128	22	1.3	**3E-10**	0.9	**4E-12**	1.2	9E-01	0.9	**2E-08**	0.9	**2E-04**	RNA methyltransferase activity	Nucleolus	RNA methyltransferase
51631	**LUC7L2**	**putative RNA-binding protein Luc7-like 2 isoform 1**	11	67	6	1.3	**1E-06**	1.0	**1E-06**	1.1	**5E-05**	1.0	**3E-06**	0.9	1E-01	Molecular function unknown	Nucleolus	Unclassified
9779	**TBC1D5**	**PREDICTED: TBC1 domain family member 5 isoform X2**	7	29	7	1.3	**8E-04**	1.1	**1E-04**	1.3	**2E-02**	1.0	**6E-04**	1.0	5E-01	Molecular function unknown	-	Unclassified
9701	**PPP6R2**	**serine/threonine-protein phosphatase 6 regulatory subunit 2 isoform 1**	5	12	5	1.3	1E+00	1.1	5E-01	1.2	2E-01	1.0	5E-01	1.1	7E-01	#N/A	#N/A	#N/A
10992	**SF3B2**	**splicing factor 3B subunit 2**	22	118	22	1.3	**3E-13**	1.0	**6E-15**	1.3	**4E-04**	1.0	**2E-09**	1.0	6E-01	RNA binding	Nucleus	RNA binding protein
93100	**NAPRT1; NAPRT**	**nicotinate phosphoribosyltransferase isoform 1**	11	66	11	1.3	**7E-11**	1.0	**1E-11**	1.2	**2E-03**	1.0	**6E-09**	1.0	7E-01	#N/A	#N/A	#N/A
1676	**DFFA**	**DNA fragmentation factor subunit alpha isoform 1**	6	28	6	1.3	**4E-05**	0.8	**1E-04**	1.2	**7E-03**	1.0	**3E-03**	0.9	7E-02	Chaperone activity	Cytoplasm	Chaperone
55759	**WDR12**	**ribosome biogenesis protein WDR12**	7	31	7	1.3	**4E-05**	0.8	**7E-07**	1.2	1E-01	0.7	7E-01	1.1	5E-01	Molecular function unknown	Nucleolus	Unclassified
92609	**TIMM50**	**mitochondrial import inner membrane translocase subunit TIM50**	8	53	8	1.3	**1E-02**	1.0	**2E-03**	1.4	7E-02	1.1	**8E-04**	1.0	5E-01	Protein tyrosine/serine/threonine phosphatase activity	Mitochondrion	Dual specificity phosphatase
6125	**RPL5**	**60S ribosomal protein L5**	15	154	15	1.3	**2E-16**	0.9	**2E-16**	1.1	**2E-03**	0.8	**2E-02**	1.0	8E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6132	**RPL8**	**60S ribosomal protein L8**	13	127	13	1.3	**2E-14**	1.0	**8E-12**	1.1	**5E-07**	0.8	**3E-03**	1.0	9E-01	Structural constituent of ribosome	Nucleolus	Ribosomal subunit
6164	**RPL34**	**PREDICTED: 60S ribosomal protein L34 isoform X1**	6	84	6	1.3	**3E-11**	1.0	**1E-10**	1.1	**1E-02**	0.8	**8E-03**	1.0	9E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
6738	**TROVE2**	**60 kDa SS-A/Ro ribonucleoprotein isoform 2**	13	83	13	1.3	**4E-10**	1.0	**1E-10**	1.3	**7E-06**	1.0	**9E-10**	0.9	1E-01	RNA binding	Cytoplasm	RNA binding protein
2237	**FEN1**	**flap endonuclease 1**	10	48	10	1.3	**1E-06**	0.8	**1E-06**	1.2	**9E-03**	0.8	2E-01	1.0	5E-01	Deoxyribonuclease activity	Nucleus	Deoxyribonuclease
51593	**SRRT**	**serrate RNA effector molecule homolog isoform a**	19	94	19	1.3	**6E-06**	0.9	**1E-05**	1.2	9E-01	0.9	**2E-03**	0.9	**9E-04**	Molecular function unknown	Nucleus	Unclassified
5547	**PRCP**	**lysosomal Pro-X carboxypeptidase isoform 1 preproprotein**	5	23	5	1.3	**7E-04**	1.4	**9E-04**	1.3	**4E-03**	1.3	**6E-04**	1.1	**3E-02**	Carboxypeptidase activity	Lysosome	Carboxypeptidase
84129	**ACAD11**	**acyl-CoA dehydrogenase family member 11**	4	15	4	1.3	**3E-02**	1.0	**2E-02**	1.3	2E-01	1.1	**7E-03**	0.9	4E-01	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase
7086	**TKT**	**transketolase isoform 2**	27	386	27	1.3	**2E-16**	1.0	**2E-16**	**1.5**	**2E-16**	1.1	**2E-16**	0.9	**5E-09**	Transferase activity, transferring aldehyde or ketonic groups	Cytoplasm	Enzyme: Transketolase
11344	**TWF2**	**twinfilin-2**	13	101	9	1.3	**1E-10**	0.9	**6E-10**	1.3	5E-01	1.0	**7E-07**	1.0	1E-01	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
11051	NUDT21	cleavage and polyadenylation specificity factor subunit 5	7	36	7	1.3	**2E-06**	0.9	**2E-07**	1.2	2E-01	0.8	1E-01	0.9	1E-01	RNA binding	Nucleus	RNA binding protein
7037	TFRC	transferrin receptor protein 1	15	62	15	1.3	**3E-05**	**0.6**	**5E-05**	0.9	**2E-03**	1.0	**4E-05**	1.0	7E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
26168	SENP3	sentrin-specific protease 3	3	16	3	1.3	**6E-05**	1.0	**7E-04**	1.4	5E-01	0.9	**3E-02**	1.0	6E-01	Peptidase activity	Nucleolus	Protease
10772	SRSF10; LOC100996657	serine/arginine-rich splicing factor 10 isoform 2	5	36	5	1.3	**3E-04**	0.9	**1E-04**	1.3	1E-01	0.9	**2E-03**	1.0	2E-01	#N/A	#N/A	#N/A
54788	DNAJB12	dnaJ homolog subfamily B member 12	2	8	2	1.3	2E-01	1.1	1E-01	0.9	9E-01	1.1	7E-02	0.9	1E-01	Molecular function unknown	-	Integral membrane protein
6137	RPL13	60S ribosomal protein L13 isoform 1*gi|15431297|ref|NP_000968.2| 60S ribosomal protein L13 isoform 1	13	161	13	1.3	**2E-10**	1.0	**2E-10**	1.1	**1E-04**	0.8	1E-01	1.0	2E-01	RNA binding	Ribosome	Ribonucleoprotein
54920	DUS2; DUS2L	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like isoform 1	6	33	5	1.3	**7E-04**	0.9	**5E-05**	1.6	2E-01	1.2	**9E-06**	1.0	5E-01	#N/A	#N/A	#N/A
7341	SUMO1	small ubiquitin-related modifier 1 isoform a	5	17	5	1.3	**4E-03**	0.9	**4E-03**	1.1	8E-01	1.0	**5E-03**	1.0	3E-01	Protein binding	Cytoplasm	Transcription regulatory protein
51477	ISYNA1	inositol-3-phosphate synthase 1 isoform 1	5	10	5	1.3	9E-02	0.9	5E-02	1.5	7E-01	1.1	**3E-02**	1.2	5E-01	Isomerase activity	-	Enzyme: Isomerase
10155	TRIM28	transcription intermediary factor 1-beta	19	171	19	1.3	**1E-13**	0.9	**2E-14**	1.2	9E-02	0.9	**1E-08**	1.0	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
84681	HINT2	histidine triad nucleotide-binding protein 2, mitochondrial	3	12	3	1.3	**7E-03**	1.3	**9E-03**	1.2	**3E-02**	1.4	**1E-02**	1.0	8E-01	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase
23406	COTL1	coactosin-like protein	9	67	9	1.3	**1E-07**	0.7	**3E-08**	1.2	**3E-04**	1.1	**4E-06**	1.0	9E-01	Molecular function unknown	Cytoplasm	Unclassified
9774	BCLAF1	bcl-2-associated transcription factor 1 isoform 1	19	89	19	1.3	**2E-07**	1.0	**1E-07**	1.2	**1E-02**	0.9	**3E-05**	1.0	3E-01	Transcription factor activity	Nucleus	Transcription factor
4179	CD46	membrane cofactor protein isoform 2	5	27	5	1.3	**1E-05**	0.9	**2E-06**	1.2	8E-01	0.9	**4E-05**	1.0	7E-01	Receptor activity	Plasma membrane	Cell surface receptor
51366	UBR5	E3 ubiquitin-protein ligase UBR5 isoform 1	8	24	8	1.3	**5E-04**	1.3	**8E-05**	1.2	**3E-03**	1.2	**2E-03**	1.2	1E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
8815	BANF1	barrier-to-autointegration factor	4	26	4	1.3	**1E-03**	1.0	**1E-03**	1.4	6E-02	1.3	**1E-03**	0.9	3E-01	DNA binding	Nucleus	DNA binding protein
83451	ABHD11	alpha/beta hydrolase domain-containing protein 11 isoform 1	4	22	4	1.3	**4E-03**	1.0	**1E-03**	1.4	2E-01	**1.6**	**1E-03**	1.1	1E-01	Molecular function unknown	-	Unclassified
5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 isoform 3	6	32	3	1.3	8E-02	1.2	1E-01	1.1	3E-01	1.2	6E-02	1.2	5E-01	Sugar-phosphatase activity	-	Enzyme: Phosphatase
10730	YME1L1	ATP-dependent zinc metalloprotease YME1L1 isoform 1	13	63	13	1.3	**2E-12**	0.8	**3E-13**	1.2	**4E-03**	**0.6**	**3E-02**	0.9	**3E-02**	Metallopeptidase activity	Mitochondrion	Metallo protease
6627	SNRPA1	U2 small nuclear ribonucleoprotein A'	11	85	11	1.3	**1E-07**	1.0	**2E-08**	1.3	**4E-02**	0.9	**2E-05**	1.0	**2E-02**	RNA binding	Nucleus	Ribonucleoprotein
1477	CSTF1	PREDICTED: cleavage stimulation factor subunit 1 isoform X1	9	38	9	1.3	**1E-05**	0.9	**1E-06**	1.3	1E+00	0.9	**2E-05**	1.0	7E-01	RNA binding	Nucleus	RNA binding protein
617	BCS1L	PREDICTED: mitochondrial chaperone BCS1 isoform X1	7	36	7	1.3	**7E-05**	1.0	**4E-05**	1.4	**2E-04**	1.4	**1E-05**	1.2	**3E-02**	Molecular function unknown	Mitochondrion	Unclassified
54973	CPSF3L	integrator complex subunit 11 isoform 1	1	6	1	1.3	5E-02	0.9	**4E-02**	1.2	4E-01	0.7	7E-01	1.0	9E-01	Endonuclease activity	Nucleus	Enzyme: Hydrolase
2194	FASN	fatty acid synthase	98	1122	97	1.3	**2E-16**	0.9	**2E-16**	1.5	1E+00	0.9	**2E-16**	0.9	**6E-07**	Catalytic activity	Cytoplasm	Enzyme: Synthase
8539	API5	apoptosis inhibitor 5 isoform a	16	93	16	1.3	**8E-13**	0.8	**2E-13**	1.3	**4E-06**	**0.6**	**2E-09**	0.9	**7E-07**	Molecular function unknown	Nucleus	Unclassified
51079	NDUFA13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	5	25	5	1.3	**1E-04**	0.9	**2E-03**	1.2	3E-01	1.1	1E-01	1.1	2E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
10589	DRAP1	dr1-associated corepressor	4	12	4	1.3	**1E-03**	0.9	**5E-03**	1.4	8E-01	0.8	5E-01	1.0	8E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
3430	IFI35	interferon-induced 35 kDa protein	1	5	1	1.3	1E-01	0.8	1E-01	1.0	1E-01	0.6	9E-02	0.9	2E-01	Molecular function unknown	Cytoplasm	Unclassified
5527	PPP2R5C	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform isoform c	6	26	1	1.3	1E-01	0.8	8E-01	1.1	1E-01	0.9	2E-01	0.8	7E-02	Phosphatase regulator activity	Chromosome;Nucleus	Enzyme regulator
55752	SEPT11	septin-11	10	67	4	1.3	6E-02	1.0	**2E-02**	1.2	7E-01	1.2	6E-02	1.1	2E-01	#N/A	#N/A	#N/A
6128	RPL6	PREDICTED: 60S ribosomal protein L6 isoform X1	18	251	18	1.3	**2E-16**	1.0	**2E-16**	1.1	**8E-06**	0.8	**6E-05**	0.9	**2E-02**	Structural constituent of ribosome	Nucleolus	Ribosomal subunit
10528	NOP56	nucleolar protein 56	19	118	19	1.3	**1E-09**	1.0	**7E-10**	1.2	**2E-05**	1.1	**5E-10**	1.0	3E-01	Molecular function unknown	Nucleolus	Unclassified
23450	SF3B3	splicing factor 3B subunit 3	26	147	26	1.3	**8E-09**	1.0	**6E-09**	1.2	**1E-05**	1.0	**2E-09**	1.0	**1E-02**	Ribonucleoprotein	Nucleus	RNA binding protein
5337;	PLD1	phospholipase D1 isoform b	7	21	6	1.3	**9E-07**	1.0	**3E-07**	1.3	**5E-02**	0.9	**2E-05**	1.0	3E-01	Phosphoric diester hydrolase activity	Cytoplasm;Nucleus	Enzyme: Phosphodiesterase
5393	EXOSC9	exosome complex component RRP45 isoform 1	5	20	5	1.3	**5E-03**	1.1	**5E-03**	1.4	2E-01	0.9	**2E-02**	1.1	**3E-02**	Ribonuclease activity	Nucleolus	Ribonuclease

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
64943	NT5DC2	5'-nucleotidase domain-containing protein 2 isoform 1	6	16	6	1.3	1E-01	1.2	2E-01	1.3	2E-01	1.0	**2E-02**	1.2	6E-02	Molecular function unknown	-	Unclassified
1.01E+08	BCL2L2-PABPN1	BCL2L2-PABPN1 protein	7	37	7	1.3	#N/A	0.9	#N/A	1.2	#N/A	1.0	#N/A	0.9	#N/A	#N/A	#N/A	#N/A
4642	MYO1D	unconventional myosin-Id isoform 1	20	93	20	1.3	**5E-11**	1.0	**3E-12**	1.3	**2E-04**	1.0	**2E-08**	1.0	5E-01	Structural molecule activity	Cytoplasm	Structural protein
10111	RAD50	DNA repair protein RAD50	34	142	34	1.3	**7E-11**	1.0	**7E-15**	1.2	**1E-04**	0.9	**1E-09**	1.0	9E-02	DNA binding	Nucleus	DNA binding protein
284119	PTRF	polymerase I and transcript release factor	13	132	13	1.3	**1E-08**	0.9	**1E-08**	1.0	6E-01	0.8	1E-01	1.1	**1E-05**	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein
1537	CYC1	cytochrome c1, heme protein, mitochondrial	6	30	6	1.3	**1E-04**	1.3	**1E-04**	1.6	**3E-03**	**1.7**	**2E-04**	1.0	5E-01	Molecular function unknown	Mitochondrion	Unclassified
55197	RPRD1A	regulation of nuclear pre-mRNA domain-containing protein 1A isoform 1	6	21	5	1.3	**2E-03**	0.9	**3E-04**	1.3	6E-01	1.0	**1E-02**	1.1	2E-01	Molecular function unknown	Nucleus	Unclassified
79080	CCDC86	coiled-coil domain-containing protein 86	2	12	2	1.3	**1E-02**	1.0	**2E-02**	1.0	5E-01	0.8	9E-01	1.2	**2E-02**	Molecular function unknown	Nucleus	Unclassified
84342	COG8	conserved oligomeric Golgi complex subunit 8	2	10	2	1.3	**3E-02**	1.0	**2E-02**	1.1	2E-01	1.1	5E-02	1.0	9E-02	Transporter activity	Golgi apparatus	Transport/cargo protein
153527	ZMAT2	zinc finger matrin-type protein 2	2	7	2	1.3	1E-01	0.8	9E-02	1.4	2E-01	0.8	4E-01	0.9	3E-01	RNA binding	Nucleus	RNA binding protein
3980	LIG3	DNA ligase 3 isoform alpha	8	24	8	1.3	**1E-02**	1.0	**1E-02**	1.3	**5E-02**	0.9	**1E-03**	1.1	5E-01	DNA ligase activity	Nucleus	DNA ligase
2021	ENDOG	endonuclease G, mitochondrial	1	6	1	1.3	6E-02	0.8	**2E-02**	1.3	**9E-03**	1.1	1E-01	0.7	1E-01	Deoxyribonuclease activity	Mitochondrion	Deoxyribonuclease
5339	PLEC	PREDICTED: plectin isoform X2	278	1689	1	1.3	**2E-16**	1.0	**2E-16**	1.2	**2E-16**	1.2	**2E-16**	1.1	**2E-16**	#N/A	#N/A	#N/A
6793	STK10	serine/threonine-protein kinase 10	16	61	14	1.3	**2E-06**	0.8	**8E-07**	1.2	**4E-02**	1.2	**4E-08**	1.1	1E-01	Protein serine/threonine kinase activity	-	Serine/threonine kinase
80324	PUS1	tRNA pseudouridine synthase A, mitochondrial isoform 1	6	33	6	1.3	**2E-04**	1.0	**9E-05**	1.2	**5E-02**	1.0	**6E-04**	1.0	4E-01	Catalytic activity	Nucleus	Enzyme: Synthase
6166	RPL36AL	60S ribosomal protein L36a-like	6	50	2	1.3	**7E-04**	1.0	**1E-03**	1.1	**3E-02**	0.8	**2E-02**	0.9	**4E-03**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
7706	TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	21	158	21	1.3	**2E-16**	0.9	**2E-16**	1.1	8E-01	1.1	**2E-16**	1.0	3E-01	Transcription factor activity	Nucleus	Transcription factor
27339	PRPF19	pre-mRNA-processing factor 19	13	88	13	1.3	**7E-13**	1.0	**9E-13**	1.3	**2E-04**	0.9	**3E-10**	0.9	1E-01	DNA repair protein	Nucleus	DNA binding protein
23047	PDS5B	sister chromatid cohesion protein PDS5 homolog B	10	37	8	1.3	**2E-07**	1.0	**1E-07**	1.2	**4E-02**	1.1	**7E-05**	1.0	3E-01	Transcription factor activity	Nucleus	Transcription factor
9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4 isoform 2	8	34	2	1.3	**9E-04**	1.0	**1E-03**	1.3	**1E-03**	1.2	**4E-04**	1.0	2E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
51692	CPSF3	cleavage and polyadenylation specificity factor subunit 3	5	22	5	1.3	**7E-03**	0.9	**7E-03**	1.2	5E-01	1.0	**1E-02**	1.0	3E-01	RNA binding	Nucleus	RNA binding protein
79868	ALG13	putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13 isoform 2	3	6	3	1.3	**3E-02**	0.8	2E-01	1.2	7E-01	1.0	2E-01	0.9	5E-01	Molecular function unknown	-	Unclassified
56941	C3orf37; HMCES	PREDICTED: embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein isoform X1	3	4	3	1.3	#N/A	1.3	#N/A	1.5	#N/A	1.7	#N/A	1.3	#N/A	#N/A	#N/A	#N/A
94005	PIGS	GPI transamidase component PIG-S	8	35	8	1.3	**5E-07**	1.0	**3E-07**	1.2	**2E-03**	1.1	**7E-07**	1.0	7E-01	Cytoskeletal anchoring activity	Microsome	Anchor protein
55173	MRPS10	28S ribosomal protein S10, mitochondrial	4	16	4	1.3	**2E-06**	1.2	**4E-04**	1.2	**3E-03**	1.1	**5E-04**	1.1	**3E-04**	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
55339	WDR33	PREDICTED: pre-mRNA 3' end processing protein WDR33 isoform X1	4	15	4	1.3	**3E-04**	0.9	**4E-05**	1.1	6E-01	0.8	2E-01	0.9	4E-01	Molecular function unknown	Nucleus	Unclassified
219988	PATL1	protein PAT1 homolog 1	7	33	7	1.3	**5E-04**	0.8	**3E-03**	1.2	**5E-02**	0.9	**1E-02**	1.0	6E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
81844	TRIM56	PREDICTED: E3 ubiquitin-protein ligase TRIM56 isoform X1	5	21	5	1.3	**2E-03**	0.9	**1E-03**	1.3	8E-01	1.0	**1E-02**	0.9	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
3482	IGF2R	cation-independent mannose-6-phosphate receptor	23	81	23	1.3	**2E-13**	0.9	**4E-12**	1.1	9E-01	0.8	**5E-03**	1.0	1E-01	Receptor activity	Plasma membrane	Cell surface receptor
10146	G3BP1	PREDICTED: ras GTPase-activating protein-binding protein 1 isoform X1	13	132	12	1.3	**1E-09**	0.8	**2E-10**	1.1	**5E-04**	0.7	**5E-04**	0.9	**3E-04**	Ribonuclease activity;RNA binding	Cytosol	RNA binding protein;Ribonuclease
4267	CD99	CD99 antigen isoform a	2	16	2	1.3	**6E-03**	0.8	**1E-02**	0.9	1E-01	0.7	2E-01	1.6	3E-01	Molecular function unknown	Integral to membrane	Unclassified
9329	GTF3C4	general transcription factor 3C polypeptide 4	7	17	7	1.3	**9E-03**	0.8	**8E-03**	1.1	**2E-02**	0.9	2E-01	1.0	6E-01	Transcription factor activity	Nucleus	Transcription factor
6256	RXRA	retinoic acid receptor RXR-alpha isoform a	2	8	2	1.3	**4E-02**	0.9	**1E-02**	1.2	6E-01	0.8	3E-01	1.0	2E-01	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor
2908	NR3C1	glucocorticoid receptor isoform alpha	3	12	3	1.3	8E-02	0.8	**4E-02**	1.1	3E-01	0.8	6E-01	0.8	2E-01	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor;Transcription factor
80789	INTS5	integrator complex subunit 5	3	9	3	1.3	1E-01	0.8	6E-02	1.3	3E-01	0.8	5E-01	0.9	1E-01	Protein binding	Nucleus	Unclassified
2197	FAU	ubiquitin-like protein fubi and ribosomal protein S30	1	18	1	1.3	**2E-03**	1.0	**6E-03**	1.0	**3E-02**	**0.6**	**1E-02**	0.9	**4E-02**	Ubiquitin-specific protease activity	Ribosome	Ubiquitin proteasome system protein

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
11183	MAP4K5	PREDICTED: mitogen-activated protein kinase kinase kinase kinase 5 isoform X1	4	12	4	1.3	**2E-03**	0.9	**6E-03**	1.0	4E-01	0.9	1E-01	1.1	6E-02	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
4731	NDUFV3	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial isoform a	6	16	6	1.3	9E-02	0.8	9E-02	1.1	3E-01	0.6	3E-01	1.0	9E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
2549	GAB1	GRB2-associated-binding protein 1 isoform a	3	10	3	1.3	1E-01	1.5	1E-01	**1.5**	**5E-03**	1.3	7E-02	1.3	5E-02	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
29894;	CPSF1	cleavage and polyadenylation specificity factor subunit 1	23	51	10	1.3	**1E-09**	1.0	**3E-09**	1.2	**4E-06**	0.9	**9E-06**	1.1	2E-01	RNA binding	Nucleus	RNA binding protein
10412	NSA2	ribosome biogenesis protein NSA2 homolog isoform 1	6	29	6	1.3	**8E-05**	0.8	**1E-04**	1.0	**4E-03**	**0.6**	**1E-02**	0.9	**7E-04**	Molecular function unknown	Nucleus	Unclassified
4809;	SNU13	NHP2-like protein 1*gi|4826860|ref|NP_004999.1| NHP2-like protein 1	4	11	4	1.3	**1E-03**	1.1	**2E-04**	1.2	**2E-02**	1.1	**1E-03**	0.9	1E-01	#N/A	#N/A	#N/A
7536	SF1	splicing factor 1 isoform 6	8	38	8	1.3	**8E-03**	0.8	**4E-03**	1.3	**2E-02**	0.7	8E-01	1.0	3E-01	RNA binding	Nucleus;Cytoplasm	RNA binding protein
90624	LYRM7	complex III assembly factor LYRM7 isoform 1	4	12	4	1.3	**2E-02**	**1.6**	**2E-02**	1.4	**2E-02**	1.2	**4E-02**	1.3	**4E-03**	Molecular function unknown	-	Unclassified
55100	WDR70	WD repeat-containing protein 70	2	5	2	1.3	7E-02	0.9	7E-02	1.1	9E-01	0.6	5E-02	0.7	**5E-03**	Molecular function unknown	Cytoplasm	Unclassified
8467	SMARCA5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	17	83	17	1.3	**8E-11**	0.9	**2E-11**	1.2	9E-02	0.9	**2E-03**	1.0	1E-01	DNA binding	Nucleus	DNA binding protein
23636	NUP62	nuclear pore glycoprotein p62	7	52	7	1.3	**5E-05**	1.1	**1E-05**	1.3	**3E-03**	1.3	**2E-05**	1.1	1E-01	Transporter activity	Nuclear membrane	Transport/cargo protein
51574	LARP7	la-related protein 7 isoform 2	10	30	10	1.3	**3E-03**	1.0	**2E-03**	1.3	**4E-02**	1.2	**2E-03**	1.0	8E-01	Molecular function unknown	-	Unclassified
10450	PPIE	peptidyl-prolyl cis-trans isomerase E isoform 1	4	16	3	1.3	7E-02	1.2	**2E-02**	1.5	2E-01	1.6	1E-01	1.3	4E-01	Isomerase activity;RNA binding	Nucleus	Enzyme: Isomerase;RNA binding protein
10556	RPP30	PREDICTED: ribonuclease P protein subunit p30 isoform X1	6	21	6	1.3	1E-01	1.0	6E-02	1.1	2E-01	0.8	8E-01	1.1	1E-01	Ribonuclease activity	Nucleus	Ribonuclease
4722	NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	8	46	8	1.3	**1E-07**	0.9	**5E-07**	1.2	3E-01	0.9	**4E-06**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
84717	HDGFRP2	hepatoma-derived growth factor-related protein 2 isoform 1	14	54	13	1.3	**3E-06**	1.0	**5E-08**	1.3	1E-01	0.9	**8E-04**	1.1	2E-01	#N/A	#N/A	#N/A
26354	GNL3	guanine nucleotide-binding protein-like 3 isoform 1	11	44	10	1.3	**2E-05**	0.9	**4E-04**	0.9	9E-01	**0.5**	**5E-03**	1.1	1E-01	GTP binding	Nucleolus	Cell cycle control protein
1479	CSTF3	cleavage stimulation factor subunit 3 isoform 1	16	59	16	1.3	**2E-05**	0.9	**1E-05**	1.2	8E-01	0.9	**9E-08**	1.0	3E-01	RNA binding	Nucleus	RNA binding protein
60488	MRPS35	28S ribosomal protein S35, mitochondrial isoform 1	6	24	6	1.3	**5E-05**	1.1	**2E-04**	1.3	**2E-02**	1.0	**3E-04**	1.0	8E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
26091	HERC4	probable E3 ubiquitin-protein ligase HERC4 isoform a	13	40	13	1.3	**1E-04**	1.0	**1E-04**	1.2	1E-01	1.2	**5E-04**	0.9	1E-01	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
9444	QKI	protein quaking isoform 1	5	13	4	1.3	**3E-04**	1.2	**5E-03**	1.1	**2E-02**	1.0	**6E-03**	1.3	3E-01	RNA binding	Cytoplasm	RNA binding protein
4725	NDUFS5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	4	22	4	1.3	**6E-04**	1.0	**9E-04**	0.9	5E-01	0.8	7E-01	1.0	4E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
5818	PVRL1; NECTIN1	nectin-1 isoform 1	3	14	3	1.3	**3E-03**	0.8	**5E-04**	1.4	6E-02	0.9	5E-01	0.9	3E-01	#N/A	#N/A	#N/A
5339	PLEC	plectin isoform 1a	282	3377	2	1.3	**2E-16**	1.0	**2E-16**	1.3	**2E-16**	1.4	**2E-16**	1.2	**2E-16**	#N/A	#N/A	#N/A
6633	SNRPD2	small nuclear ribonucleoprotein Sm D2 isoform 1	9	91	9	1.3	**1E-09**	0.9	**1E-09**	1.2	3E-01	0.8	**9E-03**	0.9	**3E-03**	RNA binding	Nucleus	RNA binding protein
2521	FUS	RNA-binding protein FUS isoform 1	9	81	6	1.3	**6E-09**	0.9	**7E-10**	1.3	9E-01	0.8	9E-01	0.9	5E-02	Nucleocytoplasmic transporter activity	Nucleus	RNA binding protein
5928	RBBP4	histone-binding protein RBBP4 isoform a	8	44	4	1.3	**6E-03**	0.9	**1E-03**	1.2	3E-01	0.9	**8E-03**	1.0	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9967	THRAP3	thyroid hormone receptor-associated protein 3	26	129	26	1.3	**3E-11**	1.0	**6E-13**	1.2	**2E-05**	0.9	**5E-07**	1.0	3E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
10658	CELF1	CUGBP Elav-like family member 1 isoform 4	5	34	5	1.3	**3E-06**	0.9	**7E-06**	1.2	2E-01	0.9	**5E-03**	0.9	8E-01	#N/A	#N/A	#N/A
51729	WBP11	WW domain-binding protein 11	10	48	10	1.3	**8E-05**	0.9	**8E-06**	1.2	8E-02	0.7	2E-01	1.1	2E-01	RNA binding	Nucleus	RNA binding protein
9136	RRP9	U3 small nucleolar RNA-interacting protein 2	8	34	8	1.3	**1E-03**	0.8	**8E-04**	1.2	6E-01	**0.6**	**4E-03**	1.0	8E-01	Ribonucleoprotein	Nucleolus	RNA binding protein
23070	CMTR1; FTSJD2	cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	4	20	3	1.3	**2E-03**	1.0	**3E-03**	1.4	3E-01	1.0	**3E-03**	1.0	5E-01	#N/A	#N/A	#N/A
3181	HNRNPA2B1	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X1	20	333	16	1.3	**3E-15**	0.9	**2E-16**	1.2	6E-01	0.8	**3E-02**	1.0	2E-01	Transcription factor binding;RNA binding	Nucleus	Ribonucleoprotein;RNA binding protein
7155	TOP2B	DNA topoisomerase 2-beta	21	78	11	1.3	**1E-05**	1.0	**2E-06**	1.3	6E-02	0.9	**1E-04**	1.0	**3E-02**	DNA topoisomerase activity	Nucleus	Enzyme: Topoisomerase
124245	ZC3H18	zinc finger CCCH domain-containing protein 18 isoform 1	12	47	12	1.3	**5E-03**	1.0	**4E-03**	1.3	5E-02	1.0	**6E-04**	1.0	7E-01	Molecular function unknown	-	Unclassified
55973	BCAP29	PREDICTED: B-cell receptor-associated protein 29 isoform X1	8	36	8	1.3	**7E-03**	1.0	**4E-03**	1.2	1E-01	1.4	**1E-02**	1.1	5E-02	Molecular function unknown	Endoplasmic reticulum membrane	Integral membrane protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
51075	**TMX2**	**thioredoxin-related transmembrane protein 2 isoform 1**	6	18	6	1.3	**2E-02**	1.2	**7E-03**	1.1	6E-02	1.2	**2E-03**	1.1	3E-01	Molecular function unknown	-	Integral membrane protein
6155	**RPL27**	**60S ribosomal protein L27**	9	124	9	1.3	**3E-08**	1.0	**5E-09**	1.1	**9E-06**	0.8	6E-02	1.0	8E-01	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
4076	**CAPRIN1**	**caprin-1 isoform 1**	8	42	8	1.3	**3E-05**	0.8	**6E-06**	1.1	**1E-02**	0.7	6E-02	0.8	**5E-03**	Molecular function unknown	Plasma membrane	Integral membrane protein
2591	**GALNT3**	**PREDICTED: polypeptide N-acetylgalactosaminyltransferase 3 isoform X1**	10	32	9	1.3	**1E-03**	0.9	**5E-04**	1.3	3E-01	1.0	**1E-04**	1.1	2E-01	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase
81572	**PDRG1**	**PREDICTED: p53 and DNA damage-regulated protein 1 isoform X1**	3	9	3	1.3	**3E-02**	1.0	**2E-02**	1.3	3E-01	0.8	2E-01	1.0	4E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
54878	**DPP8**	**PREDICTED: dipeptidyl peptidase 8 isoform X1**	3	10	3	1.3	**3E-02**	1.0	**5E-02**	1.1	9E-01	1.1	**3E-02**	1.2	1E-01	Aminopeptidase activity	Cytoplasm	Aminopeptidase
8880	**FUBP1**	**PREDICTED: far upstream element-binding protein 1 isoform X4**	22	90	16	1.3	**2E-12**	0.9	**1E-11**	1.2	5E-01	0.7	**8E-03**	0.9	**2E-03**	Transcription regulator activity	Nucleus	Transcription regulatory protein
7105	**TSPAN6**	**tetraspanin-6 isoform a**	3	19	3	1.3	**3E-04**	**0.6**	**6E-04**	1.2	**2E-04**	1.3	**1E-04**	0.9	2E-01	Receptor activity	Plasma membrane	Cell surface receptor
9360	**PPIG**	**PREDICTED: peptidyl-prolyl cis-trans isomerase G isoform X1**	8	27	8	1.3	**3E-02**	1.0	**3E-02**	1.2	**5E-03**	1.1	**2E-02**	1.0	9E-01	Isomerase activity	Nucleus	Enzyme: Isomerase
55226	**NAT10**	**N-acetyltransferase 10 isoform a**	26	124	26	1.3	**1E-08**	0.9	**8E-11**	1.3	**3E-02**	0.8	**9E-03**	0.9	**3E-02**	Acyltransferase activity	Nucleus	Enzyme: Acyltransferase
10657	**KHDRBS1**	**KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 1**	7	69	7	1.3	**2E-07**	0.9	**8E-08**	1.3	7E-02	1.0	**2E-07**	1.0	9E-01	RNA binding	Nucleus	RNA binding protein
839	**CASP6**	**caspase-6 isoform alpha preproprotein**	6	34	5	1.3	**3E-06**	0.8	**7E-06**	1.3	**5E-02**	1.0	**9E-04**	0.9	4E-01	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
79869	**CPSF7**	**cleavage and polyadenylation specificity factor subunit 7 isoform 1**	8	40	8	1.3	**1E-04**	1.0	**6E-05**	1.3	**3E-03**	0.8	**6E-03**	0.9	**7E-03**	Molecular function unknown	-	Unclassified
1777	**DNASE2**	**deoxyribonuclease-2-alpha**	5	25	5	1.3	**2E-04**	**0.7**	**3E-04**	1.4	**1E-04**	0.8	**2E-02**	0.9	**1E-02**	Deoxyribonuclease activity	Lysosome	Deoxyribonuclease
55168	**MRPS18A**	**28S ribosomal protein S18a, mitochondrial isoform 1**	2	6	2	1.3	**2E-02**	1.0	**3E-03**	1.2	**3E-02**	1.1	**1E-02**	1.0	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
8624	**PSMG1**	**proteasome assembly chaperone 1 isoform a**	4	12	4	1.3	1E-01	1.1	1E-01	1.4	1E-01	0.9	1E-01	1.1	2E-01	Molecular function unknown	Plasma membrane	Unclassified
6159	**RPL29**	**60S ribosomal protein L29**	4	47	4	1.3	**5E-07**	0.9	**9E-08**	1.1	3E-01	**0.7**	**2E-02**	0.8	**2E-03**	Structural constituent of ribosome	Plasma membrane	Ribosomal subunit
25926	**NOL11**	**nucleolar protein 11 isoform 1**	9	29	9	1.3	**4E-04**	0.9	**1E-04**	1.2	4E-01	0.8	2E-01	1.0	2E-01	Molecular function unknown	Nucleolus	Unclassified
374291	**NDUFS7**	**NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial**	4	16	4	1.3	**2E-03**	0.8	**1E-05**	1.1	6E-02	0.9	**3E-02**	0.9	3E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
6646	**SOAT1**	**PREDICTED: sterol O-acyltransferase 1 isoform X1**	4	14	4	1.3	**2E-02**	0.8	**5E-02**	1.2	4E-01	0.7	3E-01	1.3	**4E-02**	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase
79577	**CDC73**	**parafibromin**	7	25	7	1.3	**2E-04**	0.8	**1E-03**	1.4	**4E-02**	0.9	1E-01	0.9	**4E-02**	Molecular function unknown	Nucleolus;Nucleus	Unclassified
6733	**SRPK2**	**SRSF protein kinase 2 isoform a**	11	43	7	1.3	**5E-04**	1.0	**6E-04**	1.0	4E-01	1.0	**5E-02**	0.9	9E-02	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
112574	**SNX18**	**sorting nexin-18 isoform b**	4	16	3	1.3	**3E-03**	1.0	**2E-03**	1.3	5E-01	1.1	**6E-04**	0.9	2E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
51755	**CDK12**	**cyclin-dependent kinase 12 isoform 1**	6	28	5	1.3	**9E-03**	1.2	**2E-02**	1.1	2E-01	1.2	**4E-02**	1.1	2E-01	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
2936	**GSR**	**glutathione reductase, mitochondrial isoform 1**	4	12	4	1.3	**3E-02**	1.1	**2E-02**	1.1	**2E-02**	0.9	**5E-02**	0.9	**9E-03**	Catalytic activity	Mitochondrion	Enzyme: Reductase
8896	**BUD31**	**protein BUD31 homolog**	6	25	6	1.3	5E-02	1.1	**4E-02**	1.2	2E-01	1.0	2E-01	1.1	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
2068	**ERCC2**	**TFIIH basal transcription factor complex helicase XPD subunit isoform 1**	3	16	3	1.3	5E-02	1.0	6E-02	1.5	3E-01	1.0	1E-01	1.1	4E-01	DNA repair protein	Nucleus	DNA repair protein
9826	**ARHGEF11**	**rho guanine nucleotide exchange factor 11 isoform 2**	3	6	3	1.3	2E-01	0.9	**4E-02**	1.1	6E-01	1.1	**2E-03**	0.9	7E-01	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor
64969	**MRPS5**	**28S ribosomal protein S5, mitochondrial**	8	40	8	1.3	**1E-04**	1.2	**5E-06**	1.2	**8E-04**	1.0	**9E-05**	0.9	4E-01	Ribonucleoprotein	Mitochondrion	RNA binding protein
9533	**POLR1C**	**DNA-directed RNA polymerases I and III subunit RPAC1**	5	24	5	1.3	**1E-03**	0.9	**5E-04**	1.3	7E-01	0.9	**5E-04**	0.9	9E-02	DNA-directed RNA polymerase activity	Nucleolus	RNA polymerase
6232	**RPS27**	**40S ribosomal protein S27**	4	42	2	1.3	**2E-03**	0.9	**5E-03**	1.0	6E-01	0.8	**5E-02**	0.9	9E-02	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit
205428	**C3orf58**	**deleted in autism protein 1 isoform a**	2	8	2	1.3	**3E-02**	1.2	5E-02	1.4	3E-01	1.2	**5E-02**	1.3	4E-01	Molecular function unknown	-	Unclassified
55072	**RNF31**	**E3 ubiquitin-protein ligase RNF31**	4	5	4	1.3	**4E-02**	1.1	1E-01	1.3	4E-01	**1.6**	**3E-02**	1.3	1E-01	Molecular function unknown	-	Unclassified
26145	**IRF2BP1**	**interferon regulatory factor 2-binding protein 1**	3	8	3	1.3	2E-01	1.2	**6E-04**	1.4	3E-01	1.0	**3E-02**	1.4	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
5635	**PRPSAP1**	**phosphoribosyl pyrophosphate synthase-associated protein 1**	7	28	5	1.3	**2E-05**	1.1	**5E-05**	1.4	3E-01	1.1	**4E-03**	1.0	3E-01	Enzyme regulator activity	Cytoplasm	Regulatory/other subunit

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
6629	SNRPB2	U2 small nuclear ribonucleoprotein B''*gi|4507123|ref|NP_003083.1| U2 small nuclear ribonucleoprotein B''	6	44	4	1.3	**6E-03**	0.9	**3E-03**	1.3	5E-02	0.8	**6E-03**	1.0	7E-01	RNA binding	Nucleus	Ribonucleoprotein
9635	CLCA2	calcium-activated chloride channel regulator 2	6	21	6	1.3	**6E-03**	0.9	2E-01	0.7	3E-01	**0.4**	**7E-03**	0.7	**8E-03**	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
79691	QTRTD1; QTRT2	queuine tRNA-ribosyltransferase subunit QTRTD1 isoform 2	3	12	3	1.3	**1E-02**	0.9	**7E-03**	1.2	9E-01	1.1	6E-02	1.0	6E-01	#N/A	#N/A	#N/A
64425	POLR1E	DNA-directed RNA polymerase I subunit RPA49 isoform 1	6	26	6	1.3	**2E-04**	0.7	**2E-05**	1.2	**2E-03**	0.7	2E-01	1.0	7E-01	Transcription factor activity	Nucleolus	Transcription factor
9584	RBM39	RNA-binding protein 39 isoform a	9	49	9	1.3	**2E-08**	0.9	**2E-09**	1.4	7E-01	1.0	**4E-07**	1.0	5E-01	RNA binding;Transcription regulator activity	Nucleus	RNA binding protein;Transcription regulatory protein
11157	LSM6	U6 snRNA-associated Sm-like protein LSm6	4	17	4	1.3	**5E-06**	0.9	**2E-05**	1.5	3E-01	1.1	**7E-04**	1.0	8E-01	RNA binding	Cytoplasm	RNA binding protein
10954	PDIA5	protein disulfide-isomerase A5	8	39	8	1.3	**9E-06**	0.9	**5E-06**	1.4	5E-01	1.1	**1E-05**	1.0	8E-02	Chaperone activity	Endoplasmic reticulum	Chaperone
5198	PFAS	phosphoribosylformylglycinamidine synthase	11	51	11	1.3	**2E-05**	0.8	**3E-06**	1.3	2E-01	1.0	3E-01	1.0	4E-01	Ligase activity	Cytoplasm	Enzyme: Synthase
3150	HMGN1	non-histone chromosomal protein HMG-14	7	50	7	1.3	**7E-05**	1.0	**2E-05**	1.3	**1E-03**	0.8	8E-02	1.0	4E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
79001	VKORC1	PREDICTED: vitamin K epoxide reductase complex subunit 1 isoform X1	2	12	2	1.3	**4E-03**	**1.6**	**2E-03**	1.3	**4E-02**	**2.1**	**2E-02**	1.4	9E-02	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase;Coagulation factor
84261	FBXW9	F-box/WD repeat-containing protein 9	3	6	2	1.3	**3E-02**	1.3	**3E-04**	1.7	6E-02	1.1	7E-02	1.0	9E-01	Molecular function unknown	-	Unclassified
23476	BRD4	PREDICTED: bromodomain-containing protein 4 isoform X1	6	19	5	1.3	**3E-02**	0.9	**1E-02**	1.2	4E-01	0.9	**1E-03**	1.0	9E-01	Chromatin binding	Nucleus;Cytoplasm	Cell cycle control protein
7464	CORO2A	PREDICTED: coronin-2A isoform X1	12	64	11	1.3	**2E-10**	0.9	**3E-10**	1.4	8E-01	1.2	**6E-07**	1.1	**3E-02**	Molecular function unknown	Nucleus	Unclassified
6118	RPA2	replication protein A 32 kDa subunit isoform 3	4	18	4	1.3	**8E-03**	1.0	**2E-03**	1.3	2E-01	0.8	3E-01	0.8	**2E-03**	DNA binding	Nucleus	DNA binding protein
10153	CEBPZ	CCAAT/enhancer-binding protein zeta	13	55	13	1.3	**6E-06**	0.8	**4E-05**	1.3	7E-02	0.7	9E-01	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
65117;	RSRC2	arginine/serine-rich coiled-coil protein 2	8	19	2	1.3	**4E-05**	0.9	**5E-06**	1.4	**9E-05**	1.0	**2E-05**	0.9	2E-01	Molecular function unknown;Transcription factor activity	Nucleus	Unclassified
23154	NCDN	neurochondrin isoform 1	3	6	3	1.3	**5E-02**	1.0	**2E-03**	1.2	9E-01	0.8	4E-01	0.8	7E-02	Molecular function unknown	Cytoplasm	Unclassified
22934	LOC101060545; RPIA	ribose-5-phosphate isomerase	1	5	1	1.3	**5E-02**	0.9	1E-01	1.2	1E+00	0.9	4E-01	1.0	3E-01	#N/A	#N/A	#N/A
4436	MSH2	DNA mismatch repair protein Msh2 isoform 1	9	31	9	1.3	**5E-05**	0.9	**5E-05**	1.3	7E-01	0.8	5E-01	1.1	1E-01	DNA repair protein	Nucleus	DNA repair protein
9295	SRSF11	serine/arginine-rich splicing factor 11 isoform 1	4	22	4	1.3	**6E-04**	0.9	**9E-05**	1.3	1E-01	1.0	**2E-04**	1.0	5E-01	#N/A	#N/A	#N/A
92745	SLC38A5	sodium-coupled neutral amino acid transporter 5	3	11	3	1.3	**1E-02**	0.9	**3E-02**	1.0	5E-01	0.7	4E-01	1.1	6E-02	Transporter activity	Plasma membrane	Transport/cargo protein
23378	RRP8	ribosomal RNA-processing protein 8	6	17	6	1.3	**2E-02**	1.1	**2E-02**	1.5	**1E-02**	0.9	**3E-02**	1.1	2E-01	Methyltransferase activity	Nucleolus	Enzyme: Methyltransferase
123207	C15orf40	UPF0235 protein C15orf40 isoform b	2	10	2	1.3	6E-02	1.2	5E-02	1.4	1E-01	1.2	6E-02	0.9	2E-01	Molecular function unknown	-	Unclassified
85439	STON2	stonin-2 isoform 2	3	7	3	1.3	9E-02	0.7	2E-01	1.1	8E-01	0.6	4E-01	1.1	3E-01	Molecular function unknown	Plasma membrane	Unclassified
57018	CCNL1	cyclin-L1	2	6	2	1.3	5E-02	1.1	1E-01	1.2	**8E-03**	1.2	2E-01	1.2	1E-01	RNA binding	Nucleus	RNA binding protein
25929	GEMIN5	gem-associated protein 5 isoform 1	15	51	15	1.3	**2E-10**	0.8	**6E-11**	1.2	**3E-03**	0.8	**1E-02**	1.0	5E-01	Ribonucleoprotein	Cytoplasm	Unclassified
51236	FAM203B; FAM203A; HGH1	protein HGH1 homolog	6	24	6	1.3	**4E-04**	0.8	**3E-04**	1.1	3E-01	0.9	**2E-02**	0.9	7E-01	#N/A	#N/A	#N/A
112970	KTI12	protein KTI12 homolog	4	16	4	1.3	**2E-03**	0.8	**2E-03**	1.2	2E-01	1.1	**2E-03**	1.0	8E-01	ATP binding	-	Unclassified
54606	DDX56	probable ATP-dependent RNA helicase DDX56 isoform 1	5	17	5	1.3	**2E-03**	0.8	**3E-02**	1.1	7E-02	**0.6**	**4E-02**	1.0	6E-01	Helicase activity	Nucleolus	RNA helicase
4736	RPL10A	60S ribosomal protein L10a	9	150	9	1.3	**2E-16**	1.0	**1E-13**	1.1	**2E-03**	0.7	**2E-02**	1.0	7E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
80224	NUBPL	iron-sulfur protein NUBPL isoform 1	1	6	1	1.3	**5E-02**	1.2	**2E-02**	1.4	1E-01	1.2	**3E-02**	**1.5**	**8E-05**	Molecular function unknown	-	Unclassified
6726; 653226	SRP9; SRP9P1	signal recognition particle 9 kDa protein isoform 2	5	48	5	1.3	**2E-04**	0.8	**3E-04**	1.5	**2E-02**	0.8	2E-01	0.8	**9E-04**	#N/A	#N/A	#N/A
5723	PSPH	PREDICTED: phosphoserine phosphatase isoform X1	6	30	6	1.3	**9E-03**	0.8	**1E-02**	1.1	**3E-02**	0.8	2E-01	1.0	4E-01	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase
24142	NAT6	N-acetyltransferase 6 isoform 1	2	12	2	1.3	**5E-02**	1.1	**8E-03**	1.8	1E-01	1.3	**3E-03**	1.0	4E-01	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase
65008	MRPL1	PREDICTED: 39S ribosomal protein L1, mitochondrial isoform X1	6	24	6	1.3	**9E-03**	1.0	**2E-03**	1.3	6E-02	1.0	**1E-02**	1.1	5E-02	Structural constituent of ribosome	Mitochondrion	RNA binding protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
840	CASP7	caspase-7 isoform e	4	10	4	1.3	1E-01	0.7	**3E-02**	0.9	1E-01	0.7	5E-01	0.9	2E-01	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
84285	EIF1AD	probable RNA-binding protein EIF1AD*gi|335334939|ref|NP_001229411.1| probable RNA-binding protein EIF1AD*gi|335334941|ref|NP_001229410.1| probable RNA-binding protein EIF1AD*gi|335334945|ref|NP_001229412.1| probable RNA-binding protein EIF1AD*gi|335334947|ref|NP_001229413.1| probable RNA-binding protein EIF1AD*gi|335334949|ref|NP_001229414.1| probable RNA-binding protein EIF1AD*gi|335334951|ref|NP_001229415.1| probable RNA-binding protein EIF1AD	3	8	3	1.3	1E-01	0.9	1E-01	1.2	7E-01	1.0	9E-02	1.0	3E-01	Molecular function unknown	-	Unclassified
2673	GFPT1	glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 isoform 1	26	175	26	1.3	**4E-16**	0.8	**2E-16**	1.2	**3E-10**	1.4	**2E-16**	1.0	**5E-02**	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase
3187	HNRNPH1	heterogeneous nuclear ribonucleoprotein H*gi|5031753|ref|NP_005511.1| heterogeneous nuclear ribonucleoprotein H	11	186	5	1.3	**2E-11**	0.9	**8E-12**	1.3	2E-01	0.9	**1E-11**	1.0	5E-01	Ribonucleoprotein	Nucleus	Ribonucleoprotein
2091	FBL	rRNA 2'-O-methyltransferase fibrillarin	11	98	11	1.3	**1E-10**	1.0	**9E-08**	1.3	**2E-04**	1.0	**1E-09**	1.0	**2E-02**	Ribonucleoprotein	Nucleolus	Ribonucleoprotein
6154	RPL26	PREDICTED: 60S ribosomal protein L26 isoform X1	8	107	2	1.3	**4E-10**	1.1	**2E-09**	1.0	**5E-06**	0.8	**3E-04**	0.9	**4E-02**	Structural constituent of ribosome	Ribosome	Ribosomal subunit
5589	PRKCSH	glucosidase 2 subunit beta isoform 3*gi|574280236|ref|NP_001276033.1| glucosidase 2 subunit beta isoform 3	15	139	15	1.3	**5E-08**	1.1	**3E-09**	1.3	**1E-04**	1.2	**2E-10**	1.0	4E-01	Glucosidase activity	Endoplasmic reticulum	Regulatory/other subunit
55622	TTC27	tetratricopeptide repeat protein 27 isoform 1	4	16	4	1.3	**5E-04**	0.9	**1E-05**	1.2	2E-01	0.9	**5E-03**	1.0	9E-01	Molecular function unknown	-	Unclassified
51639	SF3B14; SF3B6	splicing factor 3B subunit 6	3	15	3	1.3	**1E-02**	1.0	**1E-02**	1.2	3E-01	0.9	8E-02	1.2	6E-02	#N/A	#N/A	#N/A
10541	ANP32B	acidic leucine-rich nuclear phosphoprotein 32 family member B	9	106	4	1.3	**1E-09**	0.9	**8E-10**	1.2	3E-01	0.9	**9E-08**	1.1	3E-01	Molecular function unknown	Nucleus	Unclassified
3157	HMGCS1	hydroxymethylglutaryl-CoA synthase, cytoplasmic	16	94	16	1.3	**4E-08**	0.8	**2E-08**	1.4	**1E-04**	**0.7**	**2E-03**	0.9	**4E-06**	CoA-ligase activity	Cytoplasm	Enzyme: Synthase
55696	RBM22	pre-mRNA-splicing factor RBM22	9	41	9	1.3	**4E-06**	0.9	**5E-06**	1.2	8E-01	0.9	**3E-04**	1.0	6E-01	Molecular function unknown	-	Unclassified
84545	MRPL43	39S ribosomal protein L43, mitochondrial isoform d	6	29	6	1.3	**1E-05**	1.1	**4E-05**	1.2	**2E-03**	1.0	**1E-03**	1.1	3E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
1810	DR1	protein Dr1	2	10	2	1.3	**4E-03**	1.0	**4E-03**	1.4	4E-01	0.8	8E-01	1.0	1E+00	Transcription regulator activity	Nucleus	Transcription regulatory protein
54840	APTX	aprataxin isoform e	1	5	1	1.3	1E-01	1.0	8E-02	1.1	**3E-03**	0.7	1E-01	0.9	2E-01	Protein binding;Hydrolase activity	Nucleoplasm	DNA repair protein
857	CAV1	caveolin-1 isoform alpha	11	134	11	1.3	**7E-14**	0.9	**7E-07**	0.8	**3E-02**	**0.6**	**3E-08**	1.1	**9E-03**	Structural molecule activity	Plasma membrane	Structural protein
9982	FGFBP1	fibroblast growth factor-binding protein 1	7	72	7	1.3	**3E-09**	0.9	**3E-09**	1.4	1E-01	0.9	**2E-06**	1.1	**1E-03**	Chaperone activity	Extracellular	Chaperone
2274	FHL2	four and a half LIM domains protein 2	8	45	8	1.3	**4E-05**	1.0	**1E-05**	0.9	**1E-02**	0.7	7E-02	0.9	**2E-02**	Protein binding	Nucleus	Adapter molecule
26119	LDLRAP1	low density lipoprotein receptor adapter protein 1	3	10	3	1.3	6E-02	1.0	9E-02	1.4	9E-01	1.0	1E-01	1.1	9E-01	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule
8878	SQSTM1	sequestosome-1 isoform 1	3	11	3	1.3	2E-01	0.9	1E-01	1.1	3E-01	1.1	1E-01	1.0	3E-01	Ubiquitin-specific protease activity	Cytoplasm;Nucleus	Ubiquitin proteasome system protein
27089	UQCRQ	cytochrome b-c1 complex subunit 8	3	24	3	1.3	**5E-03**	0.9	**3E-03**	0.9	2E-01	0.7	1E-01	0.9	5E-02	Molecular function unknown	-	Unclassified
23167	EFR3A	protein EFR3 homolog A	2	10	2	1.3	5E-02	1.2	**1E-02**	1.3	8E-02	1.0	5E-02	1.0	3E-01	Molecular function unknown	-	Unclassified
3726	JUNB	transcription factor jun-B	7	46	6	1.3	**4E-04**	1.2	**5E-05**	**1.6**	**1E-04**	1.0	**3E-04**	1.2	**8E-04**	Transcription factor activity	Nucleus	Transcription factor
8323	FZD6	frizzled-6 isoform a	3	12	3	1.3	**3E-02**	1.0	**2E-02**	1.4	6E-01	1.1	2E-01	1.1	2E-01	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor
22827	PUF60	poly(U)-binding-splicing factor PUF60 isoform b	15	74	15	1.3	**1E-12**	0.9	**8E-12**	1.2	1E-01	0.8	2E-01	0.9	**5E-04**	RNA binding	Nucleus	RNA binding protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
26121	**PRPF31**	**PREDICTED: U4/U6 small nuclear ribonucleoprotein Prp31 isoform X1**	10	42	10	1.3	**1E-04**	0.9	**7E-05**	1.2	5E-01	1.0	**3E-03**	1.0	6E-01	RNA binding	Nucleus	RNA binding protein
4522	**MTHFD1**	**C-1-tetrahydrofolate synthase, cytoplasmic**	39	230	38	1.3	**2E-16**	1.0	**2E-16**	1.3	**2E-09**	1.1	**2E-16**	1.0	1E-01	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase
26227	**PHGDH**	**D-3-phosphoglycerate dehydrogenase**	19	183	19	1.3	**2E-16**	0.7	**2E-16**	1.4	**2E-09**	1.3	**2E-16**	0.9	**5E-05**	Catalytic activity	Extracellular	Enzyme: Dehydrogenase
9987	**HNRNPDL; HNRPDL**	**heterogeneous nuclear ribonucleoprotein D-like isoform a**	13	127	11	1.3	**4E-06**	0.9	**2E-06**	1.3	1E-01	0.8	1E-01	0.9	**3E-03**	#N/A	#N/A	#N/A
84154	**RPF2**	**ribosome production factor 2 homolog isoform 1**	4	31	4	1.3	**3E-04**	1.0	**1E-04**	1.1	4E-01	0.6	1E-01	1.1	7E-02	Molecular function unknown	Nucleolus	Unclassified
51303	**FKBP11**	**peptidyl-prolyl cis-trans isomerase FKBP11 isoform 1**	2	12	2	1.3	**6E-03**	0.9	**4E-03**	1.4	4E-01	1.2	**1E-03**	1.1	7E-01	Isomerase activity	Integral to membrane	Enzyme: Isomerase
29997	**GLTSCR2**	**glioma tumor suppressor candidate region gene 2 protein**	1	8	1	1.3	**7E-03**	0.7	**2E-02**	1.0	**1E-02**	0.6	6E-02	1.0	8E-01	Molecular function unknown	Nucleus	Unclassified
118460	**EXOSC6**	**exosome complex component MTR3**	5	27	5	1.3	**2E-02**	0.9	**2E-02**	1.3	6E-01	0.8	**2E-02**	1.0	7E-01	Ribonuclease activity	Nucleus	Ribonuclease
10514	**MYBBP1A**	**myb-binding protein 1A isoform 1**	25	128	25	1.3	**1E-15**	1.0	**2E-16**	1.2	6E-02	**0.6**	**8E-04**	1.0	5E-01	Transcription regulator activity	Nucleolus	Transcription regulatory protein
3615	**IMPDH2**	**inosine-5'-monophosphate dehydrogenase 2**	20	147	18	1.3	**2E-14**	0.9	**1E-14**	1.4	1E+00	1.3	**6E-16**	0.9	**5E-04**	Catalytic activity	Cytosol;Cytoplasm	Enzyme: Dehydrogenase
10969	**EBNA1BP2**	**probable rRNA-processing protein EBP2 isoform 1**	13	63	13	1.3	**6E-08**	0.9	**4E-09**	1.2	4E-01	0.7	2E-01	1.0	1E-01	Molecular function unknown	Nucleolus	Unclassified
140823	**ROMO1**	**reactive oxygen species modulator 1**	1	8	1	1.3	**1E-03**	0.8	**2E-03**	1.2	2E-01	1.0	**6E-03**	0.9	1E-01	Molecular function unknown	-	Unclassified
10026	**PIGK**	**GPI-anchor transamidase**	5	14	5	1.3	**6E-03**	1.0	**1E-04**	1.2	1E-01	1.2	**2E-03**	0.9	4E-01	Cysteine-type peptidase activity	Endoplasmic reticulum	Cysteine protease
25902	**MTHFD1L**	**monofunctional C1-tetrahydrofolate synthase, mitochondrial isoform 1**	17	86	16	1.3	**2E-11**	1.0	**1E-11**	1.2	**1E-03**	1.1	**2E-10**	1.0	2E-01	Catalytic activity	Mitochondrion	Enzyme: Ligase
3182	**HNRNPAB**	**heterogeneous nuclear ribonucleoprotein A/B isoform b**	14	133	12	1.3	**5E-11**	0.9	**3E-12**	1.3	1E-01	**0.7**	**4E-02**	1.0	**4E-02**	MRNA binding	Nucleolus	Ribonucleoprotein
55612	**FERMT1**	**fermitin family homolog 1**	20	136	17	1.3	**2E-06**	0.8	**2E-07**	**1.6**	**8E-10**	1.4	**2E-07**	1.0	2E-01	Structural molecule activity	Cytoplasm	Structural protein
92399	**MRRF**	**ribosome-recycling factor, mitochondrial isoform 1**	7	31	7	1.3	**1E-05**	1.2	**2E-06**	1.3	**2E-07**	1.0	**2E-06**	1.0	**2E-02**	Molecular function unknown	Mitochondrion	Unclassified
65265	**C8orf33**	**UPF0488 protein C8orf33**	3	11	3	1.3	**2E-02**	1.0	**9E-03**	1.2	8E-01	1.0	5E-02	1.4	2E-01	Molecular function unknown	-	Unclassified
2967	**GTF2H3**	**general transcription factor IIH subunit 3 isoform a**	1	5	1	1.3	**2E-02**	1.0	**4E-02**	1.4	8E-02	0.9	**3E-02**	0.8	3E-01	Transcription factor activity	Nucleus	Transcription factor
4067	**LYN**	**PREDICTED: tyrosine-protein kinase Lyn isoform X1**	5	44	2	1.3	6E-02	0.8	**2E-02**	1.4	6E-01	1.1	1E-01	1.3	6E-02	Protein-tyrosine kinase activity	Plasma membrane	Tyrosine kinase
5511	**PPP1R8**	**nuclear inhibitor of protein phosphatase 1 isoform alpha**	3	12	3	1.3	**2E-03**	0.9	**3E-03**	1.3	3E-01	0.9	3E-01	0.9	8E-01	RNA binding	Nucleus	Ribonuclease
6566	**SLC16A1**	**PREDICTED: monocarboxylate transporter 1 isoform X1**	5	13	5	1.3	**3E-03**	0.9	**1E-03**	1.1	8E-01	**0.6**	**2E-02**	0.9	7E-02	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
220988	**HNRNPA3**	**heterogeneous nuclear ribonucleoprotein A3**	15	202	12	1.3	**3E-09**	1.1	**3E-10**	1.4	**1E-04**	1.4	**2E-06**	1.0	3E-01	RNA binding	Nucleus	Ribonucleoprotein
6635	**SNRPE**	**small nuclear ribonucleoprotein E isoform 1**	1	14	1	1.3	**3E-04**	1.0	**1E-03**	1.4	**2E-02**	0.9	**5E-04**	1.2	**2E-02**	Ribonucleoprotein	Nucleus	Ribonucleoprotein
2817	**GPC1**	**glypican-1**	8	28	8	1.3	**3E-03**	0.9	**3E-02**	0.9	3E-01	**0.7**	**4E-02**	0.9	**4E-03**	Receptor activity	Plasma membrane	Cell surface receptor
5018	**OXA1L**	**mitochondrial inner membrane protein OXA1L**	3	14	3	1.3	9E-02	1.1	**4E-02**	1.5	1E-01	1.1	9E-02	1.1	1E+00	Catalytic activity	Mitochondrion	Enzyme: Oxidase
9811	**CTIF**	**PREDICTED: CBP80/20-dependent translation initiation factor isoform X2**	2	6	2	1.3	1E-01	0.7	1E-01	1.4	5E-01	0.7	6E-01	1.2	5E-01	#N/A	#N/A	#N/A
1915	**EEF1A1**	**PREDICTED: elongation factor 1-alpha 1 isoform X1**	24	707	24	1.3	**2E-16**	0.8	**2E-16**	1.1	**3E-05**	1.0	**2E-16**	1.0	8E-01	Transcription regulator activity	Cytoplasm	Transcription regulatory protein
64283	**ARHGEF28**	**PREDICTED: rho guanine nucleotide exchange factor 28 isoform X1**	3	10	3	1.3	**2E-03**	0.9	**2E-02**	1.1	6E-01	0.9	2E-01	1.2	9E-02	#N/A	#N/A	#N/A
4869	**NPM1**	**nucleophosmin isoform 1**	15	421	15	1.3	**2E-16**	0.7	**2E-16**	1.2	**2E-04**	**0.6**	**2E-05**	1.0	6E-01	Chaperone activity	Nucleolus;Nucleus;Cytoplasm	Chaperone
11340	**EXOSC8**	**exosome complex component RRP43**	5	22	5	1.3	**2E-04**	1.0	**1E-04**	1.3	1E-01	1.0	**1E-03**	1.0	4E-01	Ribonuclease activity	Nucleolus	Ribonuclease
51605	**TRMT6**	**tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 isoform 1**	9	38	9	1.3	**5E-04**	1.0	**2E-04**	1.2	**5E-02**	1.0	**1E-02**	1.0	9E-01	Molecular function unknown	-	Unclassified
51018	**RRP15**	**RRP15-like protein**	5	22	5	1.3	**6E-04**	0.8	**2E-03**	1.1	3E-01	0.6	2E-01	0.9	2E-01	Molecular function unknown	Nucleolus	Unclassified
5033	**P4HA1**	**prolyl 4-hydroxylase subunit alpha-1 isoform 1**	13	57	13	1.3	**1E-06**	**0.6**	**2E-08**	1.0	**6E-05**	0.9	**1E-07**	1.0	1E-01	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Hydroxylase
10438	**C1D**	**nuclear nucleic acid-binding protein C1D**	1	6	1	1.3	**3E-03**	0.9	**2E-02**	1.4	7E-01	1.0	3E-01	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
80222	**TARS2**	**threonine--tRNA ligase, mitochondrial isoform a**	7	24	7	1.3	**5E-04**	1.1	**1E-04**	1.4	**4E-03**	0.9	**5E-03**	1.0	8E-01	Ligase activity	-	Enzyme: Ligase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
81037	**CLPTM1L**	**cleft lip and palate transmembrane protein 1-like protein**	2	12	2	1.3	**1E-02**	1.1	**7E-03**	1.1	**4E-02**	1.0	**3E-02**	1.1	1E-01	Molecular function unknown	Integral to membrane	Integral membrane protein
23304	**UBR2**	**E3 ubiquitin-protein ligase UBR2 isoform 1**	3	11	3	1.3	**5E-02**	0.9	**1E-02**	1.2	5E-01	0.7	8E-01	1.0	8E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
4001	**LMNB1**	**lamin-B1 isoform 1**	27	191	24	1.3	**2E-16**	1.0	**2E-16**	1.3	**4E-07**	1.3	**2E-16**	1.0	**3E-02**	Structural molecule activity	Nucleus	Structural protein
6773	**STAT2**	**signal transducer and activator of transcription 2 isoform 1**	7	21	7	1.3	**2E-03**	0.9	**5E-04**	1.0	**5E-02**	0.7	5E-01	1.0	9E-01	Transcription factor activity	Cytoplasm	Transcription factor
2555	**GABRA2**	**gamma-aminobutyric acid receptor subunit alpha-2 isoform b**	1	4	1	1.3	9E-02	1.0	**3E-02**	1.3	1E-01	1.1	5E-02	1.1	2E-01	Ion channel activity	-	Ion channel
123263	**MTFMT**	**methionyl-tRNA formyltransferase, mitochondrial**	2	8	2	1.3	**3E-02**	1.1	**5E-03**	1.3	7E-02	0.9	7E-02	1.0	1E+00	Transferase activity	Mitochondrion	Enzyme: Transferase
63931	**MRPS14**	**28S ribosomal protein S14, mitochondrial**	2	8	2	1.3	5E-02	1.2	**3E-02**	1.3	**2E-02**	1.1	**3E-02**	0.9	3E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
5591	**PRKDC**	**DNA-dependent protein kinase catalytic subunit isoform 1**	127	741	127	1.3	**2E-16**	1.1	**2E-16**	1.3	**2E-16**	1.0	**2E-16**	1.0	**1E-04**	Protein serine/threonine kinase activity;DNA repair protein	Nucleus	Serine/threonine kinase;DNA repair protein
9319	**TRIP13**	**PREDICTED: pachytene checkpoint protein 2 homolog isoform X1**	9	51	9	1.3	**5E-05**	0.8	**2E-06**	1.3	**6E-04**	0.8	**1E-02**	1.0	7E-01	ATPase activity	Nucleus	ATPase
4705	**NDUFA10**	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial**	9	34	9	1.3	**2E-04**	0.9	**8E-04**	1.1	9E-02	0.8	**4E-02**	1.0	5E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
55140	**ELP3**	**elongator complex protein 3 isoform 1**	7	22	7	1.3	**6E-03**	0.9	**9E-04**	1.3	8E-01	1.0	**2E-03**	1.0	5E-01	Acyltransferase activity	Nucleus	Enzyme: Acyltransferase
118429	**ANTXR2**	**anthrax toxin receptor 2 isoform 2**	3	10	3	1.3	**1E-02**	0.7	7E-02	1.1	**3E-02**	0.7	8E-01	1.3	**3E-02**	Cytoskeletal protein binding	Endoplasmic reticulum	Cytoskeletal associated protein
10117;	**ENAM**	**enamelin**	3	8	3	1.3	**2E-02**	0.5	6E-02	0.8	1E-01	0.5	9E-02	1.1	**2E-02**	Structural molecule activity	Extracellular	Structural protein
8161	**COIL**	**coilin**	2	12	2	1.3	7E-02	1.0	**3E-02**	1.4	1E+00	1.1	**5E-02**	1.0	4E-01	RNA binding	Nucleus	RNA binding protein
4728	**NDUFS8**	**PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial isoform X1**	3	18	3	1.3	**7E-07**	1.0	**1E-07**	1.3	2E-01	1.0	**1E-04**	1.0	2E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
253782	**CERS6**	**ceramide synthase 6 isoform 1**	2	8	2	1.3	**5E-03**	1.0	**5E-03**	1.2	8E-02	0.8	3E-01	1.0	6E-01	#N/A	#N/A	#N/A
23168	**RTF1**	**RNA polymerase-associated protein RTF1 homolog**	4	11	4	1.3	**2E-02**	1.0	**2E-02**	1.4	5E-01	0.9	**2E-02**	0.9	6E-01	Molecular function unknown	-	Unclassified
54439	**RBM27**	**RNA-binding protein 27**	5	17	5	1.3	**2E-02**	1.0	**2E-02**	1.2	2E-01	1.0	6E-02	0.9	7E-01	RNA binding	-	RNA binding protein
125950	**RAVER1**	**ribonucleoprotein PTB-binding 1**	5	11	5	1.3	**2E-02**	1.0	**9E-03**	1.5	8E-01	1.0	3E-01	1.3	6E-01	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein
23223	**RRP12**	**RRP12-like protein isoform 1**	23	81	23	1.3	**5E-09**	0.9	**2E-11**	1.1	9E-02	**0.6**	**2E-04**	1.0	5E-01	Molecular function unknown	Nucleolus	Unclassified
10054	**UBA2**	**SUMO-activating enzyme subunit 2**	10	60	10	1.3	**2E-07**	1.1	**9E-08**	1.3	**1E-04**	0.9	**8E-05**	1.0	1E-01	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein
4907	**NT5E**	**5'-nucleotidase isoform 1 preproprotein**	9	45	9	1.3	**5E-07**	**0.4**	**3E-06**	1.1	**2E-06**	0.9	**2E-07**	1.3	**5E-06**	Hydrolase activity	Plasma membrane	Enzyme: Hydrolase
10947	**AP3M2**	**AP-3 complex subunit mu-2**	4	19	1	1.3	**2E-05**	1.0	**2E-05**	1.2	6E-01	0.8	**4E-03**	1.0	6E-01	Transporter activity	Golgi apparatus	Transport/cargo protein
2683	**B4GALT1**	**beta-1,4-galactosyltransferase 1**	2	10	2	1.3	**2E-02**	0.8	**1E-02**	1.1	3E-01	0.7	4E-01	1.0	5E-01	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase
55066	**PDPR**	**PREDICTED: pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial isoform X1**	6	15	6	1.3	**3E-02**	1.0	8E-02	1.2	5E-01	1.0	1E-01	1.0	9E-01	#N/A	#N/A	#N/A
1736	**DKC1**	**H/ACA ribonucleoprotein complex subunit 4 isoform 1**	13	86	13	1.3	**5E-08**	1.1	**1E-08**	1.3	**2E-04**	1.1	**3E-08**	1.1	2E-01	RNA binding	Nucleus	RNA binding protein
23404	**EXOSC2**	**exosome complex component RRP4 isoform 1**	5	29	5	1.3	**5E-06**	0.9	**2E-06**	1.3	7E-01	0.8	1E-01	0.9	7E-02	Ribonuclease activity	Nucleus	Ribonuclease
89941	**RHOT2**	**mitochondrial Rho GTPase 2**	9	44	7	1.3	**1E-03**	1.3	**3E-04**	1.3	**7E-04**	1.3	**1E-03**	1.0	5E-01	GTPase activity	Mitochondrion	GTPase
64978	**MRPL38**	**39S ribosomal protein L38, mitochondrial**	4	22	4	1.3	**1E-03**	1.1	**1E-03**	1.2	**9E-03**	1.1	**1E-02**	1.0	3E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
10270	**AKAP8**	**A-kinase anchor protein 8**	3	16	3	1.3	**4E-03**	1.0	**1E-02**	1.4	6E-01	1.1	**5E-03**	1.0	5E-01	Chromatin binding	Nucleus	Cell cycle control protein
55902	**ACSS2**	**acetyl-coenzyme A synthetase, cytoplasmic isoform 2**	13	64	13	1.3	**9E-09**	1.2	**7E-12**	**2.3**	**5E-07**	**1.6**	**9E-11**	1.0	5E-01	Catalytic activity	Cytoplasm	Enzyme: Ligase
10643	**IGF2BP3**	**insulin-like growth factor 2 mRNA-binding protein 3**	11	52	8	1.3	**9E-04**	0.9	**3E-04**	1.2	5E-01	1.2	**5E-04**	1.0	2E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
5634	**PRPS2**	**ribose-phosphate pyrophosphokinase 2 isoform 1**	10	57	4	1.3	**2E-02**	1.1	**3E-03**	1.5	1E-01	0.9	6E-02	1.0	6E-01	Ligase activity	Cytoplasm	Enzyme: Ligase
84365	**MKI67IP; NIFK**	**MKI67 FHA domain-interacting nucleolar phosphoprotein**	6	25	6	1.3	6E-02	0.9	**3E-02**	1.1	2E-01	0.7	3E-01	0.9	6E-02	#N/A	#N/A	#N/A
51251	**NT5C3; NT5C3A**	**cytosolic 5'-nucleotidase 3A isoform 1**	3	12	3	1.3	**4E-03**	0.9	**5E-03**	1.1	9E-01	1.2	**1E-02**	0.9	6E-01	#N/A	#N/A	#N/A
11103	**KRR1**	**KRR1 small subunit processome component homolog**	5	18	5	1.3	**2E-02**	0.9	**5E-03**	1.3	9E-01	0.8	3E-01	1.0	4E-01	DNA binding	Nucleolus	DNA binding protein
55364	**IMPACT**	**protein IMPACT**	5	14	5	1.3	5E-02	1.1	**4E-02**	1.3	7E-02	0.9	7E-02	0.9	5E-01	Molecular function unknown	-	Unclassified

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
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Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
3190	**HNRNPK**	**heterogeneous nuclear ribonucleoprotein K isoform b**	21	296	21	1.3	**2E-16**	0.9	**2E-16**	1.2	1E+00	0.8	**9E-06**	1.0	4E-01	Ribonucleoprotein	Nucleus	Ribonucleoprotein
2222	**FDFT1**	**squalene synthase isoform 1**	14	107	14	1.3	**2E-10**	0.9	**5E-11**	1.9	1E-01	**0.7**	**8E-04**	0.9	**2E-08**	Transferase activity	Endoplasmic reticulum	Enzyme: Synthase
26010	**SPATS2L**	**SPATS2-like protein isoform d**	9	43	9	1.3	**7E-07**	0.9	**1E-05**	1.0	1E-01	0.9	**2E-05**	0.9	**8E-03**	Molecular function unknown	Nucleus	Unclassified
6168	**RPL37A**	**60S ribosomal protein L37a**	5	67	5	1.3	**2E-06**	1.0	**1E-06**	1.1	**4E-04**	0.8	1E+00	0.9	9E-02	Structural constituent of ribosome	Ribosome	Ribosomal subunit
1947	**EFNB1**	**ephrin-B1**	5	26	5	1.3	**3E-06**	0.8	**2E-06**	1.2	7E-02	0.8	4E-01	1.0	4E-01	Receptor binding	Plasma membrane	Ligand
9184	**BUB3**	**mitotic checkpoint protein BUB3 isoform a**	10	56	10	1.3	**2E-05**	0.9	**1E-06**	1.2	**4E-02**	0.9	**3E-05**	0.9	**8E-03**	Protein transporter activity	Cytoplasm	Cell cycle control protein
5538	**PPT1**	**palmitoyl-protein thioesterase 1 isoform 1**	6	20	6	1.3	**7E-05**	0.8	**9E-05**	1.4	**3E-02**	0.9	8E-02	1.0	8E-01	Hydrolase activity	Lysosome	Enzyme: Hydrolase
51649	**MRPS23**	**28S ribosomal protein S23, mitochondrial**	6	40	6	1.3	**6E-07**	1.0	**5E-09**	1.2	6E-02	1.0	**2E-04**	1.1	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
4802	**NFYC**	**nuclear transcription factor Y subunit gamma isoform 1**	2	12	2	1.3	**7E-05**	**0.7**	**9E-04**	1.3	**2E-02**	0.9	**2E-02**	1.0	5E-01	Transcription factor activity	Nucleus	Transcription factor
4698	**NDUFA5**	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform 1**	3	22	3	1.3	**9E-05**	0.9	**4E-05**	1.2	8E-01	0.9	**8E-03**	1.0	8E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
80145	**THOC7**	**THO complex subunit 7 homolog isoform 1**	4	18	4	1.3	**5E-04**	0.9	**3E-04**	1.3	1E-01	1.0	**4E-03**	0.9	9E-01	Molecular function unknown	Cytoplasm	Unclassified
5947	**RBP1**	**retinol-binding protein 1 isoform a**	7	30	7	1.3	**1E-04**	0.9	**7E-05**	1.4	6E-01	1.1	**8E-06**	1.1	**1E-02**	Transporter activity	Cytoplasm	Transport/cargo protein
132299	**OCIAD2**	**OCIA domain-containing protein 2 isoform 1**	5	38	5	1.3	**9E-04**	**0.4**	**4E-04**	0.9	**2E-03**	**0.6**	**5E-03**	0.8	**8E-04**	Molecular function unknown	-	Unclassified
55720	**TSR1**	**pre-rRNA-processing protein TSR1 homolog**	8	31	8	1.3	**1E-02**	0.8	**5E-03**	1.2	3E-01	0.7	5E-01	1.0	4E-01	Molecular function unknown	Nucleus	Unclassified
5783	**PTPN13**	**tyrosine-protein phosphatase non-receptor type 13 isoform 4**	4	12	4	1.3	**9E-04**	0.9	7E-02	0.9	1E-01	0.8	2E-01	1.1	4E-01	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase
3988	**LIPA**	**lysosomal acid lipase/cholesteryl ester hydrolase isoform 1*gi|51317399|ref|NP_000226.2| lysosomal acid lipase/cholesteryl ester hydrolase isoform 1**	4	25	4	1.3	**2E-02**	**0.4**	**2E-02**	1.1	**2E-02**	**0.5**	**5E-02**	0.9	8E-02	Lipase activity	Lysosome	Enzyme: Lipase
27440	**CECR5**	**cat eye syndrome critical region protein 5 isoform 2**	6	39	6	1.3	**1E-05**	1.2	**4E-06**	1.4	**1E-04**	1.2	**3E-06**	1.0	8E-01	Molecular function unknown	Mitochondrion	Unclassified
11222	**MRPL3**	**39S ribosomal protein L3, mitochondrial**	6	26	6	1.3	**5E-04**	1.3	**1E-05**	1.4	**1E-04**	1.1	**1E-04**	1.1	**2E-02**	Structural constituent of ribosome	Nucleolus	Ribosomal subunit
376267;	**RAB15**	**ras-related protein Rab-15**	3	38	1	1.3	8E-02	1.1	**2E-02**	1.2	6E-01	1.0	2E-01	1.5	2E-01	GTPase activity	Endosome	GTPase
6158	**RPL28**	**60S ribosomal protein L28 isoform 2**	9	108	9	1.3	**2E-16**	1.0	**2E-16**	1.2	**2E-02**	0.8	7E-01	1.0	6E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
7112	**TMPO**	**thymopoietin isoform beta**	8	34	4	1.3	**5E-04**	1.0	**1E-03**	1.2	**1E-02**	1.1	**1E-03**	0.9	4E-01	Molecular function unknown	Nucleus;Nuclear membrane;Mitochondrion;Cytoplasm	Peptide hormone
25942	**SIN3A**	**PREDICTED: paired amphipathic helix protein Sin3a isoform X1**	4	9	4	1.3	**6E-03**	0.9	**4E-02**	1.3	7E-01	0.9	**3E-02**	0.9	9E-01	Transcription regulator activity;DNA binding	Nucleus	Transcription regulatory protein
23405	**DICER1**	**endoribonuclease Dicer isoform 1**	5	12	5	1.3	5E-02	0.8	8E-02	1.1	3E-01	0.7	5E-01	0.9	6E-02	Ribonuclease activity	Cytoplasm	Ribonuclease
10236	**HNRNPR**	**heterogeneous nuclear ribonucleoprotein R isoform 2**	25	219	17	1.3	**4E-13**	1.0	**1E-13**	1.3	**5E-05**	0.9	**8E-14**	0.9	2E-01	RNA binding	Nucleus	RNA binding protein
5984	**RFC4**	**replication factor C subunit 4**	6	16	6	1.3	1E-01	1.0	9E-02	1.1	3E-01	0.8	3E-01	1.1	2E-01	DNA binding	Nucleus	DNA binding protein
6117	**RPA1**	**replication protein A 70 kDa DNA-binding subunit**	12	64	12	1.3	**3E-08**	1.0	**6E-08**	1.3	**1E-03**	0.8	**3E-02**	0.9	**2E-03**	DNA binding	Nucleus	DNA binding protein
11325	**DDX42**	**PREDICTED: ATP-dependent RNA helicase DDX42 isoform X1**	12	45	12	1.3	**6E-06**	0.9	**1E-05**	1.3	3E-01	0.8	6E-01	0.9	**5E-03**	RNA binding	Nucleus	RNA binding protein
8544	**PIR**	**pirin**	7	41	7	1.3	**1E-05**	**1.7**	**2E-05**	**2.1**	**2E-05**	**1.6**	**3E-05**	0.8	6E-02	Transcription regulator activity;Transcription cofactor activity	Nuclear matrix	Transcription regulatory protein
23350	**U2SURP**	**U2 snRNP-associated SURP motif-containing protein**	12	50	12	1.3	**4E-05**	1.0	**3E-05**	1.3	**2E-03**	0.9	**9E-04**	1.0	4E-01	#N/A	#N/A	#N/A
10197	**PSME3**	**proteasome activator complex subunit 3 isoform 2**	10	96	10	1.3	**5E-12**	0.9	**7E-13**	1.2	5E-01	0.8	7E-01	0.8	**9E-06**	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein
54976	**C20orf27**	**UPF0687 protein C20orf27 isoform 1**	1	8	1	1.3	**2E-02**	0.8	**3E-02**	1.2	1E-01	0.7	1E-01	0.9	2E-01	Molecular function unknown	-	Unclassified
79719	**AAGAB**	**alpha- and gamma-adaptin-binding protein p34 isoform 1**	3	6	3	1.3	7E-02	1.1	**4E-02**	1.1	7E-01	1.0	2E-01	1.0	8E-01	Molecular function unknown	Nucleus	Unclassified
4486	**MST1R**	**macrophage-stimulating protein receptor isoform 1 preproprotein**	4	13	3	1.3	2E-01	0.8	1E-01	1.0	5E-01	0.9	2E-01	1.1	4E-01	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase
10102	**TSFM**	**elongation factor Ts, mitochondrial isoform 1**	5	34	5	1.3	**4E-03**	1.1	**3E-03**	1.3	**2E-03**	0.8	3E-01	1.0	5E-01	Translation regulator activity	Mitochondrion	Translation regulatory protein
10592	**SMC2**	**PREDICTED: structural maintenance of chromosomes protein 2 isoform X1**	10	32	10	1.3	**7E-03**	0.7	**4E-03**	1.2	**1E-02**	0.7	2E-01	0.9	6E-01	Molecular function unknown	Nucleus	Unclassified
200081	**TXLNA**	**alpha-taxilin**	10	44	10	1.3	**2E-05**	0.8	**6E-05**	1.1	**4E-02**	0.7	5E-01	0.9	1E-01	Molecular function unknown	Cytoplasm	Unclassified

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10975	UQCR11	cytochrome b-c1 complex subunit 10	1	6	1	1.3	5E-02	1.4	8E-02	1.4	**3E-02**	1.4	**6E-03**	1.3	**2E-02**	Catalytic activity	Mitochondrion	Enzyme: Reductase
10212	DDX39A	PREDICTED: ATP-dependent RNA helicase DDX39A isoform X1	13	110	3	1.3	**2E-07**	0.9	**2E-08**	1.4	9E-01	0.9	**4E-06**	1.0	**2E-02**	#N/A	#N/A	#N/A
57552	NCEH1	neutral cholesterol ester hydrolase 1 isoform a	9	40	9	1.3	**1E-04**	1.0	**1E-05**	1.3	9E-01	**1.5**	**5E-04**	1.1	**4E-02**	Molecular function unknown	-	Unclassified
9129	PRPF3	U4/U6 small nuclear ribonucleoprotein Prp3	8	43	8	1.3	**6E-04**	0.9	**4E-04**	1.3	6E-01	0.9	**1E-03**	1.0	7E-01	RNA binding	Nucleus	RNA binding protein
51503	CWC15	spliceosome-associated protein CWC15 homolog	3	12	3	1.3	**4E-03**	1.0	**4E-04**	1.2	**4E-02**	0.7	8E-01	1.1	1E+00	Molecular function unknown	Nucleus	Unclassified
81537	SGPP1	sphingosine-1-phosphate phosphatase 1	3	11	3	1.3	**2E-02**	0.8	**8E-03**	1.2	1E-01	0.9	3E-01	1.0	3E-01	Lipid phosphatase activity	Endoplasmic reticulum	Lipid phosphatase
9070	ASH2L	set1/Ash2 histone methyltransferase complex subunit ASH2 isoform a	3	13	3	1.3	**2E-02**	0.9	**3E-02**	1.5	4E-01	0.9	**2E-03**	0.8	8E-02	DNA binding	Nucleus	DNA binding protein
84135	UTP15	PREDICTED: U3 small nucleolar RNA-associated protein 15 homolog isoform X1	8	36	8	1.3	**1E-07**	0.9	**2E-06**	1.2	6E-01	0.8	3E-01	1.0	5E-02	Molecular function unknown	-	Unclassified
91289	LMF2	lipase maturation factor 2	4	11	4	1.3	**1E-03**	0.9	**1E-02**	1.3	3E-01	**0.6**	**8E-03**	0.9	**3E-02**	Molecular function unknown	Integral to membrane	Unclassified
25814	ATXN10	ataxin-10 isoform 1	7	33	7	1.3	**2E-03**	0.8	**3E-03**	1.0	**1E-02**	**0.6**	**7E-05**	0.8	**3E-04**	Molecular function unknown	-	Unclassified
55003	PAK1IP1	p21-activated protein kinase-interacting protein 1	11	32	11	1.3	**2E-03**	0.8	**2E-04**	1.3	5E-01	0.7	1E-01	0.9	1E-01	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein
9651	PLCH2	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2 isoform 1	5	19	5	1.3	**4E-03**	1.3	**6E-03**	1.4	**9E-03**	1.1	**2E-02**	1.2	**2E-02**	Phospholipase activity	Plasma membrane	Enzyme: Phospholipase
132001	TAMM41	phosphatidate cytidylyltransferase, mitochondrial isoform a	5	15	5	1.3	**5E-03**	1.1	**4E-03**	1.3	3E-01	1.2	**3E-02**	1.1	2E-01	#N/A	#N/A	#N/A
5127	CDK16	cyclin-dependent kinase 16 isoform 3	7	36	4	1.3	**1E-02**	0.9	**5E-03**	1.3	7E-01	1.0	**5E-03**	1.0	8E-01	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase
23091	ZC3H13	PREDICTED: zinc finger CCCH domain-containing protein 13 isoform X2	4	5	4	1.3	7E-02	1.0	7E-02	1.3	2E-01	0.9	**3E-02**	1.1	8E-01	Transcription regulator activity	-	Transcription regulatory protein
55157	DARS2	aspartate--tRNA ligase, mitochondrial	17	72	17	1.3	**6E-07**	1.2	**3E-08**	**1.5**	**1E-04**	**1.7**	**4E-08**	1.1	**9E-03**	Molecular function unknown	Mitochondrion	Unclassified
1059	CENPB	major centromere autoantigen B	2	5	2	1.3	**9E-04**	0.8	**2E-03**	1.3	**4E-02**	1.0	2E-01	1.0	6E-01	DNA binding	Nucleus	DNA binding protein
51300	TIMMDC1	complex I assembly factor TIMMDC1, mitochondrial	4	15	4	1.3	**2E-02**	0.9	**1E-02**	1.3	2E-01	1.1	**3E-02**	0.9	3E-01	#N/A	#N/A	#N/A
84191	FAM96A	MIP18 family protein FAM96A isoform a	1	8	1	1.3	**3E-02**	1.0	7E-02	1.1	7E-01	1.0	2E-01	1.0	1E+00	Molecular function unknown	-	Unclassified
54512	EXOSC4	exosome complex component RRP41	3	14	3	1.3	**3E-02**	0.9	**4E-02**	1.5	9E-01	0.9	1E-01	0.9	1E-01	Ribonuclease activity	Nucleolus	Ribonuclease
56647	BCCIP	BRCA2 and CDKN1A-interacting protein isoform BCCIPbeta	6	29	6	1.3	**4E-04**	0.8	**2E-03**	**1.5**	**6E-03**	0.7	3E-01	0.9	4E-01	Peptide binding	Nucleus	Cell cycle control protein
836	CASP3	PREDICTED: caspase-3 isoform X1	5	38	4	1.3	**3E-03**	0.8	**2E-03**	1.5	4E-01	1.1	5E-02	1.0	4E-01	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease
23383	MAU2	MAU2 chromatid cohesion factor homolog	1	6	1	1.3	**5E-03**	1.0	**1E-02**	1.3	**1E-02**	1.2	1E-01	1.1	8E-01	#N/A	#N/A	#N/A
3491	CYR61	protein CYR61	6	18	6	1.3	9E-02	1.1	8E-02	1.3	1E-01	1.4	1E-01	1.3	1E-01	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein
7019	TFAM	transcription factor A, mitochondrial isoform 1	11	55	11	1.3	**2E-06**	1.1	**2E-06**	**1.5**	**1E-04**	1.2	**4E-06**	1.1	**2E-03**	Transcription factor activity	Mitochondrion	Transcription factor
23560	GTPBP4	nucleolar GTP-binding protein 1	20	98	20	1.3	**1E-14**	0.8	**2E-14**	1.1	**2E-03**	**0.6**	**5E-08**	1.0	9E-02	GTPase activity	Nucleus	GTPase
3185	HNRNPF	heterogeneous nuclear ribonucleoprotein F	11	135	9	1.3	**4E-09**	0.8	**7E-09**	1.2	**8E-03**	0.8	2E-01	0.9	**3E-02**	Ribonucleoprotein	Nucleus	Ribonucleoprotein
3073	HEXA	beta-hexosaminidase subunit alpha preproprotein	12	65	11	1.3	**3E-08**	1.3	**5E-09**	**1.5**	**3E-08**	**1.5**	**2E-08**	0.9	**5E-02**	Hydrolase activity	Lysosome	Enzyme: Hydrolase
81554	WBSCR16; RCC1L	Williams-Beuren syndrome chromosomal region 16 protein isoform 1	2	8	2	1.3	**2E-02**	1.2	1E-01	1.2	1E-01	1.0	1E-01	0.9	8E-01	#N/A	#N/A	#N/A
51350	KRT76	keratin, type II cytoskeletal 2 oral	24	4991	4	1.3	**1E-11**	**2.8**	**6E-06**	**0.4**	**2E-14**	**0.6**	**4E-02**	**3.0**	**4E-12**	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein
9933	KIAA0020; PUM3	pumilio domain-containing protein KIAA0020	7	31	7	1.3	**8E-04**	0.8	**6E-04**	1.0	**5E-02**	0.7	3E-01	1.0	3E-01	#N/A	#N/A	#N/A
90957	DHX57	PREDICTED: putative ATP-dependent RNA helicase DHX57 isoform X1	8	45	5	1.3	**8E-04**	1.4	**9E-05**	**1.5**	**2E-03**	1.2	**7E-04**	1.0	4E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
967	CD63	CD63 antigen isoform A	2	32	2	1.3	**9E-03**	**0.5**	**7E-03**	1.2	**1E-03**	0.8	5E-01	1.0	6E-01	Molecular function unknown	Lysosome	Integral membrane protein
10128	LRPPRC	leucine-rich PPR motif-containing protein, mitochondrial	60	386	60	1.4	**2E-16**	1.1	**2E-16**	1.3	**2E-16**	0.8	**1E-07**	1.0	6E-01	RNA binding	Nucleus	RNA binding protein
103	ADAR	double-stranded RNA-specific adenosine deaminase isoform a	30	157	30	1.4	**1E-14**	0.9	**2E-16**	1.2	**1E-02**	0.8	**4E-02**	0.9	**2E-02**	Deaminase activity	Nucleus	Enzyme: Deaminase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
4926	**NUMA1**	**PREDICTED: nuclear mitotic apparatus protein 1 isoform X2**	39	150	3	1.4	**2E-08**	1.0	**4E-10**	1.2	**1E-08**	1.0	**6E-11**	1.0	8E-01	Structural molecule activity	Nucleus	Structural protein
9984	**THOC1**	**THO complex subunit 1**	6	15	6	1.4	**7E-04**	1.2	**2E-03**	1.4	**1E-02**	1.1	**2E-02**	1.0	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9019	**MPZL1**	**myelin protein zero-like protein 1 isoform a**	4	18	4	1.4	**6E-03**	0.9	**9E-03**	1.2	7E-01	**0.6**	**5E-02**	0.9	2E-01	Binding	Integral to membrane	Unclassified
6631	**SNRPC**	**U1 small nuclear ribonucleoprotein C**	3	12	3	1.4	**3E-02**	0.9	5E-02	1.2	4E-01	0.7	2E-01	0.9	3E-01	RNA binding	Nucleus	Ribonucleoprotein
6949	**TCOF1**	**treacle protein isoform d**	33	148	33	1.4	**2E-15**	0.9	**2E-15**	1.3	5E-01	0.9	**2E-11**	1.1	**8E-09**	Transcription regulator activity	Nucleolus	Transcription regulatory protein
8241	**RBM10**	**RNA-binding protein 10 isoform 5**	5	26	3	1.4	**4E-04**	0.9	**7E-04**	1.1	5E-01	1.0	**2E-03**	1.1	2E-01	RNA binding	Nucleus	RNA binding protein
1603	**DAD1**	**dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1**	4	31	4	1.4	**1E-02**	1.4	**4E-03**	1.3	**4E-02**	1.4	**4E-03**	1.3	6E-02	Receptor signaling complex scaffold activity	Endoplasmic reticulum	Adapter molecule
3607	**FOXK2**	**forkhead box protein K2**	1	6	1	1.4	**3E-02**	1.1	6E-02	1.5	2E-01	1.2	**2E-02**	1.4	9E-02	Transcription factor activity;DNA binding	Nucleus	Transcription factor;DNA binding protein
51142	**CHCHD2**	**coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial**	2	8	2	1.4	7E-02	1.1	8E-02	1.6	2E-01	1.5	7E-02	0.9	2E-01	Molecular function unknown	-	Unclassified
140890	**SREK1**	**splicing regulatory glutamine/lysine-rich protein 1 isoform a**	4	14	4	1.4	**7E-03**	1.0	**2E-02**	1.2	1E-01	1.0	**5E-02**	1.2	2E-01	#N/A	#N/A	#N/A
55651	**NHP2**	**H/ACA ribonucleoprotein complex subunit 2 isoform a**	5	20	5	1.4	**8E-03**	1.1	**7E-03**	1.3	1E-01	1.1	**3E-02**	1.0	6E-01	RNA binding	Nucleolus	Ribonucleoprotein
64318	**NOC3L**	**nucleolar complex protein 3 homolog**	12	50	12	1.4	**2E-03**	0.9	**1E-03**	1.3	**2E-02**	0.7	6E-02	0.9	2E-01	Molecular function unknown	-	Unclassified
10978	**CLP1**	**polyribonucleotide 5'-hydroxyl-kinase Clp1 isoform 1**	5	12	5	1.4	**4E-02**	1.0	**4E-02**	1.3	5E-01	0.8	9E-02	1.1	**4E-02**	RNA binding	Integral to membrane	RNA binding protein
3192	**HNRNPU**	**heterogeneous nuclear ribonucleoprotein U isoform a**	31	273	31	1.4	**2E-16**	0.9	**2E-16**	1.3	**1E-02**	0.9	**3E-09**	1.0	7E-01	RNA binding	Nucleus;Cytoplasm	Ribonucleoprotein
22913	**RALY**	**RNA-binding protein Raly isoform 2**	15	98	15	1.4	**3E-14**	0.8	**4E-14**	1.2	**4E-05**	**0.7**	**5E-03**	1.0	4E-01	RNA binding	Mitochondrion;Nucleus;Cytoplasm	RNA binding protein
79718	**TBL1XR1**	**PREDICTED: F-box-like/WD repeat-containing protein TBL1XR1 isoform X1**	6	27	6	1.4	**7E-05**	1.0	**4E-05**	1.3	1E-01	0.8	2E-01	0.9	7E-02	Transcription regulator activity	Nucleus	Transcription regulatory protein
977	**CD151**	**CD151 antigen**	8	35	8	1.4	**2E-04**	0.8	**6E-04**	0.9	**8E-03**	**0.4**	**4E-04**	1.0	3E-01	Receptor activity	Plasma membrane	Cell surface receptor
55813	**UTP6**	**U3 small nucleolar RNA-associated protein 6 homolog**	5	14	5	1.4	**3E-02**	1.1	**6E-03**	1.1	1E-01	1.0	5E-01	1.0	1E-01	Molecular function unknown	Nucleolus	Unclassified
10618	**TGOLN2**	**trans-Golgi network integral membrane protein 2 isoform 2**	4	9	4	1.4	2E-01	1.8	2E-01	1.1	2E-01	1.1	2E-01	1.3	2E-01	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein
81034	**SLC25A32**	**mitochondrial folate transporter/carrier**	2	8	2	1.4	5E-01	1.2	2E-01	1.5	2E-01	1.4	6E-01	1.1	2E-01	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein
1825	**DSC3**	**desmocollin-3 isoform Dsc3a preproprotein**	16	84	16	1.4	**4E-09**	0.9	**1E-07**	1.0	6E-01	**0.6**	**3E-05**	0.8	**2E-05**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
355	**FAS**	**tumor necrosis factor receptor superfamily member 6 isoform 1**	2	8	2	1.4	**3E-02**	0.9	**1E-02**	1.1	4E-01	0.6	3E-01	1.1	2E-01	Receptor activity;Binding	Plasma membrane	Cell surface receptor;Unclassified
6430	**SRSF5**	**serine/arginine-rich splicing factor 5**	3	9	3	1.4	#N/A	0.8	#N/A	1.3	#N/A	0.7	#N/A	0.8	#N/A	#N/A	#N/A	#N/A
51202	**DDX47**	**probable ATP-dependent RNA helicase DDX47 isoform 1**	5	27	5	1.4	**6E-05**	0.9	**3E-06**	1.4	6E-01	0.7	5E-01	1.0	5E-01	Molecular function unknown	Nucleus	Unclassified;RNA helicase
56257	**MEPCE**	**7SK snRNA methylphosphate capping enzyme isoform A**	6	18	6	1.4	**2E-03**	1.1	**7E-04**	1.4	**1E-03**	1.4	**2E-03**	1.0	2E-01	Molecular function unknown	-	Unclassified
2639	**GCDH**	**glutaryl-CoA dehydrogenase, mitochondrial isoform a**	5	17	5	1.4	**3E-03**	1.1	**3E-03**	1.4	**1E-02**	**1.5**	**1E-03**	1.0	3E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
5000	**ORC4**	**origin recognition complex subunit 4 isoform 1*gi|32454746|ref|NP_859525.1|origin recognition complex subunit 4 isoform 1*gi|32454748|ref|NP_859526.1|origin recognition complex subunit 4 isoform 1*gi|32454750|ref|NP_002543.2|origin recognition complex subunit 4 isoform 1**	3	9	3	1.4	5E-02	0.8	**3E-02**	1.1	3E-01	0.6	2E-01	0.8	7E-02	#N/A	#N/A	#N/A
57456	**KIAA1143**	**uncharacterized protein KIAA1143**	2	10	2	1.4	6E-02	0.7	**3E-02**	1.3	5E-02	0.6	1E-01	0.8	7E-02	Molecular function unknown	-	Unclassified
2734	**GLG1**	**Golgi apparatus protein 1 isoform 1**	22	90	22	1.4	**4E-08**	1.0	**9E-11**	1.0	**6E-07**	1.4	**6E-11**	1.1	**9E-04**	Receptor binding	Golgi apparatus	Integral membrane protein
2787	**GNG5**	**guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5**	2	8	2	1.4	**2E-02**	1.0	**2E-02**	1.8	4E-01	0.7	6E-02	0.8	3E-01	GTPase activity	Integral to membrane	G protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
7913	DEK	protein DEK isoform 1	10	67	10	1.4	**9E-06**	0.9	**4E-06**	1.5	6E-01	1.1	**3E-08**	1.0	7E-01	DNA binding	Nucleus	DNA binding protein
3052	HCCS	cytochrome c-type heme lyase	4	10	4	1.4	**8E-03**	1.2	**6E-04**	1.4	**2E-02**	**1.9**	**5E-04**	1.2	1E-01	Lyase activity	Mitochondrion	Enzyme: Synthase
50810	HDGFRP3	hepatoma-derived growth factor-related protein 3	3	12	2	1.4	**3E-02**	1.1	**1E-02**	1.2	8E-02	1.2	**1E-02**	0.9	**3E-02**	#N/A	#N/A	#N/A
59339	PLEKHA2	PREDICTED: pleckstrin homology domain-containing family A member 2 isoform X1	2	6	2	1.4	3E-01	0.8	3E-01	1.2	9E-01	1.1	2E-01	1.1	6E-01	#N/A	#N/A	#N/A
7525	YES1	tyrosine-protein kinase Yes	9	60	3	1.4	**3E-06**	0.7	**9E-07**	1.3	9E-01	1.0	**1E-04**	1.0	9E-01	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase
4702	NDUFA8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	5	21	5	1.4	**5E-06**	0.9	**5E-05**	1.1	**3E-02**	0.8	**4E-02**	1.0	7E-01	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase
6636	SNRPF	small nuclear ribonucleoprotein F	4	33	4	1.4	**3E-04**	1.0	**5E-05**	1.3	9E-02	0.9	**2E-02**	1.1	3E-01	RNA binding	Nucleus	Ribonucleoprotein
51678	MPP6	MAGUK p55 subfamily member 6	4	21	3	1.4	**3E-04**	0.9	**2E-05**	1.2	9E-01	1.1	**6E-04**	1.2	7E-02	Molecular function unknown	Plasma membrane	Unclassified
57459	GATAD2B	PREDICTED: transcriptional repressor p66-beta isoform X1	6	18	4	1.4	**3E-03**	1.0	**4E-04**	1.2	1E-01	1.1	**2E-02**	1.0	1E+00	Transcription regulator activity	Nucleus	Transcription regulatory protein
6837	MED22	mediator of RNA polymerase II transcription subunit 22 isoform b	3	9	3	1.4	5E-02	1.0	7E-02	1.4	7E-01	1.1	6E-02	1.0	3E-01	Molecular function unknown	Cytoplasm	Unclassified
64783	RBM15	PREDICTED: putative RNA-binding protein 15 isoform X2	5	15	4	1.4	6E-02	1.0	**4E-02**	1.4	7E-01	1.0	**1E-02**	1.1	9E-02	RNA binding	-	RNA binding protein
8243	SMC1A	structural maintenance of chromosomes protein 1A isoform 1	15	51	15	1.4	**1E-05**	1.0	**1E-05**	1.3	**4E-02**	1.1	**8E-06**	1.0	3E-01	Chromatin binding	Nucleus	Cell cycle control protein
84950	PRPF38A	pre-mRNA-splicing factor 38A	7	23	7	1.4	**7E-03**	1.3	**4E-02**	1.3	4E-01	1.0	3E-01	0.9	4E-01	Molecular function unknown	-	Unclassified
56252	YLPM1	YLP motif-containing protein 1	8	25	7	1.4	**1E-03**	0.9	**8E-04**	1.2	6E-01	0.9	**2E-02**	1.0	4E-01	Molecular function unknown	Nucleus	Unclassified
9112	MTA1	metastasis-associated protein MTA1 isoform MTA1	6	24	2	1.4	7E-02	1.0	**5E-02**	1.2	5E-01	0.6	8E-01	0.9	2E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
51388	NIP7	60S ribosome subunit biogenesis protein NIP7 homolog isoform 1	5	30	5	1.4	**6E-07**	0.8	**7E-07**	1.3	**1E-02**	0.7	9E-02	0.9	6E-02	RNA binding	Nucleolus	RNA binding protein
4839	NOP2	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 3	15	69	15	1.4	**5E-06**	0.9	**4E-06**	1.4	7E-01	0.9	**6E-03**	1.1	**4E-03**	Molecular function unknown	Nucleolus	Unclassified
54928	IMPAD1	inositol monophosphatase 3	4	22	4	1.4	**1E-05**	1.0	**3E-05**	1.2	**6E-03**	1.1	**3E-05**	1.0	1E-01	Catalytic activity	-	Enzyme: Phosphatase
92675	DTD1	D-tyrosyl-tRNA(Tyr) deacylase 1	6	35	6	1.4	**2E-04**	1.1	**2E-04**	1.4	**2E-02**	1.1	**4E-04**	1.0	5E-01	ATPase activity	Nucleus	Enzyme: Ligase
30836	DNTTIP2	deoxynucleotidyltransferase terminal-interacting protein 2	8	25	8	1.4	**3E-04**	0.9	**4E-05**	1.1	5E-01	0.7	1E+00	1.2	1E-01	DNA binding	Nucleus	DNA binding protein
2926	GRSF1	G-rich sequence factor 1 isoform 1	4	17	4	1.4	**1E-03**	0.9	**1E-03**	1.2	1E+00	0.8	8E-01	0.9	1E-01	RNA binding	Cytoplasm	RNA binding protein
134147	CMBL	carboxymethylenebutenolidase homolog	4	18	4	1.4	**2E-02**	0.8	**3E-02**	1.2	**4E-02**	0.8	8E-02	1.2	9E-02	Molecular function unknown	-	Unclassified
4717	NDUFC1	NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial	1	5	1	1.4	5E-02	0.9	**4E-02**	1.0	9E-01	0.9	3E-01	0.8	1E-01	Molecular function unknown	Mitochondrion	Unclassified
79228	THOC6	THO complex subunit 6 homolog isoform 1	1	6	1	1.4	7E-02	0.9	**3E-02**	1.8	5E-01	1.2	2E-01	1.2	6E-01	Molecular function unknown	-	Unclassified
7385	UQCRC2	cytochrome b-c1 complex subunit 2, mitochondrial	18	107	18	1.4	**2E-16**	1.0	**8E-11**	1.0	**1E-05**	0.8	6E-02	1.0	5E-01	Catalytic activity	Mitochondrion	Enzyme: Reductase
9111	NMI	N-myc-interactor	4	10	4	1.4	**1E-03**	0.9	9E-02	1.1	4E-01	0.9	3E-01	1.1	3E-01	Transcription factor activity	Cytoplasm	Transcription factor
51650	MRPS33	28S ribosomal protein S33, mitochondrial	3	14	3	1.4	**2E-03**	1.4	**5E-03**	1.4	**3E-03**	1.3	**6E-03**	1.0	7E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
26589	MRPL46	39S ribosomal protein L46, mitochondrial	3	18	3	1.4	**8E-03**	1.1	**3E-03**	1.3	**2E-02**	1.0	6E-02	1.1	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
57109	REXO4	RNA exonuclease 4 isoform 1	3	9	3	1.4	2E-01	0.8	2E-01	1.3	3E-01	0.7	3E-01	1.2	2E-01	Translation regulator activity	Nucleus	Translation regulatory protein
60528	ELAC2	zinc phosphodiesterase ELAC protein 2 isoform 1	2	8	2	1.4	**2E-02**	1.0	7E-02	1.4	5E-01	0.8	4E-01	1.1	9E-02	Molecular function unknown	Nucleus	Unclassified
4700	NDUFA6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	4	17	4	1.4	**4E-02**	0.9	**3E-03**	1.1	7E-01	1.0	1E-01	1.1	3E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
29088	MRPL15	39S ribosomal protein L15, mitochondrial	4	18	4	1.4	**4E-05**	1.1	**5E-04**	1.4	**5E-02**	1.0	**2E-02**	1.0	5E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
8881	CDC16	cell division cycle protein 16 homolog*gi|118402580|ref|NP_003894.3| cell division cycle protein 16 homolog	5	25	5	1.4	**9E-05**	0.8	**3E-04**	1.1	6E-02	**0.6**	**1E-02**	0.9	**5E-03**	Protein binding	Centrosome	Cell cycle control protein

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8359; 8361; 8360; 8363; 8370; 554313; 8365; 8364; 121504; 8367; 8294; 8366; 8362; 8368	**HIST1H4A; HIST1H4F; HIST1H4D; HIST1H4J; HIST2H4A; HIST2H4B; HIST1H4H; HIST1H4C; HIST4H4; HIST1H4E; HIST1H4I; HIST1H4B; HIST1H4K; HIST1H4L**	**histone H4**	7	1038	7	1.4	**2E-16**	1.0	**2E-16**	1.4	**2E-07**	1.3	**2E-16**	1.1	**7E-06**	#N/A	#N/A	#N/A
84951	**TNS4**	**tensin-4**	11	53	11	1.4	**1E-04**	0.9	**3E-05**	1.1	7E-01	0.7	8E-01	0.9	1E-01	Molecular function unknown	Plasma membrane	Unclassified
7444	**VRK2**	**PREDICTED: serine/threonine-protein kinase VRK2 isoform X1**	5	18	5	1.4	**8E-03**	0.9	**1E-02**	1.3	8E-01	0.8	**2E-02**	1.1	**2E-02**	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase
55526	**DHTKD1**	**probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial**	9	35	9	1.4	**4E-05**	1.3	**6E-06**	1.6	**2E-03**	**1.6**	**1E-05**	1.0	7E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
55319	**TMA16**	**translation machinery-associated protein 16**	3	12	3	1.4	**5E-02**	0.8	**2E-02**	1.4	3E-01	0.7	8E-01	1.0	4E-01	#N/A	#N/A	#N/A
2618	**GART**	**trifunctional purine biosynthetic protein adenosine-3 isoform 1**	35	209	35	1.4	**2E-16**	0.9	**2E-16**	1.2	2E-01	0.8	**4E-02**	1.0	1E+00	Ligase activity	Cytosol	Enzyme: Transferase
9908	**G3BP2**	**PREDICTED: ras GTPase-activating protein-binding protein 2 isoform X1**	10	46	9	1.4	**2E-08**	0.8	**2E-07**	1.1	**2E-02**	0.8	2E-01	0.9	**2E-02**	Molecular function unknown	Cytoplasm;Nucleus	Unclassified
10209	**EIF1**	**eukaryotic translation initiation factor 1**	5	19	5	1.4	**3E-04**	1.0	**8E-04**	1.2	**3E-02**	0.8	5E-01	1.0	3E-01	Translation regulator activity	Cytoplasm	Translation regulatory protein
55848	**PLGRKT**	**PREDICTED: plasminogen receptor (KT) isoform X1**	5	22	5	1.4	**3E-04**	1.1	**9E-04**	1.3	**2E-03**	1.4	**9E-04**	1.0	9E-01	#N/A	#N/A	#N/A
29956	**CERS2**	**PREDICTED: ceramide synthase 2 isoform X1**	4	18	4	1.4	**6E-04**	0.9	**1E-04**	1.3	7E-01	1.1	**2E-03**	1.0	6E-01	#N/A	#N/A	#N/A
4712	**NDUFB6**	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 isoform 1**	2	10	2	1.4	**1E-02**	0.8	**5E-03**	1.1	**5E-02**	1.1	**2E-02**	1.1	7E-01	Electron transporter activity	Mitochondrial membrane	Regulatory/other subunit
3691	**ITGB4**	**PREDICTED: integrin beta-4 isoform X7**	58	209	2	1.4	**2E-16**	0.9	**2E-16**	1.2	**2E-16**	0.9	**2E-05**	**1.8**	**2E-16**	Cell adhesion molecule activity	Integral to membrane;Nucleus	Adhesion molecule
3178	**HNRNPA1**	**heterogeneous nuclear ribonucleoprotein A1 isoform a**	16	316	11	1.4	**3E-16**	0.9	**2E-15**	1.2	1E+00	0.9	**4E-05**	1.0	6E-01	RNA binding	Nucleus	RNA binding protein
79811	**SLTM**	**SAFB-like transcription modulator isoform a**	11	47	11	1.4	**2E-05**	1.1	**1E-05**	1.3	**1E-04**	1.2	**1E-05**	1.0	**8E-03**	Nucleic acid binding	Nucleus	DNA binding protein
9440	**MED17**	**mediator of RNA polymerase II transcription subunit 17**	4	9	4	1.4	**1E-02**	0.9	**3E-02**	1.3	7E-01	1.0	**2E-02**	1.2	3E-01	Transcription factor activity	Nucleus	Transcription factor
10573	**MRPL28**	**PREDICTED: 39S ribosomal protein L28, mitochondrial isoform X1**	4	11	4	1.4	5E-02	1.1	7E-02	1.2	**3E-02**	1.0	**3E-02**	1.1	6E-02	Structural molecule activity;Ribonucleoprotein	Mitochondrion	Structural protein
8833	**GMPS**	**GMP synthase [glutamine-hydrolyzing]**	23	131	23	1.4	**5E-14**	1.0	**2E-16**	1.4	**2E-04**	0.9	**2E-08**	1.0	**3E-02**	Amidinotransferase activity	-	Enzyme: Amidinotransferase
2273	**FHL1**	**four and a half LIM domains protein 1 isoform 5**	15	91	4	1.4	**4E-11**	0.8	**1E-11**	1.5	**5E-04**	1.2	**3E-10**	1.1	**4E-02**	Molecular function unknown	Cytoplasm	Unclassified
9801	**MRPL19**	**39S ribosomal protein L19, mitochondrial**	7	30	7	1.4	**8E-06**	1.1	**4E-06**	1.2	**2E-03**	0.9	**2E-05**	1.0	9E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
3251	**HPRT1**	**hypoxanthine-guanine phosphoribosyltransferase**	9	65	8	1.4	**3E-05**	0.9	**1E-05**	1.5	7E-01	1.1	**3E-07**	0.9	**2E-02**	Catalytic activity	Cytoplasm	Enzyme: Ribosyltransferase
7756	**ZNF207**	**BUB3-interacting and GLEBS motif-containing protein ZNF207 isoform c**	3	14	3	1.4	**9E-03**	0.8	**8E-03**	1.2	**1E-02**	0.8	8E-02	0.9	6E-02	DNA binding;Transcription factor activity	Nucleus	DNA binding protein
1488	**CTBP2**	**C-terminal-binding protein 2 isoform 2**	6	36	3	1.4	**2E-04**	0.8	**3E-04**	1.1	1E-01	0.8	1E+00	1.0	3E-01	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule;Transcription regulatory protein
84303	**CHCHD6**	**MICOS complex subunit MIC25**	5	28	5	1.4	**1E-03**	1.3	**3E-04**	1.5	**2E-03**	**1.5**	**1E-03**	1.1	**3E-02**	Molecular function unknown	-	Unclassified
116496	**FAM129A**	**protein Niban**	13	49	13	1.4	**3E-05**	0.7	**5E-05**	1.0	**1E-03**	0.7	7E-02	0.9	**2E-02**	Molecular function unknown	-	Unclassified
55646	**LYAR**	**PREDICTED: cell growth-regulating nucleolar protein isoform X1**	11	54	11	1.4	**5E-05**	0.9	**1E-05**	1.5	9E-01	1.1	**3E-06**	1.0	4E-01	Transcription regulator activity	Nucleolus	Transcription regulatory protein
23160	**WDR43**	**WD repeat-containing protein 43**	11	44	11	1.4	**7E-05**	0.9	**3E-04**	1.3	6E-01	0.8	6E-01	1.1	**2E-02**	Molecular function unknown	-	Unclassified
54919	**HEATR2; DNAAF5**	**dynein assembly factor 5, axonemal**	10	31	10	1.4	**2E-04**	0.9	**5E-05**	1.2	9E-01	0.7	1E-01	0.9	8E-02	#N/A	#N/A	#N/A
348262	**FAM195B; MCRIP1**	**protein FAM195B isoform 1**	3	14	3	1.4	**2E-03**	0.9	**6E-03**	1.3	9E-01	0.9	**2E-02**	1.0	7E-01	#N/A	#N/A	#N/A

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
10940	**POP1**	**ribonucleases P/MRP protein subunit POP1**	9	33	9	1.4	**2E-05**	1.0	**3E-05**	1.2	7E-02	0.8	2E-01	1.0	4E-01	Ribonuclease activity	Nucleolus	Regulatory/other subunit
84991	**RBM17**	**splicing factor 45**	7	32	7	1.4	**2E-05**	1.0	**9E-06**	1.3	6E-02	0.9	**1E-03**	0.9	**1E-02**	RNA binding	Nucleus	RNA binding protein
5394	**EXOSC10**	**exosome component 10 isoform 1**	9	37	9	1.4	**5E-05**	0.8	**7E-06**	1.3	6E-02	0.8	5E-01	0.9	1E-01	Protein serine/threonine kinase activity	Nucleolus	Unclassified
55154	**MSTO1**	**protein misato homolog 1 isoform a**	3	14	3	1.4	**1E-03**	0.9	**9E-04**	1.1	1E-01	0.8	8E-01	0.9	2E-01	Molecular function unknown	-	Unclassified
51116	**MRPS2**	**28S ribosomal protein S2, mitochondrial**	5	23	5	1.4	**2E-03**	1.1	**2E-04**	1.3	**1E-03**	1.0	**8E-04**	1.0	6E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
4350	**MPG**	**DNA-3-methyladenine glycosylase isoform a**	2	7	2	1.4	**2E-03**	0.8	**1E-02**	1.4	1E+00	1.2	1E-01	1.1	1E-01	Hydrolase activity	Nucleus	Enzyme: Glycosylase
3276	**PRMT1**	**protein arginine N-methyltransferase 1 isoform 1**	11	91	11	1.4	**9E-11**	0.9	**1E-10**	1.1	**2E-03**	**0.7**	**7E-05**	1.0	**9E-03**	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase
55661	**DDX27**	**probable ATP-dependent RNA helicase DDX27**	15	73	15	1.4	**7E-10**	0.8	**6E-11**	1.2	**4E-04**	**0.6**	**4E-05**	0.9	1E-01	Helicase activity	Nucleus	RNA helicase
79892	**MCMBP**	**mini-chromosome maintenance complex-binding protein isoform 1**	7	35	7	1.4	**3E-04**	0.8	**6E-04**	1.4	**1E-02**	0.7	2E-01	0.9	6E-02	#N/A	#N/A	#N/A
126382	**NR2C2AP**	**nuclear receptor 2C2-associated protein isoform 1**	2	10	2	1.4	6E-02	0.9	2E-01	1.2	5E-01	0.9	1E-01	1.0	4E-01	Molecular function unknown	Nucleus	Unclassified
2730	**GCLM**	**glutamate--cysteine ligase regulatory subunit**	7	27	7	1.4	**7E-06**	0.8	**5E-05**	1.6	6E-02	1.3	**1E-05**	1.0	3E-01	Ligase activity	-	Enzyme: Ligase
55421	**C17orf85; NCBP3**	**uncharacterized protein C17orf85**	3	8	3	1.4	**4E-02**	1.3	1E-01	1.2	9E-02	1.3	7E-02	1.2	**3E-02**	#N/A	#N/A	#N/A
54555	**DDX49**	**probable ATP-dependent RNA helicase DDX49**	3	5	3	1.4	#N/A	0.8	#N/A	1.3	#N/A	0.7	#N/A	1.0	#N/A	Helicase activity	Nucleus	RNA helicase
56943	**ENY2**	**transcription and mRNA export factor ENY2 isoform 1**	3	12	3	1.4	**1E-05**	0.9	**9E-05**	1.2	6E-01	0.7	3E-01	0.8	**2E-02**	Transcription factor activity	Nucleus	Transcription factor
29093	**MRPL22**	**39S ribosomal protein L22, mitochondrial isoform a**	4	22	4	1.4	**5E-04**	1.1	**1E-04**	1.2	**2E-03**	1.0	**2E-05**	1.1	5E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
8563	**THOC5**	**THO complex subunit 5 homolog*gi|50959102|ref|NP_001002877.1| THO complex subunit 5 homolog*gi|50959110|ref|NP_001002878.1| THO complex subunit 5 homolog*gi|50959115|ref|NP_001002879.1| THO complex subunit 5 homolog**	4	10	4	1.4	**5E-04**	1.3	**3E-04**	1.5	**2E-02**	1.0	**2E-03**	1.1	1E-01	Molecular function unknown	Nucleus	Unclassified
444	**ASPH**	**aspartyl/asparaginyl beta-hydroxylase isoform a**	13	50	13	1.4	**6E-04**	0.9	**4E-04**	1.2	3E-01	0.8	**1E-02**	1.1	**3E-03**	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase
4851	**NOTCH1**	**neurogenic locus notch homolog protein 1 preproprotein**	11	32	9	1.4	**2E-02**	1.0	**1E-02**	1.0	8E-02	0.7	6E-01	1.3	7E-01	Transcription regulator activity	Plasma membrane	Cell surface receptor
64963	**MRPS11**	**28S ribosomal protein S11, mitochondrial isoform a**	2	10	2	1.4	**3E-02**	1.3	**3E-02**	1.5	**4E-02**	1.2	**4E-02**	1.0	6E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
51010	**EXOSC3**	**exosome complex component RRP40 isoform 1**	1	5	1	1.4	6E-02	0.9	**2E-02**	1.5	8E-01	1.5	3E-01	0.9	2E-01	Ribonuclease activity	Nucleolus	Ribonuclease
790	**CAD**	**CAD protein**	41	239	37	1.4	**2E-16**	0.9	**2E-16**	1.3	7E-01	0.9	**2E-16**	1.0	9E-02	Ligase activity	Cytoplasm	Enzyme: Ligase
10607	**TBL3**	**transducin beta-like protein 3**	12	57	12	1.4	**3E-07**	0.8	**3E-08**	1.2	2E-01	0.7	2E-01	1.0	2E-01	Molecular function unknown	Nucleolus	Unclassified
2961	**GTF2E2**	**transcription initiation factor IIE subunit beta**	5	20	5	1.4	**2E-04**	0.9	**1E-04**	1.3	1E-01	0.7	1E+00	0.9	3E-01	Transcription factor activity	Nucleus	Transcription factor
6541	**SLC7A1**	**PREDICTED: high affinity cationic amino acid transporter 1 isoform X1**	4	18	4	1.4	**4E-03**	0.8	**1E-03**	1.0	2E-01	0.9	4E-01	1.2	5E-02	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
91582	**RPS19BP1**	**active regulator of SIRT1**	1	6	1	1.4	**5E-03**	0.9	1E-01	1.3	8E-01	0.7	3E-01	1.0	8E-01	Molecular function unknown	Nucleolus	Unclassified
55153	**SDAD1**	**protein SDA1 homolog isoform 1**	7	23	2	1.4	2E-01	0.9	2E-01	1.4	7E-01	0.4	5E-01	0.9	6E-02	Molecular function unknown	Nucleolus	Unclassified
29081	**METTL5**	**methyltransferase-like protein 5**	3	15	3	1.4	**1E-02**	0.8	**2E-02**	1.4	3E-01	0.9	**4E-02**	1.0	5E-01	Molecular function unknown	-	Unclassified
3134	**HLA-F**	**PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X1**	3	11	1	1.4	#N/A	0.8	#N/A	1.1	#N/A	0.6	#N/A	0.8	#N/A	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein
65003	**MRPL11**	**39S ribosomal protein L11, mitochondrial isoform a**	3	15	3	1.4	**3E-03**	1.1	**1E-03**	1.2	**3E-02**	1.1	**1E-03**	1.0	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
60481	**ELOVL5**	**elongation of very long chain fatty acids protein 5 isoform 2**	2	14	2	1.4	**1E-02**	0.9	**7E-03**	1.0	4E-01	0.9	6E-01	0.9	5E-01	Molecular function unknown	Integral to membrane	Unclassified
63915	**BLOC1S5**	**biogenesis of lysosome-related organelles complex 1 subunit 5 isoform 1**	2	5	2	1.4	3E-01	0.9	3E-01	1.4	6E-01	1.2	3E-01	1.4	1E-01	#N/A	#N/A	#N/A
55127	**HEATR1**	**HEAT repeat-containing protein 1**	24	83	24	1.4	**6E-07**	0.9	**7E-08**	1.2	8E-01	0.8	1E+00	1.0	3E-01	Molecular function unknown	-	Unclassified
79954	**NOL10**	**nucleolar protein 10 isoform 1**	6	29	5	1.4	**2E-03**	0.8	**3E-03**	1.3	6E-01	0.7	8E-01	1.0	8E-01	Molecular function unknown	Nucleolus	Unclassified
9784	**SNX17**	**sorting nexin-17 isoform 1**	2	5	2	1.4	#N/A	0.7	#N/A	1.1	#N/A	0.7	#N/A	1.0	#N/A	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule
24138	**IFIT5**	**interferon-induced protein with tetratricopeptide repeats 5**	6	12	5	1.4	**1E-02**	0.8	**3E-03**	1.0	**8E-03**	0.7	2E-01	1.0	8E-01	Molecular function unknown	-	Unclassified

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Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
54940	**OCIAD1**	**OCIA domain-containing protein 1 isoform 4**	6	19	6	1.4	**2E-02**	0.9	**1E-02**	1.2	7E-01	0.9	**5E-02**	0.8	7E-01	Molecular function unknown	Nucleus;Cytoplasm	Unclassified
51004	**COQ6**	**ubiquinone biosynthesis monooxygenase COQ6 isoform a**	2	6	2	1.4	1E-01	0.8	7E-02	1.4	1E+00	1.1	**4E-02**	1.0	1E+00	FAD binding	-	Unclassified
6881	**TAF10**	**transcription initiation factor TFIID subunit 10**	1	6	1	1.4	9E-02	1.1	1E-01	1.3	9E-01	0.9	5E-02	1.3	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
23212	**RRS1**	**ribosome biogenesis regulatory protein homolog**	11	39	11	1.4	**9E-07**	1.0	**6E-08**	1.2	**6E-03**	0.6	9E-02	1.0	5E-01	Ribonucleoprotein;Molecular function unknown	Nucleus	Unclassified
51110	**LACTB2**	**beta-lactamase-like protein 2**	4	22	4	1.4	**2E-04**	1.1	**2E-05**	1.4	**7E-03**	1.2	**4E-05**	1.1	8E-01	Molecular function unknown	-	Unclassified
55505	**NOP10**	**H/ACA ribonucleoprotein complex subunit 3**	2	8	2	1.4	**7E-03**	1.0	**6E-03**	1.3	2E-01	0.9	6E-02	0.7	3E-01	Ribonucleoprotein	Nucleolus	Ribonucleoprotein
57187	**THOC2**	**THO complex subunit 2**	13	36	13	1.4	**1E-02**	0.9	**6E-03**	1.3	9E-01	0.9	**2E-05**	0.9	2E-01	Transcription factor activity	Nucleus	Transcription factor
79590	**MRPL24**	**39S ribosomal protein L24, mitochondrial**	6	9	6	1.4	**6E-03**	1.1	**6E-03**	1.2	**3E-02**	0.9	**4E-02**	1.0	8E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
3149	**HMGB3**	**high mobility group protein B3 isoform b**	5	25	4	1.4	**8E-03**	0.9	**7E-03**	1.6	9E-01	0.8	**8E-03**	1.0	9E-01	DNA binding	Nucleus	DNA binding protein
692312	**PPAN-P2RY11**	**PPAN-P2RY11 protein isoform 1**	6	21	6	1.4	#N/A	0.9	#N/A	1.2	#N/A	0.7	#N/A	1.0	#N/A	Molecular function unknown	-	Unclassified
22894	**DIS3**	**exosome complex exonuclease RRP44 isoform a**	12	48	12	1.4	**4E-05**	1.0	**2E-05**	1.4	5E-02	1.0	**6E-04**	1.0	5E-01	RNA binding	Nucleus	RNA binding protein
6867	**TACC1**	**transforming acidic coiled-coil-containing protein 1 isoform 1**	5	14	2	1.4	2E-01	0.8	2E-01	1.2	7E-01	1.2	**1E-02**	1.1	4E-01	Molecular function unknown	Centrosome	Cell cycle control protein
2196	**FAT2**	**PREDICTED: protocadherin Fat 2 isoform X1**	6	16	6	1.4	**6E-03**	0.8	**3E-03**	1.0	1E-01	0.7	1E+00	0.9	5E-01	Cell adhesion molecule activity	-	Adhesion molecule
5359	**PLSCR1**	**PREDICTED: phospholipid scramblase 1 isoform X1**	2	10	2	1.4	6E-02	**0.6**	**3E-02**	0.6	6E-02	**0.4**	**4E-02**	1.0	8E-01	Protein binding	Plasma membrane	Integral membrane protein
26155	**NOC2L**	**nucleolar complex protein 2 homolog**	8	39	8	1.4	**4E-05**	0.9	**7E-05**	1.4	2E-01	0.7	9E-01	1.0	5E-01	Molecular function unknown	Nucleolus	Unclassified
10735	**STAG2**	**PREDICTED: cohesin subunit SA-2 isoform X1**	8	28	8	1.4	**2E-04**	1.2	**1E-04**	1.2	6E-02	1.0	**2E-03**	1.2	**4E-02**	Molecular function unknown	Nucleus	Cell cycle control protein
10849	**CD3EAP**	**DNA-directed RNA polymerase I subunit RPA34 isoform 1**	3	10	3	1.4	**2E-02**	0.9	**1E-02**	1.4	2E-01	0.9	2E-01	1.0	9E-01	Transcription regulator activity	Nucleolus	Transcription regulatory protein
10765	**KDM5B**	**lysine-specific demethylase 5B**	3	7	3	1.4	7E-02	1.2	2E-01	1.0	3E-01	0.8	6E-01	0.9	1E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
4691	**NCL**	**nucleolin**	39	481	39	1.4	**2E-16**	0.8	**2E-16**	1.3	**5E-11**	**0.7**	**7E-11**	1.0	**2E-02**	RNA binding	Nucleolus	RNA binding protein
3145	**HMBS**	**porphobilinogen deaminase isoform 1**	11	33	11	1.4	**9E-03**	1.0	**2E-03**	1.4	**3E-03**	1.0	**3E-02**	1.0	8E-01	Transferase activity	Cytoplasm	Enzyme: Synthase
28998	**MRPL13**	**39S ribosomal protein L13, mitochondrial**	5	24	5	1.4	**9E-05**	1.2	**2E-05**	1.4	**6E-04**	1.1	**3E-04**	1.1	6E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
79707	**NOL9**	**polynucleotide 5'-hydroxyl-kinase NOL9**	5	18	5	1.4	**4E-03**	1.0	**6E-04**	1.4	1E-01	1.1	**2E-03**	1.1	2E-01	Molecular function unknown	Nucleolus	Unclassified
84236	**RHBDD1**	**rhomboid-related protein 4**	1	6	1	1.4	9E-02	1.1	2E-01	1.0	6E-01	1.1	3E-01	1.2	5E-01	Molecular function unknown	-	Unclassified
65993	**MRPS34**	**28S ribosomal protein S34, mitochondrial isoform 1**	5	35	5	1.4	**9E-06**	1.2	**3E-06**	**1.5**	**6E-04**	1.0	**1E-04**	1.1	5E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
84311	**MRPL45**	**39S ribosomal protein L45, mitochondrial isoform 1**	8	33	8	1.4	**1E-03**	1.1	**5E-04**	1.3	**5E-04**	1.0	**2E-04**	0.9	8E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
51433	**ANAPC5**	**anaphase-promoting complex subunit 5 isoform a**	2	8	2	1.4	**5E-02**	1.0	**4E-02**	1.2	**4E-02**	1.0	1E-01	1.0	2E-01	Ubiquitin-specific protease activity	Nucleus	Cell cycle control protein
552889	**ATXN7L3B**	**putative ataxin-7-like protein 3B**	1	6	1	1.4	1E-01	0.6	9E-02	1.0	2E-01	0.6	2E-01	0.8	6E-02	#N/A	#N/A	#N/A
9611	**NCOR1**	**nuclear receptor corepressor 1 isoform 1**	1	6	1	1.4	2E-01	1.0	**3E-02**	1.3	4E-01	0.9	**9E-03**	1.0	9E-01	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor
8270	**LAGE3**	**EKC/KEOPS complex subunit LAGE3**	2	8	2	1.4	2E-01	1.1	1E-01	1.4	2E-01	1.1	2E-01	1.0	7E-01	Molecular function unknown	-	Unclassified
25852	**ARMC8**	**PREDICTED: armadillo repeat-containing protein 8 isoform X1**	3	6	3	1.4	2E-01	0.8	2E-01	1.1	4E-01	0.9	4E-01	1.0	8E-01	Molecular function unknown	-	Unclassified
6382	**SDC1**	**syndecan-1*gi|55749480|ref|NP_001006947.1|syndecan-1**	4	25	4	1.4	**2E-03**	0.8	**2E-03**	1.2	**2E-02**	**0.5**	**1E-02**	0.9	7E-02	Receptor activity	Plasma membrane	Cell surface receptor
57496	**MKL2**	**PREDICTED: MKL/myocardin-like protein 2 isoform X1**	6	13	4	1.4	**2E-02**	1.0	7E-02	1.1	2E-01	1.0	**3E-02**	1.0	7E-01	Transcription factor activity	Nucleus	Transcription factor
871	**SERPINH1**	**serpin H1**	18	140	18	1.4	**4E-14**	0.7	**1E-11**	1.2	**2E-05**	**0.5**	**1E-07**	1.0	1E-01	Heat shock protein activity	Endoplasmic reticulum	Heat shock protein
54795	**TRPM4**	**transient receptor potential cation channel subfamily M member 4 isoform 1**	5	15	5	1.4	**8E-07**	1.4	**5E-05**	**1.5**	**6E-05**	1.0	**2E-03**	1.2	**5E-03**	Intracellular ligand-gated ion channel activity	Plasma membrane	Intracellular ligand gated channel
29105	**C16orf80; CFAP20**	**cilia- and flagella-associated protein 20**	4	14	4	1.4	**2E-02**	0.9	**4E-02**	1.5	9E-01	1.0	9E-02	1.0	7E-01	#N/A	#N/A	#N/A
3105	**HLA-A**	**PREDICTED: HLA class I histocompatibility antigen, A-1 alpha chain isoform X2**	5	19	2	1.4	#N/A	0.9	#N/A	0.9	#N/A	0.7	#N/A	1.2	#N/A	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein
27333	**GOLIM4**	**Golgi integral membrane protein 4**	3	9	3	1.4	**5E-02**	1.1	5E-02	1.2	1E-01	1.0	**1E-02**	1.3	**4E-02**	Molecular function unknown	Golgi apparatus	Integral membrane protein

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
359948	**IRF2BP2**	**interferon regulatory factor 2-binding protein 2 isoform B**	6	24	4	1.4	**1E-02**	1.1	**3E-03**	1.3	6E-02	**0.7**	**1E-03**	1.0	8E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9692	**KIAA0391**	**mitochondrial ribonuclease P protein 3 isoform 2**	5	14	5	1.4	6E-02	1.2	**2E-02**	1.6	8E-02	1.1	5E-01	1.2	1E-01	Molecular function unknown	Mitochondrion	Unclassified
4234	**METTL1**	**tRNA (guanine-N(7)-)-methyltransferase isoform a**	2	6	2	1.4	1E-01	1.0	7E-02	1.3	2E-01	1.0	2E-01	1.0	3E-01	RNA methyltransferase activity	-	RNA methyltransferase
55299	**BRIX1**	**ribosome biogenesis protein BRX1 homolog**	10	44	10	1.4	**4E-06**	0.9	**4E-06**	1.2	8E-01	**0.6**	**3E-05**	1.1	**2E-03**	Molecular function unknown	Nucleolus	Unclassified
5471	**PPAT**	**amidophosphoribosyltransferase proprotein**	9	35	9	1.4	**6E-05**	0.8	**6E-06**	1.3	3E-01	0.9	2E-01	1.0	3E-01	Catalytic activity	Nucleus	Enzyme: Ribosyltransferase
163351	**GBP6**	**guanylate-binding protein 6**	4	10	4	1.4	**1E-03**	1.1	**1E-02**	1.0	9E-02	0.9	5E-02	1.0	3E-01	GTPase activity	-	GTPase
64710	**NUCKS1**	**nuclear ubiquitous casein and cyclin-dependent kinase substrate 1**	3	16	3	1.4	**6E-03**	1.1	**3E-03**	1.5	9E-02	0.7	6E-01	1.0	7E-01	DNA binding	Nucleus	DNA binding protein
51106	**TFB1M**	**dimethyladenosine transferase 1, mitochondrial**	4	16	4	1.4	**4E-02**	1.0	**3E-02**	1.3	2E-01	0.9	2E-01	1.0	4E-01	Transcription factor activity	Mitochondrion	Transcription factor
10523	**CHERP**	**calcium homeostasis endoplasmic reticulum protein**	7	43	7	1.4	**2E-06**	0.9	**1E-07**	1.3	**2E-02**	0.9	**1E-04**	1.0	5E-01	Molecular function unknown	Endoplasmic reticulum membrane	Unclassified
6235	**RPS29**	**40S ribosomal protein S29 isoform 2**	4	21	4	1.4	**3E-04**	1.0	**1E-03**	1.2	6E-02	0.7	2E-01	0.9	1E-01	Structural constituent of ribosome	Ribosome	Ribosomal subunit
54108	**CHRAC1**	**chromatin accessibility complex protein 1**	1	3	1	1.4	**9E-03**	0.8	**2E-02**	1.4	7E-02	0.7	8E-02	0.9	4E-01	DNA binding	Nucleus	DNA binding protein
7866	**IFRD2**	**interferon-related developmental regulator 2**	3	8	3	1.4	6E-02	0.8	9E-02	1.5	1E-01	0.6	5E-02	1.2	3E-01	Molecular function unknown	Nucleus	Unclassified
1362	**CPD**	**carboxypeptidase D isoform 1**	12	53	12	1.4	**4E-08**	0.9	**1E-08**	1.3	9E-02	0.7	6E-01	1.1	5E-02	Carboxypeptidase activity	Plasma membrane	Carboxypeptidase
55871	**CBWD1**	**COBW domain-containing protein 1 isoform 1**	3	6	3	1.4	**4E-03**	1.2	**3E-03**	**1.6**	**2E-03**	1.3	2E-01	1.3	3E-01	Molecular function unknown	-	Unclassified
23215	**PRRC2C**	**protein PRRC2C**	19	77	18	1.4	**5E-05**	1.1	**3E-05**	1.3	**9E-03**	1.0	**4E-03**	1.1	2E-01	#N/A	#N/A	#N/A
4704	**NDUFA9**	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial**	8	23	8	1.4	**1E-03**	0.8	**2E-02**	1.1	**2E-02**	1.0	**3E-02**	1.0	4E-01	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase
7515	**XRCC1**	**DNA repair protein XRCC1**	3	14	3	1.4	**2E-03**	1.1	**4E-03**	**1.6**	**5E-02**	1.0	7E-02	1.3	8E-02	DNA repair protein	Nucleus	DNA repair protein
5982	**RFC2**	**replication factor C subunit 2 isoform 1**	4	17	4	1.4	5E-02	0.9	**4E-02**	1.3	6E-01	0.8	8E-01	1.1	3E-01	DNA binding	Nucleolus	DNA binding protein
740;	**MRPL49**	**39S ribosomal protein L49, mitochondrial**	4	9	4	1.4	**8E-06**	1.2	**4E-06**	1.2	**4E-02**	1.1	**2E-03**	1.2	7E-02	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
8985	**PLOD3**	**procollagen-lysine,2-oxoglutarate 5-dioxygenase 3**	16	70	16	1.4	**9E-05**	0.8	**8E-05**	1.4	**8E-03**	1.0	**1E-05**	1.0	2E-01	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase
6597	**SMARCA4**	**transcription activator BRG1 isoform A**	13	52	8	1.4	**3E-04**	1.2	**3E-04**	1.4	**1E-04**	1.1	**6E-03**	1.1	6E-01	Transcription factor activity	Nucleus	Transcription factor
9567	**GTPBP1**	**GTP-binding protein 1**	4	17	4	1.4	**4E-04**	1.0	**9E-04**	1.5	1E-01	1.2	**1E-03**	1.0	6E-01	GTPase activity	Cytoplasm	GTPase
5431	**POLR2B**	**DNA-directed RNA polymerase II subunit RPB2 isoform 1**	19	76	19	1.4	**7E-06**	0.9	**4E-06**	1.4	6E-01	0.8	**4E-02**	1.0	8E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
135228	**CD109**	**PREDICTED: CD109 antigen isoform X1**	6	31	6	1.4	**5E-04**	1.0	**1E-03**	1.0	**5E-03**	0.8	**3E-02**	1.1	**3E-02**	Molecular function unknown	Plasma membrane	Unclassified
79882	**ZC3H14**	**zinc finger CCCH domain-containing protein 14 isoform 1**	4	16	4	1.4	**3E-02**	0.9	**2E-02**	1.3	2E-01	0.8	1E-01	1.0	1E+00	RNA binding	Nucleus	RNA binding protein
2969	**GTF2I**	**general transcription factor II-I isoform 1**	19	69	19	1.4	**8E-05**	1.0	**3E-05**	1.3	**9E-03**	0.9	**4E-04**	0.9	**2E-02**	Transcription factor activity	Nucleus	Transcription factor
64327	**LMBR1**	**limb region 1 protein homolog**	1	6	1	1.4	9E-02	1.8	1E-01	1.7	9E-02	1.7	2E-01	1.3	**3E-02**	Receptor activity	Plasma membrane	Cell surface receptor
23481	**PES1**	**pescadillo homolog isoform 1**	15	68	15	1.4	**2E-05**	0.8	**3E-07**	1.2	**2E-02**	**0.6**	**3E-02**	1.0	8E-01	Protein binding	Nucleus	Cell cycle control protein
27316	**RBMX**	**RNA-binding motif protein, X chromosome isoform 1**	18	125	6	1.4	**2E-14**	1.0	**1E-14**	1.2	**4E-02**	0.8	**4E-04**	1.3	2E-01	RNA binding	Nucleus	RNA binding protein
117159	**DCD**	**dermcidin isoform 2 preproprotein**	4	20	4	1.4	**2E-04**	1.3	**7E-04**	**1.7**	**3E-04**	**1.9**	**3E-04**	**2.2**	**8E-04**	Molecular function unknown	Extracellular	Secreted polypeptide
51253	**MRPL37**	**39S ribosomal protein L37, mitochondrial**	6	25	6	1.4	**4E-04**	1.1	**5E-05**	1.3	**4E-05**	1.0	**1E-04**	1.1	1E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
2956	**MSH6**	**DNA mismatch repair protein Msh6 isoform 1**	7	28	7	1.4	**8E-04**	0.9	**3E-04**	1.4	9E-01	0.8	9E-01	1.0	2E-01	DNA binding	Nucleus	DNA repair protein
285855	**RPL7L1**	**PREDICTED: 60S ribosomal protein L7-like 1 isoform X1**	4	21	4	1.4	**3E-06**	0.8	**8E-06**	1.2	**1E-02**	**0.6**	**3E-04**	1.0	6E-01	Structural constituent of ribosome	-	Ribosomal subunit
22938	**SNW1**	**SNW domain-containing protein 1**	9	44	9	1.4	**2E-05**	0.9	**1E-05**	1.3	6E-01	0.8	3E-01	1.0	5E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
9249	**DHRS3**	**short-chain dehydrogenase/reductase 3**	2	6	2	1.4	2E-01	1.1	2E-01	**1.5**	**4E-02**	2.1	1E-01	1.2	4E-01	Catalytic activity	-	Enzyme: Dehydrogenase
3151	**HMGN2**	**non-histone chromosomal protein HMG-17**	2	16	2	1.4	**1E-04**	0.9	**1E-04**	1.4	7E-01	**0.6**	**5E-02**	1.1	**4E-02**	Transcription regulator activity	Nucleus	Transcription regulatory protein
400506	**C16orf88; KNOP1**	**PREDICTED: lysine-rich nucleolar protein 1 isoform X1**	4	13	4	1.4	**6E-04**	0.8	**3E-03**	1.3	4E-01	0.6	4E-01	0.9	3E-01	#N/A	#N/A	#N/A
11198	**SUPT16H**	**FACT complex subunit SPT16**	33	156	33	1.4	**8E-08**	0.9	**7E-08**	1.4	1E+00	0.8	1E+00	1.0	4E-01	Transcription factor activity	Nucleus	Transcription factor
2182	**ACSL4**	**PREDICTED: long-chain-fatty-acid--CoA ligase 4 isoform X1**	11	46	8	1.4	**6E-05**	0.8	**1E-04**	1.3	2E-01	0.9	**8E-03**	1.0	**4E-02**	Ligase activity	Microsome	Enzyme: Ligase

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						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
8091	**HMGA2**	**high mobility group protein HMGI-C isoform c**	5	24	5	1.4	**9E-04**	0.8	**5E-05**	1.7	2E-01	**1.7**	**1E-04**	1.1	**5E-03**	Transcription factor activity	Nucleus	Transcription factor
5441	**POLR2L**	**DNA-directed RNA polymerases I, II, and III subunit RPABC5**	1	8	1	1.4	**4E-03**	0.8	**1E-02**	1.3	3E-01	0.8	9E-01	0.8	5E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
54539	**NDUFB11**	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial isoform 1**	2	10	2	1.4	6E-02	0.9	**4E-02**	1.2	5E-01	1.0	**3E-02**	1.0	6E-01	Oxidoreductase activity	-	Enzyme: Oxidoreductase
55703	**POLR3B**	**DNA-directed RNA polymerase III subunit RPC2 isoform 1**	2	8	2	1.4	1E-01	1.0	1E-01	1.1	6E-01	0.8	6E-01	1.0	9E-01	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase
79971	**WLS**	**protein wntless homolog isoform 1**	3	7	3	1.4	**3E-02**	0.8	**1E-02**	1.1	3E-01	0.7	9E-01	0.9	5E-01	#N/A	#N/A	#N/A
11342	**RNF13**	**E3 ubiquitin-protein ligase RNF13**	3	10	3	1.4	6E-02	0.7	5E-02	**1.6**	**1E-02**	1.1	**4E-02**	0.9	5E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
10051	**SMC4**	**structural maintenance of chromosomes protein 4 isoform 1**	9	27	9	1.4	**4E-03**	0.7	**2E-02**	1.1	**7E-03**	0.6	3E-01	1.0	8E-01	Structural constituent of chromatin	Nucleus	Structural protein
51069	**MRPL2**	**39S ribosomal protein L2, mitochondrial isoform 1**	3	10	3	1.4	**3E-02**	1.1	**2E-02**	1.3	**2E-02**	1.1	**2E-02**	1.0	1E+00	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
6391	**SDHC**	**succinate dehydrogenase cytochrome b560 subunit, mitochondrial isoform 1**	2	12	2	1.4	1E-01	1.3	1E-01	1.3	2E-01	1.1	9E-02	1.1	5E-01	Catalytic activity	Mitochondrial membrane	Enzyme: Dehydrogenase
3105	**HLA-A**	**HLA class I histocompatibility antigen, A-1 alpha chain**	5	37	1	1.4	#N/A	0.8	#N/A	0.8	#N/A	0.4	#N/A	0.9	#N/A	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein
7384	**UQCRC1**	**cytochrome b-c1 complex subunit 1, mitochondrial**	16	105	15	1.4	**4E-05**	1.0	**9E-06**	1.0	**1E-02**	0.8	1E-01	1.0	1E-01	Catalytic activity	Mitochondrion	Enzyme: Reductase
4668	**NAGA**	**PREDICTED: alpha-N-acetylgalactosaminidase isoform X1**	2	8	2	1.4	7E-02	**1.7**	**4E-02**	1.8	7E-02	2.0	6E-02	1.1	4E-01	Catalytic activity	Lysosome	Enzyme: Glycosidase
114880	**OSBPL6**	**oxysterol-binding protein-related protein 6 isoform c**	2	8	2	1.4	**3E-02**	1.3	**2E-02**	1.3	3E-01	1.0	2E-01	1.0	2E-01	Transporter activity;Lipid binding	Cytoplasm	Transport/cargo protein
51096	**UTP18**	**U3 small nucleolar RNA-associated protein 18 homolog**	5	14	5	1.4	**2E-04**	1.0	**7E-03**	1.2	1E-01	1.0	**2E-02**	1.1	7E-02	Molecular function unknown	Nucleolus	Unclassified
2720	**GLB1**	**beta-galactosidase isoform a preproprotein**	7	32	7	1.4	**3E-04**	1.2	**1E-04**	**1.6**	**6E-03**	**1.6**	**1E-04**	1.0	3E-01	Catalytic activity	Lysosome	Enzyme: Hydroxylase
10519	**CIB1**	**calcium and integrin-binding protein 1 isoform a**	2	10	2	1.4	**1E-02**	1.0	**8E-03**	1.6	4E-01	0.8	**5E-02**	1.0	7E-01	Calcium ion binding	Nucleus	Calcium binding protein
8795	**TNFRSF10B**	**tumor necrosis factor receptor superfamily member 10B isoform 1**	2	10	2	1.4	**2E-02**	0.8	6E-02	1.1	7E-02	0.9	9E-02	1.3	1E-01	Receptor activity	Plasma membrane	Cell surface receptor
26873	**OPLAH**	**5-oxoprolinase**	8	22	8	1.4	**3E-02**	1.4	**1E-02**	**1.6**	**4E-02**	**1.5**	**1E-02**	1.1	**5E-02**	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase
10196	**PRMT3**	**protein arginine N-methyltransferase 3 isoform 1**	7	31	7	1.4	**6E-04**	0.9	**3E-04**	1.4	4E-01	0.9	**2E-03**	1.0	9E-02	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase
1211	**CLTA**	**clathrin light chain A isoform b**	8	43	7	1.4	**1E-05**	**0.7**	**9E-05**	**1.8**	**5E-04**	1.3	**5E-05**	1.0	6E-01	Structural molecule activity	Cytoplasm	Structural protein
6727	**SRP14**	**signal recognition particle 14 kDa protein**	7	45	7	1.4	**7E-05**	0.9	**2E-05**	1.6	3E-01	0.9	**3E-02**	0.9	**2E-03**	RNA binding	Cytoplasm	RNA binding protein
28973	**MRPS18B**	**28S ribosomal protein S18b, mitochondrial**	3	18	3	1.4	**7E-03**	1.2	**2E-03**	1.4	**7E-04**	0.8	8E-01	0.9	3E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
64960	**MRPS15**	**28S ribosomal protein S15, mitochondrial**	5	18	5	1.4	**2E-02**	1.3	**3E-03**	1.3	**5E-03**	1.2	**5E-03**	1.2	1E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
57515	**SERINC1**	**serine incorporator 1**	2	8	2	1.4	**4E-03**	0.8	**3E-02**	1.0	3E-01	0.9	2E-01	1.2	3E-01	Protein binding	Plasma membrane	Integral membrane protein
84298	**LLPH**	**protein LLP homolog**	1	8	1	1.4	5E-02	0.8	**4E-02**	1.1	2E-01	**0.5**	**1E-02**	0.8	6E-02	Molecular function unknown	-	Unclassified
6749	**SSRP1**	**FACT complex subunit SSRP1**	17	92	17	1.4	**8E-07**	0.8	**6E-07**	1.4	4E-01	0.7	1E+00	0.9	6E-02	Transcription factor activity	Nucleus	Transcription factor
54433	**GAR1**	**H/ACA ribonucleoprotein complex subunit 1**	5	41	5	1.4	**2E-04**	1.2	**2E-04**	1.3	**2E-03**	1.1	**7E-04**	1.1	**4E-02**	Ribonucleoprotein	Nucleolus	Enzyme: Reductase
29127	**RACGAP1**	**PREDICTED: rac GTPase-activating protein 1 isoform X1**	2	8	2	1.4	6E-02	0.6	1E-01	1.2	6E-02	0.8	3E-01	1.4	2E-01	GTPase activator activity	Nucleus	GTPase activating protein
23268	**DNMBP**	**dynamin-binding protein**	4	11	4	1.4	5E-02	1.0	2E-01	1.2	8E-01	0.8	3E-01	1.0	5E-01	Guanyl-nucleotide exchange factor activity	Extracellular	Guanine nucleotide exchange factor
22803	**XRN2**	**5'-3' exoribonuclease 2**	15	55	14	1.4	**4E-07**	1.0	**7E-08**	1.3	**6E-04**	0.8	2E-01	1.0	1E-01	Ribonuclease activity	Nucleolus;Nucleus;Cytoplasm	Ribonuclease
1E+08	**JMJD7**	**jmjC domain-containing protein 7**	2	8	2	1.4	5E-02	1.4	**2E-02**	**2.0**	**4E-02**	**1.8**	**3E-02**	0.9	2E-01	Molecular function unknown	-	Unclassified
7818	**DAP3**	**28S ribosomal protein S29, mitochondrial isoform 1*gi|315434212|ref|NP_001186778.1| 28S ribosomal protein S29, mitochondrial isoform 1*gi|4758118|ref|NP_004623.1| 28S ribosomal protein S29, mitochondrial isoform 1**	6	26	6	1.4	**4E-03**	1.1	**8E-03**	1.3	**1E-03**	0.9	**3E-03**	1.0	3E-01	Ribonucleoprotein	Mitochondrion	Ribosomal subunit
56942	**CMC2**	**COX assembly mitochondrial protein 2 homolog**	2	9	2	1.4	**8E-03**	1.0	**2E-02**	1.5	2E-01	**1.5**	**4E-02**	1.1	8E-02	#N/A	#N/A	#N/A

Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract – a role for antioxidants in skin health
Supplementary table 1: List of proteins quantified in this study

Entrez Gene ID	Gene Symbol	Description	# Peptides	# PSMs	# Unique Peptides	[NHEK-Ad-DPE-V / NHEK-Ad]		[NHEK-Ad-DPE-V-Vit E / NHEK-Ad]		[NHEK-Ad-DPE / NHEK-Ad]		[NHEK-Ad-DPE-Vit E / NHEK-Ad]		[NHEK-Ad-Vit E / NHEK-Ad]		Molecular Function	Primary Localization	Molecular Class
						Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value	Median Fold change	p-value			
22992	**KDM2A**	**lysine-specific demethylase 2A isoform a**	2	8	2	1.4	8E-02	0.8	1E-01	1.3	3E-01	0.8	8E-01	0.9	6E-01	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein
7386	**UQCRFS1**	**cytochrome b-c1 complex subunit Rieske, mitochondrial**	7	29	7	1.4	**8E-04**	1.4	**6E-03**	1.2	**4E-03**	1.3	**1E-03**	1.2	**8E-04**	Catalytic activity	Mitochondrion	Enzyme: Reductase
6558	**SLC12A2**	**solute carrier family 12 member 2 isoform 1**	3	7	3	1.4	**2E-02**	1.0	**4E-02**	1.2	7E-01	0.7	7E-01	1.0	8E-01	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein
11137	**PWP1**	**periodic tryptophan protein 1 homolog**	4	10	3	1.4	8E-02	1.0	5E-02	1.3	9E-01	0.7	6E-01	0.9	7E-01	Transcription regulator activity	Nucleus	Transcription regulatory protein
1001	**CDH3**	**cadherin-3 preproprotein**	5	30	4	1.4	**4E-03**	0.8	**5E-05**	1.2	**6E-03**	0.6	8E-02	1.1	**2E-02**	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule
284695	**ZNF326**	**DBIRD complex subunit ZNF326 isoform 1**	4	11	4	1.4	8E-02	1.0	5E-02	1.4	6E-01	1.0	2E-01	1.0	8E-01	DNA binding	Nucleolus	DNA binding protein
7162	**TPBG**	**trophoblast glycoprotein*gi|5729718|ref|NP_006661.1| trophoblast glycoprotein**	5	36	5	1.4	**2E-04**	0.7	**6E-05**	1.4	**3E-02**	0.8	3E-01	1.1	2E-01	Molecular function unknown	Plasma membrane	Integral membrane protein
23107	**MRPS27**	**28S ribosomal protein S27, mitochondrial isoform 1**	11	57	11	1.4	**2E-04**	1.1	**3E-05**	1.4	**1E-03**	0.9	**8E-06**	0.9	2E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
5452;	**POU2F2**	**POU domain, class 2, transcription factor 2 isoform 4**	4	8	4	1.4	**2E-02**	0.9	**2E-02**	1.3	4E-01	0.9	2E-01	1.0	3E-01	Transcription factor activity	Nucleus	Transcription factor
4089	**SMAD4**	**mothers against decapentaplegic homolog 4**	3	13	3	1.4	**5E-02**	0.9	**2E-02**	1.3	7E-01	0.9	**1E-02**	0.9	4E-01	Transcription factor activity	Nucleus	Transcription factor
667	**DST**	**dystonin isoform 1e**	113	681	63	1.4	**2E-16**	1.2	**9E-07**	**0.6**	**2E-16**	**0.3**	**2E-16**	0.7	**2E-16**	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein
5496	**PPM1G**	**protein phosphatase 1G**	8	34	8	1.4	**5E-03**	0.9	**4E-03**	1.4	3E-01	0.7	2E-01	0.9	**3E-02**	Protein serine/threonine phosphatase activity	Nucleoplasm	Serine/threonine phosphatase
64965	**MRPS9**	**28S ribosomal protein S9, mitochondrial**	6	30	6	1.4	**7E-06**	1.0	**1E-05**	1.4	**1E-02**	1.0	**3E-04**	1.0	9E-01	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit
567	**B2M**	**beta-2-microglobulin**	3	18	3	1.4	**2E-02**	0.7	7E-02	0.8	**3E-02**	**0.4**	**3E-02**	0.9	**5E-02**	MHC class I receptor activity;MHC class II receptor activity	Extracellular	MHC complex protein