Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
AHSG	197	alpha-2-HS-glycoprotein preproprotein	NP_001613.2	1	2	2	3	**16.16**	**23.57**	6.5	6.43	284	987.7	2	2	727	197	alpha-2-HS-glycoprotein	Defense/immunity protein activity	Extracellular	Secreted polypeptide	Cell communication;Signal transduction	CYSTATIN;SP	Yes
GFPT2	9945	glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2	NP_005101.1	1	1	4	6	**12.97**	**9.75**					1	1	4842	9945	glutamine-fructose-6-phosphate transaminase 2	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase	Metabolism;Energy pathways	SIS	Yes
OR5AC2	81050	olfactory receptor 5AC2	NP_473447.1	1	1	1	3	**11.84**	**11.24**					1	1	15030	81050	olfactory receptor, family 5, subfamily AC,member 2	G-protein coupled receptor activity	Integral to membrane	G protein coupled receptor	Cell communication;Signal transduction	TM	Yes
WDR78	79819	WD repeat-containing protein 78 isoform 1	NP_079039.4	2	1	1	1	**6.25**	**5.9**					1	1	8017	79819	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;WD40	Yes
TMOD2	29767	tropomodulin-2 isoform a	NP_055363.1	2	1	2	6	**5.87**	**6.3**					1	1	4237	29767	tropomodulin 2 (neuronal)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
RNGTT	8732	mRNA-capping enzyme isoform a	NP_003791.3	3	2	2	7	**5.11**	**3.25**	1.01	0.74	8.9	4.2	3	3	4621	8732	RNA guanylyltransferase and 5`-phosphatase	Catalytic activity	Nucleus	Enzyme: Adenosyltransferase	Metabolism;Energy pathways	DSPC	Yes
JRK	8629	jerky protein homolog isoform a	NP_003715.3	2	1	1	1	**4.72**	**4.09**					1	1	4442	8629	jerky homolog (mouse)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
LOC100506514	100506514	uncharacterized protein LOC100506514	XP_011538667.1	1	1	1	1	**4.55**	**4.11**					1	1									
CPNE2	221184	copine-2	NP_689940.3	10	1	2	6	**3.9**	**6.59**					1	1	5015	221184	copine II	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	C2;VWA	Yes
PTGS2	5743	prostaglandin G/H synthase 2 precursor	NP_000954.1	1	1	1	1	**3.59**	**4.88**					1	1	2599	5743	prostaglandin-endoperoxide synthase 2(prostaglandin G/H synthase and cyclooxygenase)	Peroxidase activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	SP;EGF	Yes
SCG3	29106	secretogranin-3 isoform 1 precursor	NP_037375.2	2	1	1	2	**3.44**	**2.31**					1	1	11538	29106	secretogranin III	Molecular function unknown	Secretory granule	Secreted polypeptide	Protein metabolism	SP	Yes
SURF4	6836	surfeit locus protein 4 isoform 1	NP_149351.1	5	4	4	27	**3.28**	**4.03**	22.56	18.1	141.1	137.9	2	2	1715	6836	surfeit 4	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	TM	Yes
MAPK12	6300	mitogen-activated protein kinase 12 isoform 1	NP_002960.2	7	1	2	4	**3.16**	**5.57**					1	1	3868	6300	mitogen-activated protein kinase 12	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
CYR61	3491	protein CYR61 precursor	NP_001545.2	1	10	10	23	**3.13**	**3.25**	2.89	9.86	34.9	179	14	14	9089	3491	cysteine-rich, angiogenic inducer, 61	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell communication;Signal transduction	SP;IB;VWC;TSP1;CT	Yes
GSTM2	2946	glutathione S-transferase Mu 2 isoform 1	NP_000839.1	3	1	2	3	**3.12**	**4.98**					1	1	710	2946	glutathione S-transferase M2 (muscle)	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase	Metabolism;Energy pathways	-	No
TDO2	6999	tryptophan 2,3-dioxygenase	NP_005642.1	1	1	1	2	**3.03**	**4.15**	1.85	1.46	7.9	8.6	2	2	1847	6999	tryptophan 2,3-dioxygenase	Catalytic activity	Cytoplasm	Enzyme: Mutase	Metabolism;Energy pathways	CC	Yes
MDK	4192	midkine isoform a precursor	NP_002382.1	2	3	3	5	**2.97**	**3.14**	0.07	13	0.4	80.6	3	3	1200	4192	midkine (neurite growth-promoting factor 2)	Cytokine activity	Extracellular	Cytokine	Cell communication;Signal transduction	SP	Yes
STAU1	6780	double-stranded RNA-binding protein Staufen homolog 1 isoform c	NP_001032405.1	1	1	17	42	**2.97**	**2.36**					1	1	3422	6780	staufen, RNA binding protein (Drosophila)	RNA binding;Transporter activity	Endoplasmic reticulum	RNA binding protein;Transport/cargo protein	Protein metabolism	DSRM	Yes
CELA3A	10136	chymotrypsin-like elastase family member 3A preproprotein	NP_005738.4	1	1	1	1	**2.89**	**3.26**					1	1	6497	10136	elastase 3A, pancreatic (protease E)	Peptidase activity	Extracellular	Protease	Protein metabolism	SP;TRYPSIN	Yes
ALDH1A1	216	retinal dehydrogenase 1	NP_000680.2	1	6	8	39	**2.86**	**2.21**	3.82	4.33	50.4	43.6	19	19	1	216	aldehyde dehydrogenase 1 family, member A1	Aldehyde dehydrogenase activity	-	Enzyme: Dehydrogenase	Aldehyde metabolism	A2M	Yes
CCDC175	729665	coiled-coil domain-containing protein 175	NP_001157871.1	1	1	1	2	**2.73**	**3.55**					1	1									
DDX53	168400	DEAD box protein 53	NP_874358.2	1	1	1	1	**2.73**	**3.29**					1	1	6466	168400	DEAD (Asp-Glu-Ala-Asp) box polypeptide 53	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH;DEXDc;HELIC	No
RCN3	57333	reticulocalbin-3 precursor	NP_065701.2	1	8	8	19	**2.64**	**2.2**	8.62	6.01	77.2	41.3	9	9	17962	57333	reticulocalbin 3, EF-hand calcium binding domain	Calcium ion binding	-	Calcium binding protein	Biological_process unknown	SP;EF	Yes
ICAM1	3383	intercellular adhesion molecule 1 precursor	NP_000192.2	1	15	15	48	**2.57**	**2.62**	5.67	6.54	75	92.4	21	21	996	3383	intercellular adhesion molecule 1 (CD54), humanrhinovirus receptor	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	Ig_LIKE;IG;TM;SP	Yes
FOSL1	8061	fos-related antigen 1 isoform 1	NP_005429.1	3	1	1	4	**2.47**	**2.21**	25.2	28.98	108	112.9	2	2	643	8061	FOS-like antigen 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 1	NP_001273510.1	4	1	1	1	**2.43**	**2.9**					1	1	13870	57661	None	Molecular function unknown	-	Unclassified	Biological_process unknown	RING	Yes
KYNU	8942	kynureninase isoform a	NP_003928.1	2	14	14	30	**2.35**	**3.57**	5.1	2.69	50.8	39.9	16	16	8940	8942	kynureninase (L-kynurenine hydrolase)	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
ZNF318	24149	zinc finger protein 318	NP_055160.2	1	1	1	2	**2.33**	**2.1**					1	1	11707	24149	zinc finger protein 318	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;ZNFC2	No

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ABCA2	20	ATP-binding cassette sub-family A member 2 isoform b	NP_997698.1	2	1	1	1	**2.31**	**2.91**					1	1	8967	20	ATP-binding cassette, sub-family A (ABC1),member 2	Transporter activity	Lysosome	Transport/cargo protein	Transport	TM;AAA	Yes
AKAP12	9590	A-kinase anchor protein 12 isoform 1	NP_005091.2	2	35	35	87	**2.28**	**2.45**	3.7	3.51	59.2	60.2	42	42	5263	9590	A kinase (PRKA) anchor protein (gravin) 12	Cytoskeletal anchoring activity	Cytoplasm;Nucleus	Anchor protein	Cell growth and/or maintenance	PkinA_anch	Yes
CTSL	1514	cathepsin L1 isoform 1 preproprotein	NP_001244900.1	1	1	1	1	**2.24**	**2.14**					1	1									
POU2F2	5452	POU domain, class 2, transcription factor 2 isoform 1	NP_001193954.1	6	1	2	3	**2.23**	**2.07**					1	1	1251	5452	POU domain, class 2, transcription factor 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	POU;HOX	No
WRAP53	55135	telomerase Cajal body protein 1	NP_001137463.1	1	1	1	1	**2.2**	**3.5**					1	1	7670	55135	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	WD40	No
NUMBL	9253	numb-like protein isoform a	NP_004747.1	2	1	3	4	**2.15**	**3.41**					1	1	4931	9253	numb homolog (Drosophila)-like	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	PTB;CC	Yes
C11orf84	144097	uncharacterized protein C11orf84	NP_612480.1	1	1	1	2	**2.11**	**2.34**					1	1	14064	144097	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
TFPI2	7980	tissue factor pathway inhibitor 2 isoform 1 precursor	NP_006519.1	3	8	8	46	**2.08**	**2.24**	6.86	7	73.2	77.1	21	19	8962	7980	tissue factor pathway inhibitor 2	Protease inhibitor activity	Extracellular	Protease inhibitor	Protein metabolism	SP;KUNITZ	No
KRT23	25984	keratin, type I cytoskeletal 23 isoform 1	NP_056330.3	8	15	17	50	**2.07**	**2.78**	5.75	3.99	65	60	25	25	5863	25984	keratin 23 (histone deacetylase inducible)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	Yes
GTF2H2C_2	730394	general transcription factor IIH subunit 2-like protein	NP_001035955.1	2	1	1	1	**2.06**	**2.45**					1	1									
UQCC3	790955	ubiquinol-cytochrome-c reductase complex assembly factor 3	NP_001078841.1	1	1	1	2	**2.06**	**2.13**					1	1									
TRIML2	205860	probable E3 ubiquitin-protein ligase TRIML2 isoform 1	NP_001290348.1	2	2	2	4	**2.01**	**4.42**	16.84	20.37	50.7	201.3	2	2	8696	205860	None	Molecular function unknown	-	Unclassified	Biological_process unknown	PRY;SPRY	No
COL17A1	1308	collagen alpha-1(XVII) chain	NP_000485.3	2	26	26	69	**0.5**	**0.43**	13.12	16.26	42.4	45.4	39	39	223	1308	collagen, type XVII, alpha 1	Structural molecule activity	Plasma membrane	Anchor protein	Cell adhesion	TM;COLL	Yes
KRT17	3872	keratin, type I cytoskeletal 17	NP_000413.1	2	27	48	425	**0.5**	**0.29**	15	24.72	92.1	89.6	111	111	1019	3872	keratin 17	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
DOCK1	1793	dedicator of cytokinesis protein 1 isoform 1	NP_001277152.1	2	2	3	5	**0.5**	**0.24**					1	1	3240	1793	dedicator of cytokinesis 1	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	SH3;CC	Yes
DST	667	dystonin isoform 1e precursor	NP_001714.1	1	36	59	139	**0.49**	**0.48**	14.27	11.61	47.5	37.1	42	42	222	667	dystonin	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;CC;SPECTRIN;SH3;EF;PLEC;GAS2	Yes
DNAH10	196385	dynein heavy chain 10, axonemal	NP_997320.2	1	1	1	2	**0.49**	**0.38**	1.37	15.59	0.9	8.4	2	2	13473	196385	dynein, axonemal, heavy polypeptide 10	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	CC;AAA	Yes
TMPRSS5	80975	transmembrane protease serine 5 isoform 1	NP_110397.2	3	1	1	1	**0.49**	**0.26**					1	1	5995	80975	transmembrane protease, serine 5 (spinesin)	Serine-type peptidase activity	Plasma membrane	Serine protease	Protein metabolism	TM;SR;TRYPSIN	No
AIG1	51390	androgen-induced gene 1 protein isoform a	NP_057192.2	2	1	1	2	**0.49**	**0.18**					1	1	16346	51390	androgen-induced 1	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
KRT6B	3854	keratin, type II cytoskeletal 6B	NP_005546.2	5	5	50	709	**0.46**	**0.31**	26.5	41.06	42.6	44.9	11	11	1012	3854	keratin 6B	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
PLEKHG3	26030	pleckstrin homology domain-containing family G member 3	NP_001295076.1	1	1	1	1	**0.45**	**0.47**					1	1	17861	26030	pleckstrin homology domain containing, familyG (with RhoGef domain) member 3	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH	No
KRT6A	3853	keratin, type II cytoskeletal 6A	NP_005545.1	6	3	51	793	**0.45**	**0.39**	17.33	26.04	44.4	59.4	30	30	1011	3853	keratin 6A	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
COL14A1	7373	collagen alpha-1(XIV) chain precursor	NP_066933.1	1	2	2	5	**0.45**	**0.29**	20.56	125.71	18.6	83.4	4	4	379	7373	collagen, type XIV, alpha 1 (undulin)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	VWA;TSPN;COLL;SP;FN3	Yes
C14orf2	9556	6.8 kDa mitochondrial proteolipid isoform 2	NP_001120865.1	2	1	1	2	**0.45**	**0.25**					1	1	5199	9556	chromosome 14 open reading frame 2	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
TRIM29	23650	tripartite motif-containing protein 29	NP_036233.2	1	6	6	8	**0.44**	**0.47**	9.69	8.12	9.5	8.6	5	5	10280	23650	tripartite motif-containing 29	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BBOX;CC	Yes
DSC3	1825	desmocollin-3 isoform Dsc3a preproprotein	NP_001932.2	2	10	10	19	**0.44**	**0.4**	11.82	19	19.8	29.3	14	14	2604	1825	desmocollin 3	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	SP;Cadherin;TM	Yes
EBP	10682	3-beta-hydroxysteroid-Delta(8), Delta(7)-isomerase	NP_006570.1	1	1	1	6	**0.44**	**0.25**	46.2	86.24	36.2	39.4	3	3	2192	10682	emopamil binding protein (sterol isomerase)	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase	Metabolism;Energy pathways	TM	No
RAB25	57111	ras-related protein Rab-25	NP_065120.2	1	2	2	4	**0.42**	**0.42**	1.28	15.06	0.8	9.1	2	2	6698	57111	RAB25, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB	No
TMEM40	55287	transmembrane protein 40 isoform a	NP_001271335.1	3	1	1	2	**0.4**	**0.47**					1	1	8559	55287	transmembrane protein 40	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No
SLC37A3	84255	sugar phosphate exchanger 3 isoform 2	NP_115671.1	1	1	1	1	**0.4**	**0.37**					1	1	15381	84255	solute carrier family 37(glycerol-3-phosphate transporter), member 3	Transporter activity	Integral to membrane	Membrane transport protein	Transport	TM	No

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FAM188B	84182	protein FAM188B	NP_115598.2	1	1	1	1	**0.39**	**0.31**					1	1	13387	84182	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
STUB1	10273	E3 ubiquitin-protein ligase CHIP isoform a	NP_005852.2	2	2	2	6	**0.39**	**0.26**	39.54	106.68	27.1	50.2	3	3	6232	10273	STIP1 homology and U-box containing protein 1	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	TPR;UBOX;CC	No
KRT15	3866	keratin, type I cytoskeletal 15	NP_002266.2	2	17	29	227	**0.38**	**0.33**	34.85	46.38	110.1	133.9	45	43	1009	3866	keratin 15	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
ZSWIM8	23053	zinc finger SWIM domain-containing protein 8 isoform 3	NP_001229417.1	3	2	2	4	**0.38**	**0.2**	236.47	729.39	197.1	824.5	2	2									
ZNF185	7739	zinc finger protein 185 isoform 1	NP_001171577.1	8	4	4	8	**0.37**	**0.38**	43.34	21.15	32.6	16.2	4	4	2306	7739	zinc finger protein 185 (LIM domain)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LIM	Yes
FAM213A	84293	redox-regulatory protein FAM213A isoform 1 precursor	NP_001230709.1	3	1	1	6	**0.37**	**0.27**	6.53	177.5	4.2	97.5	3	3									
LAD1	3898	ladinin-1	NP_005549.2	1	21	21	54	**0.36**	**0.45**	18.18	21.43	33.8	51.5	25	25	3815	3898	ladinin 1	Cytoskeletal anchoring activity	Plasma membrane	Anchor protein	Cell growth and/or maintenance	-	Yes
SYTL1	84958	synaptotagmin-like protein 1 isoform 1	NP_001180237.1	2	2	2	3	**0.36**	**0.37**					1	1	12156	84958	synaptotagmin-like 1	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown;Vesicle docking	SP;C2	Yes
CALML3	810	calmodulin-like protein 3	NP_005176.1	1	4	4	7	**0.36**	**0.31**	17.26	75.11	12.3	49.4	4	4	244	810	calmodulin-like 3	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
SDPR	8436	serum deprivation-response protein	NP_004648.1	1	1	1	2	**0.34**	**0.49**					1	1	9470	8436	serum deprivation response (phosphatidylserinebinding protein)	Serine-type peptidase activity	Cytoplasm	Serine protease	Cell growth and/or maintenance	CC	Yes
KRT14	3861	keratin, type I cytoskeletal 14	NP_000517.2	3	22	50	677	**0.34**	**0.41**	26.38	19.29	160.8	128.8	163	153	1017	3861	keratin 14 (epidermolysis bullosa simplex,Dowling-Meara, Koebner)	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
PKP1	5317	plakophilin-1 isoform 1b	NP_000290.2	2	9	9	16	**0.33**	**0.33**	103.95	91.4	127.1	102.2	8	8	3579	5317	plakophilin 1 (ectodermal dysplasia/skinfragility syndrome)	Cell adhesion molecule activity	Nucleus	Cell junction protein	Intercellular junction assembly and/or maintenance	ARM	Yes
IGSF3	3321	immunoglobulin superfamily member 3 isoform 2 precursor	NP_001007238.1	1	1	1	3	**0.33**	**0.17**					1	1	4602	3321	immunoglobulin superfamily, member 3	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	IG;SP;TM	No
IFIT2	3433	interferon-induced protein with tetratricopeptide repeats 2	NP_001538.4	2	1	2	3	**0.33**	**0.16**					1	1	913	3433	interferon-induced protein withtetratricopeptide repeats 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	TPR	Yes
SERPINB13	5275	serpin B13 isoform 1	NP_001294852.1	2	1	1	2	**0.32**	**0.5**					1	1	5118	5275	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 13	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism	SERPIN	Yes
ITGB6	3694	integrin beta-6 isoform a precursor	NP_000879.2	6	5	5	13	**0.31**	**0.31**	19.96	37.11	16.5	31.1	7	7	947	3694	integrin, beta 6	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;PSI;VWA;EGFL;TM	Yes
KRT16	3868	keratin, type I cytoskeletal 16	NP_005548.2	3	21	38	278	**0.31**	**0.25**	51.01	93.02	112.5	218.3	32	32	1018	3868	keratin 16 (focal non-epidermolyticpalmoplantar keratoderma)	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
ANPEP	290	aminopeptidase N precursor	NP_001141.2	1	11	11	22	**0.3**	**0.29**	79.34	75.25	89.2	77.7	10	10	1055	290	alanyl (membrane) aminopeptidase(aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	Metallopeptidase activity	Plasma membrane	Metallo protease	Protein metabolism	TM	Yes
SYNRG	11276	synergin gamma isoform 1	NP_009178.3	7	2	2	2	**0.3**	**0.16**					1	1	6291	11276	AP1 gamma subunit binding protein 1	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	CC;EH	Yes
CLCA2	9635	calcium-activated chloride channel regulator 2 precursor	NP_006527.1	1	2	2	5	**0.28**	**0.28**	8.54	63.1	3.4	25.7	2	2	4923	9635	chloride channel, calcium activated, familymember 2	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM;VWA;SP	Yes
KRT5	3852	keratin, type II cytoskeletal 5	NP_000415.2	4	33	52	793	**0.27**	**0.29**	22.39	23.49	121.2	147	249	248	1010	3852	keratin 5 (epidermolysis bullosa simplex,Dowling-Meara/Kobner/Weber-Cockayne types)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
ARHGAP6	395	rho GTPase-activating protein 6 isoform 1	NP_038286.2	3	1	1	1	**0.26**	**0.13**					1	1	2124	395	Rho GTPase activating protein 6	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	RHOGAP;SH3	Yes
GPNMB	10457	transmembrane glycoprotein NMB isoform a precursor	NP_001005340.1	2	2	2	4	**0.25**	**0.31**	287.97	154.66	138.3	75	2	2	5081	10457	glycoprotein (transmembrane) nmb	Molecular function unknown	Plasma membrane	Integral membrane protein;Unclassified	Cell communication;Signal transduction;Biological_process unknown	SP;PKD;TM	Yes
VSNL1	7447	visinin-like protein 1	NP_003376.2	1	6	6	15	**0.25**	**0.25**	37.96	91.83	25.3	67.1	7	7	2890	7447	visinin-like 1	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	EF	Yes

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LAMC3	10319	laminin subunit gamma-3 precursor	NP_006050.3	1	1	1	1	**0.22**	**0.21**					1	1	5069	10319	laminin, gamma 3	Structural molecule activity	Extracellular	Structural protein	Cell growth and/or maintenance	LAMNT;EGFLAM;LAMB;SP;CC	Yes
SYNE2	23224	nesprin-2 isoform 5	NP_878918.2	2	1	1	2	**0.21**	**0.32**					1	1	9763	23224	spectrin repeat containing, nuclear envelope 2	Structural constituent of cytoskeleton	Nucleus;Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	NLS;LZ;CH;CC;SPECTRIN;TM	Yes
KRT84	3890	keratin, type II cuticular Hb4	NP_149034.2	3	2	6	32	**0.21**	**0.17**	47.11	146.02	26.1	72.3	7	7	9098	3890	keratin, hair, basic, 4	Structural molecule activity	-	Structural protein	Cell growth and/or maintenance	-	Yes
GPR27	2850	probable G-protein coupled receptor 27	NP_061844.1	1	1	1	1	**0.2**	**0.09**					1	1	5542	2850	G protein-coupled receptor 27	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Cell communication;Signal transduction	TM	Yes
KRT78	196374	keratin, type II cytoskeletal 78 isoform 1	NP_775487.2	3	1	4	13	**0.19**	**0.21**	77.34	230.67	21.5	78.8	2	2	17171	196374	None	Structural molecule activity	-	Structural protein	Cell growth and/or maintenance	CC	Yes
NOTCH4	4855	neurogenic locus notch homolog protein 4 preproprotein	NP_004548.3	1	1	1	1	**0.19**	**0.11**					1	1	1290	4855	Notch homolog 4 (Drosophila)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;EGFCA;EGF;ANK;TM;NOTCH;PEST	Yes
IGSF22	283284	immunoglobulin superfamily member 22	NP_775859.3	1	1	1	1	**0.17**	**0.1**					1	1	8229	283284	None	Molecular function unknown	-	Unclassified	Biological_process unknown	IG;FN3	No
SPRY4	81848	protein sprouty homolog 4 isoform 1	NP_112226.2	2	1	1	1	**0.17**	**0.09**					1	1	10466	81848	sprouty homolog 4 (Drosophila)	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
KIF27	55582	kinesin-like protein KIF27 isoform A	NP_060046.1	4	1	2	4	**0.17**	**0.06**					1	1	11179	55582	kinesin family member 27	Motor activity	-	Motor protein	Cell growth and/or maintenance	CC	Yes
ANKRD35	148741	ankyrin repeat domain-containing protein 35 isoform 1	NP_653299.4	3	1	2	3	**0.14**	**0.03**					1	1	8050	148741	ankyrin repeat domain 35	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK;CC	Yes
FAM168B	130074	myelin-associated neurite-outgrowth inhibitor	NP_001009993.2	1	1	1	1	**0.13**	**0.03**					1	1	17295	130074	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ZBTB9	221504	zinc finger and BTB domain-containing protein 9	NP_689948.1	1	1	1	1	**0.09**	**0.04**					1	1	15695	221504	zinc finger and BTB domain containing 9	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BTB;ZNFC2	Yes
TENM2	57451	teneurin-2	NP_001116151.1	1	2	2	3	**0.08**	**0.05**					1	1									
SERPINA7	6906	thyroxine-binding globulin precursor	NP_000345.2	1	1	1	1	**2.05**	**0.29**					1	1	2438	6906	serine (or cysteine) proteinase inhibitor,clade A (alpha-1 antiproteinase, antitrypsin), member 7	Protease inhibitor activity	Extracellular	Protease inhibitor	Protein metabolism	SERPIN;SP	Yes
SLFN11	91607	schlafen family member 11	NP_001098057.1	2	1	3	6	**0.48**	**27.19**					1	1	8178	91607	None	Growth factor activity	-	Cell cycle control protein	Cell development;Cell growth and/or maintenance	-	No
C19orf52	90580	uncharacterized protein C19orf52	NP_612367.1	1	1	1	2	**0.4**	**4.48**					1	1	14275	90580	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RHOA	387	transforming protein RhoA precursor	NP_001655.1	2	2	9	50	**0.34**	**3.51**	70	10.05	57.4	92.8	5	5	1323	387	ras homolog gene family, member A	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	RHO	No
SELENBP1	8991	selenium-binding protein 1 isoform 3	NP_001245218.1	3	1	1	1	**0.31**	**4.51**					1	1	5007	8991	selenium binding protein 1	Molecular function unknown	Cytoplasm	Unclassified	Protein metabolism	-	Yes
HSPB6	126393	heat shock protein beta-6	NP_653218.1	1	1	1	16	**0.26**	**2.55**	141.75	13.11	97.4	75	5	4	8130	126393	heat shock protein, alpha-crystallin-related,B6	Chaperone activity	-	Chaperone	Protein metabolism	-	Yes
LONRF1	91694	LON peptidase N-terminal domain and RING finger protein 1	NP_689484.3	1	1	1	1	**0.21**	**6.06**					1	1	8674	91694	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	RING;TPR	No
PYDC2	152138	pyrin domain-containing protein 2	NP_001076777.1	1	1	1	1	**7.81**	0.58					1	1	19279	152138	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Biological_process unknown;Regulation of signal transduction	-	No
PLA2G6	8398	85/88 kDa calcium-independent phospholipase A2 isoform a	NP_003551.2	2	1	1	2	**7.66**	0.65					1	1	4675	8398	phospholipase A2, group VI (cytosolic,calcium-independent)	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase	Lipid metabolism	ANK	Yes
MYH14	79784	myosin-14 isoform 3	NP_001139281.1	11	2	14	179	**5.92**						1		10543	79784	myosin, heavy polypeptide 14	Structural molecule activity	-	Structural protein	Cell growth and/or maintenance	MYOSIN;IQ;CC	Yes
C21orf59	56683	UPF0769 protein C21orf59	NP_067077.1	1	3	3	3	**5.67**	1.27	30.11	1	1847.8	1.8	2	2	10756	56683	chromosome 21 open reading frame 59	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
PBK	55872	lymphokine-activated killer T-cell-originated protein kinase isoform 2	NP_001265874.1	2	2	2	11	**5.09**	0.62	11.4	23.48	255.7	37.1	6	6	17822	55872	PDZ binding kinase	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
LACTB2	51110	beta-lactamase-like protein 2	NP_057111.1	1	1	1	9	**4.67**	1.46	8.88	5.09	116.9	16.7	5	5	13955	51110	lactamase, beta 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
CRYBG3	131544	very large A-kinase anchor protein	NP_705833.3	1	1	1	4	**4.1**	0.92	20.35	36.85	173.9	51	2	2	19091	131544	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;XTAL;RICIN	No
RSPH9	221421	radial spoke head protein 9 homolog isoform 1	NP_689945.2	1	1	1	2	**4**	0.7					1	1	12875	221421	chromosome 6 open reading frame 206	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
ANGPTL4	51129	angiopoietin-related protein 4 isoform a precursor	NP_647475.1	1	1	1	2	**3.85**	1.87					1	1	16173	51129	angiopoietin-like 4	Molecular function unknown	Extracellular	Secreted polypeptide	Anti-apoptosis	SP;CC;FBG	Yes

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PAQR7	164091	membrane progestin receptor alpha	NP_848509.1	1	1	1	2	**3.51**	0.92					1	1	9692	164091	progestin and adipoQ receptor family member VII	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM	No
NEB	4703	nebulin isoform 4	NP_001258137.1	3	1	1	1	**3.42**	1.85					1	1	1196	4703	nebulin	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	NEBULIN;SH3	Yes
PARP10	84875	poly [ADP-ribose] polymerase 10	NP_116178.2	1	2	2	3	**3.41**	0.67					1	1	15100	84875	poly (ADP-ribose) polymerase family, member 10	Molecular function unknown	-	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
FAAH	2166	fatty-acid amide hydrolase 1	NP_001432.2	1	1	1	2	**2.96**	0.69					1	1	4244	2166	fatty acid amide hydrolase	Hydrolase activity	Plasma membrane	Enzyme: Hydrolase	Metabolism;Energy pathways	TM	Yes
CUTC	51076	copper homeostasis protein cutC homolog	NP_057044.2	1	1	1	4	**2.95**	0.87	7	6.41	29.9	7.9	2	2	13100	51076	cutC copper transporter homolog (E.coli)	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes
NUDT4	11163	diphosphoinositol polyphosphate phosphohydrolase 2 isoform beta	NP_950241.1	6	1	1	3	**2.77**	0.86	16.17	7.41	70.3	9.1	2	2	14850	11163	nudix (nucleoside diphosphate linked moietyX)-type motif 4	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ARMC12	221481	armadillo repeat-containing protein 12 isoform a	NP_659465.2	3	1	1	2	**2.75**	0.56					1	1									
HMGN5	79366	high mobility group nucleosome-binding domain-containing protein 5	NP_110390.1	1	2	2	3	**2.61**	0.76	13.69	31.26	53.9	34.4	2	2	2310	79366	nucleosomal binding protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
DDAH1	23576	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 isoform 1	NP_036269.1	2	1	1	6	**2.56**	1.14	0.49	5.54	2.2	11	3	3	9203	23576	dimethylarginine dimethylaminohydrolase 1	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	CC;CYCLIN	Yes
DMWD	1762	dystrophia myotonica WD repeat-containing protein	NP_004934.1	1	1	1	1	**2.55**	0.58					1	1	13235	1762	dystrophia myotonica-containing WD repeat motif	Molecular function unknown	-	Unclassified	Cell growth and/or maintenance;Biological_process unknown	WD40	Yes
IQGAP3	128239	ras GTPase-activating-like protein IQGAP3	NP_839943.2	3	2	5	13	**2.51**	1.43					1	1	11051	128239	IQ motif containing GTPase activating protein3	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	CH;IQ;RASGAP	Yes
PHIP	55023	PH-interacting protein	NP_060404.3	1	3	3	3	**2.5**	0.7					1	1	10152	55023	pleckstrin homology domain interacting protein	Receptor binding	-	Ligand	Cell communication;Signal transduction	WD40;CC;BROMO	No
VTN	7448	vitronectin precursor	NP_000629.3	1	2	2	3	**2.48**	1.7	23.28	55.65	97.6	222.9	2	2	1902	7448	vitronectin (serum spreading factor, somatomedinB, complement S-protein)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	SOM;HX;SP	Yes
UCHL1	7345	ubiquitin carboxyl-terminal hydrolase isozyme L1	NP_004172.2	1	7	7	14	**2.45**	1.85	4.77	4.68	34	24.8	8	8	1877	7345	ubiquitin carboxyl-terminal esterase L1(ubiquitin thiolesterase)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
CROCC	9696	rootletin	NP_055490.4	1	3	4	6	**2.39**	1.9					1	1	16758	9696	ciliary rootlet coiled-coil, rootletin	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	No
MAN1A1	4121	mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	NP_005898.2	1	2	2	4	**2.38**	0.83					1	1	5066	4121	mannosidase, alpha, class 1A, member 1	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase	Metabolism;Energy pathways	TM;CC	Yes
PIP5K1C	23396	phosphatidylinositol 4-phosphate 5-kinase type-1 gamma isoform 3	NP_001287778.1	3	1	1	2	**2.35**	0.62					1	1	5834	23396	phosphatidylinositol-4-phosphate 5-kinase,type I, gamma	Lipid kinase activity	Cytoplasm	Lipid Kinase	Cell communication;Signal transduction	PIPKc	No
NPM1	4869	nucleophosmin isoform 3	NP_001032827.1	3	1	16	125	**2.26**	0.57					1	1	1246	4869	nucleophosmin (nucleolar phosphoprotein B23,numatrin)	Chaperone activity	Nucleolus;Nucleus;Cytoplasm	Chaperone	Protein metabolism	-	Yes
DNAJB6	10049	dnaJ homolog subfamily B member 6 isoform a	NP_490647.1	3	1	2	4	**2.16**	1					1	1	7107	10049	DnaJ (Hsp40) homolog, subfamily B, member 6	Chaperone activity	Cytoplasm;Nucleus	Chaperone	Protein metabolism;Protein folding	DNAJ	Yes
TMEM132A	54972	transmembrane protein 132A isoform a precursor	NP_060340.2	2	1	1	2	**2.15**	1.27					1	1	11034	54972	heat shock 70kDa protein 5(glucose-regulated protein, 78kDa) binding protein 1	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	CC;TM	No
TNFAIP8	25816	tumor necrosis factor alpha-induced protein 8 isoform c	NP_001273743.1	4	1	1	2	**2.15**	0.6					1	1	18204	25816	tumor necrosis factor, alpha-induced protein8	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	DED	No
TSSC4	10078	protein TSSC4 isoform a	NP_005697.2	2	1	1	1	**2.09**	1.61					1	1	10357	10078	tumor suppressing subtransferable candidate 4	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
HMGA2	8091	high mobility group protein HMGI-C isoform c	NP_001287847.1	4	5	5	26	**2.07**	1.68	3.31	3.42	26.1	21.7	14	14	2827	8091	high mobility group AT-hook 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AT_hook	Yes
RHBDD2	57414	rhomboid domain-containing protein 2 isoform a	NP_001035546.1	1	2	2	2	**2.07**	1.49					1	1	11492	57414	rhomboid, veinlet-like 7 (Drosophila)	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
ATP6V0C	527	V-type proton ATPase 16 kDa proteolipid subunit	NP_001185498.1	1	1	1	2	**2.06**	1.03	2.34	136.1	6.8	715.1	2	2	162	527	ATPase, H+ transporting, lysosomal 16kDa, V0subunit c	ATPase activity	Lysosome	ATPase	Transport	TM;SP	Yes

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UCHL5	51377	ubiquitin carboxyl-terminal hydrolase isozyme L5 isoform 1	NP_057068.1	1	1	9	18	**2.06**	0.57					1	1	10293	51377	ubiquitin carboxyl-terminal hydrolase L5	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
ZBTB34	403341	zinc finger and BTB domain-containing protein 34	NP_001092740.1	1	1	1	1	**2.04**	0.67					1	1	19419	403341	zinc finger and BTB domain containing 34	Transcription regulator activity	Nucleus	Transcription regulatory protein	Transcription	BTB;ZNFC2	Yes
ZFP91	80829	E3 ubiquitin-protein ligase ZFP91 isoform 1	NP_444251.1	2	1	1	2	**2.02**	1.66					1	1	11700	80829	zinc finger protein 91 homolog (mouse)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;ZNFC2	Yes
AKAP3	10566	A-kinase anchor protein 3	NP_006413.3	1	1	1	1	**2.01**	0.69					1	1	5256	10566	A kinase (PRKA) anchor protein 3	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein	Cell growth and/or maintenance	-	Yes
LCP1	3936	plastin-2	NP_002289.2	1	8	12	40	1.91	**2.25**	6.46	6.14	40.6	45.9	10	10	1082	3936	lymphocyte cytosolic protein 1 (L-plastin)	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF;CH	Yes
PPP4R4	57718	serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform 1	NP_478144.1	1	1	1	2	1.87	**3.56**					1	1	13878	57718	KIAA1622	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	No
CYBA	1535	cytochrome b-245 light chain	NP_000092.2	1	1	1	1	1.86	**2.1**					1	1	1989	1535	cytochrome b-245, alpha polypeptide	Catalytic activity	Plasma membrane	Enzyme: Oxidase	Metabolism;Energy pathways	TM	Yes
GARNL3	84253	GTPase-activating Rap/Ran-GAP domain-like protein 3 isoform a	NP_115669.3	2	1	1	1	1.85	**2.16**					1	1	13567	84253	GTPase activating Rap/RanGAP domain-like 3	GTPase activator activity	-	GTPase activating protein	Biological_process unknown	CNH	No
MCFD2	90411	multiple coagulation factor deficiency protein 2 isoform A precursor	NP_644808.1	3	1	1	2	1.84	**3.42**					1	1	9693	90411	multiple coagulation factor deficiency 2	Molecular function unknown	Extracellular	Unclassified	Cell communication;Signal transduction	SP	Yes
ENG	2022	endoglin isoform 1 precursor	NP_001108225.1	3	1	1	1	1.83	**2.2**					1	1	565	2022	endoglin (Osler-Rendu-Weber syndrome 1)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	ZP;TM;RGD;SP	Yes
HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform b	NP_112420.1	2	1	20	67	1.8	**2.48**					1	1	1242	3178	heterogeneous nuclear ribonucleoprotein A1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
IL1B	3553	interleukin-1 beta proprotein	NP_000567.1	1	6	6	12	1.8	**2.21**	13.86	21.17	60.6	141.4	5	5	985	3553	interleukin 1, beta	Cytokine activity	Extracellular	Cytokine	Immune response	IL1	Yes
BTBD16	118663	BTB/POZ domain-containing protein 16	NP_653188.2	1	1	1	1	1.74	**2.21**					1	1	12594	118663	chromosome 10 open reading frame 87	Molecular function unknown	-	Unclassified	Biological_process unknown	BTB	No
CYP1A1	1543	cytochrome P450 1A1	NP_000490.1	1	4	4	16	1.65	**2.08**	13.22	8.19	68.3	51	8	8	148	1543	cytochrome P450, family 1, subfamily A,polypeptide 1	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Metabolism;Energy pathways	SP	Yes
KNDC1	85442	protein very KIND	NP_689856.6	1	1	1	1	1.65	**2.04**					1	1	13931	85442	kinase non-catalytic C-lobe domain (KIND)containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;RasGEFN;RasGEF	No
MAN1A2	10905	mannosyl-oligosaccharide 1,2-alpha-mannosidase IB	NP_006690.1	1	1	1	2	1.62	**2.19**					1	1	5067	10905	mannosidase, alpha, class 1A, member 2	Hydrolase activity	Golgi apparatus	Enzyme: Hydrolase	Metabolism;Energy pathways	TM;CC	Yes
KDELC2	143888	KDEL motif-containing protein 2 precursor	NP_714916.3	1	1	1	1	1.61	**2.72**					1	1	13773	143888	KDEL (Lys-Asp-Glu-Leu) containing 2	Molecular function unknown	Extracellular	Unclassified	Biological_process unknown	SP;IGFLMN	No
UBXN1	51035	UBX domain-containing protein 1 isoform 1	NP_056937.2	3	3	3	5	1.58	**2.03**	11.26	10.73	25.5	31.6	2	2	11266	51035	None	Ubiquitin binding	-	Ubiquitin proteasome system protein	Proteolysis and peptidolysis	UBX;UBA;CC	Yes
HBG1	3047	hemoglobin subunit gamma-1	NP_000550.2	3	2	3	18	1.57	**3.21**					1	1	789	3047	hemoglobin, gamma A	Transporter activity	-	Transport/cargo protein	Transport	-	Yes
ABCB8	11194	ATP-binding cassette sub-family B member 8, mitochondrial isoform a	NP_001269220.1	4	1	1	2	1.56	**2.3**					1	1	10400	11194	ATP-binding cassette, sub-family B (MDR/TAP),member 8	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	AAA	Yes
SLC2A6	11182	solute carrier family 2, facilitated glucose transporter member 6 isoform 1	NP_060055.2	2	1	1	1	1.56	**2.04**					1	1	6010	11182	solute carrier family 2 (facilitated glucosetransporter), member 6	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
CORO1A	11151	coronin-1A	NP_009005.1	1	13	13	28	1.5	**2.79**	5.86	3.14	33.9	34.9	14	15	5414	11151	coronin, actin binding protein, 1A	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC;WD40	Yes
COL16A1	1307	collagen alpha-1(XVI) chain precursor	NP_001847.3	1	1	1	1	1.48	**4.16**					1	1	381	1307	collagen, type XVI, alpha 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	TSPN;COLL;SP	Yes
POLG	5428	DNA polymerase subunit gamma-1	NP_002684.1	1	1	1	2	1.47	**3.13**					1	1	1438	5428	polymerase (DNA directed), gamma	DNA-directed DNA polymerase activity	Mitochondrion	DNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
GLRX	2745	glutaredoxin-1	NP_002055.1	1	2	2	3	1.45	**2.35**	35.86	21.52	85	81.7	2	2	2707	2745	glutaredoxin (thioltransferase)	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
MRPL33	9553	39S ribosomal protein L33, mitochondrial isoform a	NP_004882.1	1	1	1	1	1.44	**3.02**					1	1	14753	9553	mitochondrial ribosomal protein L33	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	Yes
BCCIP	56647	BRCA2 and CDKN1A-interacting protein isoform BCCIPbeta	NP_510868.1	3	9	9	29	1.42	**2.44**	4.93	5.53	26.6	53.8	14	14	16542	56647	BRCA2 and CDKN1A interacting protein	Peptide binding	Nucleus	Cell cycle control protein	Cell growth and/or maintenance;Signal transduction;DNA repair	CC;NLS	No
MTTP	4547	microsomal triglyceride transfer protein large subunit isoform 2	NP_001287714.1	2	1	1	2	1.4	**2.85**					1	1	1144	4547	microsomal triglyceride transfer protein (largepolypeptide, 88kDa)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	SP	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
ANKRD11	29123	ankyrin repeat domain-containing protein 11	NP_001243111.1	1	1	1	2	1.4	**2.26**					1	1	12456	29123	ankyrin repeat domain 11	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ANK;CC	Yes
GSTM1	2944	glutathione S-transferase Mu 1 isoform 1	NP_000552.2	1	1	1	2	1.39	**2.6**					1	1	707	2944	glutathione S-transferase M1	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase	Energy pathways;Metabolism;Xenobiotic metabolism	-	Yes
ACAD10	80724	acyl-CoA dehydrogenase family member 10 isoform a	NP_001130010.1	2	1	1	2	1.39	**2.58**					1	1	10625	80724	acyl-Coenzyme A dehydrogenase family, member10	Catalytic activity	-	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
KLF5	688	Krueppel-like factor 5 isoform 1	NP_001721.2	2	2	2	4	1.38	**2.08**	27.79	7.99	58.6	23.9	2	2	4212	688	Kruppel-like factor 5 (intestinal)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
UBAC1	10422	ubiquitin-associated domain-containing protein 1	NP_057256.2	1	2	2	5	1.37	**3.66**	8.59	5.37	20.7	35	3	3	12170	10422	ubiquitin associated domain containing 1	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	UBA;STI1	No
SEC11C	90701	signal peptidase complex catalytic subunit SEC11C isoform 1	NP_150596.1	2	2	2	4	1.35	**2.25**	6.44	23.17	12.3	84.9	2	2	15310	90701	SEC11-like 3 (S. cerevisiae)	Aminopeptidase activity	Microsome	Aminopeptidase	Protein metabolism	TM	Yes
USP48	84196	ubiquitin carboxyl-terminal hydrolase 48 isoform a	NP_115612.4	1	1	1	2	1.34	**2.74**					1	1	15637	84196	ubiquitin specific protease 48	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC;UCH;DUSP; UBQ;TM	Yes
CD40	958	tumor necrosis factor receptor superfamily member 5 isoform 1 precursor	NP_001241.1	3	1	1	1	1.34	**2.36**					1	1	178	958	CD40 antigen (TNF receptor superfamily member 5)	Receptor activity	Cytoplasm	Cell surface receptor	Cell communication;Signal transduction	TM;TNFR;SP	Yes
FAM21C	253725	WASH complex subunit FAM21C isoform 1	NP_056077.2	3	1	16	32	1.27	**2.54**					1	1	11094	253725	family with sequence similarity 21, member C	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	No
FHL1	2273	four and a half LIM domains protein 1 isoform 1	NP_001153174.1	5	1	1	2	1.27	**2.15**					1	1	2157	2273	four and a half LIM domains 1	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	LIM	Yes
SLC12A7	10723	solute carrier family 12 member 7	NP_006589.2	1	2	2	4	1.26	**2.11**	28.76	7.24	54.9	21.9	2	2	9221	10723	solute carrier family 12 (potassium/chloridetransporters), member 7	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	NP_665906.1	2	3	3	10	1.23	**2.51**	1.66	2.78	4.6	15.7	5	5	2829	3159	high mobility group AT-hook 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AT_hook	No
BCL2L1	598	bcl-2-like protein 1 isoform 1	NP_612815.1	2	2	2	5	1.22	**2.16**	15.79	10.62	34.4	41.3	3	3	2497	598	BCL2-like 1	Receptor signaling complex scaffold activity	Mitochondrial membrane	Adapter molecule	Apoptosis	TM;BH4;BCL	Yes
SOD2	6648	superoxide dismutase [Mn], mitochondrial isoform A precursor	NP_000627.2	2	2	2	15	1.22	**2.14**	3.44	2.38	11.9	14.5	8	8	938	6648	superoxide dismutase 2, mitochondrial	Superoxide dismutase activity	Mitochondrion	Enzyme: Superoxide dismutase	Cell proliferation;Anti-apoptosis;Cell growth and/or maintenance	-	Yes
GRPEL2	134266	grpE protein homolog 2, mitochondrial precursor	NP_689620.2	1	1	1	2	1.2	**2.99**					1	1	17079	134266	GrpE-like 2, mitochondrial (E. coli)	Chaperone activity	Mitochondrion	Chaperone	Protein metabolism	CC	No
FUS	2521	RNA-binding protein FUS isoform 1	NP_004951.1	3	5	7	25	1.2	**2.05**	4.55	1.07	15.5	6.2	8	8	660	2521	fusion (involved in t(12;16) in malignantliposarcoma)	Nucleocytoplasmic transporter activity	Nucleus	RNA binding protein	RNA localization	RRM;ZnF_RBZ	Yes
HELZ	9931	probable helicase with zinc finger domain	NP_055692.2	1	2	2	3	1.19	**2.22**	1.68	10.87	3.5	43.6	3	3	10452	9931	helicase with zinc finger	Helicase activity	Nucleus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1	Yes
POLR3C	10623	DNA-directed RNA polymerase III subunit RPC3 isoform 2	NP_001290385.1	2	1	1	6	1.17	**2.3**	5.11	15.66	10.4	68.9	3	3	17880	10623	polymerase (RNA) III (DNA directed)polypeptide C (62kD)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
HM13	81502	minor histocompatibility antigen H13 isoform 1	NP_110416.1	4	4	4	26	1.16	**2.18**	7.29	6.26	31.1	52.4	13	13	6166	81502	histocompatibility (minor) 13	Peptidase activity	Integral to membrane	Protease	Immune response	TM	Yes
TNFRSF6B	8771	tumor necrosis factor receptor superfamily member 6B precursor	NP_003814.1	1	2	2	7	1.15	**2.79**	3.26	18.92	7.5	143.5	4	4	4527	8771	tumor necrosis factor receptor superfamily,member 6b, decoy	Cytokine activity;Protein binding	Extracellular	Secreted polypeptide;Cytokine	Immune response;Anti-apoptosis;Apoptosis	TNFR;SP	Yes
MT1G	4495	metallothionein-1G isoform 2	NP_001288196.1	6	1	1	1	1.13	**2.57**					1	1	11827	4495	metallothionein 1G	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
KIAA1429	25962	protein virilizer homolog isoform 1	NP_056311.2	2	2	2	4	1.13	**2.06**	9.26	22.78	14.8	74.4	2	2	10889	25962	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	Yes
SRBD1	55133	S1 RNA-binding domain-containing protein 1	NP_060549.4	1	1	1	1	1.12	**2.36**					1	1	7669	55133	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC;HHH;S1	No
SI	6476	sucrase-isomaltase, intestinal	NP_001032.2	1	2	2	46	1.12	**2.05**	3.61	3.01	19.7	30.4	23	23	1962	6476	sucrase-isomaltase (alpha-glucosidase)	Glucosidase activity	Plasma membrane	Enzyme: Glucosidase	Metabolism;Energy pathways	Trefoil;TM	Yes
NINJ1	4814	ninjurin-1	NP_004139.2	1	1	1	6	1.1	**2.78**	31	2.97	64.6	14.4	3	3	3639	4814	ninjurin 1	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	TM	No

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HNRNPA0	10949	heterogeneous nuclear ribonucleoprotein A0	NP_006796.1	1	10	12	35	1.07	**2**	5.62	5.78	24.3	48.8	16	16	17112	10949	heterogeneous nuclear ribonucleoprotein A0	RNA binding	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
KRT10	3858	keratin, type I cytoskeletal 10	NP_000412.3	5	14	20	80	1.06	**2.05**	4.07	5.71	21.4	62.6	24	24	1021	3858	keratin 10 (epidermolytic hyperkeratosis;keratosis palmaris et plantaris)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
KRIT1	889	krev interaction trapped protein 1 isoform 1	NP_004903.2	2	1	1	2	1.05	**2.71**					1	1	5020	889	KRIT1, ankyrin repeat containing	Molecular function unknown	Tubulin	Unclassified	Signal transduction	ANK;B41;NLS	Yes
ANP32B	10541	acidic leucine-rich nuclear phosphoprotein 32 family member B	NP_006392.1	1	4	7	46	1.05	**2.42**	19.29	10.68	71.2	97.7	10	10	9803	10541	acidic (leucine-rich) nuclear phosphoprotein32 family, member B	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	LRR;NLS	Yes
KRT9	3857	keratin, type I cytoskeletal 9	NP_000217.2	1	9	10	22	1.04	**3.64**	12.53	1.92	40.8	21.2	9	9	6351	3857	keratin 9 (epidermolytic palmoplantarkeratoderma)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
SHANK3	85358	SH3 and multiple ankyrin repeat domains protein 3	NP_277052.1	1	1	1	1	1.02	**2.28**					1	1	18979	85358	SH3 and multiple ankyrin repeat domains 3	Receptor signaling complex scaffold activity	Dendrite	Cytoskeletal associated protein	Signal transduction	ANK;SH3;PDZ;SAM	No
P3H3	10536	prolyl 3-hydroxylase 3 precursor	NP_055077.2	1	3	4	8	1.02	**2.11**	1.33	11.47	2.7	51.3	4	4									
LSM5	23658	U6 snRNA-associated Sm-like protein LSm5 isoform a	NP_036454.1	2	1	1	2	0.98	**2.1**					1	1	6285	23658	LSM5 homolog, U6 small nuclear RNA associated(S. cerevisiae)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
GIT2	9815	ARF GTPase-activating protein GIT2 isoform 1	NP_476510.1	6	2	4	6	0.97	**2.16**					1	1	9779	9815	G protein-coupled receptor kinase interactor 2	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	CC;ARFGAP	Yes
PRSS1	5644	trypsin-1 preproprotein	NP_002760.1	5	2	2	54	0.95	**3.61**	13.73	8.07	77.6	312.9	28	28	2039	5644	protease, serine, 1 (trypsin 1)	Serine-type peptidase activity	Extracellular	Serine protease	Protein metabolism	TRYPSIN;SP	Yes
THG1L	54974	probable tRNA(His) guanylyltransferase	NP_060342.2	1	1	1	4	0.95	**2.03**	27.8	9.61	38.6	28.1	2	2	13726	54974	None	Molecular function unknown	Cytoplasm	Cell cycle control protein	Cell growth and/or maintenance	-	No
MAP2K4	6416	dual specificity mitogen-activated protein kinase kinase 4 isoform 2	NP_001268364.1	2	4	4	4	0.94	**2.31**	19.9	30.03	33.1	180.2	3	3	3213	6416	mitogen-activated protein kinase kinase 4	Protein threonine/tyrosine kinase activity	Cytoplasm;Plasma membrane	Dual specificity kinase	Cell communication;Signal transduction	S_T_Y_Kinase	Yes
KLHDC10	23008	kelch domain-containing protein 10	NP_055812.1	1	2	2	3	0.93	**2.2**					1	1	17182	23008	None	Molecular function unknown	-	Unclassified	Biological_process unknown	KELCH	No
KRT2	3849	keratin, type II cytoskeletal 2 epidermal	NP_000414.2	1	8	17	177	0.93	**2.07**	6.92	2.65	17.2	14.6	7	7	2560	3849	keratin 2A (epidermal ichthyosis bullosa ofSiemens)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
KRT1	3848	keratin, type II cytoskeletal 1	NP_006112.3	1	17	19	58	0.92	**2.38**	2.9	4.02	14.2	54	28	28	763	3848	keratin 1 (epidermolytic hyperkeratosis)	Structural molecule activity	Plasma membrane	Structural protein	Cell growth and/or maintenance	CC	Yes
HNRNPA3	220988	heterogeneous nuclear ribonucleoprotein A3	NP_919223.1	1	13	16	36	0.9	**2.42**	10.31	5.27	40.9	58.4	18	18	5644	220988	heterogeneous nuclear ribonucleoprotein A3	RNA binding	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;NES	Yes
SEPHS1	22929	selenide, water dikinase 1 isoform 1	NP_036379.2	3	2	2	2	0.88	**2.01**	19.5	27.71	24.6	92.5	2	2	2944	22929	selenophosphate synthetase 1	ATP binding	-	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
ADIPOR1	51094	adiponectin receptor protein 1	NP_057083.2	1	2	2	3	0.87	**2.4**					1	1	6402	51094	adiponectin receptor 1	Protein-hormone receptor activity	Plasma membrane	Integral membrane protein	Metabolism;Energy pathways;Fatty acid metabolism	TM	Yes
DCAF7	10238	DDB1- and CUL4-associated factor 7	NP_005819.3	1	1	1	2	0.85	**2.57**					1	1	9340	10238	WD repeat domain 68	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown;Signal transduction	WD40	Yes
FGFR1OP	11116	FGFR1 oncogene partner isoform a	NP_008976.1	3	2	2	3	0.85	**2.43**					1	1	10392	11116	FGFR1 oncogene partner	Molecular function unknown	-	Unclassified	Cell growth and/or maintenance	LISH	No
ANKDD1A	348094	ankyrin repeat and death domain-containing protein 1A	NP_874362.3	1	1	1	2	0.85	**2.12**					1	1	14178	348094	None	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK;DEATH	No
MMP3	4314	stromelysin-1 preproprotein	NP_002413.1	1	1	1	1	0.84	**2.02**					1	1	1703	4314	matrix metalloproteinase 3 (stromelysin 1,progelatinase)	Metallopeptidase activity	Extracellular	Metallo protease	Protein metabolism	ZnMc;HX;SP	Yes
HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	NP_002127.1	2	1	20	104	0.83	**3.77**	24.67	1.68	29.6	9	2	2	1242	3178	heterogeneous nuclear ribonucleoprotein A1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
RBBP4	5928	histone-binding protein RBBP4 isoform a	NP_005601.1	3	3	9	25	0.83	**2.07**	41.15	23.69	77.3	127.2	4	4	4232	5928	retinoblastoma binding protein 4	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
PDSS1	23590	decaprenyl-diphosphate synthase subunit 1	NP_055132.2	1	1	1	2	0.82	**2.24**					1	1	9591	23590	trans-prenyltransferase	Transferase activity	Endoplasmic reticulum	Enzyme: Transferase	Metabolism;Energy pathways	-	No
ANAPC2	29882	anaphase-promoting complex subunit 2	NP_037498.1	1	1	1	2	0.8	**2.22**					1	1	7367	29882	anaphase promoting complex subunit 2	Ligase activity	-	Cell cycle control protein	Cell communication;Signal transduction	CULL	Yes
VPS8	23355	vacuolar protein sorting-associated protein 8 homolog isoform a	NP_001009921.1	2	1	1	2	0.8	**2.13**					1	1	11111	23355	KIAA0804	Molecular function unknown	-	Unclassified	Biological_process unknown	RING	No

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VASP	7408	vasodilator-stimulated phosphoprotein	NP_003361.1	1	7	7	17	0.8	**2.13**	9.65	6.27	24.9	44.2	10	10	3415	7408	vasodilator-stimulated phosphoprotein	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cytoskeleton organization and biogenesis	WH1;CC	Yes
NACC2	138151	nucleus accumbens-associated protein 2	NP_653254.1	1	1	1	1	0.71	**2.05**					1	1	9831	138151	BTB (POZ) domain containing 14A	Molecular function unknown	-	Unclassified	Biological_process unknown	BTB	No
METTL3	56339	N6-adenosine-methyltransferase 70 kDa subunit	NP_062826.2	1	2	2	2	0.66	**3.16**					1	1	14389	56339	methyltransferase like 3	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
TFB2M	64216	dimethyladenosine transferase 2, mitochondrial	NP_071761.1	1	3	3	6	0.65	**3.59**	84.92	26.36	91.1	223.9	2	2	9520	64216	transcription factor B2, mitochondrial	Transcription factor activity	Mitochondrion	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
CIAO1	9391	probable cytosolic iron-sulfur protein assembly protein CIAO1	NP_004795.1	1	2	2	3	0.64	**2.58**	33	30.03	30.8	152.5	2	2	16057	9391	WD repeat domain 39	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
GNA15	2769	guanine nucleotide-binding protein subunit alpha-15	NP_002059.3	1	1	1	1	0.64	**2.52**					1	1	760	2769	guanine nucleotide binding protein (G protein),alpha 15 (Gq class)	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	-	Yes
UBE2E1	7324	ubiquitin-conjugating enzyme E2 E1 isoform 1	NP_003332.1	2	1	1	2	0.62	**2.93**	25.98	5.96	23.2	25.1	2	2	4225	7324	ubiquitin-conjugating enzyme E2E 1 (UBC4/5homolog, yeast)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBC	Yes
POTEJ	653781	POTE ankyrin domain family member J	NP_001264012.1	1	1	10	103	0.6	**2.32**					1	1									
ACTBL2	345651	beta-actin-like protein 2	NP_001017992.1	1	2	12	370	0.6	**2.24**	110.87	33.3	118.5	143.1	2	2	18598	345651	None	Molecular function unknown	-	Unclassified	Biological_process unknown	ACTIN	Yes
BTF3	689	transcription factor BTF3 isoform B	NP_001198.2	1	1	11	110	0.58	**6.28**					1	1	3966	689	basic transcription factor 3	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SH3RF2	153769	putative E3 ubiquitin-protein ligase SH3RF2	NP_689763.3	1	1	1	1	0.56	**3.48**					1	1	10229	153769	SH3 domain containing ring finger 2	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	RING;SH3	Yes
PROSC	11212	proline synthase co-transcribed bacterial homolog protein	NP_009129.1	1	2	2	3	0.56	**3.11**	55.65	25.1	46.4	154	2	2	16060	11212	proline synthetase co-transcribed homolog(bacterial)	Racemase and epimerase activity	Cytoplasm	Enzyme: Racemase	Metabolism;Energy pathways	-	No
HEXDC	284004	hexosaminidase D	NP_775891.2	1	1	1	1	0.56	**2.75**					1	1	8677	284004	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TMED5	50999	transmembrane emp24 domain-containing protein 5 isoform 1 precursor	NP_057124.3	1	1	1	4	0.56	**2.72**	7.3	0.25	5.8	1	2	2	13028	50999	transmembrane emp24 protein transport domaincontaining 5	Molecular function unknown	Membrane fraction	Unclassified	Biological_process unknown	SP;TM	No
Mar-05	54708	E3 ubiquitin-protein ligase MARCH5	NP_060294.1	1	2	2	4	0.54	**2.16**	4.73	21.22	3.6	72.5	2	2									
MBNL1	4154	muscleblind-like protein 1 isoform c	NP_997176.1	10	3	3	4	0.53	**2.44**	7.65	3.39	5.7	11.7	2	2	7355	4154	muscleblind-like (Drosophila)	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of gene expression, epigenetic	ZnF_C3H1;ZnF_C4	Yes
TNFRSF12A	51330	tumor necrosis factor receptor superfamily member 12A precursor	NP_057723.1	1	1	1	2	**0.5**	1.35					1	1	5801	51330	tumor necrosis factor receptor superfamily,member 12A	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;SP	Yes
GINS4	84296	DNA replication complex GINS protein SLD5	NP_115712.1	1	2	2	2	**0.5**	0.92					1	1	11583	84296	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	No
ATP6	4508	ATP synthase F0 subunit 6	YP_003024031.1	1	1	1	4	**0.5**	0.82					1	1									
FLNC	2318	filamin-C isoform a	NP_001449.3	2	5	17	84	**0.49**	1.12	43.15	9.44	84.3	38	12	12	18	2318	filamin C, gamma (actin binding protein 280)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;IGFLMN	Yes
NNT	23530	NAD(P) transhydrogenase, mitochondrial	NP_036475.3	1	2	2	7	**0.49**	0.64	34.03	29.75	29.8	34.1	3	3	9715	23530	nicotinamide nucleotide transhydrogenase	Oxidoreductase activity	Mitochondrial membrane	Enzyme: Oxidoreductase	Energy pathways	TM	Yes
SERPINB3	6317	serpin B3	NP_008850.1	1	2	2	3	**0.48**	0.81	90.91	118.82	68.7	230.6	2	2	2745	6317	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 3	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism	SERPIN	Yes
MPDU1	9526	mannose-P-dolichol utilization defect 1 protein	NP_004861.2	1	1	1	5	**0.48**	0.78	28.33	0.05	19.2	0.1	2	2	4951	9526	mannose-P-dolichol utilization defect 1	Molecular function unknown	Integral to membrane	Integral membrane protein	Metabolism;Energy pathways	CTNS;TM	No
SH3D19	152503	SH3 domain-containing protein 19 isoform 1	NP_001009555.3	3	1	1	5	**0.48**	0.77	18.16	43.79	12.4	50.3	2	2	16364	152503	None	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	SH3;SH2	No
CYB5R1	51706	NADH-cytochrome b5 reductase 1	NP_057327.2	1	9	9	20	**0.48**	0.52	40.28	23.03	75.9	43.1	12	12	6434	51706	NAD(P)H:quinone oxidoreductase type 3,polypeptide A2	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase	Metabolism;Energy pathways	SP	No
KNTC1	9735	kinetochore-associated protein 1	NP_055523.1	1	1	1	2	**0.47**	0.84					1	1	9561	9735	kinetochore associated 1	Chromatin binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction;Chromosome segregation	-	Yes

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DOPEY2	9980	protein dopey-2	NP_005119.2	1	1	1	2	**0.47**	0.78					1	1	7271	9980	chromosome 21 open reading frame 5	Molecular function unknown	-	Unclassified	Cell growth and/or maintenance	-	Yes
TAGLN	6876	transgelin	NP_003177.2	1	2	2	4	**0.47**	0.7	35.27	16.42	23.7	16.3	2	2	2891	6876	transgelin	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Muscle development	CH	Yes
STOM	2040	erythrocyte band 7 integral membrane protein isoform a	NP_004090.4	4	8	8	52	**0.47**	0.54	43.53	14.83	142.8	43.3	27	27	585	2040	stomatin	Channel regulator activity	Cytoplasmic vesicle	Integral membrane protein	Cell communication;Signal transduction	PHB;TM	Yes
ATE1	11101	arginyl-tRNA--protein transferase 1 isoform 2	NP_008972.2	5	1	1	1	**0.46**	0.87					1	1	6979	11101	arginyltransferase 1	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase	Protein metabolism	-	Yes
KDF1	126695	keratinocyte differentiation factor 1	NP_689578.2	1	1	1	2	**0.45**	0.89					1	1									
SUMF2	25870	sulfatase-modifying factor 2 isoform e precursor	NP_001123541.1	4	2	2	4	**0.45**	0.78	47.37	5.17	31	5.7	2	2	6400	25870	sulfatase modifying factor 2	Molecular function unknown	Endoplasmic reticulum	Unclassified	Protein metabolism	SP;TM	Yes
NF2	4771	merlin isoform 1	NP_000259.1	6	2	2	3	**0.45**	0.75					1	1	6980	4771	neurofibromin 2 (bilateral acoustic neuroma)	Structural constituent of cytoskeleton	Cytoplasm;Nucleus;Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	B41;ERM;CC	Yes
KRT72	140807	keratin, type II cytoskeletal 72 isoform 1	NP_542785.1	3	1	7	61	**0.45**	0.66					1	1	9746	140807	None	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
SRR	63826	serine racemase isoform a	NP_068766.1	2	1	1	2	**0.45**	0.58					1	1	10451	63826	serine racemase	Racemase and epimerase activity	Cytoplasm	Enzyme: Racemase	Metabolism;Energy pathways	-	Yes
GSN	2934	gelsolin isoform b	NP_001121134.1	6	24	24	97	**0.45**	0.55	14.73	10.37	50.4	42.7	51	51	674	2934	gelsolin (amyloidosis, Finnish type)	Structural constituent of cytoskeleton	Extracellular	Cytoskeletal protein	Cell growth and/or maintenance	GEL;SP	Yes
ARPC3	10094	actin-related protein 2/3 complex subunit 3 isoform 1	NP_001265485.1	2	6	6	19	**0.44**	1.98	33.65	7.87	46.3	49.4	9	9	9175	10094	actin related protein 2/3 complex, subunit 3,21kDa	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
SYNPO2	171024	synaptopodin-2 isoform a	NP_597734.2	4	1	1	4	**0.44**	1.4	30.55	10.91	19.1	21.8	2	2	15456	171024	synaptopodin 2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	PDZ	Yes
ANLN	54443	actin-binding protein anillin isoform 1	NP_061155.2	3	1	1	2	**0.44**	0.79					1	1	9799	54443	anillin, actin binding protein (scraps homolog,Drosophila)	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	CC;PH	Yes
MBOAT2	129642	lysophospholipid acyltransferase 2	NP_620154.2	1	1	1	2	**0.44**	0.54					1	1	11410	129642	O-acyltransferase (membrane bound) domaincontaining 2	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM	No
TSPO	706	translocator protein	NP_000705.2	1	2	2	2	**0.43**	1.25					1	1	15913	706	benzodiazapine receptor (peripheral)	Receptor activity	Mitochondrion	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
CCNT2	905	cyclin-T2 isoform a	NP_001232.1	2	2	2	6	**0.42**	0.79	66.98	2.24	40.9	2.5	2	2	4839	905	cyclin T2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CYCLIN	Yes
MAP2K7	5609	dual specificity mitogen-activated protein kinase kinase 7 isoform 1	NP_001284484.1	3	1	1	1	**0.42**	0.56					1	1	4309	5609	mitogen-activated protein kinase kinase 7	Protein threonine/tyrosine kinase activity	Cytoplasm	Dual specificity kinase	Signal transduction	S_T_Y_Kinase;CC;S_T_kinase	Yes
TPM1	7168	tropomyosin alpha-1 chain isoform Tpm1.4sm	NP_001018007.1	2	2	14	1087	**0.41**	1.13	4.45	1.13	43.1	29.2	502	502	1839	7168	tropomyosin 1 (alpha)	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
CRABP2	1382	cellular retinoic acid-binding protein 2	NP_001869.1	2	5	5	13	**0.41**	0.56	48.03	53.87	60.6	102.3	8	8	8353	1382	cellular retinoic acid binding protein 2	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
VANGL1	81839	vang-like protein 1 isoform 1	NP_620409.1	2	2	2	2	**0.39**	1.31					1	1	18279	81839	vang-like 1 (van gogh, Drosophila)	Protein binding	Integral to membrane	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
RAB29	8934	ras-related protein Rab-7L1 isoform 1	NP_003920.1	3	2	3	11	**0.39**	1.13					1	1									
HACD4	401494	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 4	NP_001010915.2	1	1	1	2	**0.39**	0.59					1	1									
PLSCR1	5359	phospholipid scramblase 1	NP_066928.1	4	1	1	1	**0.38**	0.62					1	1	8855	5359	phospholipid scramblase 1	Protein binding	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
SORBS1	10580	sorbin and SH3 domain-containing protein 1 isoform 3	NP_001030126.1	12	2	2	8	**0.37**	1.03	59.11	11.93	46.4	21.5	4	3	5587	10580	sorbin and SH3 domain containing 1	Cell adhesion molecule activity	Cell junction	Cell junction protein	Signal transduction;Cytoskeleton organization and biogenesis	SORB;SH3	Yes
PRNP	5621	major prion protein preproprotein	NP_000302.1	1	4	4	7	**0.37**	0.76	27.56	61.43	17.7	96.7	3	3	1453	5621	prion protein (p27-30) (Creutzfeld-Jakobdisease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	Molecular function unknown	Plasma membrane	Membrane bound ligand	Metabolism	SP;TM	Yes
GSTT1	2952	glutathione S-transferase theta-1 isoform a	NP_000844.2	5	2	2	4	**0.31**	1.09					1	1	2700	2952	glutathione S-transferase theta 1	Glutathione transferase activity	Nucleus	Enzyme: Glutathione transferase	Metabolism;Energy pathways	-	No
GLS2	27165	glutaminase liver isoform, mitochondrial isoform 1 precursor	NP_037399.2	1	1	1	1	**0.31**	1.05					1	1	5901	27165	glutaminase 2 (liver, mitochondrial)	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase	Metabolism;Energy pathways	ANK	Yes
LZIC	84328	protein LZIC	NP_115744.2	1	1	1	2	**0.31**	0.67					1	1	14340	84328	leucine zipper and CTNNBIP1 domain containing	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No

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S100A10	6281	protein S100-A10	NP_002957.1	1	3	3	9	**0.31**	0.52	39.13	11.08	30.2	14.1	6	6	232	6281	S100 calcium binding protein A10 (annexin IIligand, calpactin I, light polypeptide (p11)) [Homo sapiens]Other Aliases:HGNC:10487, 42C, ANX2L, ANX2LG, CAL1L, CLP11, Ca	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	S_100;TM	Yes
CNN1	1264	calponin-1 isoform 1	NP_001290.2	2	2	2	11	**0.3**	1.34	52.88	13.9	28	33	3	3	2884	1264	calponin 1, basic, smooth muscle	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH	Yes
HACD2	201562	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	NP_940684.1	1	1	1	2	**0.26**	0.76					1	1									
SYNM	23336	synemin isoform A	NP_663780.2	1	1	1	4	**0.18**	1.5	179.37	16.07	47.8	35	2	2	7305	23336	desmuslin	Structural constituent of cytoskeleton	Intermediate filament;Nucleus; Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
PREX1	57580	phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	NP_065871.2	1	1	1	1	**0.13**	0.79					1	1	6066	57580	None	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH;DSH;PDZ;CC	Yes
UBQLN2	29978	ubiquilin-2	NP_038472.2	1	2	3	12	**0.1**	0.6					1	1	2224	29978	ubiquilin 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBQ;STI1;UBA	Yes
TRPM2	7226	transient receptor potential cation channel subfamily M member 2	NP_003298.1	1	1	1	1	**0.03**						1		4777	7226	transient receptor potential cation channel,subfamily M, member 2	Intracellular ligand-gated ion channel activity	Plasma membrane	Intracellular ligand gated channel	Ion transport	TM	Yes
BBS1	582	Bardet-Biedl syndrome 1 protein	NP_078925.3	1	2	2	2	**0.03**						1		1950	582	Bardet-Biedl syndrome 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
MUC2	4583	mucin-2 precursor	NP_002448.3	1	2	2	3	1.99	**0.24**					1	1	11828	4583	mucin 2, intestinal/tracheal	Molecular function unknown	Endoplasmic reticulum	Secreted polypeptide	Biological_process unknown	SP;VWD;VWC;CT	Yes
TCEB3B	51224	RNA polymerase II transcription factor SIII subunit A2	NP_057511.2	1	1	1	2	1.8	**0.5**	25.75	57.06	73.2	42.3	2	2	18169	51224	transcription elongation factor B polypeptide3B (elongin A2)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TFS	Yes
ZYG11B	79699	protein zyg-11 homolog B	NP_078922.1	1	1	1	1	1.79	**0.45**					1	1	13356	79699	zyg-11 homolog (C. elegans)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
UCHL5	51377	ubiquitin carboxyl-terminal hydrolase isozyme L5 isoform 2	NP_001186190.1	3	1	9	25	1.74	**0.32**	0.46	27.8	1.4	15.4	3	3	10293	51377	ubiquitin carboxyl-terminal hydrolase L5	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
RNASET2	8635	ribonuclease T2 precursor	NP_003721.2	1	1	1	4	1.7	**0.46**	4.24	10.13	10.2	6.6	2	2	10197	8635	ribonuclease T2	Ribonuclease activity	Cytoplasm	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP	Yes
YIF1B	90522	protein YIF1B isoform 5	NP_001034761.1	6	2	2	3	1.63	**0.5**	17.85	106.81	43	87.7	2	2	11277	90522	Yip1 interacting factor homolog B (S.cerevisiae)	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
FGG	2266	fibrinogen gamma chain isoform gamma-B precursor	NP_068656.2	2	1	1	448	1.45	**0.32**	1.42	10.6	31.2	53	218	219	621	2266	fibrinogen, gamma polypeptide	Protein binding	Extracellular	Coagulation factor	Protein metabolism	FBG;SP;CC	Yes
KNG1	3827	kininogen-1 isoform 1 precursor	NP_001095886.1	2	1	1	9	1.41	**0.4**	7.39	79.88	23.6	81.2	5	5	1970	3827	kininogen 1	Protease inhibitor activity	Extracellular	Coagulation factor	Protein metabolism	CYSTATIN;SP	Yes
HIST1H2AD	3013	histone H2A type 1-D	NP_066409.1	2	1	7	168	1.36	**0.48**	0.41	13.75	1	11.4	3	3	7534	3013	histone 1, H2ad	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
NDUFA3	4696	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	NP_004533.1	1	1	1	1	1.31	**0.5**					1	1	4830	4696	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 3, 9kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	Yes
CNGA1	1259	cGMP-gated cation channel alpha-1 isoform 1	NP_001136036.1	2	1	1	1	1.3	**0.49**					1	1	445	1259	cyclic nucleotide gated channel alpha 1	Intracellular ligand-gated ion channel activity	Plasma membrane	Intracellular ligand gated channel	Transport	TM;CNMP;CC	Yes
CLINT1	9685	clathrin interactor 1 isoform 1	NP_001182484.1	2	1	11	30	1.29	**0.4**					1	1	6273	9685	None	Transporter activity	Golgi apparatus;Nucleus;Cytoplasm	Transport/cargo protein	Transport	CC	Yes
ADAMDEC1	27299	ADAM DEC1 isoform 1 precursor	NP_055294.1	2	1	1	1	1.25	**0.48**					1	1	7070	27299	ADAM-like, decysin 1	Metallopeptidase activity	Extracellular	Metallo protease	Cell communication;Signal transduction	SP;REP;DISINT	Yes
OSBPL11	114885	oxysterol-binding protein-related protein 11	NP_073613.2	1	2	3	5	1.25	**0.37**					1	1	9481	114885	oxysterol binding protein-like 11	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	PH	Yes
FAM3D	131177	protein FAM3D precursor	NP_620160.1	1	1	1	2	1.24	**0.44**	3.48	53.87	6.1	34.9	2	2	12271	131177	family with sequence similarity 3, member D	Cytokine activity	Extracellular	Cytokine	Cell communication;Signal transduction	SP	Yes
PLG	5340	plasminogen isoform 1 precursor	NP_000292.1	1	1	1	4	1.23	**0.48**	11.65	97.85	20.5	73.7	2	2	1417	5340	plasminogen	Peptidase activity	Extracellular	Protease	Protein metabolism	PAN;KRINGLE;TRYPSIN;SP	Yes
GLIPR2	152007	Golgi-associated plant pathogenesis-related protein 1 isoform e	NP_001273942.1	4	1	1	1	1.22	**0.48**					1	1	6187	152007	chromosome 9 open reading frame 19	Molecular function unknown	-	Unclassified	Biological_process unknown	SCP	Yes
GPA33	10223	cell surface A33 antigen precursor	NP_005805.1	1	1	1	1	1.21	**0.43**					1	1	3704	10223	glycoprotein A33 (transmembrane)	Antigen binding	Plasma membrane	Immunoglobulin	Immune response	IGV;Ig_LIKE;TM	Yes
POSTN	10631	periostin isoform 1 precursor	NP_006466.2	7	3	3	30	1.21	**0.17**	7.55	109.04	35.2	80.8	14	14	12295	10631	periostin, osteoblast specific factor	Cell adhesion molecule activity	-	Adhesion molecule	Cell communication;Signal transduction	SP	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
MYPOP	339344	myb-related transcription factor, partner of profilin	NP_001012661.1	1	1	1	2	1.2	**0.37**					1	1	17352	339344	None	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT	No
WDFY1	57590	WD repeat and FYVE domain-containing protein 1	NP_065881.1	1	2	2	3	1.19	**0.48**					1	1	15663	57590	WD repeat and FYVE domain containing 1	Molecular function unknown	Endosome	Unclassified	Biological_process unknown	WD40;FYVE	Yes
KRT3	3850	keratin, type II cytoskeletal 3	NP_476429.2	2	3	11	64	1.16	**0.11**	11.07	582.62	44.7	875.9	11	11	1013	3850	keratin 3	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
BGN	633	biglycan preproprotein	NP_001702.1	1	2	2	22	1.13	**0.42**	9.07	43.48	29.6	55.4	8	8	2359	633	biglycan	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	LRR;SP	Yes
CLMN	79789	calmin	NP_079010.2	1	2	2	3	1.06	**0.44**					1	1	13076	79789	calmin (calponin-like, transmembrane)	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	CH;TM	Yes
MRPL10	124995	39S ribosomal protein L10, mitochondrial isoform b	NP_683685.1	2	3	3	6	1.03	**0.5**	12.05	41.34	21.7	37	3	3	14738	124995	mitochondrial ribosomal protein L10	Structural constituent of ribosome	Mitochondrion	RNA binding protein	Protein metabolism	-	No
MRPL12	6182	39S ribosomal protein L12, mitochondrial	NP_002940.2	1	5	5	32	1.03	**0.45**	7.28	53.26	27.5	104.5	13	13	3849	6182	mitochondrial ribosomal protein L12	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
GPATCH8	23131	G patch domain-containing protein 8 isoform 1	NP_001002909.1	3	4	4	5	1.02	**0.49**	11.13	6.14	19.8	5.2	3	3	11089	23131	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	G_PATCH;ZNFC2;CC	Yes
JCHAIN	3512	immunoglobulin J chain precursor	NP_653247.1	1	1	1	8	1.02	**0.33**	2.37	47.11	4.8	31.6	4	4									
PRELP	5549	prolargin precursor	NP_002716.1	1	2	2	3	1.01	**0.5**	19.17	5.72	27.9	4.1	2	2	3556	5549	proline arginine-rich end leucine-rich repeatprotein	Cytoskeletal anchoring activity	Extracellular matrix	Anchor protein	Cell growth and/or maintenance	LRR;SP	Yes
MYL9	10398	myosin regulatory light polypeptide 9 isoform a	NP_006088.2	2	1	6	68	1.01	**0.45**					1	1	17619	10398	myosin, light polypeptide 9, regulatory	Molecular function unknown	-	Unclassified	Muscle contraction	EF	Yes
ACTA1	58	actin, alpha skeletal muscle	NP_001091.1	1	1	26	727	0.99	**0.44**	6.73	48.86	19	67	8	8	30	58	actin, alpha 1, skeletal muscle	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	ACTIN	Yes
SLC39A14	23516	zinc transporter ZIP14 isoform b precursor	NP_056174.2	3	1	1	2	0.99	**0.34**					1	1	12288	23516	solute carrier family 39 (zinc transporter),member 14	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	Yes
HBD	3045	hemoglobin subunit delta	NP_000510.1	1	1	2	24	0.96	**0.26**	12.39	127.02	27.1	85.4	5	5	787	3045	hemoglobin, delta	Transporter activity	-	Transport/cargo protein	Transport	-	Yes
FLII	2314	protein flightless-1 homolog isoform 3	NP_001243194.1	2	1	35	94	0.9	**0.5**	7.72	13.42	9.8	9.4	2	2	2647	2314	flightless I homolog (Drosophila)	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	GEL;CC;LRR	Yes
MCM10	55388	protein MCM10 homolog isoform 1	NP_877428.1	2	1	1	1	0.89	**0.26**					1	1	11297	55388	MCM10 minichromosome maintenance deficient 10(S. cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
MPV17	4358	protein Mpv17	NP_002428.1	1	1	1	9	0.85	**0.31**	27.68	2.75	42.3	1.2	3	2	8847	4358	MpV17 transgene, murine homolog,glomerulosclerosis	Molecular function unknown	Peroxisome;Mitochondrion	Integral membrane protein	Biological_process unknown	TM	Yes
TCEB2	6923	transcription elongation factor B polypeptide 2 isoform a	NP_009039.1	2	5	5	11	0.84	**0.49**	11.34	23.28	25.6	30.9	7	7	2874	6923	transcription elongation factor B (SIII),polypeptide 2 (18kDa, elongin B)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBQ	Yes
PIK3CG	5294	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform	NP_002640.2	1	1	1	2	0.84	**0.4**					1	1	3135	5294	phosphoinositide-3-kinase, catalytic, gammapolypeptide	Lipid kinase activity	Plasma membrane	Lipid Kinase	Cell communication;Signal transduction	PI3KC2;PI3KA;PI3KC	Yes
VTI1A	143187	vesicle transport through interaction with t-SNAREs homolog 1A	NP_660207.2	1	1	1	1	0.83	**0.48**					1	1	18290	143187	vesicle transport through interaction witht-SNAREs homolog 1A (yeast)	Transporter activity	Integral to membrane	Transport/cargo protein	Transport	t_SNARE;CC;TM	Yes
MPG	4350	DNA-3-methyladenine glycosylase isoform a	NP_002425.2	3	1	1	2	0.81	**0.44**					1	1	6766	4350	N-methylpurine-DNA glycosylase	Hydrolase activity	Nucleus	Enzyme: Glycosylase	DNA repair	TM	Yes
SRSF2	6427	serine/arginine-rich splicing factor 2	NP_003007.2	1	2	2	11	0.79	**0.47**	35.44	51.7	60.8	51.4	4	4									
ZBTB45	84878	zinc finger and BTB domain-containing protein 45	NP_116181.1	1	1	1	1	0.79	**0.31**					1	1	15808	84878	zinc finger protein 499	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;BTB	Yes
CD99	4267	CD99 antigen isoform a precursor	NP_002405.1	2	1	1	2	0.78	**0.46**					1	1	2434	4267	CD99 antigen	Molecular function unknown	Integral to membrane	Unclassified	Immune response	SP;TM	Yes
S100A2	6273	protein S100-A2	NP_005969.1	1	6	6	28	0.78	**0.44**	17.38	34.99	60.5	70.1	17	17	1508	6273	S100 calcium binding protein A2	Calcium ion binding	Nucleus	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
MUC5AC	4586	mucin-5AC precursor	NP_001291288.1	1	1	1	1	0.78	**0.36**					1	1									
NEMF	9147	nuclear export mediator factor NEMF isoform 1	NP_004704.2	2	1	1	1	0.77	**0.5**					1	1									
CLHC1	130162	clathrin heavy chain linker domain-containing protein 1 isoform 1	NP_689598.2	2	1	1	1	0.77	**0.39**					1	1									
HBB	3043	hemoglobin subunit beta	NP_000509.1	1	1	2	451	0.76	**0.3**	3.03	12.43	34.2	58.2	207	207	786	3043	hemoglobin, beta	Transporter activity	Extracellular	Transport/cargo protein	Transport	-	Yes
ACSF3	197322	acyl-CoA synthetase family member 3, mitochondrial isoform 1 precursor	NP_777577.2	2	4	4	8	0.75	**0.5**	22.25	42.78	34.5	44.8	4	4	14117	197322	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
RPS27L	51065	40S ribosomal protein S27-like	NP_057004.1	1	1	3	23	0.75	**0.45**					1	1	18003	51065	ribosomal protein S27-like	Molecular function unknown	Ribosome	Unclassified	Biological_process unknown	-	No
VMP1	81671	vacuole membrane protein 1	NP_112200.2	1	1	1	6	0.74	**0.4**	14.96	21	19.4	11.8	3	2									
SNX33	257364	sorting nexin-33	NP_695003.1	1	2	2	3	0.74	**0.34**	2.8		2.9		2	1	11331	257364	None	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	SH3;PX	Yes
MAL2	114569	protein MAL2	NP_443118.1	1	1	1	1	0.74	**0.31**					1	1	14351	114569	mal, T-cell differentiation protein 2	Transporter activity	Endosome	Transport/cargo protein	Transport	TM	Yes
MANBAL	63905	protein MANBAL	NP_071360.1	1	1	1	2	0.73	**0.47**					1	1	14356	63905	mannosidase, beta A, lysosomal-like	Molecular function unknown	Integral to membrane	Integral membrane protein;Unclassified	Biological_process unknown	TM	No
NDUFB8	4714	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial isoform 1 precursor	NP_004995.1	3	1	1	2	0.73	**0.22**					1	1	11886	4714	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 8, 19kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	Yes
C8A	731	complement component C8 alpha chain preproprotein	NP_000553.1	1	1	1	1	0.72	**0.09**					1	1	409	731	complement component 8, alpha polypeptide	Complement activity	Extracellular	Complement protein	Immune response	TSP1;LDLA;SP	Yes
VPS13A	23230	vacuolar protein sorting-associated protein 13A isoform A	NP_150648.2	4	2	2	2	0.71	**0.48**					1	1	5814	23230	vacuolar protein sorting 13A (yeast)	Transporter activity	-	Transport/cargo protein	Protein metabolism;Transport	CC	Yes
S100A11	6282	protein S100-A11	NP_005611.1	1	6	6	32	0.7	**0.47**	10.24	22.72	31.1	47.6	18	18	4385	6282	S100 calcium binding protein A11(calgizzarin)	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
VPS18	57617	vacuolar protein sorting-associated protein 18 homolog	NP_065908.1	1	2	2	4	0.7	**0.44**	37.25	36.27	38.3	23	2	2	9776	57617	vacuolar protein sorting protein 18	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC	Yes
IFIH1	64135	interferon-induced helicase C domain-containing protein 1	NP_071451.2	1	2	2	12	0.7	**0.38**	23.96	110.79	43.1	120	6	5	9507	64135	interferon induced with helicase C domain 1	ATPase activity	Cytoplasm	ATPase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	No
KRT19	3880	keratin, type I cytoskeletal 19	NP_002267.2	2	26	40	412	0.67	**0.34**	5.17	17.85	43.8	86.2	147	147	1007	3880	keratin 19	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
RNF170	81790	E3 ubiquitin-protein ligase RNF170 isoform a	NP_001153695.1	2	1	1	2	0.66	**0.5**					1	1	13165	81790	ring finger protein 170	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;RING;TM	No
LPCAT2	54947	lysophosphatidylcholine acyltransferase 2	NP_060309.2	1	2	2	4	0.66	**0.45**	20.96	133.46	19.6	101.8	2	2	7913	54947	None	Molecular function unknown	-	Unclassified	Biological_process unknown	PISC;EF;TM	No
MARK1	4139	serine/threonine-protein kinase MARK1 isoform 2	NP_061120.3	7	2	5	10	0.65	**0.38**	0.57	95.97	0.5	54.7	2	2	7353	4139	MAP/microtubule affinity-regulating kinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;UBA	No
PLGRKT	55848	plasminogen receptor (KT)	NP_060935.2	1	1	1	1	0.65	**0.34**					1	1									
DYNLL2	140735	dynein light chain 2, cytoplasmic	NP_542408.1	1	3	4	8	0.64	**0.48**	2.86	68.78	3.2	62.4	3	3	6489	140735	None	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	-	No
CLTB	1212	clathrin light chain B isoform b	NP_009028.1	2	6	6	22	0.64	**0.47**	3.18	7.3	6.8	11.4	11	11	352	1212	clathrin, light polypeptide (Lcb)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	-	Yes
IFITM3	10410	interferon-induced transmembrane protein 3	NP_066362.2	3	2	2	5	0.63	**0.45**	59.05	62.03	56.2	41.4	2	2	5719	10410	interferon induced transmembrane protein 3(1-8U)	Molecular function unknown	Plasma membrane	Integral membrane protein	Immune response	TM	No
PHLPP1	23239	PH domain leucine-rich repeat-containing protein phosphatase 1	NP_919431.2	1	1	1	1	0.63	**0.31**					1	1	15145	23239	PH domain and leucine rich repeat proteinphosphatase	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	PH;LRR;PP2C;LZ	No
SLC37A2	219855	sugar phosphate exchanger 2 isoform 1	NP_938018.1	1	1	1	1	0.6	**0.44**					1	1	15380	219855	solute carrier family 37(glycerol-3-phosphate transporter), member 2	Auxiliary transport protein activity	Integral to membrane	Membrane transport protein	Transport	TM	No
CBR4	84869	carbonyl reductase family member 4	NP_116172.2	1	1	1	2	0.58	**0.44**					1	1	7859	84869	None	Molecular function unknown	-	Unclassified	Biological_process unknown	KRINGLE	No
SMN1	6606	survival motor neuron protein isoform d	NP_000335.1	4	2	2	2	0.57	**0.45**	140.48	189.19	159.3	184.2	2	2	2646	6606	survival of motor neuron 1, telomeric	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TUDOR	Yes
CD82	3732	CD82 antigen isoform 1	NP_002222.1	1	1	1	1	0.57	**0.42**					1	1	9004	3732	CD82 antigen	Receptor activity;Receptor regulator activity	Plasma membrane	Integral membrane protein;Cell surface receptor	Cell communication;Signal transduction	TM	Yes
SLC35F6	54978	solute carrier family 35 member F6 precursor	NP_060347.2	1	2	2	3	0.57	**0.32**	14.96	155.82	12.1	78.8	2	2									
KRT4	3851	keratin, type II cytoskeletal 4	NP_002263.3	1	2	4	63	0.56	**0.27**	42.64	135.31	104.8	211.7	13	13	478	3851	keratin 4	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
TACSTD2	4070	tumor-associated calcium signal transducer 2 precursor	NP_002344.2	1	7	7	23	0.55	**0.5**	21.91	33.1	41.6	59.2	11	11	672	4070	tumor-associated calcium signal transducer 2	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	THYRO;TM;SP	Yes
OCIAD2	132299	OCIA domain-containing protein 2 isoform 1	NP_001014446.1	3	6	6	26	0.54	**0.48**	12.69	19.1	26.2	35.5	14	14	14873	132299	OCIA domain containing 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TPM4	7171	tropomyosin alpha-4 chain isoform Tpm4.1cy	NP_001138632.1	2	3	23	67	0.54	**0.47**	10.35	35.16	9.6	29.2	3	3	11734	7171	tropomyosin 4	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
EFNB1	1947	ephrin-B1 precursor	NP_004420.1	1	6	6	10	0.53	**0.49**	1.27	40.39	1.3	40.8	4	4	2072	1947	ephrin-B1	Receptor binding	Plasma membrane	Ligand	Cell communication;Signal transduction	SP;TM	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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ITIH4	3700	inter-alpha-trypsin inhibitor heavy chain H4 isoform 1 precursor	NP_002209.2	2	1	1	3	0.53	**0.48**					1	1	2781	3700	inter-alpha (globulin) inhibitor H4 (plasmaKallikrein-sensitive glycoprotein)	Protease inhibitor activity	Extracellular	Protease inhibitor	Protein metabolism	VWA;SP;VIT	Yes
SERPINA3	12	alpha-1-antichymotrypsin precursor	NP_001076.2	1	1	1	1	0.52	**0.49**					1	1	120	12	serine (or cysteine) proteinase inhibitor,clade A (alpha-1 antiproteinase, antitrypsin), member 3	Protease inhibitor activity	Extracellular	Protease inhibitor	Protein metabolism	SERPIN;SP	Yes
CD9	928	CD9 antigen	NP_001760.1	1	2	2	7	0.52	**0.43**	45.63	76.21	50	73.6	4	4	880	928	CD9 antigen (p24)	Molecular function unknown	Cell surface	Unclassified	Immune response	TM	Yes
HLA-A	3105	HLA class I histocompatibility antigen, A-1 alpha chain precursor	NP_002107.3	1	1	6	24	0.52	**0.43**					1	1	826	3105	major histocompatibility complex, class I, A	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein	Immune response	IGC;SP;TM	Yes
S100A14	57402	protein S100-A14	NP_065723.1	1	7	7	30	0.51	**0.45**	14.88	22.79	32.8	46	18	18	10467	57402	S100 calcium binding protein A14	Calcium ion binding	Cytoplasm	Calcium binding protein	Biological_process unknown	EF	Yes
DSP	1832	desmoplakin isoform I	NP_004406.2	2	106	106	316	0.51	**0.43**	5.79	8.69	39.4	51.8	167	167	513	1832	desmoplakin	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	PLEC;CC;SPECTRIN	Yes
CEP44	80817	centrosomal protein of 44 kDa isoform b	NP_001138786.1	2	1	1	1	0.51	**0.39**					1	1									
FSIP2	401024	fibrous sheath-interacting protein 2	NP_775922.2	1	1	1	1	0.51	**0.33**					1	1	8177	285135	fibrous sheath interacting protein 2	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TMEM57	55219	macoilin isoform a	NP_060672.2	2	1	1	2	0.51	**0.25**					1	1	13340	55219	None	Molecular function unknown	Nuclear membrane	Integral membrane protein	Biological_process unknown	CC;ERM;TM	No
GAS6	2621	growth arrest-specific protein 6 precursor	NP_000811.1	1	1	1	2		**0.47**						1	2705	2621	growth arrest-specific 6	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	GLA;EGFL;EGFCA;LAMG;SP	Yes
EP400	57634	E1A-binding protein p400	NP_056224.3	1	1	1	1	1.99	1.89					1	1	9378	57634	E1A binding protein p400	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC;SANT	Yes
RPS6KA5	9252	ribosomal protein S6 kinase alpha-5 isoform a	NP_004746.2	2	1	1	1	1.99	0.71					1	1	6789	9252	ribosomal protein S6 kinase, 90kDa,polypeptide 5	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cytokine and chemokine mediated signaling pathway;Regulation of translation;Transcription	S_T_kinase;NLS	Yes
VAT1L	57687	synaptic vesicle membrane protein VAT-1 homolog-like	NP_065978.1	1	1	1	2	1.98	1.98					1	1	13875	57687	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
LOC642249	642249	uncharacterized protein LOC642249	XP_006725002.1	1	1	1	1	1.97	1.66					1	1									
CARKD	55739	ATP-dependent (S)-NAD(P)H-hydrate dehydratase isoform a	NP_060680.2	4	1	1	4	1.97	0.87	5.59	12.58	15.7	15.6	2	2	7698	55739	None	Transporter activity	-	Transport/cargo protein	Metabolism	SP	No
DPEP3	64180	dipeptidase 3 isoform a precursor	NP_071752.3	2	1	1	1	1.96	0.68					1	1	7012	64180	dipeptidase 3	Peptidase activity	-	Protease	Protein metabolism	SP	No
HCFC2	29915	host cell factor 2	NP_037452.1	1	1	1	1	1.95	0.87					1	1	6393	29915	host cell factor C2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KELCH;FN3	No
RBM6	10180	RNA-binding protein 6 isoform 1	NP_005768.1	2	1	1	2	1.94	0.62					1	1	6054	10180	RNA binding motif protein 6	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;G_PATCH;CC	Yes
NAA40	79829	N-alpha-acetyltransferase 40 isoform 1	NP_079047.2	2	2	2	3	1.93	1.65					1	1	7838	79829	None	Molecular function unknown	-	Unclassified	Metabolism	-	No
DAB2	1601	disabled homolog 2 isoform 1	NP_001334.2	2	1	1	2	1.92	0.81					1	1	3139	1601	disabled homolog 2, mitogen-responsivephosphoprotein (Drosophila)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PTB;CC	Yes
TMEM87A	25963	transmembrane protein 87A isoform 1 precursor	NP_056312.2	3	2	2	2	1.91	0.73					1	1	10895	25963	None	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	SP;TM	No
TIMM17A	10440	mitochondrial import inner membrane translocase subunit Tim17-A	NP_006326.1	1	4	4	10	1.9	1.4	9.33	14.36	41.1	47.5	5	5	5449	10440	translocase of inner mitochondrial membrane17 homolog A (yeast)	Catalytic activity	Mitochondrion	Enzyme: Translocase	Transport	TM	Yes
SRSF6	6431	serine/arginine-rich splicing factor 6	NP_006266.2	1	5	9	18	1.89	1.58	1.7	9.65	6.4	31.1	4	4									
COQ5	84274	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial precursor	NP_115690.3	1	1	1	1	1.89	1.31					1	1	17560	84274	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
DCAF8	50717	DDB1- and CUL4-associated factor 8	NP_056541.2	1	1	1	2	1.89	1.28					1	1	18300	50717	WD repeat domain 42A	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	CC;WD40	Yes
MAFF	23764	transcription factor MafF isoform a	NP_036455.1	2	1	1	2	1.89	1.14					1	1	5343	23764	v-maf musculoaponeurotic fibrosarcoma oncogenehomolog F (avian)	Transcription factor activity;Transcription factor binding	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes

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DPEP1	1800	dipeptidase 1 precursor	NP_001121613.1	1	1	1	2	1.89	1.13					1	1	1563	1800	dipeptidase 1 (renal)	Peptidase activity	Endoplasmic reticulum	Protease	Protein metabolism	SP	Yes
SET	6418	protein SET isoform 1	NP_001116293.1	5	3	14	48	1.88	1.8	5.9	4.83	27.7	21.5	6	6	9023	6418	SET translocation (myeloid leukemia-associated)	MHC class I receptor activity;MHC class II receptor activity	Nucleus	MHC complex protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
RAB43	339122	ras-related protein Rab-43 isoform a	NP_940892.1	10	2	3	35	1.88	1.1					1	1	17947	339122	RAB43, member RAS oncogene family	GTPase activity	-	GTPase	Cell communication;Signal transduction	RAB	Yes
METTL14	57721	N6-adenosine-methyltransferase subunit METTL14	NP_066012.1	1	2	2	2	1.87	1.99					1	1	13879	57721	None	Methyltransferase activity	-	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
ZPR1	8882	zinc finger protein ZPR1	NP_003895.1	1	7	7	21	1.86	1.47	6.97	7.69	42.7	38.9	10	11									
CAAP1	79886	caspase activity and apoptosis inhibitor 1 isoform 1	NP_079104.3	2	1	1	2	1.86	0.99					1	1									
ECI2	10455	enoyl-CoA delta isomerase 2, mitochondrial isoform 2	NP_996667.2	2	5	5	11	1.86	0.88	20.75	8.69	105.2	17.3	5	5									
SPATA20	64847	spermatogenesis-associated protein 20 isoform 1 precursor	NP_073738.2	3	1	1	2	1.86	0.68	6.62	2.72	17.6	2.6	2	2	7961	64847	spermatogenesis associated 20	Molecular function unknown	-	Unclassified	Reproduction;Embryonic development	SP	No
NACC1	112939	nucleus accumbens-associated protein 1	NP_443108.1	1	2	2	3	1.85	1.72	12.15	5.8	32.6	14.2	2	2	10692	112939	BTB (POZ) domain containing 14B	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	BTB	No
C12orf43	64897	uncharacterized protein C12orf43 isoform a	NP_001273120.1	5	1	1	2	1.85	0.97					1	1	7771	64897	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
MFAP1	4236	microfibrillar-associated protein 1	NP_005917.2	1	1	2	3	1.84	1.43					1	1	2569	4236	microfibrillar-associated protein 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	CC	Yes
OS9	10956	protein OS-9 isoform 1 precursor	NP_006803.1	8	4	4	9	1.84	1.2	2.99	1.05	9.5	2.2	3	3	17804	10956	None	Molecular function unknown	Cytoplasm;Endoplasmic reticulum	Unclassified	Biological_process unknown	SP;CC	Yes
PALM2	114299	paralemmin-2 isoform a	NP_443749.5	2	1	2	3	1.84	0.92					1	1	17817	114299	paralemmin 2	Molecular function unknown	Plasma membrane	Unclassified	Cell growth and/or maintenance	CC	No
MTMR9	66036	myotubularin-related protein 9	NP_056273.2	1	2	2	6	1.81	0.94	2.63	1.99	8.3	3.2	3	3	9377	66036	myotubularin related protein 9	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase	Cell communication;Signal transduction	CC	Yes
TRIM59	286827	tripartite motif-containing protein 59	NP_775107.1	1	1	1	2	1.81	0.62					1	1	15568	286827	tripartite motif-containing 59	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	RING;TM	No
HSPA13	6782	heat shock 70 kDa protein 13 precursor	NP_008879.3	1	2	2	8	1.8	1.99	1.14	4.95	4.1	19.9	4	4	3061	6782	stress 70 protein chaperone,microsome-associated, 60kDa	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP	Yes
MAP1B	4131	microtubule-associated protein 1B	NP_005900.2	3	46	47	134	1.8	1.79	2.66	3.13	41.2	49.2	69	69	1139	4131	microtubule-associated protein 1B	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
CCDC132	55610	coiled-coil domain-containing protein 132 isoform a	NP_060137.2	3	2	2	2	1.8	0.61					1	1	10973	55610	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
SULF2	55959	extracellular sulfatase Sulf-2 isoform a precursor	NP_061325.1	2	2	2	3	1.79	1.24	10.24	8.29	26.3	14.6	2	2	18130	55959	sulfatase 2	Catalytic activity	Extracellular	Enzyme: Sulphatase	Metabolism;Energy pathways	SP;CC;SULF	Yes
YBX3	8531	Y-box-binding protein 3 isoform a	NP_003642.3	2	3	16	47	1.79	0.78	5.19	10.31	16.2	14	3	3									
AK6	102157402	adenylate kinase isoenzyme 6 isoform b	NP_057367.1	1	1	1	6	1.79	0.7	15.98	19.59	52.6	24.1	3	3									
TXNRD1	7296	thioredoxin reductase 1, cytoplasmic isoform 3	NP_001087240.1	5	21	21	113	1.78	1.91	5.49	5.05	84.1	81.8	56	55	3068	7296	thioredoxin reductase 1	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
RTFDC1	51507	protein RTF2 homolog isoform a	NP_001269964.1	3	3	3	6	1.78	1.9	14.76	1.9	48.1	6.3	3	3									
EXOSC3	51010	exosome complex component RRP40 isoform 1	NP_057126.2	2	1	1	8	1.78	0.89	0.59	2.07	1.5	3.2	2	3	16220	51010	exosome component 3	Ribonuclease activity	Nucleolus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
POLR2H	5437	DNA-directed RNA polymerases I, II, and III subunit RPABC3 isoform 2	NP_006223.2	5	2	2	3	1.78	0.81					1	1	9082	5437	polymerase (RNA) II (DNA directed) polypeptideH	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
FGB	2244	fibrinogen beta chain isoform 1 preproprotein	NP_005132.2	2	1	1	3	1.78	0.71					1	1	620	2244	fibrinogen, B beta polypeptide	Protein binding	Extracellular	Coagulation factor	Protein metabolism	FBG;SP;CC	Yes
HMOX1	3162	heme oxygenase 1	NP_002124.1	1	4	4	11	1.77	1.27	16.96	16.15	75.4	53.4	5	6	782	3162	heme oxygenase (decycling) 1	Catalytic activity	Endoplasmic reticulum;Microsome	Enzyme: Oxygenase	Metabolism;Energy pathways	TM	Yes
HGH1	51236	protein HGH1 homolog	NP_057542.2	1	3	3	6	1.77	0.64	2.14	27.95	5.4	25.8	2	2									
IL1A	3552	interleukin-1 alpha proprotein	NP_000566.3	1	9	9	29	1.76	1.86	9.04	3.53	65.2	25	14	14	988	3552	interleukin 1, alpha	Cytokine activity	Cytoplasm	Cytokine	Immune response	IL1	Yes
C19orf33	64073	immortalization up-regulated protein	NP_277055.1	1	2	2	5	1.76	1.13	0.71	16.55	2.2	33.2	3	3	12706	64073	chromosome 19 open reading frame 33	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
HORMAD1	84072	HORMA domain-containing protein 1 isoform 1	NP_115508.2	2	1	1	1	1.76	0.85					1	1	11396	84072	HORMA domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
LOC105371592	105371592	atherin-like	XP_011507045.1	1	1	1	3	1.75	1.84	6.25	0.44	15.6	1.1	2	2									
RCN1	5954	reticulocalbin-1 precursor	NP_002892.1	1	9	9	39	1.75	1.41	3.63	6.5	30.6	45.2	22	22	4111	5954	reticulocalbin 1, EF-hand calcium binding domain	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein	Cell communication;Signal transduction	SP;EF	Yes
LOC101060458	101060458	peptidyl-prolyl cis-trans isomerase A-like isoform X1	XP_003960579.2	7	1	2	3	1.75	1.36	0.53	11.57	1.3	22.5	2	2									

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ISG20L2	81875	interferon-stimulated 20 kDa exonuclease-like 2	NP_001290024.1	1	2	2	4	1.75	1.25	6.37	1.66	15.8	2.9	2	2	7788	81875	None	Exonuclease activity	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	EXOIII	Yes
GSKIP	51527	GSK3-beta interaction protein	NP_001258833.1	1	1	1	2	1.75						1										
SLC7A11	23657	cystine/glutamate transporter	NP_055146.1	1	2	2	4	1.74	1.73	0.52	0.08	1.6	0.2	3	3	9720	23657	solute carrier family 7, (cationic amino acidtransporter, y+ system) member 11	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
EMILIN3	90187	EMILIN-3 precursor	NP_443078.1	1	1	1	1	1.74	0.72					1	1	12335	90187	elastin microfibril interfacer 3	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
AP2S1	1175	AP-2 complex subunit sigma isoform 3	NP_001288005.1	5	2	2	6	1.74	0.66					1	1	3762	1175	adaptor-related protein complex 2, sigma 1subunit	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Cell communication;Signal transduction	-	Yes
MYL6	4637	myosin light polypeptide 6 isoform 2	NP_524147.2	5	1	10	72	1.74	0.57	6.58	23.15	23.1	26.7	4	4	17618	4637	myosin, light polypeptide 6, alkali, smoothmuscle and non-muscle	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	EF	Yes
COX2	4513	cytochrome c oxidase subunit II	YP_003024029.1	1	7	7	23	1.73	1.1	9.27	15.8	47.9	52.1	8	8									
ZDHHC5	25921	palmitoyltransferase ZDHHC5	NP_056272.2	1	2	2	3	1.73	0.97	21.56	8.65	56.7	11.9	2	2	15720	25921	zinc finger, DHHC-type containing 5	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	SP;TM	Yes
EEF1B2	1933	elongation factor 1-beta	NP_001950.1	1	7	8	53	1.72	1.01	6.36	13.27	63.1	80.5	28	28	2804	1933	eukaryotic translation elongation factor 1beta 2	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
DAB2IP	153090	disabled homolog 2-interacting protein isoform 2	NP_619723.1	3	1	3	3	1.71	1.05					1	1	9903	153090	DAB2 interacting protein	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	PH;C2;RASGAP;CC	No
CHMP4B	128866	charged multivesicular body protein 4b	NP_789782.1	2	7	7	20	1.7	1.75	4.53	4.73	23.5	25.1	9	9	16642	128866	chromatin modifying protein 4B	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC	No
SAP130	79595	histone deacetylase complex subunit SAP130 isoform a	NP_001139400.1	2	1	1	2	1.7	1.11					1	1	18015	79595	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
STT3A	3703	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A isoform a	NP_689926.1	2	9	9	65	1.7	0.65	4.99	8.64	57.1	35.9	39	39	3086	3703	integral membrane protein 1	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	TM	Yes
SERPINB2	5055	plasminogen activator inhibitor 2	NP_002566.1	1	24	24	239	1.69	1.73	3.43	3.55	66.6	70.7	109	108	1420	5055	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 2	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism;Anti-apoptosis	SP;SERPIN	Yes
CPNE1	8904	copine-1 isoform b	NP_003906.2	3	15	15	46	1.69	1.4	4.87	6.01	42.8	43	25	24	5014	8904	copine I	Transporter activity	Cytoplasm	Transport/cargo protein	Vesicle-mediated transport	C2;VWA	Yes
TUBB2A	7280	tubulin beta-2A chain	NP_001060.1	2	6	34	523	1.69	0.52	10.96	46.55	95.6	142.3	19	19									
IFI30	10437	gamma-interferon-inducible lysosomal thiol reductase preproprotein	NP_006323.2	1	2	2	4	1.69	0.52	5.4	89.94	12.9	73.4	2	2	5234	10437	interferon, gamma-inducible protein 30	Catalytic activity	Lysosome	Enzyme: Reductase	Metabolism;Energy pathways	CXXC;SP	No
RAB6A	5870	ras-related protein Rab-6A isoform b	NP_942599.1	12	1	10	81	1.68	1.33	24.25	2.16	62.8	4.1	2	2	1543	5870	RAB6A, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB	No
OSBPL2	9885	oxysterol-binding protein-related protein 2 isoform 2	NP_653081.1	3	1	1	4	1.67	1.86	4.3	5.42	10.2	14.3	2	2	9473	9885	oxysterol binding protein-like 2	Lipid binding	Golgi apparatus	Transport/cargo protein	Vesicle-mediated transport	CC	No
EREG	2069	proepiregulin preproprotein	NP_001423.1	1	1	1	2	1.66	1.6					1	1	3638	2069	epiregulin	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	TM;EGF;SP	No
CPT1A	1374	carnitine O-palmitoyltransferase 1, liver isoform isoform 1	NP_001867.2	2	10	10	21	1.66	1.6	8.1	6.04	49.4	34.5	12	12	2755	1374	carnitine palmitoyltransferase 1A (liver)	Palmitoyltransferase activity	Mitochondrial membrane	Enzyme: Palmitoyltransferase	Mitochondrial transport	TM	Yes
ALDH1A2	8854	retinal dehydrogenase 2 isoform 1	NP_003879.2	4	3	7	31	1.66	1.33	8.46	0.75	32.2	2.2	5	5	4733	8854	aldehyde dehydrogenase 1 family, member A2	Catalytic activity	Extracellular	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
YBX1	4904	nuclease-sensitive element-binding protein 1	NP_004550.2	2	8	13	101	1.66	1.2	3.82	8.96	41	74.5	39	38	1095	4904	nuclease sensitive element binding protein 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CDC42SE2	56990	CDC42 small effector protein 2	NP_064625.1	1	1	1	1	1.66	0.51					1	1	16695	56990	CDC42 small effector 2	Molecular function unknown	Plasma membrane	Unclassified	Cell communication;Signal transduction	PBD	No
IGSF1	3547	immunoglobulin superfamily member 1 isoform 3 precursor	NP_001164432.1	3	3	3	4	1.64	1.93	35.46	14.66	97.9	41.8	2	2	2138	3547	immunoglobulin superfamily, member 1	Antigen binding	Plasma membrane	Immunoglobulin	Immune response	IGC2;TM;IG;SP	No
JUND	3727	transcription factor jun-D isoform JunD-FL	NP_005345.3	2	4	4	8	1.64	1.14	2.38	5.24	7.8	12	4	4	1304	3727	jun D proto-oncogene	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
FBLN5	10516	fibulin-5 precursor	NP_006320.2	1	1	1	12	1.64	0.58	10.68	29.92	45.1	44.8	6	6	5204	10516	fibulin 5	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	EGFL;EGFCA;RGD;SP	Yes
ABCA1	19	ATP-binding cassette sub-family A member 1	NP_005493.2	1	2	2	4	1.63	1.71	14.07	3.63	33.4	8.8	2	2	2501	19	ATP-binding cassette, sub-family A (ABC1),member 1	Transporter activity	Plasma membrane;Cell surface;Intracellular vesicle	Transport/cargo protein	Transport	TM;AAA;SP	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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CHKA	1119	choline kinase alpha isoform a	NP_001268.2	2	1	1	2	1.63	1.26					1	1	327	1119	choline kinase alpha	Lipid kinase activity	-	Lipid Kinase	Metabolism;Energy pathways	SP	No
SMYD4	114826	SET and MYND domain-containing protein 4	NP_443160.2	1	1	1	1	1.63	0.73					1	1	18079	114826	SET and MYND domain containing 4	Molecular function unknown	-	Unclassified	Biological_process unknown	SET;CC	No
BANF1	8815	barrier-to-autointegration factor	NP_003851.1	1	2	2	11	1.63	0.64	16.39	4.81	65.4	6.8	5	5	4817	8815	barrier to autointegration factor 1	DNA binding	Nucleus	DNA binding protein	Biological_process unknown	-	Yes
LOC105370098	105370098	uncharacterized protein LOC105370098	XP_011506705.1	1	1	1	1	1.62	1.67					1	1									
MMRN2	79812	multimerin-2 precursor	NP_079032.2	1	1	1	2	1.62	1.51					1	1	10601	79812	multimerin 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	SP;CC;C1Q	Yes
TNS3	64759	tensin-3	NP_073585.8	1	1	1	1	1.62	1.24					1	1	8438	64759	tensin 3	Receptor activity;Molecular function unknown	Integral to membrane	Integral membrane protein;Cell surface receptor	Cell communication;Signal transduction;Biological_process unknown	SH2;PTB	No
YBX3	8531	Y-box-binding protein 3 isoform b	NP_001138898.1	2	1	14	42	1.62	1.19					1	1									
ACOX3	8310	peroxisomal acyl-coenzyme A oxidase 3 isoform a	NP_003492.2	2	4	4	4	1.62	0.85	35.45	25.07	96.9	30.9	2	2	4552	8310	acyl-Coenzyme A oxidase 3, pristanoyl	Catalytic activity	Peroxisome	Enzyme: Oxidase	Metabolism;Energy pathways	-	Yes
CASC3	22794	protein CASC3	NP_031385.2	1	1	1	1	1.61	0.74					1	1	16225	22794	cancer susceptibility candidate 3	Molecular function unknown	Cytoplasm	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
TF	7018	serotransferrin precursor	NP_001054.1	1	9	9	13	1.6	1.56	4.31	10.8	19.7	50.6	8	8	1811	7018	transferrin	Transporter activity	Extracellular	Transport/cargo protein	Transport	SP;TR_FER	Yes
CLTA	1211	clathrin light chain A isoform a	NP_001824.1	8	7	7	19	1.6	1.4	8.24	5.12	38.6	20.5	8	8	351	1211	clathrin, light polypeptide (Lca)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
KIAA0430	9665	meiosis arrest female protein 1 isoform 2	NP_001171927.1	3	1	1	1	1.6	1.07					1	1	13992	9665	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
FBXO30	84085	F-box only protein 30	NP_115521.3	1	1	1	4	1.6	0.84	16.7	7.72	39.1	9.2	2	2	10953	84085	F-box protein 30	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	F_BOX;CC	Yes
FCGBP	8857	IgGFc-binding protein precursor	NP_003881.2	1	1	1	8	1.6	0.72	4.48	5.37	16.1	8.6	5	5	10956	8857	Fc fragment of IgG binding protein [Homosapiens]Other Aliases: HGNC:13572, FC(GAMMA)BP Other Designations: Human Fc gammaBP [AA 1-2843]; IgG Fc binding protein; IgG Fc binding protein	Molecular function unknown	Extracellular	Unclassified	Immune response	SP;VWD	Yes
SHPK	23729	sedoheptulokinase	NP_037408.2	1	1	1	1	1.6	0.7					1	1	5451	23729	carbohydrate kinase-like	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
GCLM	2730	glutamate--cysteine ligase regulatory subunit isoform 1	NP_002052.1	2	5	5	13	1.59	1.96	2.54	1.94	11.5	10.8	8	8	3106	2730	glutamate-cysteine ligase, modifier subunit	Ligase activity	-	Enzyme: Ligase	Metabolism;Energy pathways	ALDKR	No
DDX31	64794	probable ATP-dependent RNA helicase DDX31 isoform 1	NP_073616.6	2	3	3	3	1.59	1.89	3.43	15.42	7.7	43.1	2	2	10860	64794	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	RNA binding	Nucleolus	RNA binding protein;RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	No
HYOU1	10525	hypoxia up-regulated protein 1 precursor	NP_006380.1	2	43	43	221	1.59	1.87	3.39	3.68	63.2	85.3	115	116	3448	10525	hypoxia up-regulated 1	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP	Yes
FNBP4	23360	formin-binding protein 4	NP_056123.2	1	4	4	6	1.59	1.67	10.01	7.56	32.6	25.6	4	4	10996	23360	formin binding protein 4	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	WW;CC	No
PVR	5817	poliovirus receptor isoform alpha precursor	NP_006496.4	4	2	2	6	1.59	1.5	4.15	3.67	13.3	11.1	4	4	1434	5817	poliovirus receptor	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;IGV;IG;TM;Ig_LIKE	Yes
PPHLN1	51535	periphilin-1 isoform 1	NP_057572.5	4	1	1	2	1.59	0.75					1	1	10488	51535	periphilin 1	Structural molecule activity	Nucleus;Cytoplasm	Structural protein	Cell growth and/or maintenance	NES;NLS	Yes
CYP27B1	1594	25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial	NP_000776.1	1	2	2	3	1.58	1.94					1	1	2031	1594	cytochrome P450, family 27, subfamily B,polypeptide 1	Catalytic activity	Mitochondrion	Enzyme: Hydroxylase	Metabolism;Energy pathways	-	Yes
PGAM4	441531	phosphoglycerate mutase 4	NP_001025062.1	1	1	8	57	1.58	1.7					1	1	18831	441531	Phosphoglycerate mutase family 4	Isomerase activity	-	Enzyme: Mutase	Metabolism	-	No
NAMPT	10135	nicotinamide phosphoribosyltransferase precursor	NP_005737.1	1	15	15	60	1.58	1.49	3.43	3.59	31.4	31	32	32	9938	10135	pre-B-cell colony enhancing factor 1	Transferase activity	Extracellular	Cytokine	Anti-apoptosis	-	Yes
COPS8	10920	COP9 signalosome complex subunit 8 isoform 1	NP_006701.1	2	2	2	22	1.58	0.91	8.37	8.89	43.8	26	10	10	16737	10920	COP9 constitutive photomorphogenic homologsubunit 8 (Arabidopsis)	Molecular function unknown	Cytoplasm	Regulatory/other subunit	Regulation of signal transduction	-	Yes
THEMIS	387357	protein THEMIS isoform 1	NP_001158157.1	3	1	1	1	1.58	0.59					1	1	16662	387357	chromosome 6 open reading frame 190	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
FBN1	2200	fibrillin-1 precursor	NP_000129.3	2	2	2	5	1.57	0.69	9.85	18.09	27.3	21.8	3	3	618	2200	fibrillin 1 (Marfan syndrome)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	EGF;EGFCA;EGFL;SP	Yes

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HRC	3270	sarcoplasmic reticulum histidine-rich calcium-binding protein precursor	NP_002143.1	1	1	1	1	1.57	0.6					1	1	818	3270	histidine rich calcium binding protein	Calcium ion binding	Sarcoplasmic reticulum	Calcium binding protein	Cell communication;Signal transduction	SP;CC	Yes
PPOX	5498	protoporphyrinogen oxidase	NP_000300.1	1	1	1	3	1.57	0.59		13.95		11.6	1	2	2953	5498	protoporphyrinogen oxidase	Catalytic activity	Mitochondrion	Enzyme: Oxidase	Metabolism;Energy pathways	SP	Yes
G6PD	2539	glucose-6-phosphate 1-dehydrogenase isoform a	NP_000393.4	2	33	33	123	1.56	1.74	3.61	3.26	48.8	49	67	67	2377	2539	glucose-6-phosphate dehydrogenase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
OPN4	94233	melanopsin isoform 2	NP_001025186.1	2	1	1	1	1.56	1.54					1	1	5977	94233	opsin 4 (melanopsin)	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Cell communication;Signal transduction	TM	Yes
DCK	1633	deoxycytidine kinase	NP_000779.1	1	1	1	2	1.56	1.39					1	1	507	1633	deoxycytidine kinase	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
MAGED2	10916	melanoma-associated antigen D2	NP_803182.1	9	13	13	34	1.56	1.23	2.63	8.6	16	42.9	15	15	6630	10916	melanoma antigen family D, 2	Molecular function unknown	Nucleus	Unclassified	Cell growth and/or maintenance	MAGE	Yes
NHSL1	57224	NHS-like protein 1 isoform 1	NP_065197.1	2	2	2	5	1.56	1.09	4.07	17.84	11.1	34.6	3	3	19619	57224	NHS-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
LYN	4067	tyrosine-protein kinase Lyn isoform A	NP_002341.1	52	5	7	28	1.56	0.98	8.32	12.68	32.7	31.1	6	6	1301	4067	v-yes-1 Yamaguchi sarcoma viral related oncogenehomolog	Protein-tyrosine kinase activity	Plasma membrane	Tyrosine kinase	Cell communication;Signal transduction	SH3;SH2;Tyr_Kinase	Yes
C17orf64	124773	uncharacterized protein C17orf64	NP_859058.2	1	1	1	1	1.56	0.77					1	1	14029	124773	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
FN1	2335	fibronectin isoform 3 preproprotein	NP_002017.1	10	33	33	96	1.55	1.76	4.22	4.26	48.5	56.4	49	49	626	2335	fibronectin 1	Extracellular matrix structural constituent	Extracellular;Nucleus	Extracellular matrix protein	Cell growth and/or maintenance	FN1;FN2;FN3;RGD;SP	Yes
HSP90B1	7184	endoplasmin precursor	NP_003290.1	1	40	42	356	1.55	1.49	1.95	2.85	42.2	61.9	180	180	1860	7184	tumor rejection antigen (gp96) 1	Heat shock protein activity	Endoplasmic reticulum	Heat shock protein	Protein metabolism	SP;CC	Yes
DOLK	22845	dolichol kinase	NP_055723.1	1	1	1	1	1.55	1.35					1	1	15525	22845	transmembrane protein 15	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
MARCKSL1	65108	MARCKS-related protein	NP_075385.1	1	4	5	23	1.55	1.33	5.78	3.32	25.8	12.5	8	8	4247	65108	MARCKS-like 1	Receptor signaling complex scaffold activity	-	Adapter molecule	Cell communication;Signal transduction	-	Yes
EEF1A2	1917	elongation factor 1-alpha 2	NP_001949.1	1	2	13	131	1.55	1.14	20.85	8.04	48.1	13	2	2	4265	1917	eukaryotic translation elongation factor 1alpha 2	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	GTP_EFTU;GTP_EFTU_D2;GTP_EFTU_D3	Yes
PRPH	5630	peripherin	NP_006253.2	2	1	5	26	1.55	1.02	26.85	13.48	64.6	19.7	2	2	1365	5630	peripherin	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
CCDC59	29080	thyroid transcription factor 1-associated protein 26	NP_054886.2	1	1	1	2	1.55	0.78					1	1	13696	29080	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TGFB2	7042	transforming growth factor beta-2 isoform 1 precursor	NP_001129071.1	2	2	2	5	1.54	1.46	11.3	23.77	25	52.3	2	2	1828	7042	transforming growth factor, beta 2	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	TGFB;SP;TM	No
CLNS1A	1207	methylosome subunit pICln	NP_001284.1	1	6	6	47	1.54	1.33	4.73	4.19	37	27.7	24	24	3694	1207	chloride channel, nucleotide-sensitive, 1A	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	Yes
CPSF3L	54973	integrator complex subunit 11 isoform 2	NP_060341.2	5	3	3	3	1.54	1.21	17.46	14.43	39.6	25	2	2	13377	54973	cleavage and polyadenylation specific factor3-like	Endonuclease activity	Nucleus	Enzyme: Hydrolase	Regulation of cell cycle	-	Yes
SCYL1	57410	N-terminal kinase-like protein isoform A	NP_065731.3	2	6	6	10	1.54	1.18	2.97	5.1	10.2	13.5	5	5	6414	57410	SCY1-like 1 (S. cerevisiae)	Transcription regulator activity	Centrosome	Cell cycle control protein	Cell communication;Signal transduction;Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HEAT;S_T_Y_Kinase	No
OXA1L	5018	mitochondrial inner membrane protein OXA1L	NP_005006.3	1	4	4	7	1.54	1	6.22	13.43	19.3	27.3	4	4	3043	5018	oxidase (cytochrome c) assembly 1-like	Catalytic activity	Mitochondrion	Enzyme: Oxidase	Metabolism;Energy pathways	TM	Yes
DDX39A	10212	ATP-dependent RNA helicase DDX39A	NP_005795.2	1	8	17	58	1.54	0.85	4.93	8.54	23.1	21.9	9	9									
PCID2	55795	PCI domain-containing protein 2 isoform 2	NP_001245141.1	3	4	4	7	1.54	0.82	5.75	6.81	20	12.6	5	5	7749	55795	None	Molecular function unknown	-	Unclassified	Biological_process unknown	PCI	No
VPS33A	65082	vacuolar protein sorting-associated protein 33A	NP_075067.2	1	1	1	1	1.54	0.6					1	1	15651	65082	vacuolar protein sorting 33A (yeast)	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	Yes
CKB	1152	creatine kinase B-type	NP_001814.2	1	9	10	34	1.53	1.61	6.93	8.86	45.8	64.2	17	17	423	1152	creatine kinase, brain	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 2 precursor	NP_001193769.1	4	1	1	2	1.53	1.52					1	1	4343	10618	trans-golgi network protein 2	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	SP;TM	Yes
DFFB	1677	DNA fragmentation factor subunit beta isoform 1	NP_001269598.1	2	1	1	2	1.53	1.35					1	1	3532	1677	DNA fragmentation factor, 40kDa, betapolypeptide (caspase-activated DNase)	Deoxyribonuclease activity	Nucleus	Deoxyribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
GYS1	2997	glycogen [starch] synthase, muscle isoform 1	NP_002094.2	3	14	14	33	1.53	1.18	4.43	8.39	28.4	42.5	17	17	721	2997	glycogen synthase 1 (muscle)	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes

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RBM15B	29890	putative RNA-binding protein 15B	NP_037418.3	1	2	3	4	1.53	0.99	15	4.64	33.4	6.5	2	2	11486	29890	RNA binding motif protein 15B	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	No
ASF1A	25842	histone chaperone ASF1A	NP_054753.1	1	1	1	2	1.53	0.98					1	1	16459	25842	ASF1 anti-silencing function 1 homolog A (S.cerevisiae)	Chaperone activity	Nucleus	Chaperone	Protein metabolism	-	No
RWDD1	51389	RWD domain-containing protein 1 isoform a	NP_057036.2	2	3	3	4	1.53	0.92	4.07	10.08	12.5	18.6	4	4	15286	51389	RWD domain containing 1	Molecular function unknown	-	Unclassified	Biological_process	RWD;CC	Yes
IFT122	55764	intraflagellar transport protein 122 homolog isoform 1	NP_443711.2	2	1	1	2	1.53	0.74					1	1	6922	55764	WD repeat domain 10	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	WD40	Yes
NQO1	1728	NAD(P)H dehydrogenase [quinone] 1 isoform a	NP_000894.1	4	11	11	47	1.52	1.85	5.73	5.6	46.7	56.8	26	26	518	1728	NAD(P)H dehydrogenase, quinone 1	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways;Synaptic transmission;Xenobiotic metabolism	-	Yes
PROSER2	254427	proline and serine-rich protein 2	NP_694988.3	1	6	6	9	1.52	1.47	12.42	7.91	44	26.4	5	5									
TOX4	9878	TOX high mobility group box family member 4 isoform 1	NP_055643.1	5	4	4	7	1.52	1.25	2.59	9.89	7.9	25.2	4	4	12661	9878	chromosome 14 open reading frame 92	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG	Yes
KMT2A	4297	histone-lysine N-methyltransferase 2A isoform 1 precursor	NP_001184033.1	2	2	2	3	1.52	0.83					1	1									
HNRNPCL3	649330	heterogeneous nuclear ribonucleoprotein C-like 3	NP_001139653.1	3	1	9	183	1.52	0.53	4.71	37.12	10.1	28.6	2	2									
AHCY	191	adenosylhomocysteinase isoform 1	NP_000678.1	2	20	22	92	1.51	1.41	3.57	4.28	38.2	43.3	47	47	1621	191	S-adenosylhomocysteine hydrolase	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
STK11	6794	serine/threonine-protein kinase STK11	NP_000446.1	1	2	2	4	1.51	1.31	41.05	29.87	107.5	59.6	2	2	3740	6794	serine/threonine kinase 11 (Peutz-Jegherssyndrome)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
AFTPH	54812	aftiphilin isoform a	NP_982261.2	3	3	3	3	1.51	1.12	0.17	5.56	0.5	10.8	3	3	10635	54812	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
FKBP11	51303	peptidyl-prolyl cis-trans isomerase FKBP11 isoform 1 precursor	NP_057678.1	2	1	1	4	1.51	1.08	5.43	3.9	14.3	7.3	3	3	11170	51303	FK506 binding protein 11, 19 kDa	Isomerase activity	Integral to membrane	Enzyme: Isomerase	Metabolism;Energy pathways	SP;TM	Yes
RBBP6	5930	E3 ubiquitin-protein ligase RBBP6 isoform 1	NP_008841.2	3	2	2	2	1.51	0.75					1	1	2964	5930	retinoblastoma binding protein 6	Ubiquitin-specific protease activity	Nucleus;Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	ZnF_C2HC;RING;CC	No
EIF5	1983	eukaryotic translation initiation factor 5	NP_001960.2	1	12	12	40	1.5	1.66	4.76	4.37	34.4	35.2	22	22	3417	1983	eukaryotic translation initiation factor 5	Translation regulator activity;GTPase activator activity	Cytoplasm	Translation regulatory protein;GTPase activating protein	Protein metabolism	-	Yes
P4HB	5034	protein disulfide-isomerase precursor	NP_000909.2	1	36	36	244	1.5	1.6	1.77	2.09	30.8	38.8	127	126	7181	5034	procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfideisomerase-associated 1)	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase	Protein metabolism	SP	Yes
RDH13	112724	retinol dehydrogenase 13 isoform 1 precursor	NP_001139443.1	2	5	5	16	1.5	1.52	8.68	8.53	38.2	37.8	8	8	17963	112724	retinol dehydrogenase 13 (all-trans and 9-cis)	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
C17orf85	55421	uncharacterized protein C17orf85	NP_001107590.1	1	3	3	6	1.5	1.14	12.95	5.04	34.6	10	3	3	17116	55421	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	CC	Yes
SLC39A7	7922	zinc transporter SLC39A7 isoform 1 precursor	NP_008910.2	2	1	1	1	1.5	1.09					1	1	9028	7922	solute carrier family 39 (zinc transporter),member 7	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM;SP	Yes
CRBN	51185	protein cereblon isoform 1	NP_057386.2	2	1	1	3	1.5	0.86					1	1	16750	51185	cereblon	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
PSMB3	5691	proteasome subunit beta type-3	NP_002786.2	1	8	8	57	1.5	0.81	5.58	5.42	50.3	25.4	32	32	3709	5691	proteasome (prosome, macropain) subunit, betatype, 3	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
NF1	4763	neurofibromin isoform 1	NP_001035957.1	2	1	1	2	1.5	0.67					1	1	1203	4763	neurofibromin 1 (neurofibromatosis, vonRecklinghausen disease, Watson disease)	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	RASGAP;SEC14	Yes
LPGAT1	9926	acyl-CoA:lysophosphatidylglycerol acyltransferase 1	NP_055688.1	1	1	1	3	1.49	1.61	40.72	33.64	104	89.4	2	2	14304	9926	lysophosphatidylglycerol acyltransferase 1	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM;PISC	Yes
UTP11L	51118	probable U3 small nucleolar RNA-associated protein 11	NP_057121.2	1	5	5	7	1.49	1.22	2.78	14.05	8.3	35.3	4	4	16711	51118	None	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
GSK3A	2931	glycogen synthase kinase-3 alpha	NP_063937.2	1	3	5	8	1.49	1.09	2.87	2.92	7.4	5.5	3	3	6002	2931	glycogen synthase kinase 3 alpha	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
C5orf24	134553	UPF0461 protein C5orf24 isoform 1	NP_689622.2	2	2	2	3	1.49	0.79	7.45	29.23	15.8	33.5	2	2	8226	134553	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
ALDH1A3	220	aldehyde dehydrogenase family 1 member A3 isoform 1	NP_000684.2	2	28	32	293	1.48	1.82	2.15	1.53	40.1	34.9	148	148	2713	220	aldehyde dehydrogenase 1 family, member A3	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
CFL1	1072	cofilin-1	NP_005498.1	3	10	10	49	1.48	1.56	3.49	3.05	27.3	25.1	27	27	3261	1072	cofilin 1 (non-muscle)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	ADF;NLS	Yes
CLIP2	7461	CAP-Gly domain-containing linker protein 2 isoform 1	NP_003379.3	2	2	3	5	1.48	1.52	1.98	6.46	4.2	13.9	2	2	9140	7461	cytoplasmic linker 2	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell communication;Signal transduction	CC	Yes
SEMA3C	10512	semaphorin-3C precursor	NP_006370.1	1	9	9	14	1.48	1.42	4.28	10.66	16.9	41.6	7	7	4034	10512	sema domain, immunoglobulin domain (Ig), shortbasic domain, secreted, (semaphorin) 3C	Receptor binding	Extracellular	Ligand	Cell communication;Signal transduction	SP;SEMA;PSI;IG	Yes
NOL4L	140688	nucleolar protein 4-like isoform 1	NP_001243727.1	8	3	3	4	1.48	1.38	7.44	22.6	15.7	46.3	2	2									
SLC38A1	81539	sodium-coupled neutral amino acid transporter 1 isoform 2	NP_001265319.1	2	2	2	5	1.48	1.35	4.41	2.58	11.3	6.1	3	3	12245	81539	solute carrier family 38, member 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
CHCHD1	118487	coiled-coil-helix-coiled-coil-helix domain-containing protein 1	NP_976043.1	1	1	1	2	1.48	1.34					1	1	12313	118487	coiled-coil-helix-coiled-coil-helix domaincontaining 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
CMIP	80790	C-Maf-inducing protein isoform C-Mip	NP_938204.2	2	2	2	2	1.48	1.25					1	1									
NFRKB	4798	nuclear factor related to kappa-B-binding protein isoform 2	NP_006156.2	2	1	1	1	1.48	1.23					1	1	1240	4798	nuclear factor related to kappaB bindingprotein	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
SZT2	23334	protein SZT2	NP_056099.3	1	1	1	1	1.48	0.86					1	1									
PAAF1	80227	proteasomal ATPase-associated factor 1 isoform 2	NP_079431.1	3	2	2	2	1.47	1.44					1	1	7761	80227	WD repeat domain 71	Protein binding	-	Ubiquitin proteasome system protein	Proteolysis and peptidolysis	WD40	No
GNAO1	2775	guanine nucleotide-binding protein G(o) subunit alpha isoform b	NP_620073.2	9	3	6	43	1.47	1.35	1.35	4.87	3.4	11.4	3	3	757	2775	guanine nucleotide binding protein (G protein),alpha activating activity polypeptide O	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	-	Yes
AKT1S1	84335	proline-rich AKT1 substrate 1 isoform a	NP_115751.3	2	2	2	3	1.47	1.19	1.48	14.81	3.1	25.3	2	2	12441	84335	AKT1 substrate 1 (proline-rich)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
PLEKHG4	25894	puratrophin-1 isoform 1	NP_001123200.1	2	1	1	1	1.47	1.13					1	1	10890	25894	pleckstrin homology domain containing, familyG (with RhoGef domain) member 4	Molecular function unknown	-	Unclassified	Biological_process unknown	RHOGEF;PH	No
ANP32A	8125	acidic leucine-rich nuclear phosphoprotein 32 family member A	NP_006296.1	3	5	8	51	1.47	1.12	10.03	12.37	49.3	45.8	10	10	9014	8125	acidic (leucine-rich) nuclear phosphoprotein32 family, member A	MHC class I receptor activity;MHC class II receptor activity	Nucleus	MHC complex protein	Immune response	LRR	Yes
MED17	9440	mediator of RNA polymerase II transcription subunit 17	NP_004259.3	1	2	2	4	1.47	0.91	3.5	6.4	7.3	8.3	2	2	4816	9440	cofactor required for Sp1 transcriptionalactivation, subunit 6, 77kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PDCD2L	84306	programmed cell death protein 2-like	NP_115722.1	1	1	1	2	1.47	0.81					1	1	17480	84306	None	Molecular function unknown	Cytoplasm	Unclassified	Apoptosis	-	No
TALDO1	6888	transaldolase	NP_006746.1	1	18	18	80	1.46	1.84	2.16	1.92	21.3	24	45	45	3640	6888	transaldolase 1	Transferase activity, transferring aldehyde or ketonic groups	Nucleus	Enzyme: Transaldolase	Metabolism;Energy pathways	-	Yes
GCLC	2729	glutamate--cysteine ligase catalytic subunit isoform a	NP_001489.1	2	14	14	42	1.46	1.38	4.31	4.92	28.7	30.2	20	19	6032	2729	glutamate-cysteine ligase, catalytic subunit	Ligase activity	-	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
C3	718	complement C3 precursor	NP_000055.2	1	14	14	42	1.46	1.28	4.26	10.34	30.6	70.1	23	23	400	718	complement component 3	Complement activity	Extracellular	Complement protein	Immune response	ANATO;A2M;C345C;SP	Yes
C8orf33	65265	UPF0488 protein C8orf33	NP_075568.1	1	2	2	4	1.46	1.18	7.6	1.02	15.8	1.7	2	2	7951	65265	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PEX19	5824	peroxisomal biogenesis factor 19 isoform a	NP_002848.1	2	2	2	3	1.46	1.16	3.16	9.2	6.5	15.1	2	2	2610	5824	peroxisomal biogenesis factor 19	Protein binding	Cytoplasm	Integral membrane protein	Cell communication;Signal transduction	CAAX	No
UAP1L1	91373	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	NP_997192.2	1	2	3	8	1.46	1.11					1	1	15596	91373	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	No
CTDP1	9150	RNA polymerase II subunit A C-terminal domain phosphatase isoform 1	NP_004706.3	2	1	1	2	1.46	0.96					1	1	5377	9150	CTD (carboxy-terminal domain, RNA polymeraseII, polypeptide A) phosphatase, subunit 1	Transcription factor binding	Nucleus;Cytoplasm	Enzyme: Phosphatase	Transcription	BRCT;CPDc	Yes
COL12A1	1303	collagen alpha-1(XII) chain long isoform precursor	NP_004361.3	2	3	3	6	1.46	0.95	12.09	51.25	25.4	77.9	2	2	377	1303	collagen, type XII, alpha 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	FN3;VWA;TSPN;COLL;SP	Yes
FLNB	2317	filamin-B isoform 1	NP_001157789.1	1	2	142	804	1.46	0.64	14.42	118.13	30.4	146.3	2	2	4543	2317	filamin B, beta (actin binding protein 278)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;IGFLMN	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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PPP1R2	5504	protein phosphatase inhibitor 2 isoform 1	NP_001278433.1	3	2	2	4	1.46	0.62	19.67	56.69	42.2	53.4	2	2	3478	5504	protein phosphatase 1, regulatory (inhibitor)subunit 2	Protein binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	No
HDGFRP2	84717	hepatoma-derived growth factor-related protein 2 isoform 1	NP_001001520.1	2	9	10	20	1.45	1.39	3.89	10.53	18	48.9	10	10									
GOSR1	9527	Golgi SNAP receptor complex member 1 isoform 1	NP_004862.1	3	2	2	4	1.45	1.36	23.01	3.97	49.9	7.7	2	2	4936	9527	golgi SNAP receptor complex member 1	Auxiliary transport protein activity	Golgi apparatus;Nucleus	Membrane transport protein	Transport	TM	Yes
CCDC86	79080	coiled-coil domain-containing protein 86	NP_077003.1	1	5	5	6	1.45	1.34	7.08	3.05	23.2	9.1	5	5	8322	79080	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	No
LYRM4	57128	LYR motif-containing protein 4 isoform 2	NP_001158312.1	3	1	1	4	1.45	1.21	1.81	2.05	3.7	3.5	2	2	12855	57128	chromosome 6 open reading frame 149	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
AATF	26574	protein AATF	NP_036270.1	1	7	7	17	1.45	1.2	2.64	8.07	11.6	29.7	9	9	12236	26574	apoptosis antagonizing transcription factor	Transcription factor activity	Nucleus	Transcription factor	Apoptosis	LZ;NLS	No
CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	NP_001230575.1	1	5	5	9	1.45	1.1	2.11	8.4	6.9	20.9	5	5	5127	10421	CD2 antigen (cytoplasmic tail) binding protein2	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
CWC15	51503	spliceosome-associated protein CWC15 homolog	NP_057487.2	1	3	3	9	1.45	0.91	6.09	8.77	22	19.8	6	6	13703	51503	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
CDC34	997	ubiquitin-conjugating enzyme E2 R1	NP_004350.1	1	1	2	3	1.45	0.9					1	1	306	997	cell division cycle 34	Ligase activity	Nucleus	Enzyme: Ligase	Protein metabolism	UBC	No
XIRP2	129446	xin actin-binding repeat-containing protein 2 isoform 1	NP_689594.4	2	1	1	1	1.45	0.65					1	1	10267	129446	cardiomyopathy associated 3	Cytoskeletal protein binding	-	Anchor protein;Unclassified	Cytoskeletal anchoring	CC;LIM	Yes
ALKBH5	54890	RNA demethylase ALKBH5	NP_060228.3	1	1	1	8	1.44	1.87	16.52	15.17	43	61.5	3	4	8621	54890	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 1	NP_060225.4	2	19	19	60	1.44	1.5	2.97	5.83	23.5	50	29	29	8620	54888	NOL1/NOP2/Sun domain family, member 2	RNA methyltransferase activity	Nucleolus	RNA methyltransferase	-	-	Yes
CENPV	201161	centromere protein V	NP_859067.2	1	3	3	7	1.44	1.32	16.7	10.85	43.5	25.3	3	3	12173	201161	proline rich 6	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
RAE1	8480	mRNA export factor	NP_001015885.1	1	5	5	7	1.44	1.29	2.9	18.05	8.4	49.1	4	4	11939	8480	RAE1 RNA export 1 homolog (S. pombe)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
FREM2	341640	FRAS1-related extracellular matrix protein 2 precursor	NP_997244.4	1	1	1	1	1.44	1.27					1	1	10602	341640	FRAS1 related extracellular matrix protein 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	CALXB;TM	No
PGP	283871	phosphoglycolate phosphatase	NP_001035830.1	1	7	7	15	1.44	1.15	6.71	11.97	27.9	40.4	8	8	19077	283871	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TPM3	7170	tropomyosin alpha-3 chain isoform Tpm3.12st	NP_689476.2	1	2	16	42	1.44	0.87					1	1	1840	7170	tropomyosin 3	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein;Structural protein	Cell growth and/or maintenance	CC	Yes
YY1	7528	transcriptional repressor protein YY1	NP_003394.1	3	2	2	6	1.44	0.81	19.88	6.72	42.2	7.7	2	2	2482	7528	YY1 transcription factor	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
LTF	4057	lactotransferrin isoform 1 precursor	NP_002334.2	2	1	1	2	1.44	0.63					1	1	1028	4057	lactotransferrin	Transporter activity	Secretory granule	Transport/cargo protein	Transport	SP;TR_FER;NLS	Yes
PRKCSH	5589	glucosidase 2 subunit beta isoform 3 precursor	NP_001276032.1	3	20	20	113	1.43	1.6	4.53	7.57	48.7	105.5	51	51	3518	5589	protein kinase C substrate 80K-H	Glucosidase activity	Endoplasmic reticulum	Regulatory/other subunit	Energy pathways;Metabolism	SP;LDLA;CC	Yes
SQSTM1	8878	sequestosome-1 isoform 1	NP_003891.1	2	14	14	56	1.43	1.39	4.07	6.96	32.6	57.1	30	30	3319	8878	sequestosome 1	Ubiquitin-specific protease activity	Cytoplasm;Nucleus	Ubiquitin proteasome system protein	Protein metabolism	PB1;ZnF_ZZ;UBA	No
NUP43	348995	nucleoporin Nup43	NP_942590.1	1	2	2	3	1.43	1.28					1	1	12174	348995	nucleoporin 43kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	WD40	Yes
ZC3H11A	9877	zinc finger CCCH domain-containing protein 11A	NP_055642.3	1	9	9	18	1.43	1.24	6.38	8.1	29.5	32.6	10	10	11100	9877	zinc finger CCCH-type containing 11A	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1	Yes
HBA1	3039	hemoglobin subunit alpha	NP_000549.1	2	4	4	251	1.43	0.56	1.15	3.49	21.4	25.8	167	167	784	3039	hemoglobin, alpha 1	Transporter activity	-	Transport/cargo protein	Transport	-	Yes
DVL1	1855	segment polarity protein dishevelled homolog DVL-1	NP_004412.2	1	1	1	2	1.43	0.54					1	1	3220	1855	dishevelled, dsh homolog 1 (Drosophila)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	DSH;PDZ	Yes
HNRNPDL	9987	heterogeneous nuclear ribonucleoprotein D-like isoform a	NP_112740.1	2	4	6	19	1.42	1.95	4.26	6.33	12.1	25.1	4	4									
GOLM1	51280	Golgi membrane protein 1	NP_057632.2	1	2	2	2	1.42	1.74	8.81	19.67	17.8	51.4	2	2	8428	51280	golgi phosphoprotein 2	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	CC;TM	Yes
LEO1	123169	RNA polymerase-associated protein LEO1 isoform 1	NP_620147.1	2	4	4	11	1.42	1.43	2.43	4.61	8.4	16.3	6	6	11231	123169	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	No
CEBPB	1051	CCAAT/enhancer-binding protein beta isoform a	NP_005185.2	3	1	1	2	1.42	1.36					1	1	1801	1051	CCAAT/enhancer binding protein (C/EBP), beta	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
MYADM	91663	myeloid-associated differentiation marker	NP_612382.1	1	2	2	18	1.42	1.28	8.07	13.16	35.3	54.2	9	9	14792	91663	myeloid-associated differentiation marker	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
SERPINE1	5054	plasminogen activator inhibitor 1 precursor	NP_000593.1	1	7	7	13	1.42	1.09	3.09	11.76	10.8	32.1	6	6	1418	5054	serine (or cysteine) proteinase inhibitor,clade E (nexin, plasminogen activator inhibitor type 1), member 1	Protease inhibitor activity	Extracellular	Protease inhibitor	Protein metabolism	SERPIN;SP	Yes
SNX18	112574	sorting nexin-18 isoform b	NP_443102.2	3	4	4	7	1.42	0.98	3.65	8.48	11.6	18.6	5	5	15407	112574	sorting nexin associated golgi protein 1	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	SH3;PX	Yes
RACGAP1	29127	rac GTPase-activating protein 1	NP_001119575.1	1	6	6	10	1.42	0.95	1.06	10.77	3.7	25.5	6	6	5402	29127	Rac GTPase activating protein 1	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	C1;RHOGAP;CC	No
NUCB2	4925	nucleobindin-2 precursor	NP_005004.1	1	8	8	17	1.42	0.95	7.09	10.56	30.9	30.9	9	9	9726	4925	nucleobindin 2	Calcium ion binding	Golgi apparatus;Nucleus	Calcium binding protein	Cell communication;Signal transduction	EF;CC;SP	Yes
RNPS1	10921	RNA-binding protein with serine-rich domain 1 isoform a	NP_006702.1	3	4	4	12	1.42	0.87	10.68	7.74	41.7	18	7	7	7341	10921	RNA binding protein S1, serine-rich domain	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
TRIP10	9322	cdc42-interacting protein 4 isoform 2	NP_004231.1	2	1	19	46	1.42	0.84	20.12	29.7	42.2	36.6	2	2	5142	9322	thyroid hormone receptor interactor 10	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell growth and/or maintenance	FES;CC;SH3	Yes
C17orf75	64149	protein Njmu-R1	NP_071739.2	1	1	1	5	1.42	0.8					1	1	11392	64149	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
DHX33	56919	putative ATP-dependent RNA helicase DHX33 isoform 1	NP_064547.2	2	1	1	1	1.42	0.7					1	1	13143	56919	DEAH (Asp-Glu-Ala-His) box polypeptide 33	Molecular function unknown	Nucleolus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	No
TUBB	203068	tubulin beta chain isoform b	NP_821133.1	5	6	35	951	1.42	0.64	1.03	2.33	21.2	21.5	203	203	1852	203068	tubulin, beta polypeptide	Structural constituent of cytoskeleton	Cytoplasm;Plasma membrane	Cytoskeletal protein	Cell growth and/or maintenance	TUBULIN;CC	Yes
AACS	65985	acetoacetyl-CoA synthetase	NP_076417.2	2	3	4	13	1.41	1.79	12.71	10.18	37	37.6	4	4	12391	65985	acetoacetyl-CoA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	No
TBC1D13	54662	TBC1 domain family member 13 isoform a	NP_060671.3	2	4	4	7	1.41	1.39	4.69	4.29	14.8	13.4	5	5	18163	54662	TBC1 domain family, member 13	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	TBC	Yes
CLCN7	1186	H(+)/Cl(-) exchange transporter 7 isoform a	NP_001278.1	2	1	1	2	1.41	1.37					1	1	4103	1186	chloride channel 7	Voltage-gated ion channel activity	Plasma membrane	Voltage gated channel	Transport	TM;CBS	Yes
NDRG2	57447	protein NDRG2 isoform a	NP_963293.1	5	1	1	1	1.41	1.15					1	1	17630	57447	NDRG family member 2	Hydrolase activity	Perinuclear region	Enzyme: Hydrolase	Metabolism;Energy pathways;Cell proliferation;Cell differentiation	-	Yes
LSM14B	149986	protein LSM14 homolog B	NP_653304.2	1	6	6	12	1.41	1.12	2.11	12.57	8.4	41.5	8	8	12768	149986	family with sequence similarity 61, member B	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
PTMS	5763	parathymosin	NP_002815.3	1	4	4	22	1.41	1.12	3.37	5.61	15.2	20.1	10	10	1344	5763	parathymosin	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	No
PSMB6	5694	proteasome subunit beta type-6 isoform 1 proprotein	NP_002789.1	2	5	5	11	1.41	1.1	5.03	7.28	16	18	5	5	2630	5694	proteasome (prosome, macropain) subunit, betatype, 6	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
SRSF5	6430	serine/arginine-rich splicing factor 5	NP_001034554.1	1	3	4	9	1.41	1.1	2.19	14.58	5.4	28.3	3	3									
IK	3550	protein Red	NP_006074.2	1	8	8	24	1.41	1.01	3.84	10.97	20.4	43.2	14	14	2771	3550	IK cytokine, down-regulator of HLA II	Molecular function unknown	Nucleus	Unclassified	Immune response	CC	Yes
NOP16	51491	nucleolar protein 16 isoform 3	NP_057475.2	6	3	3	6	1.41	0.88	2.49	4.58	6.1	7	3	3	13694	51491	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
UAP1	6675	UDP-N-acetylhexosamine pyrophosphorylase	NP_003106.3	1	10	11	30	1.4	1.48	8.4	8.55	46.1	50.2	14	14	4178	6675	UDP-N-acteylglucosamine pyrophosphorylase 1	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase	Metabolism;Energy pathways	-	Yes
HLTF	6596	helicase-like transcription factor	NP_620636.1	1	1	1	2	1.4	1.36					1	1	4461	6596	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 3	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;RING;HELIC;NLS	Yes
LSG1	55341	large subunit GTPase 1 homolog	NP_060855.2	1	4	4	7	1.4	1.28	0.08	1.95	0.2	4.3	3	3	7748	55341	None	Nucleotide binding;GTPase activity	Endoplasmic reticulum	GTPase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
C15orf52	388115	uncharacterized protein C15orf52	NP_997263.2	1	2	2	2	1.4	1.26					1	1	16964	388115	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
GPALPP1	55425	GPALPP motifs-containing protein 1	NP_061029.2	1	1	1	2	1.4	1.22					1	1									

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NUDT16L1	84309	protein syndesmos isoform 1	NP_115725.1	1	2	2	5	1.4	1.17	6.23	14.84	15.2	30.9	3	3	15309	84309	nudix (nucleoside diphosphate linked moietyX)-type motif 16-like 1	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	-	No
GRPEL1	80273	grpE protein homolog 1, mitochondrial precursor	NP_079472.1	1	4	4	9	1.4	1.17	1.12	3.32	3.5	8.7	5	5	7550	80273	GrpE-like 1, mitochondrial (E. coli)	Chaperone activity	Mitochondrion	Chaperone	Protein metabolism	CC	No
EHBP1L1	254102	EH domain-binding protein 1-like protein 1	NP_001092879.1	1	8	8	21	1.4	1.15	11.52	10.01	51.4	35.5	9	9	19384	254102	EH domain binding protein 1-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CH;CC	Yes
ATAD3B	83858	ATPase family AAA domain-containing protein 3B	NP_114127.3	1	2	15	25	1.4	1.13					1	1	10679	83858	ATPase family, AAA domain containing 3B	ATPase activity	Mitochondrion	ATPase	Metabolism;Energy pathways	CC;AAA	No
RPL35	11224	60S ribosomal protein L35	NP_009140.1	1	4	4	13	1.4	1	6.17	12.86	24.8	37.8	8	8	10200	11224	ribosomal protein L35	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	CC	Yes
BTF3L4	91408	transcription factor BTF3 homolog 4 isoform 1	NP_689478.1	2	1	1	10	1.4	0.91	0.79	7.02	2.5	14.3	5	5	17521	91408	basic transcription factor 3-like 4	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 2	NP_842565.2	4	1	74	218	1.4	0.9					1	1	1683	6711	spectrin, beta, non-erythrocytic 1	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	SPECTRIN;CC;PH;CH	Yes
CDK4	1019	cyclin-dependent kinase 4	NP_000066.1	46	1	2	18	1.4	0.87					1	1	447	1019	cyclin-dependent kinase 4	Kinase activity	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	S_T_kinase	Yes
TRMT61A	115708	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	NP_689520.2	1	3	3	5	1.4	0.85	4.02	51.5	7.9	68.8	2	2	8810	115708	chromosome 14 open reading frame 172	RNA methyltransferase activity	-	RNA methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
FLNB	2317	filamin-B isoform 2	NP_001448.2	3	1	141	838	1.4	0.82	7.09	27.11	38.4	94.8	14	13	4543	2317	filamin B, beta (actin binding protein 278)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;IGFLMN	Yes
SMARCB1	6598	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 isoform a	NP_003064.2	2	4	4	7	1.4	0.81	2.22	9.99	5.4	14.1	3	3	3364	6598	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily b, member 1	DNA binding	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
EHMT1	79813	histone-lysine N-methyltransferase EHMT1 isoform 1	NP_079033.4	2	3	3	5	1.4	0.69	15.44	11.17	31.3	11	2	2	7383	79813	euchromatic histone-lysine N-methyltransferase1	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ANK;SET	Yes
RABL2B	11158	rab-like protein 2B isoform 3	NP_001124395.1	7	2	2	4	1.4	0.68	31.35	7.48	68.8	7.2	2	2	10395	11158	RAB, member of RAS oncogene family-like 2B	GTPase activity	-	GTPase	Cell communication;Signal transduction	RAS;Small_GTPase	No
C1orf50	79078	uncharacterized protein C1orf50	NP_077002.2	1	1	1	2	1.4	0.59					1	1	14714	79078	chromosome 1 open reading frame 50	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
HSPA5	3309	78 kDa glucose-regulated protein precursor	NP_005338.1	3	43	45	503	1.39	1.51	1.81	1.76	40.7	43.1	242	242	682	3309	heat shock 70kDa protein 5 (glucose-regulatedprotein, 78kDa)	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP;CC	Yes
PLD3	23646	phospholipase D3	NP_036400.2	1	8	8	18	1.39	1.43	4.52	5.42	21.1	26.2	11	11	7148	23646	phospholipase D family, member 3	Phospholipase activity	Endoplasmic reticulum;Golgi apparatus	Enzyme: Phospholipase	Metabolism;Energy pathways	PLDc;TM	No
ACO1	48	cytoplasmic aconitate hydratase	NP_001265281.1	1	29	29	100	1.39	1.42	3.46	2.67	35.7	27.8	52	52	13	48	aconitase 1, soluble	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ITCH	83737	E3 ubiquitin-protein ligase Itchy homolog isoform 1	NP_001244066.1	5	13	14	28	1.39	1.42	6.73	5.11	38.8	29.5	16	16	7565	83737	itchy homolog E3 ubiquitin protein ligase(mouse)	Ubiquitin-specific protease activity	Endosome	Ubiquitin proteasome system protein	Regulation of signal transduction	C2;WW;HECT	Yes
GLTSCR2	29997	glioma tumor suppressor candidate region gene 2 protein	NP_056525.2	1	2	2	5	1.39	1.38	4.35	4.02	10.5	9.6	3	3	16142	29997	glioma tumor suppressor candidate region gene2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
NCL	4691	nucleolin	NP_005372.2	1	42	42	233	1.39	1.37	1.98	2.3	30.4	35	116	116	1245	4691	nucleolin	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
PADI6	353238	protein-arginine deiminase type-6	NP_997304.3	1	1	1	1	1.39	1.36					1	1	15095	353238	peptidyl arginine deiminase, type VI	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
BTF3	689	transcription factor BTF3 isoform A	NP_001032726.1	1	3	13	117	1.39	1.34	11.2	10.2	31.9	27.9	4	4	3966	689	basic transcription factor 3	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SERPINH1	871	serpin H1 precursor	NP_001226.2	1	24	24	110	1.39	1.34	3.49	5.39	39.2	60.9	61	61	2968	871	serine (or cysteine) proteinase inhibitor,clade H (heat shock protein 47), member 1, (collagen binding protein 1)	Heat shock protein activity	Endoplasmic reticulum	Heat shock protein	Protein metabolism	SP;SERPIN	Yes

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PPM1G	5496	protein phosphatase 1G	NP_817092.1	1	18	18	52	1.39	1.28	3.37	4.09	25.1	28.2	28	28	9237	5496	protein phosphatase 1G (formerly 2C),magnesium-dependent, gamma isoform	Protein serine/threonine phosphatase activity	Nucleoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction;Protein modification	PP2C;CC;PA2c	Yes
CCDC58	131076	coiled-coil domain-containing protein 58 isoform 1	NP_001017928.1	2	1	1	1	1.39	1.22					1	1	18548	131076	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
SNW1	22938	SNW domain-containing protein 1	NP_036377.1	1	10	10	19	1.39	1.21	1.65	5.69	8	24.2	12	12	4340	22938	SKI interacting protein	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	Yes
JPH2	57158	junctophilin-2 isoform 1	NP_065166.2	1	1	1	1	1.39	1.16					1	1	12006	57158	junctophilin 2	Cell adhesion molecule activity	Sarcoplasmic reticulum;Nucleus;Cytoplasm	Cell junction protein	Cell growth and/or maintenance	MORN;TM	Yes
BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	NP_683692.2	2	3	3	5	1.39	0.93	4.97	48.87	9.8	71.1	2	2									
BAK1	578	bcl-2 homologous antagonist/killer	NP_001179.1	1	4	4	15	1.39	0.86	11.42	11.74	40.3	22.9	6	5	2744	578	BCL2-antagonist/killer 1	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule	Apoptosis	TM;BH3;BH1;BH2	Yes
RSL24D1	51187	probable ribosome biogenesis protein RLP24	NP_057388.1	1	2	2	5	1.39	0.82	14.07	35.43	28.1	42.7	2	2	12665	51187	chromosome 15 open reading frame 15	Molecular function unknown	Ribosome	Unclassified	Biological_process unknown	TRASH	Yes
TCF20	6942	transcription factor 20 isoform 1	NP_005641.1	2	2	2	4	1.39	0.74	0.84	10.77	1.6	11.2	2	2	4378	6942	transcription factor 20 (AR1)	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;PHD	Yes
ALB	213	serum albumin preproprotein	NP_000468.1	1	3	5	23	1.39	0.52	7.21	15.46	26.9	21.5	7	7	62	213	albumin	Transporter activity	Extracellular	Transport/cargo protein	Transport	Albumin;SP	Yes
DLAT	1737	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor	NP_001922.2	1	12	12	61	1.38	1.64	4.22	4.22	34.5	40.7	33	32	10578	1737	dihydrolipoamide S-acetyltransferase (E2component of pyruvate dehydrogenase complex)	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
CTNNBL1	56259	beta-catenin-like protein 1 isoform 1	NP_110517.2	2	6	6	9	1.38	1.43	13.33	15.01	43	50.7	5	5	10850	56259	catenin, beta like 1	Molecular function unknown	Nucleus	Unclassified	Apoptosis	ARM	Yes
PTGES	9536	prostaglandin E synthase	NP_004869.1	1	2	2	3	1.38	1.38	4.37	14	8.5	27.8	2	2	5528	9536	prostaglandin E synthase	Molecular function unknown	Microsome	Enzyme: Synthase	Lipid metabolism	TM	Yes
DBNL	28988	drebrin-like protein isoform a	NP_054782.2	3	1	13	45	1.38	1.17					1	1	6588	28988	drebrin-like	Kinase regulator activity	Actin cytoskeleton	Adapter molecule	Signal transduction	ADF;CC;SH3	Yes
NEDD4L	23327	E3 ubiquitin-protein ligase NEDD4-like isoform 7	NP_001230889.1	7	4	5	13	1.38	1.17	5.08	10.84	15.8	28.9	5	5	5903	23327	neural precursor cell expressed,developmentally down-regulated 4-like	Ubiquitin-specific protease activity	Plasma membrane;Perinuclear region	Ubiquitin proteasome system protein	Protein metabolism	C2;WW;HECT	No
RSF1	51773	remodeling and spacing factor 1	NP_057662.3	1	5	5	9	1.38	1.1	8.78	1.29	27.6	3.2	5	5	10537	51773	hepatitis B virus x associated protein	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PHD;CC;NLS	Yes
CNOT3	4849	CCR4-NOT transcription complex subunit 3	NP_055331.1	1	2	2	3	1.38	1.07	9.87	2.82	19.5	4.3	2	2	5368	4849	CCR4-NOT transcription complex, subunit 3	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
SEC23B	10483	protein transport protein Sec23B isoform 1	NP_006354.2	2	9	11	37	1.38	1.06	3.23	8.73	16.7	35.8	14	14	11543	10483	Sec23 homolog B (S. cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	GEL	Yes
COL4A1	1282	collagen alpha-1(IV) chain isoform 1 preproprotein	NP_001836.3	1	1	1	2	1.38	0.99					1	1	359	1282	collagen, type IV, alpha 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	COLL;C4;SP	Yes
TXNL1	9352	thioredoxin-like protein 1	NP_004777.1	1	6	6	15	1.38	0.99	8.43	3.79	33.7	10.6	8	8	4335	9352	thioredoxin-like 1	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
RPS21	6227	40S ribosomal protein S21	NP_001015.1	1	1	1	2	1.38	0.93					1	1	1605	6227	ribosomal protein S21	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
IGFBP7	3490	insulin-like growth factor-binding protein 7 isoform 1 precursor	NP_001544.1	3	8	8	13	1.38	0.92	16.38	7.45	60	17	6	6	4183	3490	insulin-like growth factor binding protein 7	Cell adhesion molecule activity	Extracellular	Adhesion molecule	Cell communication;Signal transduction	SP;IB;KAZAL;IG	Yes
CCZ1B	221960	vacuolar fusion protein CCZ1 homolog B	NP_932765.1	1	3	3	3	1.38	0.92	2.05	22.07	4	29.3	2	2									
PEG10	23089	retrotransposon-derived protein PEG10 isoform 3	NP_001165908.1	6	1	1	3	1.38	0.71					1	1	15117	23089	paternally expressed 10	Protein binding	Nucleus	Cell cycle control protein	Apoptosis	CC;ZNFC2;ZnF_C2HC	No
SH3KBP1	30011	SH3 domain-containing kinase-binding protein 1 isoform a	NP_114098.1	3	14	14	35	1.37	1.37	6.08	5.24	36.4	31.3	18	18	2301	30011	SH3-domain kinase binding protein 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction;Regulation of signal transduction;Cell adhesion	SH3;CC	Yes
RABAC1	10567	prenylated Rab acceptor protein 1	NP_006414.2	1	1	1	2	1.37	1.37					1	1	5375	10567	Rab acceptor 1 (prenylated)	GTPase activator activity	Golgi apparatus	GTPase activating protein	Transport	TM	No
ALG2	85365	alpha-1,3/1,6-mannosyltransferase ALG2	NP_149078.1	1	4	4	7	1.37	1.26	6.13	9.73	16.9	25	4	4	9716	85365	asparagine-linked glycosylation 2 homolog(yeast, alpha-1,3-mannosyltransferase)	Mannosyltransferase activity	Endoplasmic reticulum	Enzyme: Mannosyltransferase	Metabolism;Energy pathways	TM	Yes
NOB1	28987	RNA-binding protein NOB1	NP_054781.1	1	4	4	8	1.37	1.19	4.02	5.21	11.1	12.5	4	4	11395	28987	None	Ribonuclease activity	-	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PINc	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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ZNF598	90850	zinc finger protein 598	NP_835461.2	1	5	6	12	1.37	1.19	6.27	4.25	17.3	10.1	4	4	11732	90850	zinc finger protein 598	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING	No
INPPL1	3636	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	NP_001558.3	1	1	1	2	1.37	1.14					1	1	2900	3636	inositol polyphosphate phosphatase-like 1	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase	Cell communication;Signal transduction	SH2;I_Phosphatase;SAM	No
PEX5	5830	peroxisomal biogenesis factor 5 isoform e	NP_001287718.1	5	1	1	1	1.37	0.96					1	1	2684	5830	peroxisomal biogenesis factor 5	Protein binding	Cytoplasm	Integral membrane protein	Cell communication;Signal transduction	TPR	Yes
PLTP	5360	phospholipid transfer protein isoform a precursor	NP_006218.1	4	5	5	7	1.37	0.92	21.18	38.58	53.4	67.5	3	3	1399	5360	phospholipid transfer protein	Transporter activity	Extracellular	Transport/cargo protein	Transport	SP	Yes
EEFSEC	60678	selenocysteine-specific elongation factor	NP_068756.2	1	3	3	5	1.37	0.81	18.14	27.57	45	40.2	3	3	7409	60678	eukaryotic elongation factor,selenocysteine-tRNA-specific	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	GTP_EFTU_D2	Yes
FAM98B	283742	protein FAM98B	NP_775882.2	1	5	5	12	1.37	0.79	0.36	16.02	1.3	34.4	7	7	8786	283742	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ANKRD34A	284615	ankyrin repeat domain-containing protein 34A	NP_001034977.1	1	1	1	1	1.37	0.76					1	1	19079	284615	ankyrin repeat domain 34	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK	No
TOMM5	401505	mitochondrial import receptor subunit TOM5 homolog isoform 3	NP_001127956.1	3	1	1	1	1.37	0.74					1	1	16672	401505	chromosome 9 open reading frame 105	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
CARHSP1	23589	calcium-regulated heat stable protein 1	NP_055131.2	1	1	1	4	1.37	0.66	8.33	12.48	16.3	11.8	2	2	8515	23589	calcium regulated heat stable protein 1,24kDa	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	CSP	Yes
PLEKHM1	9842	pleckstrin homology domain-containing family M member 1	NP_055613.1	1	1	1	2	1.36	1.86					1	1	11439	9842	pleckstrin homology domain containing, familyM (with RUN domain) member 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PH;C1	No
NOSIP	51070	nitric oxide synthase-interacting protein	NP_057037.1	1	4	4	6	1.36	1.72	2.04	13.2	5.5	47.9	4	4	17642	51070	nitric oxide synthase interacting protein	Transporter activity	Cytoplasmic vesicle	Transport/cargo protein	Transport	CC	No
C11orf58	10944	small acidic protein	NP_055082.1	1	3	3	27	1.36	1.4	14	14.61	69.8	76.1	11	11	18069	10944	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ACOT8	10005	acyl-coenzyme A thioesterase 8	NP_005460.2	1	2	2	7	1.36	1.38	6.8	0.83	18.6	2.3	4	4	6998	10005	peroxisomal acyl-CoA thioesterase	Hydrolase activity	Peroxisomal matrix	Enzyme: Thioesterase	Lipid metabolism	-	Yes
MRI1	84245	methylthioribose-1-phosphate isomerase isoform 1	NP_001026897.1	2	3	3	9	1.36	1.3	6.72	7.16	18.4	18.7	4	4	14548	84245	None	Translation regulator activity;Molecular function unknown	-	Translation regulatory protein;Unclassified	Protein metabolism;Biological_process unknown	-	No
HMG20A	10363	high mobility group protein 20A isoform a	NP_060670.1	2	3	3	7	1.36	1.3	8.11	6.56	19.3	14.9	3	3	16116	10363	high-mobility group 20A	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	No
FAM207A	85395	protein FAM207A	NP_478070.1	1	1	1	2	1.36	1.3					1	1									
SUGP1	57794	SURP and G-patch domain-containing protein 1	NP_757386.2	1	3	3	4	1.36	1.28	5.06	3.76	12	8.3	3	3									
GOLGA2	2801	Golgin subfamily A member 2	NP_004477.3	1	16	16	38	1.36	1.28	2.22	6.11	12.9	34.1	18	18	3989	2801	golgi autoantigen, golgin subfamily a, 2	Structural molecule activity	Golgi apparatus;Golgi membrane	Structural protein	Cell growth and/or maintenance	CC	Yes
GDA	9615	guanine deaminase isoform a	NP_001229434.1	1	1	18	47	1.36	1.27					1	1	8849	9615	guanine deaminase	Deaminase activity	Cytoplasm	Enzyme: Deaminase	Metabolism;Energy pathways	-	Yes
SRM	6723	spermidine synthase	NP_003123.2	1	7	7	19	1.36	1.22	5.78	14.72	24	58.2	9	9	1692	6723	spermidine synthase	Transferase activity;Methyltransferase activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
RALGAPA1	253959	ral GTPase-activating protein subunit alpha-1 isoform 2	NP_919277.2	4	2	2	3	1.36	1.22	0.39	0.19	0.7	0.3	2	2	12324	253959	GTPase activating Rap/RanGAP domain-like 1	GTPase activator activity	Nucleus;Cytoplasm	GTPase activating protein	Signal transduction	TM;CC;LZ	Yes
MAP2K3	5606	dual specificity mitogen-activated protein kinase kinase 3 isoform B	NP_659731.1	4	6	6	11	1.36	1.06	6.07	6.98	22.1	19.8	7	7	3816	5606	mitogen-activated protein kinase kinase 3	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Signal transduction	S_T_kinase	Yes
TBC1D10A	83874	TBC1 domain family member 10A isoform 1	NP_001191169.1	2	1	1	2	1.36	1.02					1	1	18162	83874	TBC1 domain family, member 10A	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	TBC	Yes
USP19	10869	ubiquitin carboxyl-terminal hydrolase 19 isoform 1	NP_001186089.1	4	3	3	5	1.36	1.01	20.36	2.94	50.8	5.1	3	3	18278	10869	ubiquitin specific protease 19	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	TM;UCH	Yes
PREPL	9581	prolyl endopeptidase-like isoform 1	NP_006027.2	3	1	1	2	1.36	0.94					1	1	17189	9581	prolyl endopeptidase-like	Serine-type peptidase activity	-	Serine protease	Protein metabolism	-	No
NAGA	4668	alpha-N-acetylgalactosaminidase precursor	NP_000253.1	1	1	1	1	1.36	0.92					1	1	76	4668	N-acetylgalactosaminidase, alpha-	Catalytic activity	Lysosome	Enzyme: Glycosidase	Metabolism;Energy pathways	SP	Yes
AGPAT9	84803	glycerol-3-phosphate acyltransferase 3	NP_116106.2	1	1	1	1	1.36	0.89					1	1	14417	84803	None	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Lipid metabolism;Energy pathways	TM;PISC	No
MPHOSPH10	10199	U3 small nucleolar ribonucleoprotein protein MPP10	NP_005782.1	1	9	9	18	1.36	0.89	3.4	5.15	15.4	15.2	11	11	10404	10199	M-phase phosphoprotein 10 (U3 smallnucleolar ribonucleoprotein)	Ribonucleoprotein	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	Yes
MAP7D3	79649	MAP7 domain-containing protein 3 isoform 1	NP_078873.2	3	1	1	1	1.36	0.77					1	1	9953	79649	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No

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CTSZ	1522	cathepsin Z preproprotein	NP_001327.2	1	4	4	6	1.35	1.87	13.97	14.13	39.1	56.7	4	4	4410	1522	cathepsin Z	Cysteine-type peptidase activity	Lysosome	Cysteine protease	Protein metabolism	SP;PPTC1	Yes
GPATCH4	54865	G patch domain-containing protein 4 isoform 1	NP_056405.2	2	2	2	4	1.35	1.66	2.01	10.7	3.8	25.5	2	2	13596	54865	G patch domain containing 4	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	G_PATCH	No
GOLGA3	2802	Golgin subfamily A member 3 isoform 1	NP_005886.2	2	21	21	45	1.35	1.33	4.45	2.08	30	13.6	24	24	3990	2802	golgi autoantigen, golgin subfamily a, 3	Structural molecule activity	Golgi apparatus;Nucleus	Structural protein	Cell growth and/or maintenance	CC;NLS	Yes
DNTTIP1	116092	deoxynucleotidyltransferase terminal-interacting protein 1	NP_443183.1	1	2	2	4	1.35	1.23					1	1	16831	116092	deoxynucleotidyltransferase, terminal,interacting protein 1	DNA binding	Nucleus	DNA binding protein	Immune response	NLS	Yes
KIF23	9493	kinesin-like protein KIF23 isoform 1	NP_612565.1	3	9	9	16	1.35	1.23	0.66	5.23	2.3	17.1	7	7	5455	9493	kinesin family member 23	Motor activity	Nucleus	Motor protein	Cell growth and/or maintenance	KISC;CC	Yes
TUBB3	10381	tubulin beta-3 chain isoform 1	NP_006077.2	2	6	28	491	1.35	1.19	3.92	6.03	22.8	31.3	18	18	4044	10381	tubulin, beta 3	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	TUBULIN;CC	Yes
FADS3	3995	fatty acid desaturase 3	NP_068373.1	1	1	1	1	1.35	1.1					1	1	7547	3995	fatty acid desaturase 3	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
ZNF622	90441	zinc finger protein 622	NP_219482.1	1	8	8	12	1.35	1.09	4.2	7.98	15.1	23.4	7	7	12278	90441	zinc finger protein 622	Transcription regulator activity	Nucleus	Transcription regulatory protein	Cell communication;Signal transduction	ZNFC2	Yes
TMEM147	10430	transmembrane protein 147 isoform 1	NP_116024.1	2	1	1	2	1.35	1.05					1	1	17633	10430	None	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
PISD	23761	phosphatidylserine decarboxylase proenzyme	NP_055153.1	1	2	2	4	1.35	1.05	7.53	2.45	14.4	3.6	2	2	17854	23761	phosphatidylserine decarboxylase	Carboxy-lyase activity	Mitochondrion	Enzyme: Decarboxylase	Metabolism;Energy pathways	-	Yes
RAB11FIP5	26056	rab11 family-interacting protein 5	NP_056285.1	1	3	3	7	1.35	0.98	2.36	0.31	5.5	0.5	3	3	16117	26056	RAB11 family interacting protein 5 (classI)	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	C2	Yes
COX5A	9377	cytochrome c oxidase subunit 5A, mitochondrial precursor	NP_004246.2	1	4	5	8	1.35	0.96	2.79	0.46	6.5	0.8	3	3	4799	9377	cytochrome c oxidase subunit Va	Oxidoreductase activity	Mitochondrion	Regulatory/other subunit	Metabolism;Energy pathways	-	Yes
PHKB	5257	phosphorylase b kinase regulatory subunit beta isoform a	NP_000284.1	2	2	2	4	1.35	0.77	3.79	3.71	8.9	4.9	3	3	1407	5257	phosphorylase kinase, beta	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
DDX4	54514	probable ATP-dependent RNA helicase DDX4 isoform 1	NP_077726.1	4	1	4	8	1.35	0.74					1	1	5593	54514	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
ALKBH1	8846	alkylated DNA repair protein alkB homolog 1	NP_006011.2	1	1	1	1	1.35	0.74					1	1	5634	8846	alkB, alkylation repair homolog (E. coli)	DNA repair protein	Nucleus	DNA repair protein	DNA repair	-	Yes
CTSD	1509	cathepsin D preproprotein	NP_001900.1	1	10	10	180	1.35	0.69	3.82	4.51	56.7	32.8	105	105	291	1509	cathepsin D (lysosomal aspartyl protease)	Aspartic-type signal peptidase activity	Lysosome	Aspartic protease	Protein metabolism	SP	Yes
ADA	100	adenosine deaminase	NP_000013.2	1	7	7	20	1.34	1.85	3.2	7.07	13.6	43.2	10	10	38	100	adenosine deaminase	Deaminase activity	Plasma membrane	Enzyme: Deaminase	Metabolism;Energy pathways	-	Yes
QSOX2	169714	sulfhydryl oxidase 2 precursor	NP_859052.3	1	4	4	6	1.34	1.73	6.29	4.22	14.7	12.7	3	3	17942	169714	quiescin Q6-like 1	Molecular function unknown	Plasma membrane	Unclassified	Apoptosis	TM;SP	No
ZMYND8	23613	protein kinase C-binding protein 1 isoform q	NP_001268712.1	17	4	4	7	1.34	1.53	4.94	7.82	11.5	21	3	3	10166	23613	protein kinase C binding protein 1	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PHD;BROMO;PWWP;CC	Yes
RNF2	6045	E3 ubiquitin-protein ligase RING2	NP_009143.1	2	2	2	3	1.34	1.48	9.97	18.56	19	40.5	2	2	7028	6045	ring finger protein 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	RING	No
CCDC9	26093	coiled-coil domain-containing protein 9	NP_056418.1	1	3	3	5	1.34	1.43	8.53	5.19	20	12.9	3	3	10813	26093	coiled-coil domain containing 9	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
PSME3	10197	proteasome activator complex subunit 3 isoform 2	NP_789839.1	3	10	10	42	1.34	1.42	3.71	3.02	23.6	20.4	22	22	5500	10197	proteasome (prosome, macropain) activatorsubunit 3 (PA28 gamma; Ki)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
C11orf98	102288414	uncharacterized protein C11orf98	NP_001273015.1	2	4	5	10	1.34	1.34	8.08	12.85	27.1	44.2	6	6									
SAP30	8819	histone deacetylase complex subunit SAP30	NP_003855.1	1	1	1	1	1.34	1.33					1	1	4540	8819	sin3-associated polypeptide, 30kDa	Protein binding	Nucleus	Regulatory/other subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
RRP8	23378	ribosomal RNA-processing protein 8	NP_056139.1	1	2	2	4	1.34	1.29	1.6	16.84	3.7	38.9	3	3	13800	23378	None	Methyltransferase activity	Nucleolus	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	No
PRCC	5546	proline-rich protein PRCC	NP_005964.3	1	2	2	8	1.34	1.21	3.53	4.37	9.4	10.6	4	4	1562	5546	papillary renal cell carcinoma(translocation-associated)	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	NLS	Yes
BUD13	84811	BUD13 homolog isoform 1	NP_116114.1	2	3	3	5	1.34	1.18	9.99	1.48	23.4	3	3	3	11307	84811	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	No
ASH2L	9070	set1/Ash2 histone methyltransferase complex subunit ASH2 isoform a	NP_004665.2	4	2	2	3	1.34	1.14					1	1	5309	9070	ash2 (absent, small, or homeotic)-like(Drosophila)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SPRY	Yes
RCE1	9986	CAAX prenyl protease 2 isoform 1	NP_005124.1	2	1	1	2	1.34	1.13					1	1	7289	9986	RCE1 homolog, prenyl protein protease (S.cerevisiae)	Metallopeptidase activity	Endoplasmic reticulum	Metallo protease	Protein metabolism	TM;SP	Yes
HDGFRP3	50810	hepatoma-derived growth factor-related protein 3	NP_057157.1	1	2	3	4	1.34	1.08					1	1									

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PHF14	9678	PHD finger protein 14	NP_055475.2	1	3	3	5	1.34	1.02	0.03	6.33	0.1	11.3	3	3	17845	9678	PHD finger protein 14	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	CC;PHD	Yes
TPP1	1200	tripeptidyl-peptidase 1 preproprotein	NP_000382.3	1	4	4	14	1.34	1.01	5.35	15.55	19.2	43.2	7	7	6415	1200	tripeptidyl peptidase I	Serine-type peptidase activity	Lysosome	Serine protease	Protein metabolism	SP	Yes
NUCB1	4924	nucleobindin-1 precursor	NP_006175.2	1	15	15	40	1.34	1.01	2.91	7.62	19.6	38.9	25	24	3205	4924	nucleobindin 1	Calcium ion binding	Golgi apparatus	Calcium binding protein	Cell communication;Signal transduction	SP;CC;EF	Yes
IFIT5	24138	interferon-induced protein with tetratricopeptide repeats 5	NP_036552.1	1	3	3	7	1.34	0.94	1.47	28.87	2.8	40	2	2	17130	24138	interferon-induced protein withtetratricopeptide repeats 5	Molecular function unknown	-	Unclassified	Biological_process unknown	TPR	No
NDUFAF3	25915	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 isoform a precursor	NP_951032.1	2	1	1	8	1.34	0.91	2.33	21.8	6.2	41.2	4	4	16809	25915	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TSPYL1	7259	testis-specific Y-encoded-like protein 1	NP_003300.1	1	3	3	4	1.34	0.86	5.71	27.59	10.8	34.5	2	2	5278	7259	TSPY-like 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
RANBP1	5902	ran-specific GTPase-activating protein isoform 1	NP_001265568.1	4	6	6	32	1.34	0.83	3	7.26	17.2	25.8	18	18	3110	5902	RAN binding protein 1	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	CC	Yes
CCT6A	908	T-complex protein 1 subunit zeta isoform a	NP_001753.1	5	15	15	157	1.34	0.82	4.48	5.6	59.2	44	83	83	89	908	chaperonin containing TCP1, subunit 6A (zeta 1)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
RNF113A	7737	RING finger protein 113A	NP_008909.1	1	2	2	3	1.34	0.75					1	1	6760	7737	ring finger protein 113A	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;ZnF_C3H1	No
NCKAP1L	3071	nck-associated protein 1-like isoform 1	NP_005328.2	2	1	1	2	1.34	0.54					1	1	781	3071	hematopoietic protein 1	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	-	Yes
NAP1L1	4673	nucleosome assembly protein 1-like 1 isoform 1	NP_631946.1	2	9	11	108	1.33	1.65	6.41	5.41	60.7	63.1	43	42	1248	4673	nucleosome assembly protein 1-like 1	DNA binding	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	Yes
EPS8L2	64787	epidermal growth factor receptor kinase substrate 8-like protein 2	NP_073609.2	1	13	13	53	1.33	1.52	4.53	6.46	32.1	53.4	27	26	10940	64787	EPS8-like 2	Receptor signaling complex scaffold activity	-	Adapter molecule	Cell communication;Signal transduction	SH3;PTB	No
CLPB	81570	caseinolytic peptidase B protein homolog isoform 1	NP_110440.1	4	6	6	10	1.33	1.46	3.11	12.94	10.2	48.7	6	6	11560	81570	None	ATPase activity	Nucleus	ATPase	Metabolism;Energy pathways	SP;ANK;CC;AAA	Yes
RPS24	6229	40S ribosomal protein S24 isoform d	NP_001135757.1	5	5	5	44	1.33	1.43	5.07	12.11	36.9	115.1	28	28	3877	6229	ribosomal protein S24	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	NLS	Yes
PLAUR	5329	urokinase plasminogen activator surface receptor isoform 1 precursor	NP_002650.1	4	2	2	3	1.33	1.42	6.12	2.37	11.5	4.8	2	2	1421	5329	plasminogen activator, urokinase receptor	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;LU;GPI	No
ARCN1	372	coatomer subunit delta isoform 1	NP_001646.2	2	21	21	73	1.33	1.38	3.17	4.82	27.5	44.4	41	41	2893	372	archain 1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC	Yes
PALM2-AKAP2	445815	PALM2-AKAP2 protein isoform 2	NP_671492.1	5	22	23	65	1.33	1.33	4.06	5.39	32.4	44.3	34	35	18661	445815	None	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	C-C	Yes
MCC	4163	colorectal mutant cancer protein isoform 1	NP_001078846.1	2	9	9	20	1.33	1.31	7.11	10.52	32.2	48.1	11	11	1157	4163	mutated in colorectal cancers	Molecular function unknown	Cytoplasm	Unclassified;Cell cycle control protein	Cell communication;Signal transduction	CC;EF	Yes
PGD	5226	6-phosphogluconate dehydrogenase, decarboxylating isoform 1	NP_002622.2	3	20	20	107	1.33	1.31	3.38	4.67	34.4	48	55	55	1391	5226	phosphogluconate dehydrogenase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
FAM50A	9130	protein FAM50A	NP_004690.1	2	5	5	7	1.33	1.26	14.33	15	44.5	44.1	5	5	2349	9130	family with sequence similarity 50, member A	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
NELFE	7936	negative elongation factor E	NP_002895.3	1	7	7	20	1.33	1.18	2.31	9.94	8.7	34.3	8	8									
DNAJC21	134218	dnaJ homolog subfamily C member 21 isoform 1	NP_919259.3	2	1	1	2	1.33	1.17					1	1	14056	134218	None	DNA binding	-	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;DNAJ;ZNFC2	No
ADRBK1	156	beta-adrenergic receptor kinase 1	NP_001610.2	2	3	3	5	1.33	1.13	5.92	12.92	11.2	20.8	2	2	182	156	adrenergic, beta, receptor kinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	RGS;S_T_kinase;PH;CC	Yes
DBR1	51163	lariat debranching enzyme	NP_057300.2	1	3	3	4	1.33	1.12	29.74	16.61	60.7	26.8	2	2	7384	51163	debranching enzyme homolog 1 (S. cerevisiae)	Hydrolase activity	Nucleus	Enzyme: Hydrolase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
GPR107	57720	protein GPR107 isoform 1 precursor	NP_001130029.1	4	2	2	4	1.33	1.07	11.83	20.14	22.6	31.2	2	2	17054	57720	G protein-coupled receptor 107	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Cell communication;Signal transduction	SP;TM	No
CD3EAP	10849	DNA-directed RNA polymerase I subunit RPA34 isoform 1	NP_001284519.1	2	8	8	27	1.33	1.07	2.12	6.05	8.9	20.7	10	10	125	10849	CD3E antigen, epsilon polypeptide associatedprotein	Transcription regulator activity	Nucleolus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
DDX56	54606	probable ATP-dependent RNA helicase DDX56 isoform 1	NP_061955.1	2	4	4	8	1.33	1.05	10.16	1.28	27.6	2.7	4	4	12154	54606	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	Helicase activity	Nucleolus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;NLS	Yes
ACP1	52	low molecular weight phosphotyrosine protein phosphatase isoform c	NP_004291.1	3	4	4	13	1.33	1.02	11.93	11.61	47.1	34.4	8	8	8881	52	acid phosphatase 1, soluble	Acid phosphatase activity	Cytoplasm	Enzyme: Acid phosphatase	Metabolism;Energy pathways	TM	Yes
LRIF1	55791	ligand-dependent nuclear receptor-interacting factor 1 isoform 1	NP_060842.3	2	2	2	4	1.33	1.01	16.41	24.05	31.6	35.5	2	2									
MORF4L2	9643	mortality factor 4-like protein 2	NP_001135890.1	1	1	1	2	1.33	0.98					1	1	2326	9643	mortality factor 4 like 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HLH;LZ	Yes
EPN1	29924	epsin-1 isoform a	NP_001123543.1	3	2	3	9	1.33	0.95	3.07	8.15	7.1	13.5	3	3	6270	29924	epsin 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	UIM	Yes
JUN	3725	transcription factor AP-1	NP_002219.1	1	1	1	2	1.33	0.92					1	1	1302	3725	v-jun sarcoma virus 17 oncogene homolog (avian)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;NLS;CC	Yes
MRPL48	51642	39S ribosomal protein L48, mitochondrial	NP_057139.1	1	1	1	2	1.33	0.91					1	1	14767	51642	mitochondrial ribosomal protein L48	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
LIPE	3991	hormone-sensitive lipase	NP_005348.2	1	5	5	10	1.33	0.69	2.02	9.04	6	14	5	5	1062	3991	lipase, hormone-sensitive	Lipase activity	Cytoplasm	Enzyme: Lipase	Metabolism;Energy pathways	-	Yes
AZGP1	563	zinc-alpha-2-glycoprotein precursor	NP_001176.1	1	1	1	12	1.33	0.6	3.63	10.4	11.8	15.5	6	6	1910	563	alpha-2-glycoprotein 1, zinc	Cell adhesion molecule activity	Extracellular	Adhesion molecule	Immune response	SP;IGC	Yes
FKBP14	55033	peptidyl-prolyl cis-trans isomerase FKBP14 precursor	NP_060416.1	1	2	2	4	1.32	1.39	13.21	8.97	25.1	17.8	2	2	16898	55033	FK506 binding protein 14, 22 kDa	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase	Metabolism;Energy pathways	SP	Yes
BAX	581	apoptosis regulator BAX isoform 1	NP_001278357.1	8	7	7	39	1.32	1.34	5.63	13.06	33.2	88.7	19	19	2498	581	BCL2-associated X protein	Receptor signaling complex scaffold activity	Cytoplasm;Mitochondrion	Adapter molecule	Apoptosis	BCL;TM	Yes
HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	NP_001073027.1	1	27	27	88	1.32	1.34	3.77	4.95	36.8	49.6	51	50	18952	221092	heterogeneous nuclear ribonucleoprotein U-like 2	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;SPRY	Yes
TFRC	7037	transferrin receptor protein 1	NP_003225.2	3	21	21	77	1.32	1.32	2.54	2.99	21.4	25.3	40	40	1812	7037	transferrin receptor (p90, CD71)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
FAT1	2195	protocadherin Fat 1 precursor	NP_005236.2	1	53	53	112	1.32	1.31	2.52	2.6	27	27.8	64	64	2986	2195	FAT tumor suppressor homolog 1 (Drosophila)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	Cadherin;LAMG;EGFCA;TM;SP	Yes
NIFK	84365	MKI67 FHA domain-interacting nucleolar phosphoprotein	NP_115766.3	1	8	8	24	1.32	1.28	1.86	1.79	8.8	8.3	13	13									
API5	8539	apoptosis inhibitor 5 isoform b	NP_006586.1	4	14	14	53	1.32	1.27	2.67	4.29	17	26.5	23	23	16500	8539	apoptosis inhibitor 5	Molecular function unknown	Nucleus	Unclassified	Apoptosis	-	Yes
DDX21	9188	nucleolar RNA helicase 2 isoform 1	NP_004719.2	2	36	38	134	1.32	1.23	1.94	2.7	20.7	27.1	64	65	5895	9188	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	ATPase activity	Nucleolus	ATPase	Metabolism;Energy pathways	DEXDc;HELIC	Yes
OSBP	5007	oxysterol-binding protein 1	NP_002547.1	1	12	12	32	1.32	1.19	7.57	6.35	44.2	33	18	18	1327	5007	oxysterol binding protein	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	PH;CC	Yes
UBE2M	9040	NEDD8-conjugating enzyme Ubc12	NP_003960.1	1	3	3	9	1.32	1.18	4.23	13.62	12.5	37	5	5	4414	9040	ubiquitin-conjugating enzyme E2M (UBC12homolog, yeast)	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBC	No
USP15	9958	ubiquitin carboxyl-terminal hydrolase 15 isoform 1	NP_001239007.1	3	8	10	21	1.32	1.18	7.58	3.12	32.6	11.7	10	10	5293	9958	ubiquitin specific protease 15	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	DUSP;UCH	Yes
EPN2	22905	epsin-2 isoform b	NP_055779.2	3	3	4	7	1.32	1.18	1.27	0.84	2.9	1.7	3	3	6271	22905	epsin 2	Receptor signaling complex scaffold activity;Molecular function unknown	Cytoplasmic vesicle	Unclassified;Adapter molecule	Cell communication;Signal transduction;Biological_process unknown	UIM	Yes
BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 1	NP_055554.1	4	23	23	39	1.32	1.18	4.68	6.1	28	33.1	20	20	16544	9774	BCL2-associated transcription factor 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
UBP1	7342	upstream-binding protein 1 isoform LBP-1b	NP_055332.3	2	2	3	6	1.32	1.17	14.57	15.66	27.8	26.3	2	2	10291	7342	upstream binding protein 1 (LBP-1a)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAM_PNT	No
RAD54L2	23132	helicase ARIP4	NP_055921.2	1	1	1	2	1.32	1.13					1	1	10018	23132	None	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
GRSF1	2926	G-rich sequence factor 1 isoform 1	NP_002083.3	2	6	6	14	1.32	1.13	5.03	7.81	17.7	23.6	7	7	7276	2926	G-rich RNA sequence binding factor 1	RNA binding	Cytoplasm	RNA binding protein	Protein metabolism	RRM	Yes
SPATS2	65244	spermatogenesis-associated serine-rich protein 2	NP_075559.2	1	4	4	9	1.32	1.12	4.04	13	10.7	29.9	4	4	15434	65244	spermatogenesis associated, serine-rich 2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
TSFM	10102	elongation factor Ts, mitochondrial isoform 1 precursor	NP_001166167.1	2	3	3	8	1.32	1.1	19.3	13.96	54.6	31.4	4	4	5285	10102	Ts translation elongation factor, mitochondrial	Translation regulator activity	Mitochondrion	Translation regulatory protein	Protein metabolism	UBA	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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C7orf43	55262	uncharacterized protein C7orf43 isoform 1	NP_060745.3	2	1	1	3	1.32	1.09					1	1	7716	55262	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
MIER1	57708	mesoderm induction early response protein 1 isoform b	NP_001071168.2	10	1	2	3	1.32	1.01					1	1	11362	57708	None	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT;SP;NLS	Yes
CMTR1	23070	cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	NP_055865.1	1	2	2	4	1.32	0.97	8.02	14.58	15	20.1	2	2									
PCCB	5096	propionyl-CoA carboxylase beta chain, mitochondrial isoform 2 precursor	NP_001171485.1	2	9	9	13	1.32	0.94	10.5	8.36	35	19.4	6	6	1982	5096	propionyl Coenzyme A carboxylase, betapolypeptide	Ligase activity	Mitochondrion	Enzyme: Carboxylase	Metabolism;Energy pathways	SP	Yes
CBWD1	55871	COBW domain-containing protein 1 isoform 1	NP_060961.3	4	1	1	4	1.32	0.89	8.93	5.61	16.8	7.1	2	2	16686	55871	COBW domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	AAA	No
SKP1	6500	S-phase kinase-associated protein 1 isoform b	NP_733779.1	2	10	11	65	1.32	0.77	4.85	19.07	34.9	90.9	28	28	3255	6500	S-phase kinase-associated protein 1A (p19A)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism;Regulation of cell cycle;Chromosome segregation	SKP1	Yes
PPHLN1	51535	periphilin-1 isoform 6	NP_001137259.1	1	1	1	2	1.32	0.69					1	1	10488	51535	periphilin 1	Structural molecule activity	Nucleus;Cytoplasm	Structural protein	Cell growth and/or maintenance	NES;NLS	Yes
TRAPPC13	80006	trafficking protein particle complex subunit 13 isoform 1	NP_001087224.1	4	1	1	2	1.32	0.67					1	1									
FECH	2235	ferrochelatase, mitochondrial isoform a precursor	NP_001012533.1	2	2	2	4	1.32	0.59	4.53	16.2	10.3	16.7	3	3	1509	2235	ferrochelatase (protoporphyria)	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
FAM162A	26355	protein FAM162A	NP_055182.3	1	2	2	7	1.32	0.58	7.93	48.92	21.1	61.3	4	4	6422	26355	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
RGP1	9827	RAB6A-GEF complex partner protein 2	NP_001073965.2	1	1	1	2	1.31	1.77					1	1	13790	9827	KIAA0258	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
DKK3	27122	dickkopf-related protein 3 precursor	NP_056965.3	1	2	2	3	1.31	1.68	27.12	10.98	53.5	26.6	2	2	5659	27122	dickkopf homolog 3 (Xenopus laevis)	Receptor binding;Lipid binding	Extracellular	Ligand	Cell communication;Signal transduction	SP;CC	Yes
MAPRE1	22919	microtubule-associated protein RP/EB family member 1	NP_036457.1	1	10	10	39	1.31	1.64	4.14	2.87	22	18.4	16	15	4379	22919	microtubule-associated protein, RP/EB family,member 1	Protein binding	Centrosome	Cell cycle control protein	Cell communication;Signal transduction	CH;CC	Yes
DLGAP4	22839	disks large-associated protein 4 isoform a	NP_055717.2	3	5	5	8	1.31	1.46	2.66	11.69	7.8	39.6	5	5	16826	22839	discs, large (Drosophila) homolog-associatedprotein 4	Molecular function unknown	Cytosol	Adapter molecule;Unclassified	Cell communication;Signal transduction	-	Yes
ALDH2	217	aldehyde dehydrogenase, mitochondrial isoform 1 precursor	NP_000681.2	2	14	17	53	1.31	1.44	3.81	3.66	24.8	26.2	24	24	3	217	aldehyde dehydrogenase 2 family (mitochondrial)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
PKN1	5585	serine/threonine-protein kinase N1 isoform 1	NP_998725.1	2	1	1	2	1.31	1.42					1	1	3019	5585	protein kinase N1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	HR1;C2;S_T_kinase;CC	Yes
EIF2S2	8894	eukaryotic translation initiation factor 2 subunit 2	NP_003899.2	1	18	18	65	1.31	1.36	2.01	5.09	15.9	43.4	36	36	4882	8894	eukaryotic translation initiation factor 2,subunit 2 beta, 38kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
PITPNA	5306	phosphatidylinositol transfer protein alpha isoform	NP_006215.1	1	4	4	7	1.31	1.32	1.35	10.12	3.5	27.2	4	4	2548	5306	phosphatidylinositol transfer protein, alpha	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
TIMM50	92609	mitochondrial import inner membrane translocase subunit TIM50	NP_001001563.1	1	9	9	29	1.31	1.32	5.31	7.01	28.5	38.3	16	16	12118	92609	translocase of inner mitochondrial membrane 50homolog (yeast)	Protein tyrosine/serine/threonine phosphatase activity	Mitochondrion	Dual specificity phosphatase	Cell communication;Signal transduction	CPDc	No
IGF2BP3	10643	insulin-like growth factor 2 mRNA-binding protein 3	NP_006538.2	1	18	20	73	1.31	1.3	4.07	4.41	28.3	30.5	27	27	16306	10643	None	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	RRM;KH;NLS	No
GLA	2717	alpha-galactosidase A precursor	NP_000160.1	1	4	4	9	1.31	1.26	5.13	5.76	16.6	17.9	6	6	2357	2717	galactosidase, alpha	Galactosidase activity	Endoplasmic reticulum	Enzyme: Galactosidase	Metabolism;Energy pathways	SP	Yes
SAMHD1	25939	deoxynucleoside triphosphate triphosphohydrolase SAMHD1	NP_056289.2	1	17	17	47	1.31	1.25	3.97	5.59	27	37	26	26	8418	25939	SAM domain and HD domain 1	GTPase activity	Nucleus;Cytoplasm	GTPase	Immune response	SAM;HDc	Yes
NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 1	NP_001271317.1	3	17	17	53	1.31	1.24	2.69	2.16	19.8	15	31	31	3864	9221	nucleolar and coiled-body phosphoprotein 1	Transcription factor activity	Nucleolus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LISH	Yes
XRCC4	7518	DNA repair protein XRCC4 isoform 2	NP_071801.1	2	3	3	3	1.31	1.17	4.34	4.7	9.8	9.5	3	3	15951	7518	X-ray repair complementing defective repair inChinese hamster cells 4	DNA repair protein	Nucleus	DNA repair protein	DNA repair	CC	Yes
ELMO2	63916	engulfment and cell motility protein 2	NP_877496.1	3	4	4	6	1.31	1.16	8.97	14.91	16.7	24.7	2	2	12103	63916	engulfment and cell motility 2 (ced-12 homolog,C. elegans)	Molecular function unknown	Cytoplasm	Unclassified	Signal transduction;Cell growth and/or maintenance;Cell migration	PH;LZ	Yes
SNRNP70	6625	U1 small nuclear ribonucleoprotein 70 kDa isoform 1	NP_003080.2	2	15	15	54	1.31	1.09	3.24	6.61	21.5	37.1	25	25	1617	6625	small nuclear ribonucleoprotein 70kDapolypeptide (RNP antigen)	Ribonucleoprotein;RNA binding	Nucleus	Ribonucleoprotein;RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;RRM	Yes
NOL8	55035	nucleolar protein 8 isoform a	NP_060418.4	2	3	3	3	1.31	1.06	2.85	5.37	6.5	9.9	3	3	11397	55035	nucleolar protein 8	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	No

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RNF14	9604	E3 ubiquitin-protein ligase RNF14 isoform 1	NP_001188294.1	1	1	1	2	1.31	1.03					1	1	5745	9604	ring finger protein 14	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of gene expression, epigenetic	RWD;IBR;RING	Yes
WDR77	79084	methylosome protein 50	NP_077007.1	1	3	3	8	1.31	1.01	5.54	5.06	16.4	11.5	5	5	14387	79084	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	WD40	No
EIF4EBP1	1978	eukaryotic translation initiation factor 4E-binding protein 1	NP_004086.1	1	1	1	4	1.31	0.98	16.33	3.25	31.1	4.5	2	2	3746	1978	eukaryotic translation initiation factor 4Ebinding protein 1	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
INTS2	57508	integrator complex subunit 2	NP_065799.1	1	1	2	4	1.31	0.97					1	1	11137	57508	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
GEMIN2	8487	gem-associated protein 2 isoform alpha	NP_003607.1	3	2	2	3	1.31	0.94	2.81	0.02	5.2	0	2	2									
TNFRSF10B	8795	tumor necrosis factor receptor superfamily member 10B isoform 1 precursor	NP_003833.4	2	2	2	3	1.31	0.92	11.13	24.28	20.8	32.2	2	2	4680	8795	tumor necrosis factor receptor superfamily,member 10b	Receptor activity	Plasma membrane	Cell surface receptor	Apoptosis;Cell communication;Signal transduction	TM;TNFR;DEATH	Yes
RBM8A	9939	RNA-binding protein 8A	NP_005096.1	1	6	6	17	1.31	0.9	4.25	17.12	16.8	49.1	9	9	5609	9939	RNA binding motif protein 8A	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
ADD1	118	alpha-adducin isoform b	NP_054908.2	5	3	3	8	1.31	0.88	3.7	8.96	9.7	15.9	4	4	36	118	adducin 1 (alpha)	Structural molecule activity	Nucleus;Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
POLR2G	5436	DNA-directed RNA polymerase II subunit RPB7	NP_002687.1	1	1	1	2	1.31	0.86					1	1	15995	5436	polymerase (RNA) II (DNA directed) polypeptideG	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S1	No
PFDN1	5201	prefoldin subunit 1	NP_002613.2	1	1	1	1	1.31	0.83					1	1	5357	5201	prefoldin 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CC	Yes
UCHL3	7347	ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 2	NP_005993.1	2	5	5	14	1.31	0.81	8.36	14.82	29.7	32.7	7	7	4367	7347	ubiquitin carboxyl-terminal esterase L3(ubiquitin thiolesterase)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
MAX	4149	protein max isoform a	NP_002373.3	7	1	1	2	1.31	0.8					1	1	1113	4149	MYC associated factor X	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HLH;CC;LZ	No
RPS8	6202	40S ribosomal protein S8	NP_001003.1	1	9	9	143	1.31	0.78	2.31	6.96	27.1	50.2	77	77	15969	6202	ribosomal protein S8	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	-	Yes
KIDINS220	57498	kinase D-interacting substrate of 220 kDa	NP_065789.1	1	1	1	2	1.31	0.76					1	1	17235	57498	None	Protein kinase binding	Plasma membrane	Integral membrane protein	Cell growth and/or maintenance	ANK;TM	No
RRAGC	64121	ras-related GTP-binding protein C isoform 1	NP_071440.1	3	3	3	6	1.31	0.69	1.94	18.52	4.4	22.4	3	3	12198	64121	Ras-related GTP binding C	GTPase activity	Cytoplasm	G protein	Cell communication;Signal transduction	-	No
INTS5	80789	integrator complex subunit 5	NP_085131.1	1	1	1	2	1.31	0.58					1	1	13883	80789	None	Protein binding	Nucleus	Unclassified	RNA metabolism;Transcription	-	Yes
HYI	81888	putative hydroxypyruvate isomerase isoform 3	NP_001177809.1	3	1	1	7	1.3	1.97	10.61	7	19.8	19.7	2	2	11039	81888	hydroxypyruvate isomerase homolog (E. coli)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
TOMM34	10953	mitochondrial import receptor subunit TOM34	NP_006800.2	1	9	9	25	1.3	1.89	5.14	6.1	24.4	43.5	13	13	11641	10953	translocase of outer mitochondrial membrane 34	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	TPR	Yes
UGDH	7358	UDP-glucose 6-dehydrogenase isoform 1	NP_003350.1	3	14	14	43	1.3	1.71	5.6	6.42	34.4	53.7	21	21	4535	7358	UDP-glucose dehydrogenase	Catalytic activity	-	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
DND1	373863	dead end protein homolog 1	NP_919225.1	1	1	1	2	1.3	1.41					1	1	13240	373863	dead end homolog 1 (zebrafish)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	No
DYNC2H1	79659	cytoplasmic dynein 2 heavy chain 1 isoform 2	NP_001073932.1	2	1	1	1	1.3	1.4					1	1	10344	79659	dynein, cytoplasmic, heavy polypeptide 2	Motor activity	Golgi apparatus	Motor protein	Cell growth and/or maintenance	AAA;CC	Yes
LOC101060521	101060521	DNA-directed RNA polymerase III subunit RPC5 isoform X1	XP_005276555.2	6	1	1	1	1.3	1.3					1	1									
STAU1	6780	double-stranded RNA-binding protein Staufen homolog 1 isoform b	NP_059347.2	2	1	17	41	1.3	1.28					1	1	3422	6780	staufen, RNA binding protein (Drosophila)	RNA binding;Transporter activity	Endoplasmic reticulum	RNA binding protein;Transport/ cargo protein	Protein metabolism	DSRM	Yes
DNAJC25-GNG10	552891	DNAJC25-GNG10 protein precursor	NP_004116.2	2	1	1	2	1.3	1.24					1	1									
ARID1A	8289	AT-rich interactive domain-containing protein 1A isoform a	NP_006006.3	4	6	6	14	1.3	1.23	14.52	5.95	48.8	18.1	6	6	4319	8289	AT rich interactive domain 1A (SWI- like)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRIGHT	Yes
NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 3	NP_001245238.1	4	19	19	56	1.3	1.23	2.65	3.25	19.8	23	32	32	1244	4839	nucleolar protein 1, 120kDa	Molecular function unknown	Nucleolus	Unclassified	Regulation of cell cycle;Cell proliferation	-	Yes
ATP6AP1	537	V-type proton ATPase subunit S1 precursor	NP_001174.2	1	2	2	5	1.3	1.22	0.92	7.72	2.1	16.4	3	3	2184	537	ATPase, H+ transporting, lysosomal accessoryprotein 1	Transporter activity	-	Transport/cargo protein	Transport	TM	Yes

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NAPA	8775	alpha-soluble NSF attachment protein	NP_003818.2	1	10	10	29	1.3	1.22	3.09	7.82	16.7	41	17	17	4447	8775	N-ethylmaleimide-sensitive factor attachmentprotein, alpha	Receptor signaling complex scaffold activity	Golgi apparatus	Adapter molecule	Transport	-	No
PWP2	5822	periodic tryptophan protein 2 homolog	NP_005040.2	2	6	6	21	1.3	1.22	4.48	9.43	18.6	37.5	10	10	3279	5822	PWP2 periodic tryptophan protein homolog(yeast)	Signal transducer activity	Nucleolus	Cell cycle control protein	Cell communication;Signal transduction	WD40	Yes
FEN1	2237	flap endonuclease 1	NP_004102.1	1	12	12	40	1.3	1.2	2.99	4.96	18	27.1	21	20	2670	2237	flap structure-specific endonuclease 1	Deoxyribonuclease activity	Nucleus	Deoxyribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	XPGI;HHH2;CC	Yes
FTSJ1	24140	putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase isoform a	NP_036412.1	3	3	3	5	1.3	1.17	6.51	6.56	14.7	13.4	3	3	6568	24140	FtsJ homolog 1 (E. coli)	Methyltransferase activity	Nucleolus	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
TRA2B	6434	transformer-2 protein homolog beta isoform 1	NP_004584.1	2	5	7	16	1.3	1.16	5.78	10.55	22.8	38.1	9	9	4097	6434	splicing factor, arginine/serine-rich 10(transformer 2 homolog, Drosophila)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
TOP1	7150	DNA topoisomerase 1	NP_003277.1	3	18	18	46	1.3	1.16	2.62	4.22	18.2	26.4	28	28	535	7150	topoisomerase (DNA) I	DNA topoisomerase activity	Nucleus	Enzyme: Topoisomerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
EHD1	10938	EH domain-containing protein 1 isoform 2	NP_001269374.1	2	26	27	91	1.3	1.14	3.58	4.24	32	33.4	45	45	9325	10938	EH-domain containing 1	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	EH	Yes
FKBP10	60681	peptidyl-prolyl cis-trans isomerase FKBP10 precursor	NP_068758.3	2	7	7	23	1.3	1.13	1.87	2.27	8.1	8.5	11	11	9522	60681	FK506 binding protein 10, 65 kDa	Isomerase activity	Endoplasmic reticulum	Unclassified	Protein folding	SP;EF	Yes
ACAD8	27034	isobutyryl-CoA dehydrogenase, mitochondrial	NP_055199.1	1	2	2	6	1.3	1.11	19.83	14.09	47	27.6	3	3	11985	27034	acyl-Coenzyme A dehydrogenase family, member 8	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
LCMT1	51451	leucine carboxyl methyltransferase 1 isoform a	NP_057393.2	2	2	2	3	1.3	1.1	0.96	21.83	1.8	35	2	2	17266	51451	leucine carboxyl methyltransferase 1	Methyltransferase activity	-	Enzyme: Methyltransferase	Protein modification;Metabolism;Energy pathways	-	Yes
CHD2	1106	chromodomain-helicase-DNA-binding protein 2 isoform 1	NP_001262.3	2	4	6	9	1.3	1	0.97	5.82	2.5	11.7	4	4	3669	1106	chromodomain helicase DNA binding protein 2	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CHROMO;DEXDc;HELIC;CC	Yes
AQR	9716	intron-binding protein aquarius	NP_055506.1	1	3	3	5	1.3	0.94	13.61	8.5	31.3	13.9	3	3	12468	9716	aquarius homolog (mouse)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown;RNA metabolism	-	Yes
ALYREF	10189	THO complex subunit 4	NP_005773.3	1	5	5	19	1.3	0.86	6.03	6.64	26.4	19	11	11									
REXO4	57109	RNA exonuclease 4 isoform 1	NP_065118.2	4	2	2	3	1.3	0.82	20.77	63.08	39.7	84.6	2	2	4239	57109	XPMC2 prevents mitotic catastrophe 2 homolog(Xenopus laevis)	Translation regulator activity	Nucleus	Translation regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	EXOIII	No
CALR	811	calreticulin precursor	NP_004334.1	1	21	21	171	1.29	1.55	2.96	2.66	36.1	39.1	84	84	169	811	calreticulin	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP;CC	Yes
CALU	813	calumenin isoform c precursor	NP_001186600.1	5	10	10	22	1.29	1.49	5.26	2.68	27.7	16.1	16	16	4569	813	calumenin	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein	Cell communication;Signal transduction	EF;SP	Yes
HARS	3035	histidine--tRNA ligase, cytoplasmic isoform 1	NP_002100.2	7	14	19	79	1.29	1.48	2.84	2.66	20.2	21.9	30	30	827	3035	histidyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	CC	Yes
CTTN	2017	src substrate cortactin isoform a	NP_005222.2	3	28	28	84	1.29	1.45	2.64	4.41	22.9	44.4	44	44	1268	2017	cortactin	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	SH3;CC;HS1_rep	Yes
LAMA3	3909	laminin subunit alpha-3 isoform 1 precursor	NP_937762.2	5	69	69	365	1.29	1.43	1.78	2.26	30.9	44.2	172	172	2883	3909	laminin, alpha 3	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	EGFLAM;LAMG;SP;CC;LAMNT;LAMB;TSPN	Yes
SELK	58515	selenoprotein K	NP_067060.2	1	2	2	3	1.29	1.38					1	1									
FERMT2	10979	fermitin family homolog 2 isoform 2	NP_001128471.1	3	5	6	16	1.29	1.35	5.04	2.55	14.7	7.7	5	5	6374	10979	pleckstrin homology domain containing, familyC (with FERM domain) member 1	Structural constituent of cytoskeleton	Plasma membrane;Nucleus;Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	PH;CC;B41	Yes
OGFR	11054	opioid growth factor receptor	NP_031372.2	1	14	14	28	1.29	1.35	5.27	4.85	25.9	24.9	14	14	8404	11054	opioid growth factor receptor	Ligand-dependent nuclear receptor activity	Nucleus;Cytoplasm	Nuclear receptor	Cell communication;Signal transduction	-	Yes
GTF2E2	2961	transcription initiation factor IIE subunit beta	NP_002086.1	1	3	3	4	1.29	1.32	16.97	17.49	31.8	33.5	2	2	1800	2961	general transcription factor IIE, polypeptide2, beta 34kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HLH	Yes
ACAT1	38	acetyl-CoA acetyltransferase, mitochondrial precursor	NP_000010.1	1	18	18	53	1.29	1.32	3.01	7.35	20	52.6	26	26	1946	38	acetyl-Coenzyme A acetyltransferase 1(acetoacetyl Coenzyme A thiolase)	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	SP	Yes

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IVD	3712	isovaleryl-CoA dehydrogenase, mitochondrial isoform 1 precursor	NP_002216.2	2	7	7	17	1.29	1.29	5.28	10.44	20.6	42.1	9	9	9516	3712	isovaleryl Coenzyme A dehydrogenase	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
NDRG3	57446	protein NDRG3 isoform a	NP_114402.1	2	7	7	16	1.29	1.29	4.27	8.17	15.7	30.4	8	8	12007	57446	NDRG family member 3	Molecular function unknown	Cytoplasm	Unclassified;Cell cycle control protein	Cell communication;Signal transduction;Cell differentiation	-	No
EIF1AY	9086	eukaryotic translation initiation factor 1A, Y-chromosomal isoform 1	NP_004672.2	3	6	6	13	1.29	1.28	2.18	12.73	6.9	41.6	6	6	2455	9086	eukaryotic translation initiation factor 1A,Y-linked	Translation regulator activity	-	Translation regulatory protein	Protein metabolism	-	No
XRCC1	7515	DNA repair protein XRCC1	NP_006288.2	1	7	7	9	1.29	1.27	6.42	4.75	22.3	16	7	7	1909	7515	X-ray repair complementing defective repair inChinese hamster cells 1	DNA repair protein	Nucleus	DNA repair protein	DNA repair	BRCT;NLS	Yes
CNPY2	10330	protein canopy homolog 2 isoform 1 precursor	NP_055070.1	2	7	7	16	1.29	1.25	9.55	8.85	38.3	34.1	9	9	12056	10330	transmembrane protein 4	Protein binding	Integral to membrane	Integral membrane protein	Cell growth and/or maintenance	SP	Yes
MIA3	375056	melanoma inhibitory activity protein 3 isoform 1 precursor	NP_940953.2	2	16	16	30	1.29	1.22	3.46	4.17	19.1	21.8	18	18	18918	375056	melanoma inhibitory activity family, member 3	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;SH3;CC	Yes
ZNF326	284695	DBIRD complex subunit ZNF326 isoform 1	NP_892021.1	1	5	5	15	1.29	1.21	2.19	4.31	7.5	13.9	7	7	15774	284695	zinc finger protein 326	DNA binding	Nucleolus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;CC	No
POLD2	5425	DNA polymerase delta subunit 2 isoform 2	NP_006221.2	2	2	2	3	1.29	1.19	6.56	4.94	12	8.3	2	2	15982	5425	polymerase (DNA directed), delta 2, regulatorysubunit 50kDa	DNA-directed DNA polymerase activity	Nucleus	DNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
RPL39	6170	60S ribosomal protein L39	NP_000991.1	1	1	1	2	1.29	1.18	1.57	7.68	2.9	12.8	2	2	3546	6170	ribosomal protein L39	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	No
ACSL3	2181	long-chain-fatty-acid--CoA ligase 3	NP_004448.2	1	28	31	121	1.29	1.14	2.55	4.61	24.3	39.6	53	53	3845	2181	acyl-CoA synthetase long-chain family member 3	CoA-ligase activity	Peroxisome	Enzyme: Ligase	Fatty acid metabolism	TM	Yes
NEURL1	9148	E3 ubiquitin-protein ligase NEURL1	NP_004201.3	1	1	1	1	1.29	1.13					1	1									
ITPKC	80271	inositol-trisphosphate 3-kinase C	NP_079470.1	1	7	7	13	1.29	1.12	2.76	7.76	8.7	21.6	6	6	9400	80271	inositol 1,4,5-trisphosphate 3-kinase C	Lipid kinase activity	Cytoplasm	Lipid Kinase	Cell communication;Signal transduction	PIPKc	Yes
DBNL	28988	drebrin-like protein isoform b	NP_001014436.1	2	1	13	45	1.29	1.1					1	1	6588	28988	drebrin-like	Kinase regulator activity	Actin cytoskeleton	Adapter molecule	Signal transduction	ADF;CC;SH3	Yes
HACL1	26061	2-hydroxyacyl-CoA lyase 1 isoform a	NP_036392.2	4	5	5	7	1.29	1.09	14.14	7.35	47	19.8	6	6	9183	26061	None	Lyase activity	Peroxisome	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
UBAP1	51271	ubiquitin-associated protein 1 isoform 2	NP_001164672.1	3	3	3	6	1.29	1.07	4.7	6.22	10.5	11.6	3	3	15597	51271	ubiquitin associated protein 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
BOP1	23246	ribosome biogenesis protein BOP1	NP_056016.1	1	6	6	16	1.29	1.05	5.66	10.2	20.9	30.9	8	8	16558	23246	block of proliferation 1	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	WD40	Yes
HSDL2	84263	hydroxysteroid dehydrogenase-like protein 2 isoform 1	NP_115679.2	2	13	13	34	1.29	1.05	3.44	5.8	19	26.3	18	18	13679	84263	hydroxysteroid dehydrogenase like 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
CCDC137	339230	coiled-coil domain-containing protein 137	NP_954981.1	1	2	2	2	1.29	1.04	10.07	4.97	18.6	7.4	2	2	11313	339230	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
LANCL2	55915	lanC-like protein 2	NP_061167.1	1	1	1	1	1.29	1.01					1	1	13956	55915	LanC lantibiotic synthetase component C-like 2(bacterial)	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	-	Yes
HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform a	NP_112604.2	2	1	15	245	1.29	1.01					1	1	1243	3183	heterogeneous nuclear ribonucleoprotein C(C1/C2)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;LZ;CC	Yes
C2orf47	79568	uncharacterized protein C2orf47, mitochondrial precursor	NP_078796.2	1	5	5	10	1.29	0.91	5.68	2.92	18.1	6.5	6	6	7994	79568	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TNIP1	10318	TNFAIP3-interacting protein 1 isoform 3	NP_001239320.1	6	2	2	2	1.29	0.89	20.41	12.11	38.6	15.3	2	2	9216	10318	TNFAIP3 interacting protein 1	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein	Cell growth and/or maintenance	CC	Yes
PCIF1	63935	phosphorylated CTD-interacting factor 1	NP_071387.1	1	1	1	6	1.29	0.8	8.22	13.05	18.5	18.1	3	3	12779	63935	chromosome 20 open reading frame 67	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WW;NLS	Yes
RTN4IP1	84816	reticulon-4-interacting protein 1, mitochondrial precursor	NP_116119.2	1	1	1	2	1.29	0.76					1	1	18008	84816	reticulon 4 interacting protein 1	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
BPI	671	bactericidal permeability-increasing protein precursor	NP_001716.2	1	1	1	2	1.29	0.69					1	1	174	671	bactericidal/permeability-increasing protein	Defense/immunity protein activity	Secretory granule	Integral membrane protein	Immune response	SP;TM	Yes
ATP5D	513	ATP synthase subunit delta, mitochondrial precursor	NP_001678.1	1	2	2	6	1.29	0.57	1.39	24.89	3.1	24.9	3	3	4397	513	ATP synthase, H+ transporting, mitochondrial F1complex, delta subunit	ATPase activity	Mitochondrial membrane	ATPase	Ion transport	CC;SP	Yes
MYL4	4635	myosin light chain 4	NP_002467.1	1	1	1	2	1.29	0.55					1	1	1176	4635	myosin, light polypeptide 4, alkali; atrial,embryonic	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
GTF2H1	2965	general transcription factor IIH subunit 1	NP_005307.1	1	2	2	4	1.28	1.67	19.7	26.18	36.9	68.3	2	2	1807	2965	general transcription factor IIH, polypeptide1, 62kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
YTHDC2	64848	probable ATP-dependent RNA helicase YTHDC2	NP_073739.3	1	2	2	4	1.28	1.55	11.42	41.28	21	112.5	2	2	11690	64848	YTH domain containing 2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	R3H;DEXDc;ANK;HELIC	No
RALY	22913	RNA-binding protein Raly isoform 2	NP_031393.2	2	16	16	47	1.28	1.53	3.55	3.62	23.5	28.8	26	26	11480	22913	RNA binding protein (autoantigenic,hnRNP-associated with lethal yellow)	RNA binding	Mitochondrion;Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
PRMT1	3276	protein arginine N-methyltransferase 1 isoform 1	NP_001527.3	5	18	18	70	1.28	1.41	4.22	5.93	35.7	57.5	41	41	4257	3276	HMT1 hnRNP methyltransferase-like 2 (S.cerevisiae)	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	Yes
C1QBP	708	complement component 1 Q subcomponent-binding protein, mitochondrial precursor	NP_001203.1	1	4	4	46	1.28	1.41	6.45	9.43	42	72.5	24	24	3168	708	complement component 1, q subcomponent bindingprotein	Complement receptor activity	Mitochondrion;Nucleus	Complement receptor	Immune response	SP	Yes
SEC24A	10802	protein transport protein Sec24A isoform 1	NP_068817.1	2	6	7	25	1.28	1.37	6.1	3.6	23.8	14.9	9	9	8456	10802	SEC24 related gene family, member A (S.cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	GEL	Yes
COX5B	1329	cytochrome c oxidase subunit 5B, mitochondrial precursor	NP_001853.2	1	1	1	1	1.28	1.31					1	1	467	1329	cytochrome c oxidase subunit Vb	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
Sep-08	23176	septin-8 isoform a	NP_001092281.1	7	7	9	56	1.28	1.29	1.74	7.99	6.3	29.7	8	8									
SETD7	80854	histone-lysine N-methyltransferase SETD7 isoform 1	NP_085151.1	2	3	3	5	1.28	1.23	6.84	17.31	15.2	38	3	3	16226	80854	None	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MORN;SET	Yes
WDR74	54663	WD repeat-containing protein 74 isoform 1	NP_060563.2	2	1	1	4	1.28	1.23	2.55	4.16	4.6	7.3	2	2	8548	54663	WD repeat domain 74	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	WD40	Yes
TPR	7175	nucleoprotein TPR	NP_003283.2	3	71	71	158	1.28	1.22	1.75	2.35	20.9	26.6	85	84	8927	7175	translocated promoter region (to activated METoncogene)	Molecular function unknown	Cytoplasm	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
PIK3C2A	5286	phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	NP_002636.2	1	5	5	11	1.28	1.2	9.87	2.87	28.9	7.7	5	5	4672	5286	phosphoinositide-3-kinase, class 2, alphapolypeptide	Lipid kinase activity	Cytosol	Lipid Kinase	Cell communication;Signal transduction	PI3KC2;PI3KA;PI3KC;PX;C2	Yes
SCRN1	9805	secernin-1 isoform b	NP_001138986.1	3	8	8	29	1.28	1.12	5.27	5.19	26.5	22.8	15	15	15304	9805	secernin 1	Peptidase activity	Cytoplasm	Protease	Immune response	-	Yes
PPP2R1B	5519	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform a	NP_002707.3	5	4	11	41	1.28	1.11	2.08	3.3	7.1	9.7	7	7	4384	5519	protein phosphatase 2 (formerly 2A),regulatory subunit A (PR 65), beta isoform	Protein serine/threonine phosphatase activity;Enzyme regulator activity	Cytoplasm	Regulatory/other subunit;Serine/threonine phosphatase	Cell communication;Signal transduction;Regulation of cell proliferation	HEAT	Yes
EIF2A	83939	eukaryotic translation initiation factor 2A	NP_114414.2	1	15	15	41	1.28	1.09	2.61	4.37	15.7	22.6	22	22	11739	83939	None	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC	Yes
NUDCD1	84955	nudC domain-containing protein 1 isoform 1	NP_116258.2	2	10	10	26	1.28	1.06	5.21	10.6	24.5	42.4	13	13	16200	84955	NudC domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
RPL13	6137	60S ribosomal protein L13 isoform 1	NP_000968.2	3	14	14	47	1.28	1.01	6.04	6.39	39.3	32.5	24	24	6428	6137	ribosomal protein L13	RNA binding	Ribosome	Ribonucleoprotein	Protein metabolism	-	Yes
TCEB3	6924	transcription elongation factor B polypeptide 3	NP_003189.2	1	3	3	5	1.28	0.95	1.99	6.7	3.6	9	2	2	2873	6924	transcription elongation factor B (SIII),polypeptide 3 (110kDa, elongin A)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TFS	Yes
HNRNPLL	92906	heterogeneous nuclear ribonucleoprotein L-like isoform 1	NP_612403.2	2	2	3	7	1.28	0.91					1	1									
COBLL1	22837	cordon-bleu protein-like 1 isoform 1	NP_001265387.1	4	2	2	2	1.28	0.88	6.77	38.95	12.3	51.2	2	2	10844	22837	COBL-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	WH2	Yes
SOX15	6665	protein SOX-15	NP_008873.1	1	2	2	3	1.28	0.72					1	1	3191	6665	SRY (sex determining region Y)-box 15	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG	Yes
MED24	9862	mediator of RNA polymerase II transcription subunit 24 isoform 1	NP_055630.2	2	1	1	2	1.28	0.7					1	1	6107	9862	thyroid hormone receptor associated protein 4	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SLC9A3R2	9351	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 isoform a	NP_001123484.1	2	1	1	4	1.27	1.61	2.63	2.31	4.7	5.3	2	2	5946	9351	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PDZ	Yes
CORO1B	57175	coronin-1B	NP_001018080.1	1	10	11	25	1.27	1.42	2.18	2.59	10.4	13.8	14	14	16743	57175	coronin, actin binding protein, 1B	Molecular function unknown	-	Unclassified	Cell motility	WD40	Yes
GYG1	2992	glycogenin-1 isoform 1	NP_004121.2	3	5	5	7	1.27	1.29	1.94	11.38	5.5	33.8	5	5	6805	2992	glycogenin	Molecular function unknown	-	Unclassified	Metabolism;Energy pathways	-	Yes
PLCG1	5335	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 isoform a	NP_002651.2	2	8	8	11	1.27	1.26	8.05	4.96	27.5	16.7	7	7	1398	5335	phospholipase C, gamma 1	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase	Metabolism	PH;SH2;SH3;C2;PLCXc;PLCYc	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
GPT2	84706	alanine aminotransferase 2 isoform 1	NP_597700.1	2	1	1	2	1.27	1.22					1	1	6307	84706	glutamic pyruvate transaminase (alanineaminotransferase) 2	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase	Metabolism;Energy pathways	-	No
MOCS3	27304	adenylyltransferase and sulfurtransferase MOCS3	NP_055299.1	1	5	5	13	1.27	1.2	8.31	6.36	28.6	20.4	7	7	10092	27304	molybdenum cofactor synthesis 3	Sulfotransferase activity	Cytoplasm	Enzyme: Sulphotransferase	Metabolism;Energy pathways	RHOD;CC	Yes
SRSF7	6432	serine/arginine-rich splicing factor 7 isoform 1	NP_001026854.1	2	8	9	29	1.27	1.19	8.05	12.91	41.2	65	15	15									
GNL3	26354	guanine nucleotide-binding protein-like 3 isoform 1	NP_055181.3	2	13	13	33	1.27	1.16	4.83	6.42	26.4	33.4	18	19	6419	26354	guanine nucleotide binding protein-like 3(nucleolar)	GTP binding	Nucleolus	Cell cycle control protein	Regulation of cell proliferation	CC;NLS	Yes
DNTTIP2	30836	deoxynucleotidyltransferase terminal-interacting protein 2	NP_055412.2	1	9	9	23	1.27	1.16	2.3	5.89	9.7	23	11	11	9994	30836	None	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	Yes
TP53RK	112858	TP53-regulating kinase	NP_291028.3	1	3	3	8	1.27	1.15	6.86	7.98	17.5	20.8	4	5	12276	112858	TP53 regulating kinase	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	KOW;NLS	Yes
BAG5	9529	BAG family molecular chaperone regulator 5 isoform a	NP_001015049.1	2	7	7	13	1.27	1.05	5.71	13.69	19.4	39.5	7	7	4862	9529	BCL2-associated athanogene 5	Molecular function unknown	-	Unclassified	Biological_process unknown	BAG;CC	Yes
ARHGEF35	445328	rho guanine nucleotide exchange factor 35	NP_001003702.2	1	1	2	3	1.27	1.04					1	1									
ANKLE2	23141	ankyrin repeat and LEM domain-containing protein 2	NP_055929.1	1	3	3	4	1.27	1.04	17.7	20.12	32.7	30.2	2	2	19309	23141	KIAA0692	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK;SP	No
CHMP2B	25978	charged multivesicular body protein 2b isoform 1	NP_054762.2	2	3	4	8	1.27	0.96	18.63	0.72	42.7	1.2	3	3	13174	25978	chromatin modifying protein 2B	Transporter activity	-	Transport/cargo protein	Transport	CC	No
GABPB1	2553	GA-binding protein subunit beta-1 isoform beta 1	NP_005245.2	4	1	1	1	1.27	0.95					1	1	15975	2553	GA binding protein transcription factor, betasubunit 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ANK;CC	Yes
PBRM1	55193	protein polybromo-1	NP_060783.3	1	3	3	5	1.27	0.95	0.39	22.69	0.9	38.7	3	3	7302	55193	None	Chromatin binding	Nucleus	Regulatory/other subunit	Regulation of development	BROMO;HMG;CC;BAH	Yes
UBA5	79876	ubiquitin-like modifier-activating enzyme 5 isoform 1	NP_079094.1	2	3	3	5	1.27	0.92	5.34	7.21	11.8	11.5	3	3	15598	79876	ubiquitin-activating enzyme E1-domaincontaining 1	Protein binding	Integral to membrane	Ubiquitin proteasome system protein	Protein metabolism	TM	No
TJAP1	93643	tight junction-associated protein 1 isoform a	NP_001139488.1	2	1	1	2	1.27	0.9					1	1	10269	93643	tight junction protein 4 (peripheral)	Cell adhesion molecule activity	Plasma membrane	Cell junction protein	Cell growth and/or maintenance	CC	No
RAB3A	5864	ras-related protein Rab-3A	NP_002857.1	12	2	6	54	1.27	0.8					1	1	1535	5864	RAB3A, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB	No
PSMG4	389362	proteasome assembly chaperone 4 isoform a	NP_001122064.1	3	1	1	2	1.27	0.79					1	1	19577	389362	proteasome (prosome, macropain) assembly chaperone 4	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
TRAF6	7189	TNF receptor-associated factor 6	NP_004611.1	1	1	1	2	1.27	0.71					1	1	3833	7189	TNF receptor-associated factor 6	Signal transducer activity	Cytoplasm	Adapter molecule	Signal transduction	RING;MATH;CC	Yes
B4GALT1	2683	beta-1,4-galactosyltransferase 1	NP_001488.2	2	5	5	15	1.26	1.73	3.4	5.82	9.6	22.8	5	5	659	2683	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase	Metabolism;Energy pathways	SP;TM	Yes
PPP1CA	5499	serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 3	NP_001008709.1	3	3	15	53	1.26	1.49	4.19	10.13	9.2	26.7	3	3	15942	5499	protein phosphatase 1, catalytic subunit,alpha isoform	Protein serine/threonine phosphatase activity	Cytoskeleton	Serine/threonine phosphatase	Cell proliferation	PP2A	Yes
NASP	4678	nuclear autoantigenic sperm protein isoform 2	NP_002473.2	3	29	29	89	1.26	1.34	3.95	4.43	32.8	39	41	40	4423	4678	nuclear autoantigenic sperm protein(histone-binding)	Histone binding	Nucleus;Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction;Regulation of cell cycle	TPR;CC	Yes
NMD3	51068	60S ribosomal export protein NMD3	NP_057022.2	1	5	5	8	1.26	1.29	4.55	10.18	12.9	30.1	5	5	13026	51068	NMD3 homolog (S. cerevisiae)	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
NUP50	10762	nuclear pore complex protein Nup50 isoform b	NP_009103.2	2	5	5	8	1.26	1.29	4	8.25	10.1	21.6	4	4	5226	10762	nucleoporin 50kDa	Transporter activity	Nucleoplasm	Transport/cargo protein	Transport	-	Yes
RPRD1B	58490	regulation of nuclear pre-mRNA domain-containing protein 1B	NP_067038.1	1	8	9	49	1.26	1.24	6.87	5.73	40.4	32.5	20	20	8513	58490	chromosome 20 open reading frame 77	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
OXCT1	5019	succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial precursor	NP_000427.1	2	9	9	27	1.26	1.21	3.21	7.58	15.2	35.4	14	14	2001	5019	3-oxoacid CoA transferase 1	CoA-transferase activity	Mitochondrion	Enzyme: CoA transferase	Metabolism;Energy pathways	SP	Yes
NSA2	10412	ribosome biogenesis protein NSA2 homolog isoform 1	NP_055701.1	2	5	5	16	1.26	1.17	8.09	4.97	29.3	16.5	8	8	18191	10412	None	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
WIBG	84305	partner of Y14 and mago isoform 1	NP_115721.1	2	8	8	19	1.26	1.15	6.63	5.73	26.9	21	10	10	17940	84305	within bgcn homolog (Drosophila)	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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IRF3	3661	interferon regulatory factor 3 isoform 1	NP_001562.1	6	6	6	18	1.26	1.12	8.3	9.8	35.8	35.7	11	10	4769	3661	interferon regulatory factor 3	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	IRF	Yes
CADM1	23705	cell adhesion molecule 1 isoform A precursor	NP_001287972.1	5	1	1	2	1.26	1.12					1	1	5746	23705	immunoglobulin superfamily, member 4	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;IG;Ig_LIKE;IGC2;Band 4.1	Yes
ARAP3	64411	arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3	NP_071926.4	1	4	4	6	1.26	1.1	22.03	10.23	60.1	22.7	4	4	9441	64411	centaurin, delta 3	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	-	No
SRPR	6734	signal recognition particle receptor subunit alpha isoform 1	NP_003130.2	2	16	16	46	1.26	1.09	3.56	6.7	22.7	37.7	25	25	1645	6734	signal recognition particle receptor (`dockingprotein`)	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Protein metabolism	AAA;SP	Yes
ZC3H4	23211	zinc finger CCCH domain-containing protein 4	NP_055983.1	1	8	9	25	1.26	1.05	3	3.73	12	12.4	10	10	19314	23211	chromosome 19 open reading frame 7	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;ZnF_C3H1	Yes
GTF2F1	2962	general transcription factor IIF subunit 1	NP_002087.2	1	14	14	22	1.26	1.03	2.61	11.42	11.9	44.2	13	13	1803	2962	general transcription factor IIF, polypeptide1, 74kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
HDHD3	81932	haloacid dehalogenase-like hydrolase domain-containing protein 3	NP_112496.1	1	1	1	3	1.26	1.03	6.92	2.92	12.4	4.2	2	2	13641	81932	haloacid dehalogenase-like hydrolase domaincontaining 3	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
ZCCHC8	55596	zinc finger CCHC domain-containing protein 8	NP_060082.2	1	10	10	21	1.26	0.99	6.66	6.97	28.3	23.1	11	11	11698	55596	zinc finger, CCHC domain containing 8	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;ZnF_C2HC	Yes
DCAF13	25879	DDB1- and CUL4-associated factor 13	NP_056235.4	1	5	5	10	1.26	0.96	12.71	3.91	37	8.4	5	5	8528	25879	WD repeats and SOF1 domain containing	Molecular function unknown	Nucleolus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	No
ESF1	51575	ESF1 homolog	NP_057733.2	1	4	4	8	1.26	0.95	2.59	4.26	6.5	8.1	4	4	10732	51575	chromosome 20 open reading frame 6	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	Yes
HEXIM1	10614	protein HEXIM1	NP_006451.1	3	8	8	26	1.26	0.94	4.69	9.97	20.6	33.3	12	12	9544	10614	None	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
HMGB2	3148	high mobility group protein B2	NP_001124160.1	1	3	4	18	1.26	0.9	4.31	9.86	12.2	20	5	5	1229	3148	high-mobility group box 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG	Yes
RBM26	64062	RNA-binding protein 26 isoform 2	NP_001273561.1	2	2	7	14	1.26	0.9	9.87	11.74	17.7	15	2	2	12611	64062	chromosome 13 open reading frame 10	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1;RRM;CC	Yes
DIDO1	11083	death-inducer obliterator 1 isoform c	NP_149072.2	3	8	8	20	1.26	0.89	2.22	8.75	8.9	25	10	10	10363	11083	death associated transcription factor 1	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Apoptosis	PHD;TFS2M	Yes
TRMT6	51605	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 isoform 1	NP_057023.2	2	3	3	6	1.26	0.86	6.15	19.28	13.5	29.4	3	3	13027	51605	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
ELOF1	84337	transcription elongation factor 1 homolog	NP_115753.1	1	1	1	2	1.26	0.85					1	1	14639	84337	elongation factor 1 homolog (ELF1, S.cerevisiae)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
BET1	10282	BET1 homolog	NP_005859.1	1	2	2	6	1.26	0.85	0.36	30.52	0.8	47	3	3	16107	10282	BET1 homolog (S. cerevisiae)	Protein binding	Golgi apparatus	Integral membrane protein	Transport	t_SNARE;TM	Yes
SLC2A14	144195	solute carrier family 2, facilitated glucose transporter member 14 isoform d	NP_001273166.1	5	3	3	5	1.26	0.84	18.29	19.4	41.5	28.8	3	3	11573	144195	solute carrier family 2 (facilitated glucosetransporter), member 14	Transporter activity	-	Transport/cargo protein	Transport	TM	No
CACNA1B	774	voltage-dependent N-type calcium channel subunit alpha-1B isoform 1	NP_000709.1	2	1	1	1	1.26	0.83					1	1	3005	774	calcium channel, voltage-dependent, L type,alpha 1B subunit	Voltage-gated ion channel activity	Plasma membrane	Voltage gated channel	Transport	TM;CC	Yes
SUMO1	7341	small ubiquitin-related modifier 1 isoform a precursor	NP_003343.1	2	3	3	4	1.26	0.8	2.56	2.45	5.6	3.4	3	3	3554	7341	SMT3 suppressor of mif two 3 homolog 1 (yeast)	Protein binding	Cytoplasm	Transcription regulatory protein	Regulation of cell cycle;Apoptosis;Protein modification	UBQ	Yes
EEF1D	1936	elongation factor 1-delta isoform 1	NP_115754.3	3	2	10	52	1.26	0.79	2.4	0.72	6.8	1.3	5	5	560	1936	eukaryotic translation elongation factor 1delta (guanine nucleotide exchange protein)	Guanyl-nucleotide exchange factor activity	Endoplasmic reticulum	Guanine nucleotide exchange factor	Cell communication;Signal transduction	CC	Yes
FXR2	9513	fragile X mental retardation syndrome-related protein 2	NP_004851.2	1	4	7	12	1.26	0.78	9.71	9.69	24.8	15.2	4	4	5629	9513	fragile X mental retardation, autosomal homolog2	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH;NES	Yes
MRPS21	54460	28S ribosomal protein S21, mitochondrial	NP_114107.1	1	2	2	4	1.26	0.55	7.42	35.48	13.2	28.3	2	2	14784	54460	mitochondrial ribosomal protein S21	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No

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ECE1	1889	endothelin-converting enzyme 1 isoform 1	NP_001388.1	4	5	5	15	1.25	1.74	7.94	7.8	24.6	34.1	6	6	2690	1889	endothelin converting enzyme 1	Metallopeptidase activity	Plasma membrane	Metallo protease	Protein metabolism	TM	Yes
LENG8	114823	leukocyte receptor cluster member 8	NP_443157.1	1	3	3	5	1.25	1.74					1	1	11226	114823	leukocyte receptor cluster (LRC) member 8	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NAP1L4	4676	nucleosome assembly protein 1-like 4	NP_005960.1	1	13	15	87	1.25	1.71	5.77	7.01	46.1	83.8	37	37	11873	4676	nucleosome assembly protein 1-like 4	Chaperone activity	Nucleus	Chaperone	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
GFPT1	2673	glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 isoform 1	NP_001231639.1	2	19	22	59	1.25	1.53	3.04	4.95	20.7	42.6	29	29	702	2673	glutamine-fructose-6-phosphate transaminase 1	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase	Metabolism;Energy pathways	SIS	Yes
PLA2G4A	5321	cytosolic phospholipase A2	NP_077734.1	1	2	2	5	1.25	1.45	2.8	5.37	6.1	13.6	3	3	8986	5321	phospholipase A2, group IVA (cytosolic,calcium-dependent)	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase	Metabolism;Energy pathways	C2	Yes
AGPAT1	10554	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	NP_116130.2	1	1	1	2	1.25	1.44					1	1	4372	10554	1-acylglycerol-3-phosphate O-acyltransferase 1(lysophosphatidic acid acyltransferase, alpha)	Acyltransferase activity	Endoplasmic reticulum membrane	Enzyme: Acyltransferase	Metabolism;Energy pathways	SP;TM	Yes
PMPCB	9512	mitochondrial-processing peptidase subunit beta precursor	NP_004270.2	1	10	10	21	1.25	1.36	3.71	2.27	16.1	10.7	12	12	7539	9512	peptidase (mitochondrial processing) beta	Peptidase activity	Mitochondrion	Protease	Protein metabolism	SP	Yes
PPP1R3D	5509	protein phosphatase 1 regulatory subunit 3D	NP_006233.1	1	1	1	2	1.25	1.36					1	1	4507	5509	protein phosphatase 1, regulatory subunit 3D	Molecular function unknown	Cytoplasm	Regulatory/other subunit	Metabolism;Energy pathways	-	Yes
DNAJC7	7266	dnaJ homolog subfamily C member 7 isoform 1	NP_003306.3	2	11	11	23	1.25	1.33	3.09	4.19	13.4	19.5	12	12	7046	7266	DnaJ (Hsp40) homolog, subfamily C, member 7	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism;Protein folding	TPR;DNAJ	No
C9orf64	84267	UPF0553 protein C9orf64	NP_115683.3	1	3	3	7	1.25	1.33	1.86	9.15	4	21.3	3	3	12969	84267	chromosome 9 open reading frame 64	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TLR2	7097	toll-like receptor 2 precursor	NP_003255.2	1	2	2	4	1.25	1.31	13.89	9.25	25	17.2	2	2	4323	7097	toll-like receptor 2	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;LRR;TIR	Yes
HSP90AB1	3326	heat shock protein HSP 90-beta isoform a	NP_001258898.1	3	32	54	631	1.25	1.25	2.23	3.36	34.3	53.5	143	142	6763	3326	heat shock 90kDa protein 1, beta	Chaperone activity	Cytoplasm	Chaperone	Cell communication;Signal transduction	CC	Yes
CEP350	9857	centrosome-associated protein 350	NP_055625.4	1	2	2	3	1.25	1.24	13.42	5.69	24	10	2	2	9870	9857	None	Molecular function unknown	Centrosome	Unclassified	Biological_process unknown	CC	Yes
OAT	4942	ornithine aminotransferase, mitochondrial isoform 1 precursor	NP_000265.1	3	18	19	71	1.25	1.24	3.26	3.78	23.7	28.2	33	35	2021	4942	ornithine aminotransferase (gyrate atrophy)	Transaminase activity	Mitochondrion	Enzyme: Aminotransferase	Metabolism;Energy pathways	SP	No
PDIA6	10130	protein disulfide-isomerase A6 isoform a	NP_001269633.1	5	18	18	117	1.25	1.23	2.76	2.66	28	26.4	63	63	7504	10130	protein disulfide isomerase-associated 6	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase	Protein metabolism	SP	Yes
SF3A3	10946	splicing factor 3A subunit 3	NP_006793.1	1	12	12	55	1.25	1.18	4.25	7.07	29.2	47.2	29	29	10411	10946	splicing factor 3a, subunit 3, 60kDa	RNA binding	Nucleus	RNA binding protein	Protein metabolism	ZnF_C2C2;CC	Yes
DDX5	1655	probable ATP-dependent RNA helicase DDX5	NP_004387.1	1	19	29	121	1.25	1.15	3.03	3.22	24.7	24.2	41	41	1615	1655	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
MAK16	84549	protein MAK16 homolog	NP_115898.2	1	2	2	3	1.25	1.15	4.15	2.89	7.4	4.7	2	2	15223	84549	RNA binding motif protein 13	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
FBXL18	80028	F-box/LRR-repeat protein 18	NP_079239.3	1	4	4	9	1.25	1.14	2.57	11.47	7.2	29.7	5	5	7753	80028	F-box and leucine-rich repeat protein 18	Molecular function unknown	-	Unclassified	Biological_process unknown	F_BOX;CC	No
SUPT6H	6830	transcription elongation factor SPT6	NP_003161.2	1	10	10	19	1.25	1.12	5.66	8.2	22.7	29.8	10	10	3211	6830	suppressor of Ty 6 homolog (S. cerevisiae)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S1;SH2	Yes
LOC101929876	101929876	40S ribosomal protein S26	XP_005276741.1	2	5	5	30	1.25	1.12	2.57	4.91	12.9	22.3	16	16									
ISYNA1	51477	inositol-3-phosphate synthase 1 isoform 1	NP_057452.1	3	8	8	15	1.25	1.1	3.4	4.7	13.5	16.5	10	10	17163	51477	None	Isomerase activity	-	Enzyme: Isomerase	Metabolism;Energy pathways	-	No
NANS	54187	sialic acid synthase	NP_061819.2	1	7	7	30	1.25	1.04	7.72	20.49	40.2	104	16	16	7285	54187	N-acetylneuraminic acid synthase (sialic acidsynthase)	Catalytic activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
MUC19	283463	mucin-19 precursor	NP_775871.2	1	2	2	2	1.25	1.03	14.3	38.6	25.6	60.7	2	2	11377	283463	mucin 19	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ADD3	120	gamma-adducin isoform a	NP_058432.1	2	2	2	7	1.25	0.99	6.08	20.46	15.3	42.1	4	4	3339	120	adducin 3 (gamma)	Cytoskeletal protein binding	Plasma membrane;Nucleus;Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
SLIRP	81892	SRA stem-loop-interacting RNA-binding protein, mitochondrial isoform 1 precursor	NP_112487.1	3	2	2	3	1.25	0.97	21.39	49.13	39.2	75.9	2	2									
FTSJ3	117246	pre-rRNA processing protein FTSJ3	NP_060117.3	1	12	12	32	1.25	0.96	4.76	7.87	23.4	30.9	15	16	17024	117246	FtsJ homolog 3 (E. coli)	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	Yes
CKM	1158	creatine kinase M-type	NP_001815.2	1	1	2	2	1.25	0.93					1	1	426	1158	creatine kinase, muscle	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes

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GTF2E1	2960	general transcription factor IIE subunit 1	NP_005504.2	1	3	3	8	1.25	0.92	11.26	16.15	28.8	30.3	4	4	1799	2960	general transcription factor IIE, polypeptide1, alpha 56kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
GMEB2	26205	glucocorticoid modulatory element-binding protein 2	NP_036516.1	1	1	1	2	1.25	0.91					1	1	16245	26205	glucocorticoid modulatory element bindingprotein 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAND;CC	Yes
RBM28	55131	RNA-binding protein 28 isoform 1	NP_060547.2	2	5	5	11	1.25	0.89	3.78	5.98	11.7	13.2	6	6	7668	55131	RNA binding motif protein 28	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
FUT5	2527	alpha-(1,3)-fucosyltransferase 5	NP_002025.2	3	1	1	1	1.25	0.82					1	1	650	2527	fucosyltransferase 5 (alpha (1,3)fucosyltransferase)	Fucosyltransferase activity	Plasma membrane	Enzyme: Fucosyltransferase	Metabolism;Energy pathways	TM;SP	Yes
PTPN9	5780	tyrosine-protein phosphatase non-receptor type 9	NP_002824.1	1	3	3	4	1.25	0.8	15.21	1.64	27.4	1.9	2	2	2864	5780	protein tyrosine phosphatase, non-receptor type9	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	SEC14;Tyr_Phos	Yes
EXT1	2131	exostosin-1	NP_000118.2	1	1	1	1	1.25	0.78					1	1	598	2131	exostoses (multiple) 1	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase	Metabolism;Energy pathways	SP	Yes
NUDCD3	23386	nudC domain-containing protein 3	NP_056147.2	1	7	7	17	1.25	0.72	8.18	16.2	31.4	35.9	9	9	13831	23386	NudC domain containing 3	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
GTPBP3	84705	tRNA modification GTPase GTPBP3, mitochondrial isoform IV	NP_598399.2	4	1	1	2	1.25	0.66					1	1	12255	84705	GTP binding protein 3 (mitochondrial)	GTPase activity	Mitochondrion	G protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RAS;SH3	No
XYLB	9942	xylulose kinase	NP_005099.2	1	1	1	1	1.25	0.6					1	1	6812	9942	xylulokinase homolog (H. influenzae)	Molecular function unknown	-	Unclassified	Metabolism;Energy pathways	-	No
PDIA3	2923	protein disulfide-isomerase A3 precursor	NP_005304.3	1	37	37	203	1.24	1.6	2.53	2.42	34.1	42.4	111	110	3625	2923	protein disulfide isomerase-associated 3	Isomerase activity	Endoplasmic reticulum	Enzyme: Isomerase	Protein metabolism	SP	Yes
LOXL2	4017	lysyl oxidase homolog 2 precursor	NP_002309.1	1	2	2	3	1.24	1.47	0.84	3.78	1.5	7.8	2	2	9446	4017	lysyl oxidase-like 2	Catalytic activity	Extracellular	Enzyme: Oxidase	Cell growth and/or maintenance	SP;SR	Yes
PAFAH1B3	5050	platelet-activating factor acetylhydrolase IB subunit gamma	NP_002564.1	1	4	4	13	1.24	1.4	2.79	3.72	9.2	13.8	7	7	4354	5050	platelet-activating factor acetylhydrolase,isoform Ib, gamma subunit 29kDa	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
PPIA	5478	peptidyl-prolyl cis-trans isomerase A isoform 1	NP_066953.1	9	11	12	129	1.24	1.38	2.98	4.7	21.9	39.1	34	34	457	5478	peptidylprolyl isomerase A (cyclophilin A)	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Protein folding;Peptide metabolism	-	Yes
C11orf54	28970	ester hydrolase C11orf54 isoform a	NP_001272996.1	4	1	1	4	1.24	1.36	14.09	28.58	25.1	59.2	2	2	17923	28970	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ALDH1B1	219	aldehyde dehydrogenase X, mitochondrial precursor	NP_000683.3	1	9	12	36	1.24	1.36	4.25	4.72	20.6	25.2	15	15	5	219	aldehyde dehydrogenase 1 family, member B1	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
EIF3I	8668	eukaryotic translation initiation factor 3 subunit I	NP_003748.1	1	6	7	12	1.24	1.35	4.16	6.06	12.7	20.3	6	6	4884	8668	eukaryotic translation initiation factor 3,subunit 2 beta, 36kDa	Translation regulator activity	Ribosome	Translation regulatory protein	Protein metabolism	WD40	Yes
CEP170	9859	centrosomal protein of 170 kDa isoform beta	NP_001035863.1	2	1	18	34	1.24	1.35					1	1	17172	9859	KIAA0470	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	FHA;CC	No
RPS12	6206	40S ribosomal protein S12	NP_001007.2	1	6	6	22	1.24	1.35	4.52	5.96	19.6	28.3	12	12	4714	6206	ribosomal protein S12	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PPP4R2	151987	serine/threonine-protein phosphatase 4 regulatory subunit 2	NP_777567.1	1	7	7	13	1.24	1.33	11.9	13.55	37.2	46.5	6	6	11453	151987	protein phosphatase 4, regulatory subunit 2	Protein serine/threonine phosphatase activity	Centrosome	Serine/threonine phosphatase	Cell communication;Signal transduction	CC	No
TM9SF4	9777	transmembrane 9 superfamily member 4 precursor	NP_055557.2	1	8	9	21	1.24	1.31	5	7.05	24.3	36.8	15	15	15514	9777	transmembrane 9 superfamily protein member 4	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
UBAP2	55833	ubiquitin-associated protein 2 isoform 1	NP_060919.3	3	8	8	23	1.24	1.26	2.48	4.24	10.2	17.9	11	11	6748	55833	ubiquitin associated protein 2	Molecular function unknown	-	Unclassified	Biological_process unknown	UBA	No
GATAD2A	54815	transcriptional repressor p66-alpha isoform 1	NP_001287875.1	2	4	5	10	1.24	1.26	3.79	2.14	6.6	3.8	2	2	11741	54815	GATA zinc finger domain containing 2A	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
TSEN34	79042	tRNA-splicing endonuclease subunit Sen34 isoform 2	NP_001269262.1	2	1	1	2	1.24	1.24					1	1	10038	79042	tRNA splicing endonuclease 34 homolog (SEN34,S. cerevisiae)	Endonuclease activity	-	RNA endonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PRKD2	25865	serine/threonine-protein kinase D2 isoform A	NP_057541.2	2	5	5	12	1.24	1.22	5.46	3.19	16.7	9.5	6	6	9523	25865	protein kinase D2	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	C1;PH;S_T_kinase	Yes
ASNS	440	asparagine synthetase [glutamine-hydrolyzing] isoform a	NP_001664.3	3	13	13	28	1.24	1.22	2.48	6.51	12.4	32.6	16	16	153	440	asparagine synthetase	Ligase activity	Cytoplasm	Enzyme: Synthase	Protein metabolism	-	Yes
HAUS5	23354	HAUS augmin-like complex subunit 5	NP_056117.1	1	3	3	5	1.24	1.2	4.02	11.5	8.7	24.3	3	3	19389	23354	KIAA0841	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
EIF3J	8669	eukaryotic translation initiation factor 3 subunit J isoform 1	NP_003749.2	3	9	9	23	1.24	1.18	4.25	2.62	18.3	10.8	12	12	4883	8669	eukaryotic translation initiation factor 3,subunit 1 alpha, 35kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC	Yes
ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 3	NP_001158287.1	5	29	29	63	1.24	1.13	3.46	3.45	25.8	23.3	35	35	5191	22985	apoptotic chromatin condensation inducer 1	DNA binding	Nucleus;Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;CC;RRM	Yes
GAPVD1	26130	GTPase-activating protein and VPS9 domain-containing protein 1 isoform 4	NP_056450.2	4	11	11	31	1.24	1.11	5.88	8.35	30.8	39.7	17	17	10886	26130	GTPase activating protein and VPS9 domains 1	Molecular function unknown	-	Unclassified	Biological_process unknown	RASGAP;VPS9	No
RNMTL1	55178	rRNA methyltransferase 3, mitochondrial	NP_060616.1	1	2	2	3	1.24	1.1	6.75	3.42	11.9	5.3	2	2	15266	55178	RNA methyltransferase like 1	RNA methyltransferase activity	-	RNA methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP	No
COX6C	1345	cytochrome c oxidase subunit 6C proprotein	NP_004365.1	1	1	1	4	1.24	1.09	0.14	5.33	0.2	8.2	2	2	494	1345	cytochrome c oxidase subunit VIc	Oxidoreductase activity	Mitochondrion	Regulatory/other subunit	Metabolism;Energy pathways	SP	Yes
TTPAL	79183	alpha-tocopherol transfer protein-like isoform 1	NP_077307.2	2	2	2	4	1.24	1.08	8.12	34.09	14.3	55.8	2	2	9837	79183	chromosome 20 open reading frame 121	Molecular function unknown	-	Unclassified	Transport	SEC14	Yes
ANKHD1-EIF4EBP3	404734	ANKHD1-EIF4EBP3 protein	NP_065741.3	5	14	21	48	1.24	1.07	3.52	9.43	15.8	37.7	13	13	17468	404734	None	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK;CC;KH	No
HECTD1	25831	E3 ubiquitin-protein ligase HECTD1	NP_056197.3	1	8	8	16	1.24	1.07	5.84	6.36	19.3	18.2	7	7	17098	25831	HECT domain containing 1	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	ANK;F58C;HECT	Yes
PRPF3	9129	U4/U6 small nuclear ribonucleoprotein Prp3	NP_004689.1	1	10	10	21	1.24	1.07	8.75	6.42	37.1	23.1	11	11	7389	9129	PRP3 pre-mRNA processing factor 3 homolog(yeast)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PWI	Yes
MAP1S	55201	microtubule-associated protein 1S isoform 1	NP_060644.4	2	8	8	14	1.24	1.05	7.31	7.89	24.3	22.2	7	7	10461	55201	BPY2 interacting protein 1	Structural constituent of cytoskeleton	Microtubule	Cytoskeletal protein	Cell growth and/or maintenance	-	No
FAM46C	54855	protein FAM46C	NP_060179.2	1	1	1	1	1.24	1.04					1	1	13312	54855	family with sequence similarity 46, member C	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
BYSL	705	bystin	NP_004044.3	1	6	6	11	1.24	1.03	2.69	2.78	7.5	6.4	5	5	4848	705	bystin-like	Cell adhesion molecule activity	Cytoplasm	Adhesion molecule	Cell growth and/or maintenance	-	Yes
RPL27	6155	60S ribosomal protein L27	NP_000979.1	1	6	7	39	1.24	0.99	4.79	5.44	28.4	25.6	22	22	9602	6155	ribosomal protein L27	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	KOW	No
FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 1	NP_112179.2	3	6	6	17	1.24	0.96	4.27	9.09	15.1	25	8	8	9646	81608	FIP1 like 1 (S. cerevisiae)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
GCDH	2639	glutaryl-CoA dehydrogenase, mitochondrial isoform a precursor	NP_000150.1	2	7	7	21	1.24	0.95	4.5	8.22	17.8	25.1	10	10	1977	2639	glutaryl-Coenzyme A dehydrogenase	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
PPAT	5471	amidophosphoribosyltransferase proprotein	NP_002694.3	1	8	8	14	1.24	0.95	4.26	6.51	16	18.6	9	9	1402	5471	phosphoribosyl pyrophosphate amidotransferase	Catalytic activity	Nucleus	Enzyme: Ribosyltransferase	Metabolism;Energy pathways	-	Yes
WDR33	55339	pre-mRNA 3' end processing protein WDR33 isoform 1	NP_060853.3	1	2	2	4	1.24	0.91	5.95	31.77	10.5	42.8	2	2	11680	55339	WD repeat domain 33	Molecular function unknown	Nucleus	Unclassified	Cell growth and/or maintenance	CC;WD40;COLL;TM	Yes
RPL17-C18orf32	100526842	RPL17-C18orf32 protein isoform 1	NP_001186284.1	4	11	11	63	1.24	0.88	3.57	6.5	27.9	36.2	38	38									
DAPP1	27071	dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide isoform 1	NP_055210.2	2	3	3	5	1.24	0.88	4.34	7.59	7.6	9.5	2	2	5773	27071	dual adaptor of phosphotyrosine and3-phosphoinositides	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	SH2;PH	Yes
PEX3	8504	peroxisomal biogenesis factor 3	NP_003621.1	1	2	2	3	1.24	0.87	11.08	19.73	19.7	24.5	2	2	4407	8504	peroxisomal biogenesis factor 3	Protein binding	Peroxisome	Integral membrane protein	Cell communication;Signal transduction	-	Yes
SH3BP5L	80851	SH3 domain-binding protein 5-like	NP_085148.1	1	2	2	3	1.24	0.84	7.2	37.51	12.7	46.8	2	2	13887	80851	None	Protein binding	-	Unclassified	Cell communication;Cell-cell signaling	CC	No
IKBIP	121457	inhibitor of nuclear factor kappa-B kinase-interacting protein isoform 1	NP_710154.1	2	8	12	30	1.24	0.84	7.47	8.15	33	24	12	12	8092	121457	None	Molecular function unknown	Endoplasmic reticulum	Unclassified	Apoptosis	CC;LZ	No
LOC102724594	102724594	splicing factor U2AF 35 kDa subunit isoform X1	XP_006726862.1	5	5	5	20	1.24	0.83	9.87	10.5	42.3	29.5	11	11									
HAT1	8520	histone acetyltransferase type B catalytic subunit	NP_003633.1	1	5	5	7	1.24	0.76	0.61	14.99	1.1	16.2	2	2	4339	8520	histone acetyltransferase 1	Acyltransferase activity	Nucleus	Enzyme: Acyltransferase	Metabolism	CC;NLS	Yes
TCEAL5	340543	transcription elongation factor A protein-like 5	NP_001012997.1	3	2	2	3	1.24	0.7	12.21	37.16	21.7	37.9	2	2	18502	340543	transcription elongation factor A (SII)-like 5	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
YIPF3	25844	protein YIPF3	NP_056203.2	1	2	2	4	1.24	0.69	20.89	17.48	37.8	17.2	2	2	9852	25844	chromosome 6 open reading frame 109	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
FMOD	2331	fibromodulin precursor	NP_002014.2	1	1	1	12	1.24	0.64	4.44	10.08	13.5	15.8	6	6	2591	2331	fibromodulin	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	LRR;SP	Yes
HRNR	388697	hornerin	NP_001009931.1	1	3	3	6	1.23	1.82	17.91	12.22	39.6	40	3	3	17114	388697	hornerin	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	S_100;SIS	Yes
HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 1	NP_001017963.2	2	32	53	627	1.23	1.41	2.33	3.32	36.3	62.6	152	151	777	3320	heat shock 90kDa protein 1, alpha	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CC	Yes

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Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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SIRT2	22933	NAD-dependent protein deacetylase sirtuin-2 isoform 1	NP_036369.2	3	1	1	1	1.23	1.4					1	1	10377	22933	sirtuin (silent mating type informationregulation 2 homolog) 2 (S. cerevisiae)	Deacetylase activity	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
SERPINB9	5272	serpin B9	NP_004146.1	4	4	6	10	1.23	1.39	14.43	5.49	31.4	13.3	3	3	3480	5272	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 9	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism	SERPIN	Yes
DMAP1	55929	DNA methyltransferase 1-associated protein 1	NP_061973.1	1	2	2	4	1.23	1.37	1.86	25.17	3.2	51.6	2	2	5465	55929	DNA methyltransferase 1 associated protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT;CC	Yes
SSRP1	6749	FACT complex subunit SSRP1	NP_003137.1	1	18	18	58	1.23	1.34	3.46	2.56	22.4	17.9	27	27	5061	6749	structure specific recognition protein 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	Yes
CBL	867	E3 ubiquitin-protein ligase CBL	NP_005179.2	1	5	5	9	1.23	1.31	4.81	1.2	13.2	3.5	5	5	1320	867	Cas-Br-M (murine) ecotropic retroviraltransforming sequence	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Cell communication;Signal transduction;Protein metabolism	RING;UBA	Yes
PRAF2	11230	PRA1 family protein 2	NP_009144.1	1	2	2	3	1.23	1.28					1	1	6596	11230	PRA1 domain family, member 2	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	Yes
ALDOC	230	fructose-bisphosphate aldolase C	NP_005156.1	1	12	17	135	1.23	1.26	1.18	6.44	5.8	33.3	16	16	2386	230	aldolase C, fructose-bisphosphate	Lyase activity	Mitochondrion	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
SARS	6301	serine--tRNA ligase, cytoplasmic	NP_006504.2	1	18	18	58	1.23	1.25	3.88	5.9	24.2	38.3	25	25	9605	6301	seryl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
NCBP2	22916	nuclear cap-binding protein subunit 2 isoform 1	NP_031388.2	2	1	1	1	1.23	1.24					1	1	5503	22916	nuclear cap binding protein subunit 2, 20kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
UEVLD	55293	ubiquitin-conjugating enzyme E2 variant 3 isoform a	NP_001035787.1	8	4	4	6	1.23	1.22	7.18	5.73	17.8	14	4	4	15608	55293	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBC	No
LYAR	55646	cell growth-regulating nucleolar protein	NP_060286.1	1	15	15	28	1.23	1.22	1.75	5.29	8.7	26.4	16	16	10064	55646	None	Transcription regulator activity	Nucleolus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
RMDN3	55177	regulator of microtubule dynamics protein 3	NP_060615.1	1	7	7	19	1.23	1.17	8.45	3.69	35.5	14.4	11	11									
UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 1	NP_006640.2	3	14	14	27	1.23	1.17	6.03	7.64	28.4	34.3	14	14	6712	10813	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	Molecular function unknown	Ribosome	Unclassified	Biological_process unknown	CC	Yes
AURKAIP1	54998	aurora kinase A-interacting protein	NP_060370.1	1	1	1	2	1.23	1.17					1	1	16457	54998	None	Enzyme regulator activity	Nucleus	Enzyme regulator;Cell cycle control protein	Regulation of enzyme activity;Cell communication;Signal transduction	NLS	No
DDOST	1650	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	NP_005207.2	1	10	10	43	1.23	1.17	1.21	1.98	6.8	10.6	21	21	3728	1650	dolichyl-diphosphooligosaccharide-proteinglycosyltransferase	Galactosyltransferase activity	Endoplasmic reticulum	Enzyme: Galactosyltransferase	Metabolism;Energy pathways	SP;TM	Yes
CD47	961	leukocyte surface antigen CD47 isoform 1 precursor	NP_001768.1	2	4	4	10	1.23	1.15	10.41	14.33	34.9	45.8	7	7	3017	961	CD47 antigen (Rh-related antigen,integrin-associated signal transducer)	Molecular function unknown	Plasma membrane;Cell surface	Unclassified	Immune response	TM;SP;Ig_LIKE	Yes
PRRC1	133619	protein PRRC1 isoform 1	NP_001273737.1	2	5	5	28	1.23	1.13	3.36	2.8	13.7	10.5	11	11	14052	133619	None	Molecular function unknown	Golgi apparatus	Unclassified	Biological_process unknown	-	No
NCOA5	57727	nuclear receptor coactivator 5	NP_066018.1	1	7	7	16	1.23	1.12	5.83	11.51	16.1	29.4	5	5	14813	57727	nuclear receptor coactivator 5	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
GIGYF2	26058	PERQ amino acid-rich with GYF domain-containing protein 2 isoform b	NP_056390.2	3	15	15	36	1.23	1.12	1.93	4.63	10.7	23.5	20	20	11639	26058	trinucleotide repeat containing 15	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	CC	No
ATXN3	4287	ataxin-3 reference isoform	NP_004984.2	10	4	4	6	1.23	1.1	13.46	6.33	23.7	9.9	2	2	6131	4287	ataxin 3	Ubiquitin-specific protease activity	Nucleus	Protease	Protein metabolism	UIM;CC	Yes
GNE	10020	bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase isoform 1	NP_001121699.1	5	3	3	10	1.23	1.08	8.14	8.38	22.7	20.5	5	5	4825	10020	glucosamine(UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	Racemase and epimerase activity	Cytoplasm	Enzyme: Epimerase	Metabolism;Energy pathways	-	Yes
ACBD6	84320	acyl-CoA-binding domain-containing protein 6	NP_115736.1	1	2	2	3	1.23	1.07	11	4.83	19.3	7.3	2	2	12416	84320	acyl-Coenzyme A binding domain containing 6	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK	No
STRAP	11171	serine-threonine kinase receptor-associated protein	NP_009109.3	1	13	13	34	1.23	1.06	5.85	8.3	31.3	38.6	18	18	5816	11171	serine/threonine kinase receptor associatedprotein	Receptor binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	WD40	Yes
COPZ1	22818	coatomer subunit zeta-1 isoform 4	NP_001258665.1	4	5	5	26	1.23	1.05	2.18	9.36	9.7	36.6	13	13	16738	22818	coatomer protein complex, subunit zeta 1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	No

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HSPA14	51182	heat shock 70 kDa protein 14 isoform 1	NP_057383.2	2	7	7	13	1.23	1.04	5.43	11.49	17.8	32.3	7	7	7021	51182	heat shock 70kDa protein 14	Chaperone activity	-	Chaperone	Biological_process unknown	-	No
EHMT2	10919	histone-lysine N-methyltransferase EHMT2 isoform c	NP_001276342.1	3	1	1	2	1.23	1.01					1	1	6854	10919	euchromatic histone-lysine N-methyltransferase2	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Protein modification	CC;ANK;SET;PSET;NLS;PreSET;ZFC3	Yes
TAB1	10454	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 isoform alpha	NP_006107.1	2	4	4	9	1.23	0.93	4.65	4.88	12.8	10.2	5	5									
CDC73	79577	parafibromin	NP_078805.3	1	8	8	17	1.23	0.93	4.02	17.34	13.2	44.5	7	7	9581	79577	hyperparathyroidism 2 (with jaw tumor)	Molecular function unknown	Nucleolus;Nucleus	Unclassified	Biological_process unknown	-	No
HCLS1	3059	hematopoietic lineage cell-specific protein isoform 1	NP_005326.2	2	11	11	37	1.23	0.91	5.17	7.27	29.8	31.2	21	21	3199	3059	hematopoietic cell-specific Lyn substrate 1	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	HS1_rep;CC;SH3	Yes
DDR1	780	epithelial discoidin domain-containing receptor 1 isoform 3 precursor	NP_054700.2	6	4	4	6	1.23	0.9	2.65	5	5.6	7.8	3	3	2678	780	discoidin domain receptor family, member 1	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	F58C;Tyr_Kinase;TM;NPXY;SP	Yes
CTBP2	1488	C-terminal-binding protein 2 isoform 2	NP_073713.2	2	2	5	8	1.23	0.89	1.95	7.95	3.4	10.1	2	2	4016	1488	C-terminal binding protein 2	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule;Transcription regulatory protein	Cell communication;Signal transduction	2HD	Yes
CUL1	8454	cullin-1	NP_003583.2	1	9	9	18	1.23	0.88	5.68	6.02	22.5	16.8	10	10	4389	8454	cullin 1	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CULL	Yes
TUBA1A	7846	tubulin alpha-1A chain isoform 1	NP_006000.2	4	2	31	558	1.23	0.84	1.46	12.11	5.4	32.9	9	10	3959	7846	None	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	TUBULIN	Yes
RIOK1	83732	serine/threonine-protein kinase RIO1 isoform 1	NP_113668.2	2	1	1	1	1.23	0.83					1	1	17978	83732	RIO kinase 1 (yeast)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
MECR	51102	trans-2-enoyl-CoA reductase, mitochondrial isoform a	NP_057095.3	2	1	1	1	1.23	0.83					1	1	12192	51102	mitochondrial trans-2-enoyl-CoA reductase	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	SP	Yes
ABR	29	active breakpoint cluster region-related protein isoform a	NP_068781.2	4	1	2	4	1.23	0.75	6.6	28.92	11.5	31.3	2	2	2649	29	active BCR-related gene	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	RHOGEF;PH;C2;RHOGAP;CC	Yes
PARK2	5071	E3 ubiquitin-protein ligase parkin isoform 1	NP_004553.2	3	1	1	1	1.23	0.72					1	1	3967	5071	Parkinson disease (autosomal recessive,juvenile) 2, parkin	Ubiquitin-specific protease activity	Endoplasmic reticulum	Ubiquitin proteasome system protein	Protein metabolism	UBQ;IBR	Yes
RFC1	5981	replication factor C subunit 1 isoform 2	NP_001191676.1	2	2	2	2	1.23	0.59					1	1	24	5981	replication factor C (activator 1) 1, 145kDa	DNA binding	Nucleus;Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRCT;AAA	Yes
RPLP1	6176	60S acidic ribosomal protein P1 isoform 1	NP_000994.1	2	2	3	29	1.23	0.58	4.59	10.15	19.7	20.7	12	12	1611	6176	ribosomal protein, large, P1	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
GRWD1	83743	glutamate-rich WD repeat-containing protein 1	NP_113673.3	1	6	6	10	1.22	1.43	7.4	8.9	22.4	31.9	6	6	11013	83743	glutamate-rich WD repeat containing 1	Molecular function unknown	Nucleus	Unclassified	Cell growth and/or maintenance	WD40	Yes
LAMC2	3918	laminin subunit gamma-2 isoform a precursor	NP_005553.2	2	56	56	281	1.22	1.43	2.29	3.64	33.4	66.2	136	134	1031	3918	laminin, gamma 2	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	EGFLAM;LAMB;SP;CC;EGF	Yes
BCL9L	283149	B-cell CLL/lymphoma 9-like protein	NP_872363.1	1	3	3	4	1.22	1.41	13.12	3.29	28.2	8.1	3	3	10612	283149	B-cell CLL/lymphoma 9-like	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	NLS	Yes
GALK1	2584	galactokinase	NP_000145.1	1	2	2	3	1.22	1.39	2.08	2.31	3.6	4.5	2	2	5057	2584	galactokinase 1	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
DNAJC2	27000	dnaJ homolog subfamily C member 2 isoform 1	NP_055192.1	2	6	6	8	1.22	1.36	12.03	15.72	33.8	50.6	5	5	19072	27000	zuotin related factor 1	Chaperone activity	Nucleus	Chaperone	Regulation of cell cycle	CC;DNAJ;SANT	Yes
RBM12	10137	RNA-binding protein 12	NP_690051.1	1	11	11	16	1.22	1.36	1.45	4.62	5.8	21	11	11	6212	10137	RNA binding motif protein 12	RNA binding	Mitochondrion	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;NLS;TM	Yes
TMF1	7110	TATA element modulatory factor	NP_009045.2	1	2	2	4	1.22	1.34	11.13		19.3		2	1	3081	7110	TATA element modulatory factor 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform a	NP_997636.1	3	11	11	21	1.22	1.33	2.27	4.99	9.6	23.3	12	12	1786	5573	protein kinase, cAMP-dependent, regulatory,type I, alpha (tissue specific extinguisher 1)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	CNMP	Yes
AVEN	57099	cell death regulator Aven	NP_065104.1	1	4	4	11	1.22	1.29	8.15	3.64	24.7	11.5	6	6	5588	57099	apoptosis, caspase activation inhibitor	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Apoptosis	-	Yes
AAMP	14	angio-associated migratory cell protein isoform 1	NP_001289474.1	2	8	8	16	1.22	1.26	3.93	6.26	14.5	24	9	9	4600	14	angio-associated, migratory cell protein	Cell adhesion molecule activity	Extracellular	Adhesion molecule	Cell growth and/or maintenance	WD40	Yes
NVL	4931	nuclear valosin-containing protein-like isoform 1	NP_002524.2	4	3	3	3	1.22	1.21					1	1	3887	4931	nuclear VCP-like	ATPase activity	Nucleoplasm	ATPase	Metabolism;Energy pathways	AAA	Yes
PPWD1	23398	peptidylprolyl isomerase domain and WD repeat-containing protein 1 isoform 1	NP_056157.1	4	6	6	19	1.22	1.19	4.29	4	15.7	14.3	9	9	11063	23398	peptidylprolyl isomerase domain and WD repeatcontaining 1	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 2	NP_473357.1	9	4	4	7	1.22	1.19	8.91	4.46	22	10.6	4	4									

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
EIF6	3692	eukaryotic translation initiation factor 6 isoform a	NP_002203.1	2	7	7	44	1.22	1.16	2.92	8.31	15.6	43.8	19	19	4221	3692	integrin beta 4 binding protein	Translation regulator activity	Cytoplasm	Translation regulatory protein	Regulation of translation	-	Yes
QKI	9444	protein quaking isoform 1	NP_006766.1	5	2	2	5	1.22	1.15	7.91	5.49	16.8	11	3	3	6691	9444	quaking homolog, KH domain RNA binding (mouse)	RNA binding	Cytoplasm	RNA binding protein	RNA metabolism	KH	Yes
SAFB	6294	scaffold attachment factor B1 isoform 1	NP_001188267.1	4	10	18	41	1.22	1.13	3.07	3.9	13	15.4	12	12	4205	6294	scaffold attachment factor B	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;SAP;CC	Yes
EEF1G	1937	elongation factor 1-gamma	NP_001395.1	1	13	13	88	1.22	1.12	2.33	4.23	20.7	35.2	52	52	11745	1937	eukaryotic translation elongation factor 1gamma	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
RPRD1A	55197	regulation of nuclear pre-mRNA domain-containing protein 1A isoform 1	NP_060640.2	3	3	4	11	1.22	1.12	6.56	6.87	13.9	13.4	3	3	10134	55197	None	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of cell cycle	CC	No
ZNF428	126299	zinc finger protein 428	NP_872304.2	1	2	2	3	1.22	1.12	13.67	10.7	23.8	17.1	2	2	14671	126299	None	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	No
CHORDC1	26973	cysteine and histidine-rich domain-containing protein 1 isoform a	NP_036256.2	2	6	6	14	1.22	1.11	1.63	11.75	5.3	35.6	7	7	5072	26973	cysteine and histidine-rich domain(CHORD)-containing, zinc binding protein 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
ATP2B1	490	plasma membrane calcium-transporting ATPase 1 isoform 1b	NP_001673.2	6	8	14	37	1.22	1.06	2.11	10.16	7.3	31.3	8	8	158	490	ATPase, Ca++ transporting, plasma membrane 1	ATPase activity	Plasma membrane	ATPase	Transport	TM;CC	Yes
PIGT	51604	GPI transamidase component PIG-T isoform 1 precursor	NP_057021.2	4	5	5	8	1.22	1.03	16.65	6.32	42.2	13	4	4	15136	51604	phosphatidylinositol glycan, class T	Transaminase activity	Endoplasmic reticulum	Enzyme: Aminotransferase	Protein metabolism	SP;TM	Yes
TBL3	10607	transducin beta-like protein 3	NP_006444.2	1	11	11	41	1.22	1.01	4.56	6.63	24.6	29.9	19	19	9327	10607	transducin (beta)-like 3	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	WD40	Yes
BCAT2	587	branched-chain-amino-acid aminotransferase, mitochondrial isoform a precursor	NP_001181.2	3	6	6	30	1.22	0.99	4.43	15.37	22.6	69.1	17	17	217	587	branched chain aminotransferase 2,mitochondrial	Transaminase activity	Mitochondrion	Enzyme: Aminotransferase	Metabolism;Energy pathways	SP;CXXC	Yes
PGM3	5238	phosphoacetylglucosamine mutase isoform 1	NP_001186846.1	4	15	15	33	1.22	0.99	6.85	8.28	34.5	33.8	16	16	1390	5238	phosphoglucomutase 3	Catalytic activity	Cytoplasm	Enzyme: Mutase	Metabolism;Energy pathways	CC	Yes
COG5	10466	conserved oligomeric Golgi complex subunit 5 isoform 1	NP_006339.3	3	7	7	14	1.22	0.91	8.63	15.15	28.4	37.9	7	7	8436	10466	component of oligomeric golgi complex 5	Transporter activity;Structural molecule activity	Golgi apparatus	Structural protein;Transport/cargo protein	Transport;Golgi organization and biogenesis	-	Yes
RNF31	55072	E3 ubiquitin-protein ligase RNF31	NP_060469.4	1	2	2	2	1.22	0.88	9.3	35.64	16.2	46.5	2	2	11516	55072	ring finger protein 31	Molecular function unknown	-	Unclassified	Biological_process unknown	ZnF_RBZ;UBA;IBR	Yes
POLR2F	5435	DNA-directed RNA polymerases I, II, and III subunit RPABC2 isoform 1	NP_068809.1	2	1	1	1	1.22	0.85					1	1	5105	5435	polymerase (RNA) II (DNA directed) polypeptideF	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
ZNF281	23528	zinc finger protein 281 isoform 1	NP_036614.1	2	5	5	9	1.22	0.85	8.23	13.08	22.8	25.3	5	5	11702	23528	zinc finger protein 281	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
LARP4	113251	la-related protein 4 isoform a	NP_443111.4	6	5	5	13	1.22	0.81	6.38	10.69	22.2	24.9	8	8	17289	113251	None	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LA;RRM	No
PIP4K2B	8396	phosphatidylinositol 5-phosphate 4-kinase type-2 beta	NP_003550.1	2	6	6	10	1.22	0.8	2.41	12.15	7.2	24	6	6	4463	8396	phosphatidylinositol-4-phosphate 5-kinase,type II, beta	Lipid kinase activity	Plasma membrane	Lipid Kinase	Cell communication;Signal transduction	PIPKc;CC	Yes
TRIP12	9320	E3 ubiquitin-protein ligase TRIP12 isoform a	NP_001271143.1	5	8	9	22	1.22	0.8	4.9	13.38	17	31.1	8	8	5144	9320	thyroid hormone receptor interactor 12	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HECT;CC	Yes
COL6A3	1293	collagen alpha-3(VI) chain isoform 1 precursor	NP_004360.2	5	3	3	5	1.22	0.78	25.89	9.38	59	12.7	3	3	371	1293	collagen, type VI, alpha 3	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	KUNITZ;SP;VWA;COLL	Yes
GNG5	2787	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 precursor	NP_005265.1	1	4	4	7	1.22	0.7	5.52	6.33	13.5	8.9	4	4	11865	2787	guanine nucleotide binding protein (G protein),gamma 5	GTPase activity	Integral to membrane	G protein	Cell communication;Signal transduction	-	No
PEA15	8682	astrocytic phosphoprotein PEA-15 isoform a	NP_001284505.1	3	4	4	6	1.22	0.63	1.61	10.28	3.4	11.2	3	3	4579	8682	phosphoprotein enriched in astrocytes 15	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	DED;NES	Yes
SMAD3	4088	mothers against decapentaplegic homolog 3 isoform 1	NP_005893.1	4	1	3	11	1.22	0.57	3.37	12.47	5.8	10.2	2	2	4380	4088	SMAD, mothers against DPP homolog 3(Drosophila)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MH1;MH2	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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PIK3C3	5289	phosphatidylinositol 3-kinase catalytic subunit type 3 isoform 1	NP_002638.2	2	3	3	5	1.22	0.53	1.35	26.98	2.9	25.3	3	3	4009	5289	phosphoinositide-3-kinase, class 3	Lipid kinase activity	-	Lipid Kinase	Cell communication;Signal transduction	PI3KA;PI3KC2;PI3KC	Yes
CEBPD	1052	CCAAT/enhancer-binding protein delta	NP_005186.2	1	1	1	1	1.21	1.68					1	1	297	1052	CCAAT/enhancer binding protein (C/EBP), delta	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
TST	7263	thiosulfate sulfurtransferase	NP_003303.2	1	4	4	8	1.21	1.55	15.35	5.79	43.4	20.2	5	5	1583	7263	thiosulfate sulfurtransferase (rhodanese)	Sulfotransferase activity	Mitochondrion	Enzyme: Sulphotransferase	Metabolism;Energy pathways	RHOD	No
TOR1B	27348	torsin-1B precursor	NP_055321.1	1	2	2	6	1.21	1.44	5.03	8.25	10.6	20.9	3	3	16270	27348	torsin family 1, member B (torsin B)	Chaperone activity	Perinuclear region	Chaperone	Protein metabolism	SP;AAA	Yes
UQCRH	7388	cytochrome b-c1 complex subunit 6, mitochondrial isoform 1 precursor	NP_005995.2	4	3	3	9	1.21	1.44	2.69	7.87	7.3	25.8	5	5	15629	7388	ubiquinol-cytochrome c reductase hinge protein	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	SP	Yes
CLPTM1	1209	cleft lip and palate transmembrane protein 1 isoform 2	NP_001285.1	3	8	8	18	1.21	1.4	1.75	3.33	6.7	14.9	10	10	7544	1209	cleft lip and palate associated transmembraneprotein 1	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
ME1	4199	NADP-dependent malic enzyme	NP_002386.1	1	14	14	48	1.21	1.4	6.03	6.99	37.8	52.2	25	25	1102	4199	malic enzyme 1, NADP(+)-dependent, cytosolic	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase	Metabolism;Energy pathways	CC	Yes
UXT	8409	protein UXT isoform 1	NP_705582.1	2	1	1	2	1.21	1.35					1	1	2209	8409	ubiquitously-expressed transcript	Transcription regulator activity	Nucleus	Transcription regulatory protein	Transcription;Apoptosis;Cell differentiation	-	Yes
CAPRIN1	4076	caprin-1 isoform 1	NP_005889.3	2	10	10	49	1.21	1.32	7.81	9.57	45.5	62.8	21	21	3108	4076	membrane component, chromosome 11, surfacemarker 1	Molecular function unknown	Plasma membrane	Integral membrane protein	Transport	CC	No
PABPC4	8761	polyadenylate-binding protein 4 isoform 1	NP_001129125.1	4	17	27	85	1.21	1.3	2.64	2.68	14	15.3	19	19	4557	8761	poly(A) binding protein, cytoplasmic 4(inducible form)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
NLN	57486	neurolysin, mitochondrial	NP_065777.1	1	12	12	32	1.21	1.26	7.18	12.08	34.5	64.2	15	15	7495	57486	neurolysin (metallopeptidase M3 family)	Metallopeptidase activity	Cytoplasm	Metallo protease	Protein metabolism	SP	Yes
CHML	1122	rab proteins geranylgeranyltransferase component A 2	NP_001812.2	1	1	1	2	1.21	1.25					1	1	341	1122	choroideremia-like (Rab escort protein 2)	Protein binding	Cytoplasm	Enzyme: Prenyltransferase	Metabolism;Energy pathways	-	Yes
SNAP23	8773	synaptosomal-associated protein 23 isoform SNAP23A	NP_003816.2	2	5	5	9	1.21	1.24	5.98	21.05	16.2	63.8	5	5	3962	8773	synaptosomal-associated protein, 23kDa	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	CC;t_SNARE	Yes
CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	NP_115812.1	1	6	6	8	1.21	1.24	1.99	7.05	5.4	19.8	5	5									
GBP4	115361	guanylate-binding protein 4	NP_443173.2	1	1	1	1	1.21	1.23					1	1	13570	115361	guanylate binding protein 4	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	CC	Yes
RABEP1	9135	rab GTPase-binding effector protein 1 isoform 1	NP_004694.2	4	5	5	7	1.21	1.22	7.29	14.97	19.9	42.7	5	5	4684	9135	rabaptin, RAB GTPase binding effector protein1	GTPase activator activity	Cytoplasm;Nucleus	GTPase activating protein	Cell communication;Signal transduction	CC	Yes
MANF	7873	mesencephalic astrocyte-derived neurotrophic factor precursor	NP_006001.4	1	6	6	13	1.21	1.22	3.75	3.13	13.7	11.5	9	9	3558	7873	arginine-rich, mutated in early stage tumors	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	SP;SAP	Yes
ZC3H15	55854	zinc finger CCCH domain-containing protein 15	NP_060941.2	1	9	9	24	1.21	1.19	2.49	5.44	11.3	24.6	14	14	13988	55854	None	DNA binding	Nucleus;Cytoplasm	DNA binding protein	Biological_process unknown	ZnF_C3H1;CC	No
NDUFAF7	55471	NADH dehydrogenase [ubiquinone] complex I, assembly factor 7 isoform 1	NP_653337.1	1	1	1	3	1.21	1.17	9.64	5.44	16.6	9	2	2									
HSD17B2	3294	estradiol 17-beta-dehydrogenase 2	NP_002144.1	1	2	2	8	1.21	1.15	5.62	7.47	13.6	17.3	4	4	186	3294	hydroxysteroid (17-beta) dehydrogenase 2	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM;SP	Yes
FRG1	2483	protein FRG1	NP_004468.1	4	3	3	9	1.21	1.13	3.05	6.69	7.4	15.2	4	4	3176	2483	FSHD region gene 1	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
DHX57	90957	putative ATP-dependent RNA helicase DHX57	NP_945314.1	1	1	3	6	1.21	1.13					1	1	9919	90957	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1;DEXDc;HELIC;UBA	Yes
PABPN1	8106	polyadenylate-binding protein 2	NP_004634.1	4	10	10	17	1.21	1.12	8.4	16.3	33	62.9	10	10	3787	8106	poly(A) binding protein, nuclear 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
RPL22	6146	60S ribosomal protein L22 proprotein	NP_000974.1	1	6	6	33	1.21	1.1	4.17	7.25	22.2	35.8	19	19	1602	6146	ribosomal protein L22	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
HMGB3	3149	high mobility group protein B3 isoform b	NP_001288160.1	2	5	5	12	1.21	1.09	3.07	9.97	9.8	29.3	7	7	2181	3149	high-mobility group box 3	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	Yes
LRRC47	57470	leucine-rich repeat-containing protein 47	NP_065761.1	1	14	14	60	1.21	1.07	2.99	3.13	19	17.1	27	26	13837	57470	leucine rich repeat containing 47	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	LRR;CC	Yes
ARFIP2	23647	arfaptin-2 isoform 1	NP_001229783.1	4	4	5	17	1.21	1.06	5.69	18.79	17	51.9	6	6	7209	23647	ADP-ribosylation factor interacting protein 2(arfaptin 2)	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	-	Yes
DGCR14	8220	protein DGCR14	NP_073210.1	1	1	1	2	1.21	1.03					1	1	3452	8220	DiGeorge syndrome critical region gene 14	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes

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Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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SIGMAR1	10280	sigma non-opioid intracellular receptor 1 isoform 1	NP_005857.1	6	2	2	4	1.21	1.03					1	1	3580	10280	opioid receptor, sigma 1	Transmembrane receptor activity	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	SP;TM	No
HIVEP2	3097	transcription factor HIVEP2	NP_006725.3	1	1	1	2	1.21	1					1	1	881	3097	human immunodeficiency virus type I enhancerbinding protein 2	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
GOLIM4	27333	Golgi integral membrane protein 4 isoform 1	NP_055313.1	2	5	5	6	1.21	1	8.24	16.11	22.7	37.2	5	5	8429	27333	golgi phosphoprotein 4	Molecular function unknown	Golgi apparatus	Integral membrane protein	Cell communication;Signal transduction	TM;CC	Yes
AKR1B10	57016	aldo-keto reductase family 1 member B10	NP_064695.3	1	3	3	5	1.21	0.98	11.02	29.46	23.4	53.3	3	3	5271	57016	aldo-keto reductase family 1, member B10(aldose reductase)	Catalytic activity	-	Enzyme: Reductase	Metabolism;Energy pathways	ALDKR	No
RAB2B	84932	ras-related protein Rab-2B isoform 1	NP_116235.2	2	1	8	32	1.21	0.97					1	1	6312	84932	RAB2B, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB	Yes
GTF2H3	2967	general transcription factor IIH subunit 3 isoform a	NP_001507.2	4	3	3	3	1.21	0.96	12.86	2.57	22.2	3.5	2	2	7531	2967	general transcription factor IIH, polypeptide3, 34kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
GTF2H4	2968	general transcription factor IIH subunit 4	NP_001508.1	1	2	2	4	1.21	0.95	5.44	19.82	9.4	27	2	2	3456	2968	general transcription factor IIH, polypeptide4, 52kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PTPRE	5791	receptor-type tyrosine-protein phosphatase epsilon isoform 1 precursor	NP_006495.1	2	3	3	5	1.21	0.93	7.92	20.59	16.8	34	3	3	2956	5791	protein tyrosine phosphatase, receptor type, E	Receptor signaling protein tyrosine phosphatase activity	Plasma membrane	Receptor tyrosine phosphatase	Cell communication;Signal transduction	TM;Tyr_Phos;SP	Yes
SURF1	6834	surfeit locus protein 1 isoform 1	NP_003163.1	1	1	1	2	1.21	0.89					1	1	1711	6834	surfeit 1	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	TM	No
RPRD2	23248	regulation of nuclear pre-mRNA domain-containing protein 2 isoform 1	NP_056018.2	3	6	6	9	1.21	0.88	6.19	7.19	18.6	15.6	6	6	11084	23248	KIAA0460	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
PINX1	54984	PIN2/TERF1-interacting telomerase inhibitor 1 isoform 1	NP_060354.4	1	2	2	3	1.21	0.86	4.97	6.76	8.6	8.2	2	2									
PPA1	5464	inorganic pyrophosphatase	NP_066952.1	1	9	10	32	1.21	0.84	8.49	8.91	39.9	28.7	14	14	1527	5464	pyrophosphatase (inorganic)	Catalytic activity	Cytoplasm	Enzyme: Phosphohydrolase	Metabolism;Energy pathways	-	Yes
TPM4	7171	tropomyosin alpha-4 chain isoform Tpm4.2cy	NP_003281.1	2	7	27	83	1.21	0.84	5.32	14.03	24.5	46.5	14	14	11734	7171	tropomyosin 4	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
VPS52	6293	vacuolar protein sorting-associated protein 52 homolog isoform 1	NP_072047.4	4	2	2	2	1.21	0.78	8.48	11.77	14.6	13	2	2	9142	6293	vacuolar protein sorting 52 (yeast)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	TM;CC	No
ARL6IP1	23204	ADP-ribosylation factor-like protein 6-interacting protein 1	NP_055976.1	1	2	2	3	1.21	0.7	42.46	38.69	83.4	40	2	2	9641	23204	ADP-ribosylation factor-like 6 interactingprotein	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
ECSIT	51295	evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial isoform 1 precursor	NP_057665.2	4	6	6	11	1.2	1.49	14.69	16.81	49.3	74.3	7	7	12225	51295	None	Receptor signaling complex scaffold activity	Cytoplasm;Mitochondrion	Adapter molecule	Cell communication;Signal transduction	SP	No
THBS1	7057	thrombospondin-1 precursor	NP_003237.2	1	37	38	103	1.2	1.45	3.26	3.93	29.1	43.2	53	53	1765	7057	thrombospondin 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	TSPN;VWC;TSP1;EGFCA;EGF;SP;CC	Yes
TOMM40	10452	mitochondrial import receptor subunit TOM40 homolog	NP_006105.1	1	8	8	38	1.2	1.37	7.9	15.46	35.3	93.7	13	14	16274	10452	translocase of outer mitochondrial membrane 40homolog (yeast)	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	-	Yes
ARHGEF12	23365	rho guanine nucleotide exchange factor 12 isoform 1	NP_056128.1	3	3	3	5	1.2	1.36	12.85	0.22	27.1	0.5	3	3	9207	23365	Rho guanine nucleotide exchange factor (GEF)12	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	PDZ;CC;RHOGEF;PH	Yes
SERINC3	10955	serine incorporator 3 precursor	NP_006802.1	1	1	1	1	1.2	1.32					1	1	6201	10955	tumor differentially expressed 1	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	TM	Yes
RELB	5971	transcription factor RelB	NP_006500.2	1	1	1	1	1.2	1.3					1	1	6886	5971	v-rel reticuloendotheliosis viral oncogenehomolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3(avian)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	IPT;RHD	Yes
ACADVL	37	very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 3	NP_001257376.1	4	34	34	120	1.2	1.3	2.26	3.05	21.5	32	62	62	1940	37	acyl-Coenzyme A dehydrogenase, very long chain	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Energy pathways	SP	Yes
ALG11	440138	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase	NP_001004127.2	1	1	1	1	1.2	1.28					1	1	11265	440138	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM	Yes
RPS7	6201	40S ribosomal protein S7	NP_001002.1	1	14	14	47	1.2	1.24	9.97	5.66	64.1	35.3	24	24	4712	6201	ribosomal protein S7	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
MRGBP	55257	MRG/MORF4L-binding protein	NP_060740.1	1	1	1	2	1.2	1.21					1	1									
C5orf42	65250	uncharacterized protein C5orf42	NP_075561.3	1	1	1	2	1.2	1.19	2.9	19.63	5	34	2	2	7822	65250	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
NISCH	11188	nischarin isoform 1	NP_009115.2	3	2	2	3	1.2	1.15	11.06	11.12	19	18.2	2	2	11391	11188	nischarin	Receptor activity	Plasma membrane	Cell surface receptor	Cell growth and/or maintenance	PX;LRR;CC	No

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MEF2D	4209	myocyte-specific enhancer factor 2D isoform 1	NP_005911.1	10	1	1	1	1.2	1.13					1	1	2810	4209	MADS box transcription enhancer factor 2,polypeptide D (myocyte enhancer factor 2D)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Transcription	-	Yes
APOBEC3G	60489	DNA dC->dU-editing enzyme APOBEC-3G	NP_068594.1	2	2	3	3	1.2	1.11					1	1	6172	60489	apolipoprotein B mRNA editing enzyme,catalytic polypeptide-like 3G	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SAV1	60485	protein salvador homolog 1	NP_068590.1	1	1	1	2	1.2	1.1					1	1	6229	60485	salvador homolog 1 (Drosophila)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WW;CC	Yes
KPNA2	3838	importin subunit alpha-1	NP_002257.1	1	9	9	34	1.2	1.09	2.18	4.28	11.1	20	18	18	2818	3838	karyopherin alpha 2 (RAG cohort 1, importinalpha 1)	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	ARM	Yes
ARHGEF2	9181	rho guanine nucleotide exchange factor 2 isoform 1	NP_001155855.1	3	9	9	18	1.2	1.06	4.64	10.86	18.6	39.7	11	11	10458	9181	rho/rac guanine nucleotide exchange factor(GEF) 2	Guanyl-nucleotide exchange factor activity	Cytoskeleton	Guanine nucleotide exchange factor	Cell communication;Signal transduction	CC;C1;RHOGEF;PH	Yes
APAF1	317	apoptotic protease-activating factor 1 isoform c	NP_863651.1	5	3	3	4	1.2	1.05	4	27.15	6.8	42.2	2	2	3755	317	apoptotic protease activating factor	Receptor signaling complex scaffold activity	Cytoplasm;Nucleus	Adapter molecule	Anti-apoptosis	CARD;WD40	Yes
MTR	4548	methionine synthase isoform 1	NP_000245.2	3	8	8	18	1.2	1.05	6.05	14.53	22	48.2	9	9	1136	4548	5-methyltetrahydrofolate-homocysteinemethyltransferase	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	Yes
CPSF7	79869	cleavage and polyadenylation specificity factor subunit 7 isoform 1	NP_079087.3	3	8	8	20	1.2	1.03	4.32	9.99	17.4	35	11	11	16906	79869	None	Molecular function unknown	-	Unclassified	Biological_process unknown	RRM	No
BCAP29	55973	B-cell receptor-associated protein 29 isoform a	NP_001008405.1	2	3	3	3	1.2	1.02	18.37	28.25	31.9	42.7	2	2	16541	55973	B-cell receptor-associated protein 29	Molecular function unknown	Endoplasmic reticulum membrane	Integral membrane protein	Biological_process unknown	TM;CC	Yes
SPATS2L	26010	SPATS2-like protein isoform d	NP_001269673.1	3	1	15	32	1.2	1.01					1	1	10916	26010	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
NCOR1	9611	nuclear receptor corepressor 1 isoform 1	NP_006302.2	2	3	3	9	1.2	1.01	7.46	4.47	18.1	9	4	4	2911	9611	nuclear receptor co-repressor 1	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT;CC	Yes
LIG3	3980	DNA ligase 3 isoform alpha precursor	NP_039269.2	2	4	4	8	1.2	1	5.96	1.68	14.4	3.4	4	4	2966	3980	ligase III, DNA, ATP-dependent	DNA ligase activity	Nucleus	DNA ligase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRCT	Yes
EXOSC9	5393	exosome complex component RRP45 isoform 1	NP_001029366.1	2	2	2	7	1.2	0.97	1.11	3.7	2.3	6.2	3	3	7315	5393	exosome component 9	Ribonuclease activity	Nucleolus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
BAZ2A	11176	bromodomain adjacent to zinc finger domain protein 2A isoform 1	NP_038477.2	2	1	1	3	1.2	0.96	4.95	2.2	8.4	3	2	2	10417	11176	bromodomain adjacent to zinc finger domain, 2A	Transcription regulator activity	Nucleolus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MBD;AT_hook;CC;PHD;BROMO;DDT	Yes
RICTOR	253260	rapamycin-insensitive companion of mTOR isoform 2	NP_001272368.1	3	2	2	4	1.2	0.96	10.51	1.43	17.9	1.9	2	2	10682	253260	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
PCNT	5116	pericentrin	NP_006022.3	1	2	2	3	1.2	0.94	1.33	20.72	2.3	28.1	2	2	5804	5116	pericentrin 2 (kendrin)	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
SF3B2	10992	splicing factor 3B subunit 2	NP_006833.2	1	19	19	39	1.2	0.93	3.88	7.37	23	34.5	24	24	10410	10992	splicing factor 3b, subunit 2, 145kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;CC	Yes
RCL1	10171	RNA 3'-terminal phosphate cyclase-like protein isoform a	NP_005763.3	3	6	6	9	1.2	0.92	2.4	7.08	6.4	14.6	5	5	10189	10171	RNA terminal phosphate cyclase-like 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
EIF1AD	84285	probable RNA-binding protein EIF1AD	NP_001229410.1	1	2	2	5	1.2	0.89	15.77	8.27	33.5	12.8	3	3	14411	84285	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
GTF3C4	9329	general transcription factor 3C polypeptide 4	NP_036336.2	1	8	8	13	1.2	0.89	3.87	4.91	12.3	11.6	7	7	11998	9329	general transcription factor IIIC, polypeptide4, 90kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LZ	Yes
DPH5	51611	diphthine synthase isoform a	NP_057042.2	2	3	3	5	1.2	0.86	5.66	6.84	11.8	10.2	3	3	13037	51611	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
FOXK1	221937	forkhead box protein K1	NP_001032242.1	6	10	10	16	1.2	0.86	6.53	18.23	21	43.5	7	7	18750	221937	Forkhead box K1	Transcription factor activity	Nucleus	Transcription factor	Transcription	FHA;FH;NLS	No
APOD	347	apolipoprotein D precursor	NP_001638.1	1	1	1	1	1.2	0.85					1	1	134	347	apolipoprotein D	Transporter activity	Extracellular	Transport/cargo protein	Transport	SP	Yes

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DUS3L	56931	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like isoform 1	NP_064560.2	2	2	2	5	1.2	0.84	2.71	10.52	4.6	12.6	2	2	14252	56931	dihydrouridine synthase 3-like (S. cerevisiae)	DNA binding	Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1	No
DDX19A	55308	ATP-dependent RNA helicase DDX19A	NP_060802.1	4	2	16	38	1.2	0.77	18.17	40.61	31.7	46.8	2	2	7732	55308	DEAD (Asp-Glu-Ala-As) box polypeptide 19-like	Molecular function unknown	-	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	No
CRK	1398	adapter molecule crk isoform a	NP_058431.2	2	1	1	2	1.2	0.73					1	1	1267	1398	v-crk sarcoma virus CT10 oncogene homolog (avian)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	SH2;SH3	Yes
PYROXD1	79912	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1	NP_079130.2	1	1	1	2	1.19	1.9					1	1	7976	79912	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
MLKL	197259	mixed lineage kinase domain-like protein isoform 1	NP_689862.1	1	3	3	5	1.19	1.6	3.21	0.41	5.4	0.9	2	2	8752	197259	mixed lineage kinase domain-like	Protein-tyrosine kinase activity	-	Tyrosine kinase	Cell communication;Signal transduction	CC;S_T_Y_Kinase	Yes
NIP7	51388	60S ribosome subunit biogenesis protein NIP7 homolog isoform 1	NP_057185.1	2	1	1	2	1.19	1.45					1	1	16709	51388	None	RNA binding	Nucleolus	RNA binding protein	Cell growth and/or maintenance	-	Yes
TFAP2A	7020	transcription factor AP-2-alpha isoform a	NP_003211.1	5	4	4	7	1.19	1.42	7.51	7.57	18	21.7	4	4	128	7020	transcription factor AP-2 alpha (activatingenhancer binding protein 2 alpha)	Transcription factor activity	Nucleus	Transcription factor	Development;Apoptosis;Cell differentiation;Regulation of gene expression, epigenetic	-	Yes
PANX1	24145	pannexin-1	NP_056183.2	1	4	4	12	1.19	1.39	24.76	12.91	82.8	46.2	6	6	10526	24145	pannexin 1	Cell adhesion molecule activity	Plasma membrane	Cell junction protein	Cell growth and/or maintenance	TM	Yes
GMPS	8833	GMP synthase [glutamine-hydrolyzing]	NP_003866.1	1	22	22	55	1.19	1.38	2.62	4.11	17.4	32.4	31	31	10927	8833	guanine monphosphate synthetase	Amidinotransferase activity	-	Enzyme: Amidinotransferase	Metabolism;Energy pathways	-	Yes
SART1	9092	U4/U6.U5 tri-snRNP-associated protein 1	NP_005137.1	1	18	18	48	1.19	1.37	4.41	3.99	25.6	26.8	23	23	10440	9092	squamous cell carcinoma antigen recognised by Tcells	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
ABT1	29777	activator of basal transcription 1	NP_037507.1	1	1	1	1	1.19	1.28					1	1	16469	29777	activator of basal transcription 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
KPNB1	3837	importin subunit beta-1 isoform 1	NP_002256.2	2	23	23	133	1.19	1.25	2.28	4.19	21.8	43.6	63	63	4114	3837	karyopherin (importin) beta 1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ARM;IBN_NT	Yes
SEC16A	9919	protein transport protein Sec16A isoform 2	NP_001263347.1	1	1	26	56	1.19	1.18					1	1	11075	9919	KIAA0310	Molecular function unknown	Endoplasmic reticulum	Unclassified	Cell motility;ER organization and biogenesis;Protein transport	SP	Yes
FAH	2184	fumarylacetoacetase	NP_000128.1	1	11	11	21	1.19	1.18	9.49	5.11	37	19.2	10	10	2040	2184	fumarylacetoacetate hydrolase(fumarylacetoacetase)	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
EMG1	10436	ribosomal RNA small subunit methyltransferase NEP1	NP_006322.4	1	7	7	24	1.19	1.12	2.75	9.81	10.9	37.7	11	11	12803	10436	None	Translation regulator activity	Nucleus	Translation regulatory protein	Protein metabolism	-	Yes
HIST1H2BB	3018	histone H2B type 1-B	NP_066406.1	8	2	9	541	1.19	1.12	2.12	4.3	7.1	13.6	8	8	7536	3018	histone 1, H2bb	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
SMARCD2	6603	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	NP_001091896.1	5	5	5	12	1.19	1.11	6.46	5.74	19	15.7	6	6	3439	6603	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily d, member 2	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
TMEM70	54968	transmembrane protein 70, mitochondrial isoform a	NP_060336.3	1	1	1	1	1.19	1.08					1	1	7923	54968	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	TM	No
ARL6IP6	151188	ADP-ribosylation factor-like protein 6-interacting protein 6	NP_689735.1	1	1	1	1	1.19	1.05					1	1	12485	151188	ADP-ribosylation-like factor 6 interactingprotein 6	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
MRPL9	65005	39S ribosomal protein L9, mitochondrial isoform 1	NP_113608.1	2	3	3	9	1.19	1.03	2.38	7.08	6.3	16.3	5	5	14774	65005	mitochondrial ribosomal protein L9	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
RAP2B	5912	ras-related protein Rap-2b	NP_002877.2	2	7	7	24	1.19	1.02	6.75	5.51	29.5	20.4	13	13	1548	5912	RAP2B, member of RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	No
CACYBP	27101	calcyclin-binding protein isoform 1	NP_055227.1	2	10	10	20	1.19	1.01	2.01	8.69	8.3	31	12	12	7316	27101	calcyclin binding protein	Molecular function unknown	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
IRGQ	126298	immunity-related GTPase family Q protein	NP_001007562.1	1	10	10	21	1.19	1	10.87	12.5	45.1	43.2	11	11	17161	126298	immunity-related GTPase family, Q1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RBM15	64783	putative RNA-binding protein 15 isoform 1	NP_073605.4	2	9	10	17	1.19	0.93	0.33	7.58	1.2	21.5	9	9	5832	64783	RNA binding motif protein 15	RNA binding	-	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
PEF1	553115	peflin	NP_036524.1	1	3	3	3	1.19	0.92	3.11	38.96	5.2	54.2	2	2	10143	553115	penta-EF hand domain containing 1	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	No

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CYB5R4	51167	cytochrome b5 reductase 4	NP_057314.2	1	2	2	4	1.19	0.91	1.86	62.42	3.1	94.6	2	2	12218	51167	NADPH cytochrome B5 oxidoreductase	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
GATAD2B	57459	transcriptional repressor p66-beta	NP_065750.1	1	2	3	7	1.19	0.9	5.67	33.54	9.6	44.8	2	2	15094	57459	GATA zinc finger domain containing 2B	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;ZNF_GATA	Yes
HSPA2	3306	heat shock-related 70 kDa protein 2	NP_068814.2	1	6	17	147	1.19	0.9	3.83	16.95	14.4	50.9	10	10	7174	3306	heat shock 70kDa protein 2	Heat shock protein activity	Nucleus	Heat shock protein	Protein metabolism	-	Yes
ARHGEF16	27237	rho guanine nucleotide exchange factor 16	NP_055263.2	1	3	3	5	1.19	0.89	24.5	19.72	54.1	31	3	3	12478	27237	Rho guanine exchange factor (GEF) 16	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH;SH3	No
MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 1	NP_055949.2	2	9	9	21	1.19	0.87	2.73	10.87	11.3	33.9	12	12	17591	23164	None	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Regulation of cell shape	PH;CC	No
INADL	10207	inaD-like protein	NP_795352.2	1	2	2	6	1.19	0.83	46	35.01	90.8	43.1	2	2	4434	10207	InaD-like (Drosophila)	Cell adhesion molecule activity	Plasma membrane	Cell junction protein	Cell growth and/or maintenance	L27;PDZ;CC	No
LPIN1	23175	phosphatidate phosphatase LPIN1 isoform 3	NP_001248357.1	4	3	3	4	1.19	0.83	25.7	15.75	56.9	23	3	3	9271	23175	lipin 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
PAPD5	64282	non-canonical poly(A) RNA polymerase PAPD5 isoform a	NP_001035374.2	2	1	1	2	1.19	0.8					1	1	16119	64282	PAP associated domain containing 5	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
PBDC1	51260	protein PBDC1 isoform 1	NP_057584.2	2	6	6	23	1.19	0.74	3.87	5.07	16	13	12	12									
ITM2B	9445	integral membrane protein 2B	NP_068839.1	1	1	1	1	1.19	0.71					1	1	4878	9445	integral membrane protein 2B	Molecular function unknown	Plasma membrane	Integral membrane protein	Cell growth and/or maintenance	TM	Yes
KANK2	25959	KN motif and ankyrin repeat domain-containing protein 2 isoform 1	NP_056308.3	2	2	2	2	1.19	0.7					1	1	12463	25959	ankyrin repeat domain 25	Structural molecule activity	-	Structural protein	Biological_process unknown	CC;ANK	No
GLMP	112770	glycosylated lysosomal membrane protein isoform 1 precursor	NP_653181.1	3	1	1	2	1.19	0.69					1	1									
CXorf38	159013	uncharacterized protein CXorf38	NP_659407.1	1	2	2	2	1.18	1.68					1	1	6651	159013	chromosome X open reading frame 38	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	SP;CC	No
PXDN	7837	peroxidasin homolog precursor	NP_036425.1	1	5	5	8	1.18	1.63	6.26	3.91	14.8	12.8	4	4	18965	7837	peroxidasin homolog (Drosophila)	Peroxidase activity	-	Enzyme: Peroxidase	Apoptosis	SP;LRR;IGC2;VWC	Yes
WAPAL	23063	wings apart-like protein homolog	NP_055860.1	1	2	2	3	1.18	1.4	19.84	7.92	33.9	15.8	2	2	11072	23063	KIAA0261	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;NLS;NES	No
CSE1L	1434	exportin-2 isoform 1	NP_001307.2	2	29	29	93	1.18	1.36	2.5	5.21	21.2	53.9	51	51	3217	1434	CSE1 chromosome segregation 1-like (yeast)	Transporter activity	Nucleus	Transport/cargo protein	Transport	IBN_NT	Yes
TRIP13	9319	pachytene checkpoint protein 2 homolog isoform 1	NP_004228.1	2	10	10	24	1.18	1.34	8.85	9.63	35.6	44.7	11	11	5145	9319	thyroid hormone receptor interactor 13	ATPase activity	Nucleus	ATPase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA	Yes
AKAP8	10270	A-kinase anchor protein 8	NP_005849.1	1	5	5	14	1.18	1.33	6.39	5.03	16.9	15	5	5	5258	10270	A kinase (PRKA) anchor protein 8	Chromatin binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	NLS	Yes
WDR55	54853	WD repeat-containing protein 55	NP_060176.2	1	5	5	11	1.18	1.3	6.11	8.37	17.8	27	6	6	8614	54853	WD repeat domain 55	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	No
PCNA	5111	proliferating cell nuclear antigen	NP_002583.1	1	11	11	71	1.18	1.3	5.14	4.23	38	34.5	37	37	1456	5111	proliferating cell nuclear antigen	DNA binding	Nucleus	Cell cycle control protein	DNA repair	-	Yes
FTO	79068	alpha-ketoglutarate-dependent dioxygenase FTO	NP_001073901.1	1	4	4	11	1.18	1.24	15.85	4.36	43.7	12.2	5	5	19057	79068	fat mass and obesity associated	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
DIMT1	27292	probable dimethyladenosine transferase	NP_055288.1	1	4	4	12	1.18	1.24	7.03	9.96	20.6	31	6	6									
SNRPA1	6627	U2 small nuclear ribonucleoprotein A'	NP_003081.2	1	11	11	36	1.18	1.2	2.16	6.96	11.1	37.5	19	19	4629	6627	small nuclear ribonucleoprotein polypeptide A`	RNA binding	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
WDR4	10785	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4 isoform 1	NP_061139.2	3	3	3	8	1.18	1.18	1.62	1.74	3.3	3.5	3	3	9330	10785	WD repeat domain 4	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
IWS1	55677	protein IWS1 homolog	NP_060439.2	1	3	3	8	1.18	1.16	6.6	8.33	13.5	16.9	3	3	7639	55677	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	Yes
CDC37	11140	hsp90 co-chaperone Cdc37	NP_008996.1	1	14	14	46	1.18	1.16	2.16	5.65	14.3	37.9	31	31	5456	11140	CDC37 cell division cycle 37 homolog (S.cerevisiae)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CC	Yes
PRPF6	24148	pre-mRNA-processing factor 6	NP_036601.2	1	13	13	25	1.18	1.15	2.79	5.32	12	22.4	13	13	10729	24148	chromosome 20 open reading frame 14	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	HAT	Yes
PLCB3	5331	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 isoform 1	NP_000923.1	2	28	28	54	1.18	1.14	3.29	4.54	21.6	29	30	30	2577	5331	phospholipase C, beta 3(phosphatidylinositol-specific)	Phospholipase activity	Cytoplasm	Enzyme: Phospholipase	Metabolism;Energy pathways	C2;CC	Yes
GATSL2	729438	GATS-like protein 2	NP_001138536.1	1	1	1	2	1.18	1.14					1	1	19673	729438	GATS protein-like 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
DCP1A	55802	mRNA-decapping enzyme 1A isoform a	NP_060873.4	5	2	2	6	1.18	1.12	16.46	2.39	34.7	4.7	3	3	6113	55802	decapping enzyme	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes

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TWISTNB	221830	DNA-directed RNA polymerase I subunit RPA43	NP_001002926.1	1	2	2	6	1.18	1.11	3.83	24.57	7.8	49.8	3	3	16311	221830	TWIST neighbor	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
EPCAM	4072	epithelial cell adhesion molecule precursor	NP_002345.2	1	1	1	2	1.18	1.11					1	1	1709	4072	tumor-associated calcium signal transducer 1	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;TM;THYRO	Yes
LARP4B	23185	la-related protein 4B	NP_055970.1	1	6	6	12	1.18	1.1	6.49	8.96	20.4	26.5	7	7	13787	23185	KIAA0217	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LA;RRM	No
BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 1	NP_001164185.1	9	11	11	26	1.18	1.1	3.27	9.52	13.9	39	13	13	4248	9564	breast cancer anti-estrogen resistance 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	SH3	Yes
RBM5	10181	RNA-binding protein 5	NP_005769.1	1	2	3	5	1.18	1.09	18.17	17.98	31	28.2	2	2	6052	10181	RNA binding motif protein 5	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;ZnF_RBZ;G_PATCH;CC	Yes
ATG4B	23192	cysteine protease ATG4B isoform a	NP_037457.3	2	3	3	7	1.18	1.08	5.97	14.83	14.2	32.7	4	4	16499	23192	APG4 autophagy 4 homolog B (S. cerevisiae)	Peptidase activity	Cytoplasm;Nucleus	Cysteine protease	Proteolysis and peptidolysis	-	No
MTA2	9219	metastasis-associated protein MTA2	NP_004730.2	4	16	19	43	1.18	1.08	3.63	2.93	20.3	14.9	22	22	7233	9219	metastasis associated 1 family, member 2	DNA binding	Nucleus	Regulatory/other subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Chromosome organization and biogenesis (sensu Eukarya)	SANT;ZNF_GATA	Yes
SYMPK	8189	symplekin	NP_004810.2	1	9	9	19	1.18	1.08	6.64	11.52	26.4	43.1	11	11	9090	8189	symplekin	Cell adhesion molecule activity	Plasma membrane	Cell junction protein	Cell growth and/or maintenance	HEAT	Yes
EIF2B2	8892	translation initiation factor eIF-2B subunit beta	NP_055054.1	1	6	6	13	1.18	1.07	7.16	18.13	20.9	50.3	6	6	5923	8892	eukaryotic translation initiation factor 2B,subunit 2 beta, 39kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
VAT1	10493	synaptic vesicle membrane protein VAT-1 homolog	NP_006364.2	1	11	11	44	1.18	1.05	6.17	5.72	36.8	30.2	24	24	5220	10493	vesicle amine transport protein 1 homolog (Tcalifornica)	Transporter activity	Cytoplasmic vesicle	Transport/cargo protein	Transport	-	Yes
NACA	4666	nascent polypeptide-associated complex subunit alpha isoform a	NP_001106674.2	2	7	7	89	1.18	1.05	3.96	6.69	26.4	40.7	31	31	3137	4666	nascent-polypeptide-associated complex alphapolypeptide	Chaperone activity	Nucleus	Chaperone	Protein metabolism	-	Yes
ANKRD28	23243	serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A isoform a	NP_056014.2	2	3	3	4	1.18	1.04	14.1	8.6	23.9	12.7	2	2	10651	23243	ankyrin repeat domain 28	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK	Yes
PUS7	54517	pseudouridylate synthase 7 homolog	NP_061915.2	1	6	6	9	1.18	1.03	1.41	8.61	4.1	22	6	6	7914	54517	None	Lyase activity	-	Enzyme: Lyase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
PRPF31	26121	U4/U6 small nuclear ribonucleoprotein Prp31	NP_056444.3	1	10	10	19	1.18	1.02	7.2	7.58	29.9	27.2	12	12	5917	26121	PRP31 pre-mRNA processing factor 31 homolog(yeast)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
DYNC1I2	1781	cytoplasmic dynein 1 intermediate chain 2 isoform 1	NP_001369.1	4	11	11	31	1.18	1.01	6.98	7.37	34.9	31.6	17	17	4512	1781	dynein, cytoplasmic, intermediate polypeptide 2	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	CC;WD40	Yes
POLDIP3	84271	polymerase delta-interacting protein 3 isoform 3	NP_001265586.1	3	6	6	19	1.18	1.01	5.96	5.73	22.5	18.5	10	10	17875	84271	polymerase (DNA-directed), delta interactingprotein 3	RNA binding	Nucleolus	RNA binding protein	Cell growth and/or maintenance	RRM	Yes
YLPM1	56252	YLP motif-containing protein 1	NP_062535.2	1	7	7	15	1.18	1.01	2.6	5	9.2	15.3	9	9	11688	56252	YLP motif containing 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
RIF1	55183	telomere-associated protein RIF1 isoform 1	NP_060621.3	2	5	5	8	1.18	1	6.96	5.38	16.5	10.8	4	4	10603	55183	RAP1 interacting factor homolog (yeast)	DNA repair protein	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
ANKRD27	84079	ankyrin repeat domain-containing protein 27	NP_115515.2	1	1	1	2	1.18	0.99					1	1	10650	84079	ankyrin repeat domain 27 (VPS9 domain)	Molecular function unknown	-	Unclassified	Biological_process unknown	VPS9;ANK	No
PAPSS1	9061	bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	NP_005434.4	1	11	11	21	1.18	0.97	3.3	14.04	13	47.8	11	11	9132	9061	3`-phosphoadenosine 5`-phosphosulfate synthase1	Nucleotidyltransferase activity	Nucleus	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
DDX24	57062	ATP-dependent RNA helicase DDX24	NP_065147.1	1	9	9	13	1.18	0.96	3.24	9.45	10.2	24.2	7	7	5860	57062	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Transporter activity	Nucleus	Transport/cargo protein	Transport	HELIC;DEXDc	Yes
HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	NP_004491.2	2	3	17	270	1.18	0.96	6.6	13.28	29.7	50.7	14	14	1243	3183	heterogeneous nuclear ribonucleoprotein C(C1/C2)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;LZ;CC	Yes

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TDRD7	23424	tudor domain-containing protein 7 isoform 1	NP_055105.2	2	3	3	5	1.18	0.95	3.74	16.55	6.2	22.6	2	2	11626	23424	tudor domain containing 7	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule	Cell communication;Signal transduction	TUDOR	Yes
MFGE8	4240	lactadherin isoform a preproprotein	NP_005919.2	2	8	8	13	1.18	0.95	4.74	16.6	14.9	43.6	7	7	3789	4240	milk fat globule-EGF factor 8 protein	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;EGF;F58C	Yes
TPD52L2	7165	tumor protein D54 isoform a	NP_955392.1	10	8	8	25	1.18	0.94	4.19	10.45	20.6	42.1	17	17	11947	7165	tumor protein D52-like 2	Molecular function unknown	Cytoplasm;Nucleus	Unclassified	Cell growth and/or maintenance;Biological_process unknown	CC	Yes
ATM	472	serine-protein kinase ATM	NP_000042.3	1	4	4	6	1.18	0.93	20.21	19.8	43.2	32.5	3	3	6347	472	ataxia telangiectasia mutated (includescomplementation groups A, C and D)	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	PI3KC	Yes
NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	NP_065823.1	1	13	13	27	1.18	0.91	3.65	7.36	16.8	26.3	15	15	11764	57532	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
MRPL1	65008	39S ribosomal protein L1, mitochondrial precursor	NP_064621.3	1	8	8	39	1.18	0.91	3.37	9.41	13.2	30.5	11	12	14737	65008	mitochondrial ribosomal protein L1	Structural constituent of ribosome	Mitochondrion	RNA binding protein	Protein metabolism	-	No
DYRK1A	1859	dual specificity tyrosine-phosphorylation-regulated kinase 1A isoform 1	NP_001387.2	4	1	1	2	1.18	0.91					1	1	9018	1859	dual-specificity tyrosine-(Y)-phosphorylationregulated kinase 1A	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NLS;LZ	Yes
DDX39B	7919	spliceosome RNA helicase DDX39B	NP_542165.1	2	9	17	75	1.18	0.88	6.76	15.28	37.9	68.4	21	21									
ERGIC3	51614	endoplasmic reticulum-Golgi intermediate compartment protein 3 isoform a	NP_938408.1	2	1	1	1	1.18	0.88					1	1	15306	51614	serologically defined breast cancer antigen84	Molecular function unknown	Golgi apparatus	Unclassified	Biological_process unknown	TM	Yes
THBD	7056	thrombomodulin precursor	NP_000352.1	1	5	5	12	1.18	0.87	23.15	19.23	75.5	42.7	6	6	1764	7056	thrombomodulin	Receptor activity	Plasma membrane	Cell surface receptor	Immune response	TM;LECTIN_C;EGF;EGFL;EGFCA;SP	No
TBC1D20	128637	TBC1 domain family member 20	NP_653229.1	1	1	1	2	1.18	0.85					1	1	15472	128637	TBC1 domain family, member 20	Molecular function unknown	-	Unclassified	Biological_process unknown	TBC;TM	Yes
OLFML1	283298	olfactomedin-like protein 1 precursor	NP_940876.2	1	1	1	2	1.18	0.81					1	1	17661	283298	olfactomedin-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;OLF	No
PCM1	5108	pericentriolar material 1 protein	NP_006188.3	1	6	6	9	1.18	0.8	13.68	15.76	41	31.5	6	6	2624	5108	pericentriolar material 1	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
CRLF3	51379	cytokine receptor-like factor 3	NP_057070.3	1	2	2	2	1.18	0.76	17.71	28.07	30.2	30.7	2	2	16757	51379	cytokine receptor-like factor 3	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;FN3	Yes
PFDN4	5203	prefoldin subunit 4	NP_002614.2	1	5	5	13	1.18	0.62	16.12	33.68	53.7	60.1	7	7	5358	5203	prefoldin 4	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CC	Yes
ZMIZ1	57178	zinc finger MIZ domain-containing protein 1	NP_065071.1	1	1	1	2	1.17	1.79					1	1	12115	57178	retinoic acid induced 17	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
LAMB3	3914	laminin subunit beta-3 precursor	NP_001121113.1	1	59	59	267	1.17	1.59	2.69	3.41	36.3	65.4	124	122	1032	3914	laminin, beta 3	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	LAMNT;EGFLAM;SP;CC	Yes
ARFGEF2	10564	brefeldin A-inhibited guanine nucleotide-exchange protein 2	NP_006411.2	1	4	7	13	1.17	1.51	6.42	5.96	15.1	18.2	4	4	9250	10564	ADP-ribosylation factor guaninenucleotide-exchange factor 2 (brefeldin A-inhibited)	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	-	Yes
SEC24D	9871	protein transport protein Sec24D	NP_055637.2	1	8	8	26	1.17	1.5	6.44	4.98	26.6	26.3	12	12	6218	9871	SEC24 related gene family, member D (S.cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	GEL	Yes
ECH1	1891	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	NP_001389.2	1	9	9	44	1.17	1.39	6.86	9.54	38	66.6	21	21	2825	1891	enoyl Coenzyme A hydratase 1, peroxisomal	Catalytic activity	Peroxisome	Enzyme: Hydratase	Metabolism;Energy pathways	SP	Yes
HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	NP_002129.2	4	13	15	67	1.17	1.38	5.14	6.23	34.5	50.7	31	31	3206	3184	heterogeneous nuclear ribonucleoprotein D(AU-rich element RNA binding protein 1, 37kDa)	MRNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
STARD10	10809	PCTP-like protein	NP_006636.2	1	1	1	2	1.17	1.37					1	1	18116	10809	START domain containing 10	Molecular function unknown	-	Unclassified	Biological_process unknown	START	Yes
CNNM4	26504	metal transporter CNNM4 precursor	NP_064569.3	1	1	1	4	1.17	1.37	8.66	26.21	14.5	54.2	2	2	7420	26504	cyclin M4	Molecular function unknown	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CBS;CNMP;TM;SP	No
FOXRED1	55572	FAD-dependent oxidoreductase domain-containing protein 1	NP_060017.1	1	4	4	11	1.17	1.37	4.95	5.27	14.2	17.8	6	6	13620	55572	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	No
SAAL1	113174	protein SAAL1	NP_612430.2	1	3	3	10	1.17	1.37	6.06	6.32	16	19.6	5	5	13999	113174	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PRPF19	27339	pre-mRNA-processing factor 19	NP_055317.1	1	13	13	62	1.17	1.36	5.71	4.98	35	34.8	26	25	12214	27339	PRP19/PSO4 pre-mRNA processing factor 19homolog (S. cerevisiae)	DNA repair protein	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBOX;WD40	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
IREB2	3658	iron-responsive element-binding protein 2	NP_004127.1	1	1	1	2	1.17	1.31					1	1	8858	3658	iron-responsive element binding protein 2	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PTPN1	5770	tyrosine-protein phosphatase non-receptor type 1 isoform 1	NP_002818.1	2	22	22	78	1.17	1.3	5.05	5.97	39.7	53.7	42	42	1477	5770	protein tyrosine phosphatase, non-receptor type1	Protein tyrosine phosphatase activity	Endoplasmic reticulum	Tyrosine phosphatase	Cell communication;Signal transduction	Tyr_Phos	Yes
CASP1	834	caspase-1 isoform alpha precursor	NP_150634.1	7	8	8	16	1.17	1.3	3.62	4.97	12	18.4	8	8	977	834	caspase 1, apoptosis-related cysteine protease(interleukin 1, beta, convertase)	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Apoptosis	CARD;CASc	Yes
GMPPB	29925	mannose-1-phosphate guanyltransferase beta isoform 1	NP_037466.2	2	9	9	18	1.17	1.3	12.08	6.78	51.8	31.3	12	12	13589	29925	GDP-mannose pyrophosphorylase B	Phosphorylase activity	-	Enzyme: Phosphorylase	Metabolism	-	No
HSF1	3297	heat shock factor protein 1	NP_005517.1	1	1	1	2	1.17	1.3					1	1	778	3297	heat shock transcription factor 1	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HSF;LZ	Yes
GOLGA4	2803	Golgin subfamily A member 4 isoform 1	NP_001166184.1	2	19	19	37	1.17	1.27	2.38	3.23	12.5	18.5	20	20	3941	2803	golgi autoantigen, golgin subfamily a, 4	Transporter activity	Golgi apparatus;Nucleus	Transport/cargo protein	Transport	CC	Yes
SRPK1	6732	SRSF protein kinase 1	NP_003128.3	4	4	6	19	1.17	1.27	7.52	4.55	21.8	14.2	6	6	15992	6732	SFRS protein kinase 1	Protein threonine/tyrosine kinase activity	Nucleus	Dual specificity kinase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_Y_Kinase	No
NFKB2	4791	nuclear factor NF-kappa-B p100 subunit isoform a	NP_001070962.1	2	10	11	21	1.17	1.26	2.54	5.85	9.9	24.9	11	11	1239	4791	nuclear factor of kappa light polypeptide geneenhancer in B-cells 2 (p49/p100)	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	IPT;ANK;DEATH;CC	Yes
CCS	9973	copper chaperone for superoxide dismutase	NP_005116.1	1	1	1	2	1.17	1.22					1	1	4841	9973	copper chaperone for superoxide dismutase	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
NELFCD	51497	negative elongation factor C/D	NP_945327.2	1	4	4	16	1.17	1.21	1.76	6.27	5.8	21.8	8	8									
TMEM189-UBE2V1	387522	TMEM189-UBE2V1 fusion protein	NP_954673.1	9	4	8	31	1.17	1.18	16.53	12.96	50.3	38.9	6	6	11926	387522	None	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	TM;UBC	Yes
PELO	53918	protein pelota homolog	NP_057030.3	1	9	9	15	1.17	1.18	2.25	6.11	7	20.6	7	8	9309	53918	pelota homolog (Drosophila)	Molecular function unknown	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	NLS	Yes
DDX18	8886	ATP-dependent RNA helicase DDX18	NP_006764.3	1	18	18	50	1.17	1.14	4.31	6.05	27.6	38.3	29	29	5894	8886	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Transporter activity	Nucleus	Transport/cargo protein	Transport	HELIC;DEXDc	Yes
CSTF1	1477	cleavage stimulation factor subunit 1	NP_001028693.1	1	5	5	8	1.17	1.13	5.02	6.77	10.2	13.4	3	3	2653	1477	cleavage stimulation factor, 3` pre-RNA,subunit 1, 50kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
ABCB10	23456	ATP-binding cassette sub-family B member 10, mitochondrial	NP_036221.2	1	2	2	3	1.17	1.12	11.53	6	19.3	9.5	2	2	9263	23456	ATP-binding cassette, sub-family B (MDR/TAP),member 10	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	AAA;TM	Yes
TERF2	7014	telomeric repeat-binding factor 2	NP_005643.2	1	2	2	3	1.17	1.11	2.97	27.29	4.9	44.7	2	2	3610	7014	telomeric repeat binding factor 2	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT	Yes
ST13	6767	hsc70-interacting protein isoform 1	NP_003923.2	2	14	14	48	1.17	1.11	2.51	4.49	14.7	25.4	25	25	8426	6767	suppression of tumorigenicity 13 (coloncarcinoma) (Hsp70 interacting protein)	Receptor signaling complex scaffold activity	Lysosome	Adapter molecule	Cell communication;Signal transduction	TPR;CC;STI1	Yes
EDC3	80153	enhancer of mRNA-decapping protein 3	NP_079359.2	1	3	3	6	1.17	1.1	2.41	9.37	4.9	17.9	3	3	7954	80153	None	RNA binding	Cytoplasm	RNA binding protein	Nucleobase, nucleoside, nucleotide and nucleic acid transport	-	Yes
DNM1L	10059	dynamin-1-like protein isoform 3	NP_005681.2	2	1	27	110	1.17	1.08	6.55	5.14	10.9	7.9	2	2	4833	10059	dynamin 1-like	GTPase activity	Cytoplasm	GTPase	Mitochondrion organization and biogenesis	DYNC;GED	Yes
FCHO2	115548	F-BAR domain only protein 2 isoform a	NP_620137.2	2	2	2	3	1.17	1.08	25.52	56.23	44.1	104.1	2	2	13319	115548	FCH domain only 2	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	FCH	No
RPL21	6144	60S ribosomal protein L21	NP_000973.2	1	10	10	64	1.17	1.07	3.1	11.9	21.1	84	33	33	4700	6144	ribosomal protein L21	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	No
POLD1	5424	DNA polymerase delta catalytic subunit 2	NP_001295561.1	2	6	7	11	1.17	1.06	2.44	7.3	6.4	17.5	5	5	8882	5424	polymerase (DNA directed), delta 1, catalyticsubunit 125kDa	DNA-directed DNA polymerase activity	Nucleus	DNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	Yes
EPS15	2060	epidermal growth factor receptor substrate 15 isoform A	NP_001972.1	2	11	11	20	1.17	1.06	4.51	8.98	18.5	33.9	12	12	8968	2060	epidermal growth factor receptor pathwaysubstrate 15	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	EH;CC;UIM	Yes
DHODH	1723	dihydroorotate dehydrogenase (quinone), mitochondrial	NP_001352.2	1	1	1	1	1.17	1.06					1	1	521	1723	dihydroorotate dehydrogenase	Molecular function unknown	Mitochondrion	Integral membrane protein	Biological_process unknown	TM	Yes

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
INTS7	25896	integrator complex subunit 7 isoform 1	NP_056249.1	4	2	2	11	1.17	1.06	8.01	15.85	21.1	39	5	5	8522	25896	chromosome 1 open reading frame 73	Structural molecule activity	-	Structural protein	Biological_process unknown	-	No
SUPT5H	6829	transcription elongation factor SPT5 isoform a	NP_001104490.1	2	14	14	27	1.17	1.05	5.09	8.27	22.6	33.5	14	14	3655	6829	suppressor of Ty 5 homolog (S. cerevisiae)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS;KOW	No
EMC2	9694	ER membrane protein complex subunit 2	NP_055488.1	1	6	6	17	1.17	1.03	8.76	12.4	33.2	41.9	10	10									
GPN1	11321	GPN-loop GTPase 1 isoform a	NP_009197.2	4	2	2	4	1.17	1	11.14	9.7	18.7	13.8	2	2	10308	11321	XPA binding protein 1	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	AAA;CC;SP	Yes
FAM129B	64855	niban-like protein 1 isoform 1	NP_073744.2	3	29	29	101	1.17	0.99	3.97	4.58	35.1	34.8	54	55	10804	64855	chromosome 9 open reading frame 88	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	PH	Yes
SRSF3	6428	serine/arginine-rich splicing factor 3	NP_003008.1	1	6	7	22	1.17	0.99	3.34	5.14	14.7	19.3	14	14									
MTX2	10651	metaxin-2	NP_006545.1	1	2	2	5	1.17	0.98	11.58	11.88	23.7	20.4	3	3	9777	10651	metaxin 2	Molecular function unknown	Mitochondrion	Unclassified	Transport	SP	Yes
SRPRB	58477	signal recognition particle receptor subunit beta	NP_067026.3	1	11	11	31	1.17	0.96	6.86	8.57	35.1	36.1	18	18	18105	58477	signal recognition particle receptor, B subunit	GTPase activity	Endoplasmic reticulum	GTPase	Protein metabolism	Small_GTPase	Yes
POLR2C	5432	DNA-directed RNA polymerase II subunit RPB3	NP_116558.1	1	3	3	6	1.17	0.95	6.06	21.2	14.3	42	4	4	15945	5432	polymerase (RNA) II (DNA directed) polypeptideC, 33kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RPOLD	Yes
AASDHPPT	60496	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	NP_056238.2	1	4	4	4	1.17	0.94	7.62	5.3	12.7	7.1	2	2	9675	60496	aminoadipate-semialdehydedehydrogenase-phosphopantetheinyl transferase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
TACC1	6867	transforming acidic coiled-coil-containing protein 1 isoform 1	NP_006274.2	3	3	3	5	1.17	0.94	1.51	0.08	3.1	0.1	3	3	10391	6867	transforming, acidic coiled-coil containingprotein 1	Molecular function unknown	Centrosome	Cell cycle control protein	Cell communication;Signal transduction	CC;NLS;FH2	Yes
PIK3R1	5295	phosphatidylinositol 3-kinase regulatory subunit alpha isoform 1	NP_852664.1	4	2	2	2	1.17	0.92					1	1	1381	5295	phosphoinositide-3-kinase, regulatory subunit1 (p85 alpha)	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Cell communication;Signal transduction	SH3;RHOGAP;SH2;CC	Yes
RPL8	6132	60S ribosomal protein L8	NP_150644.1	1	13	13	45	1.17	0.91	1.97	7.25	12.2	36.1	28	28	16044	6132	ribosomal protein L8	Structural constituent of ribosome	Nucleolus	Ribosomal subunit	Protein metabolism	-	Yes
MCCC1	56922	methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial isoform 1 precursor	NP_064551.3	2	3	3	7	1.17	0.88	2.17	3.73	5.1	6.6	4	4	1951	56922	methylcrotonoyl-Coenzyme A carboxylase 1(alpha)	Ligase activity	Mitochondrion	Enzyme: Carboxylase	Metabolism;Energy pathways	SP	Yes
KIF1B	23095	kinesin-like protein KIF1B isoform alpha	NP_904325.2	4	2	4	9	1.17	0.86	8.45	19.94	14.1	24.7	2	2	5818	23095	kinesin family member 1B	Motor activity	Cytoplasmic vesicle	Motor protein	Cell growth and/or maintenance	KISC;FHA;PH;CC	Yes
LZTFL1	54585	leucine zipper transcription factor-like protein 1 isoform 1	NP_065080.1	3	1	1	1	1.17	0.86					1	1	7586	54585	leucine zipper transcription factor-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	LZ	Yes
YAP1	10413	yorkie homolog isoform 9	NP_001269030.1	9	6	6	13	1.17	0.84	9.68	13.24	28.4	27.7	6	6	9424	10413	Yes-associated protein 1, 65kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WW;CC	Yes
RUNX1	861	runt-related transcription factor 1 isoform AML1c	NP_001745.2	3	3	3	4	1.17	0.84	38.96	18.11	93	26.9	3	3	1043	861	runt-related transcription factor 1 (acutemyeloid leukemia 1; aml1 oncogene)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	Runt	Yes
CHMP3	51652	charged multivesicular body protein 3 isoform 1	NP_057163.1	4	3	3	4	1.17	0.83	15.7	26.3	32.7	39	3	3									
RAB3D	9545	ras-related protein Rab-3D	NP_004274.1	11	3	8	56	1.17	0.81	2.8	26.33	5.7	38	3	3	5070	9545	RAB3D, member RAS oncogene family	GTPase activity	Secretory granule	GTPase	Transport	RAB	Yes
RPS15	6209	40S ribosomal protein S15 isoform 1	NP_001295155.1	2	3	3	68	1.17	0.81	10.37	14.75	67	65.3	25	25	1613	6209	ribosomal protein S15	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform epsilon	NP_829884.1	3	8	9	24	1.17	0.79	5.4	13.29	20.2	34.4	10	10	6181	23085	RAB6 interacting protein 2	Protein binding	Cytoplasm	Regulatory/other subunit	Energy pathways	CC	Yes
HYPK	25764	huntingtin-interacting protein K isoform 1	NP_057484.3	2	2	2	4	1.17	0.76	0.03	46.62	0	53.6	2	2									
MAP3K7	6885	mitogen-activated protein kinase kinase kinase 7 isoform A	NP_003179.1	4	3	3	4	1.17	0.69	6.3	17.8	10.4	17.4	2	2	4011	6885	mitogen-activated protein kinase kinase kinase7	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
ZBTB8OS	339487	protein archease isoform 1	NP_848642.1	5	1	1	1	1.17	0.69					1	1	12470	339487	zinc finger and BTB domain containing 8opposite strand	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ASCC2	84164	activating signal cointegrator 1 complex subunit 2 isoform 1	NP_115580.2	2	4	4	7	1.17	0.62	2.18	7.27	5.1	9.1	4	4	16515	84164	activating signal cointegrator 1 complexsubunit 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CUE	No

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Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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INTS6	26512	integrator complex subunit 6 isoform a	NP_036273.1	3	3	3	4	1.17	0.61	6.43	32.57	13.1	35.6	3	3	5063	26512	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	VWA	No
RPLP2	6181	60S acidic ribosomal protein P2	NP_000995.1	2	7	8	60	1.17	0.59	1.92	10.07	12.6	33.8	31	31	1612	6181	ribosomal protein, large P2	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	-	Yes
EWSR1	2130	RNA-binding protein EWS isoform 1	NP_053733.2	5	6	6	19	1.16	1.54	7.65	10.11	30.1	55.3	11	11	592	2130	Ewing sarcoma breakpoint region 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;ZnF_RBZ	Yes
CDK11B	984	cyclin-dependent kinase 11B isoform 1	NP_001778.2	6	1	8	16	1.16	1.49					1	1	8909	984	cell division cycle 2-like 1 (PITSLREproteins)	Protein serine/threonine kinase activity	Nucleus;Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	CC;S_T_kinase	Yes
TRIM28	10155	transcription intermediary factor 1-beta	NP_005753.1	1	30	30	135	1.16	1.43	3.32	5.5	33	73.5	69	70	3445	10155	tripartite motif-containing 28	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;BBOX;BBC;PHD;BROMO	Yes
ARF4	378	ADP-ribosylation factor 4	NP_001651.1	1	6	9	61	1.16	1.42	4.37	12.2	18.5	68.9	13	13	3107	378	ADP-ribosylation factor 4	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ARF	Yes
CDC123	8872	cell division cycle protein 123 homolog	NP_006014.2	1	2	2	5	1.16	1.4	21.64	0.11	45.6	0.3	3	3	12586	8872	chromosome 10 open reading frame 7	Molecular function unknown	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	No
RCC1	1104	regulator of chromosome condensation isoform a	NP_001041659.1	3	8	8	27	1.16	1.36	7.49	4.66	33.3	24.2	14	14	1559	1104	regulator of chromosome condensation 1	Guanyl-nucleotide exchange factor activity	Nucleus	Guanine nucleotide exchange factor	Cell communication;Signal transduction	-	Yes
AKR1B1	231	aldose reductase	NP_001619.1	1	9	10	26	1.16	1.29	4.93	8.02	19.1	35.3	11	11	71	231	aldo-keto reductase family 1, member B1(aldose reductase)	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	ALDKR	Yes
DDX27	55661	probable ATP-dependent RNA helicase DDX27	NP_060365.7	1	12	12	23	1.16	1.28	3.45	4.43	15	21.5	14	14	10859	55661	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Helicase activity	Nucleus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC	Yes
CDV3	55573	protein CDV3 homolog isoform b	NP_060018.1	6	6	6	14	1.16	1.28	7.12	3.83	23.6	13.9	8	8	13627	55573	None	Molecular function unknown	Nucleus	Unclassified	Cell proliferation	NLS	Yes
ABHD5	51099	1-acylglycerol-3-phosphate O-acyltransferase ABHD5	NP_057090.2	1	1	1	3	1.16	1.27					1	1	11986	51099	abhydrolase domain containing 5	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	ABH	No
ITSN2	50618	intersectin-2 isoform 1	NP_006268.2	3	1	1	2	1.16	1.23					1	1	9193	50618	intersectin 2	Protein domain specific binding	Endosome;Cytoplasm	Adapter molecule	Protein transport	EH;CC;SH3;RHOGEF;PH;C2	Yes
MALT1	10892	mucosa-associated lymphoid tissue lymphoma translocation protein 1 isoform a	NP_006776.1	2	1	2	3	1.16	1.23					1	1	6892	10892	mucosa associated lymphoid tissue lymphomatranslocation gene 1	Endopeptidase activity	Cytoplasm	Enzyme: Hydrolase	Regulation of signal transduction	DEATH;IGC2;Ig_LIKE	Yes
NOL3	8996	nucleolar protein 3 isoform D	NP_001263248.1	4	3	3	7	1.16	1.23	0.79	6.29	1.6	13.4	3	3	5572	8996	nucleolar protein 3 (apoptosis repressor withCARD domain)	Protease inhibitor activity	Nucleolus	Cell cycle control protein	Cell communication;Signal transduction	CARD	Yes
HNRNPUL1	11100	heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform a	NP_008971.2	2	21	21	57	1.16	1.19	4.41	6.68	28.5	45.6	30	30	10428	11100	heterogeneous nuclear ribonucleoprotein U-like 1	Ribonucleoprotein;RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;RNA metabolism;Regulation of gene expression, epigenetic	SAP;SPRY	Yes
EIF2B3	8891	translation initiation factor eIF-2B subunit gamma isoform 1	NP_065098.1	3	8	8	13	1.16	1.18	2.9	4.98	9.5	16.7	8	8	9379	8891	eukaryotic translation initiation factor 2B,subunit 3 gamma, 58kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
SDF4	51150	45 kDa calcium-binding protein isoform 2 precursor	NP_057260.2	2	4	4	7	1.16	1.18	7.1	9.18	16.6	21.9	4	4	13113	51150	stromal cell derived factor 4	Calcium ion binding	Golgi lumen	Calcium binding protein	Cell communication;Signal transduction	EF;SP	Yes
NRF1	4899	nuclear respiratory factor 1 isoform 2	NP_001280092.1	2	1	1	2	1.16	1.17					1	1	2930	4899	nuclear respiratory factor 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
WDR82	80335	WD repeat-containing protein 82	NP_079498.2	1	5	5	8	1.16	1.15	6.73	2.28	17.5	5.9	5	5	15183	80335	None	Molecular function unknown	Nucleus	Integral membrane protein	Biological_process unknown	WD40	No
SDHA	6389	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial isoform 1	NP_004159.2	2	24	24	72	1.16	1.14	2.93	3.48	20.7	24.5	36	37	2914	6389	succinate dehydrogenase complex, subunit A,flavoprotein (Fp)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
BSDC1	55108	BSD domain-containing protein 1 isoform e	NP_001287887.1	5	1	1	1	1.16	1.12					1	1	7658	55108	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TPBG	7162	trophoblast glycoprotein precursor	NP_006661.1	1	7	7	22	1.16	1.11	6.41	4.55	25.2	16.8	11	11	1837	7162	trophoblast glycoprotein	Molecular function unknown	Plasma membrane	Integral membrane protein	Cell growth and/or maintenance	SP;TM;LRR	No

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G3BP1	10146	ras GTPase-activating protein-binding protein 1	NP_005745.1	1	15	15	95	1.16	1.1	3.44	3.73	29.3	30.1	52	52	6569	10146	None	Ribonuclease activity;RNA binding	Cytosol	RNA binding protein;Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Signal transduction	RRM	Yes
BAZ1A	11177	bromodomain adjacent to zinc finger domain protein 1A isoform a	NP_038476.2	2	3	3	4	1.16	1.1	5.5	31.48	11.1	65.8	3	3	12034	11177	bromodomain adjacent to zinc finger domain, 1A	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;PHD;BROMO;AT_hook	Yes
ARFGAP1	55738	ADP-ribosylation factor GTPase-activating protein 1 isoform b	NP_783202.1	5	4	4	7	1.16	1.1	6.08	3.77	15.8	9.3	5	5	6443	55738	ADP-ribosylation factor GTPase activatingprotein 1	GTPase activator activity	Golgi apparatus	GTPase activating protein	Lipid metabolism;Protein transport	ARFGAP	Yes
WBP11	51729	WW domain-binding protein 11	NP_057396.1	1	6	6	13	1.16	1.1	4.35	5.15	13.4	15.1	7	7	18293	51729	WW domain binding protein 11	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	No
COL4A3BP	10087	collagen type IV alpha-3-binding protein isoform 3	NP_001123577.1	3	6	6	14	1.16	1.08	4.61	4.39	15.2	13.5	8	8	5246	10087	collagen, type IV, alpha 3 (Goodpastureantigen) binding protein	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Signal transduction	PH;START;CC	Yes
TSSC1	7260	protein TSSC1	NP_003301.1	1	2	2	4	1.16	1.07	1.25	23	2.1	35.9	2	2	10287	7260	tumor suppressing subtransferable candidate 1	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	No
PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	NP_060362.3	1	14	14	34	1.16	1.03	4.75	6.89	22.2	29	16	16	10995	55660	formin binding protein 3	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	FF;NLS;WW	Yes
NXF1	10482	nuclear RNA export factor 1 isoform 1	NP_006353.2	2	14	14	25	1.16	1.02	4.76	6.37	20.8	24.7	14	14	4035	10482	nuclear RNA export factor 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PSMG1	8624	proteasome assembly chaperone 1 isoform a	NP_003711.1	3	6	6	8	1.16	1.02	3.95	19.66	10.3	47.4	5	5	5598	8624	Down syndrome critical region gene 2	Molecular function unknown	Plasma membrane	Unclassified	Cell communication;Signal transduction	-	No
TRMT5	57570	tRNA (guanine(37)-N1)-methyltransferase	NP_065861.3	1	4	4	6	1.16	1.02	9.73	14.51	22.8	30.3	4	4	17213	57570	KIAA1393	Methyltransferase activity	-	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	No
CHMP5	51510	charged multivesicular body protein 5 isoform 1	NP_057494.3	2	8	8	54	1.16	1.02	6.09	4.88	34	23.8	22	22	15408	51510	chromatin modifying protein 5	Transporter activity	-	Transport/cargo protein	Transport	-	Yes
SAE1	10055	SUMO-activating enzyme subunit 1 isoform a	NP_005491.1	3	13	13	22	1.16	1.01	10.32	7.9	45.3	29.5	13	13	18010	10055	None	Ligase activity	Nucleus	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
NCAPH	23397	condensin complex subunit 2 isoform 1	NP_056156.2	4	9	9	14	1.16	1.01	5.65	8.79	19.9	27.2	9	9	3820	23397	barren homolog (Drosophila)	Molecular function unknown	Nucleolus	Cell cycle control protein	Cell growth and/or maintenance	-	Yes
ZFC3H1	196441	zinc finger C3H1 domain-containing protein	NP_659419.3	1	3	3	5	1.16	0.99	1.06	11.84	2.1	20.5	3	3	14489	196441	None	Molecular function unknown	-	Unclassified	Biological_process unknown	HAT;CC	Yes
PNPT1	87178	polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor	NP_149100.2	1	16	16	30	1.16	0.98	6.13	10.4	30	43.9	17	17	18493	87178	polyribonucleotide nucleotidyltransferase 1	Exonuclease activity	Mitochondrion	RNA exonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH;S1	No
ZNF593	51042	zinc finger protein 593	NP_056955.2	1	3	3	4	1.16	0.97	0.34	15.72	0.7	26.7	3	3	15866	51042	zinc finger protein 593	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MRPS7	51081	28S ribosomal protein S7, mitochondrial	NP_057055.2	1	7	7	18	1.16	0.96	4.24	8.08	15.6	24.9	10	10	17601	51081	mitochondrial ribosomal protein S7	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
PTGES2	80142	prostaglandin E synthase 2 isoform 1	NP_079348.1	2	10	10	33	1.16	0.96	4.34	5.58	20.4	21.6	16	16	7458	80142	prostaglandin E synthase 2	Isomerase activity	Nucleus	Enzyme: Isomerase	Metabolism;Energy pathways	-	No
RPL7A	6130	60S ribosomal protein L7a	NP_000963.1	1	15	16	83	1.16	0.95	2.62	2.82	20.2	17.7	43	43	1712	6130	ribosomal protein L7a	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	NLS	Yes
PRRC2C	23215	protein PRRC2C	NP_055987.2	1	27	30	54	1.16	0.95	3.54	3.44	21.6	17.1	27	27									
HTATSF1	27336	HIV Tat-specific factor 1	NP_055315.2	1	8	8	13	1.16	0.92	11.02	9	37.2	23.6	8	8	2282	27336	HIV TAT specific factor 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	No
SPCS2	9789	signal peptidase complex subunit 2	NP_055567.2	1	5	5	17	1.16	0.91	3.29	9.26	11.5	25.8	9	9	15435	9789	signal peptidase complex subunit 2 homolog (S.cerevisiae)	Peptidase activity	Microsome	Protease	Protein metabolism	-	Yes
HEATR5B	54497	HEAT repeat-containing protein 5B	NP_061897.1	1	1	1	2	1.16	0.9					1	1	11145	54497	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
BRI3BP	140707	BRI3-binding protein precursor	NP_542193.3	1	3	3	8	1.16	0.89	4.12	6.56	10.8	13.1	5	5	9829	140707	BRI3 binding protein	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM;CC	No
BAG6	7917	large proline-rich protein BAG6 isoform a	NP_004630.3	4	11	11	30	1.16	0.88	2.8	10.58	11.8	32.9	13	12									
RPL32	6161	60S ribosomal protein L32	NP_000985.1	1	9	9	40	1.16	0.86	6.2	10.51	30.4	38.8	17	17	17995	6161	ribosomal protein L32	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes

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TTC4	7268	tetratricopeptide repeat protein 4 isoform 1	NP_004614.3	2	6	6	9	1.16	0.85	7.49	4.03	19.6	7.7	5	5	8417	7268	tetratricopeptide repeat domain 4	Molecular function unknown	-	Unclassified	Biological_process unknown	TPR;CC	Yes
SEC23IP	11196	SEC23-interacting protein	NP_009121.1	1	9	10	21	1.16	0.82	5.25	7.67	19.4	20.1	10	10	7152	11196	SEC23 interacting protein	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	SAM;CC	No
CYB5A	1528	cytochrome b5 isoform 1	NP_683725.1	3	2	2	7	1.16	0.79	2.54	7.47	5.9	11.8	4	4	8941	1528	cytochrome b-5	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	Yes
SCRN2	90507	secernin-2 isoform 1	NP_612364.2	2	1	1	1	1.16	0.78					1	1	10213	90507	secernin 2	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	SP;CC	Yes
CECR5	27440	cat eye syndrome critical region protein 5 isoform 2 precursor	NP_149061.1	2	3	3	5	1.16	0.77	0.61	9.19	1.2	12.3	3	3	16703	27440	cat eye syndrome chromosome region, candidate 5	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	SP	Yes
MAP4K5	11183	mitogen-activated protein kinase kinase kinase kinase 5	NP_006566.2	1	3	3	3	1.16	0.77	3.18	12.73	6.4	17	3	3	5374	11183	mitogen-activated protein kinase kinase kinasekinase 5	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CNH	Yes
RABGAP1L	9910	rab GTPase-activating protein 1-like isoform C	NP_001230694.1	2	1	2	4	1.16	0.75					1	1	16464	9910	RAB GTPase activating protein 1-like	GTPase activator activity	-	GTPase activating protein	Biological_process unknown	PTB;TBC	No
RBBP7	5931	histone-binding protein RBBP7 isoform 2	NP_002884.1	2	2	8	21	1.16	0.73	24.67	9.64	52.7	12.2	3	3	4231	5931	retinoblastoma binding protein 7	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
UBR2	23304	E3 ubiquitin-protein ligase UBR2 isoform 1	NP_056070.1	2	3	3	4	1.16	0.73					1	1	9853	23304	ubiquitin protein ligase E3 component n-recognin2	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	RING;CC	Yes
FAM126A	84668	hyccin	NP_115970.2	1	2	2	3	1.16	0.71	57.5	28.67	120.4	29.4	2	2	16837	84668	None	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	No
PAN2	9924	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 isoform 1	NP_001120932.1	3	1	1	2	1.16	0.69					1	1	15640	9924	ubiquitin specific protease 52	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UCH;EXOIII	No
LHFPL2	10184	lipoma HMGIC fusion partner-like 2 protein	NP_005770.1	1	1	1	2	1.16	0.62					1	1	17272	10184	lipoma HMGIC fusion partner-like 2	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM	No
RAD23A	5886	UV excision repair protein RAD23 homolog A isoform 2	NP_001257291.1	3	3	5	26	1.16	0.57		19.5		15.8	1	2	7191	5886	RAD23 homolog A (S. cerevisiae)	DNA binding	Nucleus	DNA repair protein	DNA repair	UBQ;UBA;STI1	Yes
THBS2	7058	thrombospondin-2 precursor	NP_003238.2	1	1	2	4	1.15	1.92					1	1	1766	7058	thrombospondin 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	TSPN;VWC;TSP1;EGF;TSP3	Yes
COASY	80347	bifunctional coenzyme A synthase isoform c	NP_001035997.2	2	3	3	4	1.15	1.79	2.58	22.23	4.2	61.1	2	2	13080	80347	Coenzyme A synthase	Transferase activity	Cytoplasm	Enzyme: Transferase	Metabolism;Energy pathways	SP	Yes
SCARB1	949	scavenger receptor class B member 1 isoform 1	NP_005496.4	2	5	5	9	1.15	1.61	5.35	8.32	15.2	33.6	6	6	3024	949	scavenger receptor class B, member 1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;TM	No
UPP1	7378	uridine phosphorylase 1 isoform a	NP_001274355.1	2	15	15	40	1.15	1.57	8.86	3.41	50.6	25.5	22	22	8932	7378	uridine phosphorylase 1	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase	Metabolism;Energy pathways;Pyrimidine salvage	-	Yes
LAMC1	3915	laminin subunit gamma-1 precursor	NP_002284.3	1	22	22	54	1.15	1.5	4.73	6.43	30	55.5	29	29	1030	3915	laminin, gamma 1 (formerly LAMB2)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	LAMNT;EGFLAM;LAMB;SP;CC	Yes
EML3	256364	echinoderm microtubule-associated protein-like 3 isoform 1	NP_001287722.1	3	2	2	3	1.15	1.49					1	1	8193	256364	echinoderm microtubule associated protein like 3	Cytoskeletal protein binding	-	Cytoskeletal associated protein	Cytoskeleton organization and biogenesis	CC;WD40	Yes
WDR92	116143	WD repeat-containing protein 92 isoform 1	NP_612467.1	2	1	1	1	1.15	1.48					1	1	14012	116143	None	Calcium ion binding;Caspase activator activity	Nucleus	Calcium binding protein	Cell communication;Signal transduction;Regulation of cell cycle;RNA metabolism;Transcription;Apoptosis	WD40	Yes
PFN1	5216	profilin-1	NP_005013.1	1	11	11	127	1.15	1.45	4.9	4.27	47.7	52.8	64	64	1452	5216	profilin 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	PROF	Yes
FABP1	2168	fatty acid-binding protein, liver	NP_001434.1	1	2	2	19	1.15	1.41	6.37	2.75	19.6	11	7	8	612	2168	fatty acid binding protein 1, liver	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
CARS	833	cysteine--tRNA ligase, cytoplasmic isoform c	NP_001014437.1	4	23	23	54	1.15	1.36	3.71	2.53	24.2	19.3	31	31	464	833	cysteinyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	CC	Yes
BZW1	9689	basic leucine zipper and W2 domain-containing protein 1 isoform 2	NP_001193997.1	4	10	13	42	1.15	1.35	6.33	5.34	34.2	33.8	21	21	16570	9689	basic leucine zipper and W2 domains 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
UQCC1	55245	ubiquinol-cytochrome-c reductase complex assembly factor 1 isoform a	NP_060714.3	3	2	2	3	1.15	1.32	12.88	1.28	26	2.9	3	3									
ADRM1	11047	proteasomal ubiquitin receptor ADRM1 isoform 1	NP_008933.2	2	7	7	23	1.15	1.31	6.74	8.03	27.3	37.7	12	12	6440	11047	adhesion regulating molecule 1	Receptor activity;Molecular function unknown	Cytoplasm;Microsome	Adhesion molecule;Cell surface receptor	Cell communication;Signal transduction	SP;TM	Yes
ALDH7A1	501	alpha-aminoadipic semialdehyde dehydrogenase isoform 2	NP_001188306.1	3	29	29	195	1.15	1.3	2.97	2.61	34.8	34.2	97	96	124	501	aldehyde dehydrogenase 7 family, member A1	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
RBMS2	5939	RNA-binding motif, single-stranded-interacting protein 2	NP_002889.1	3	3	3	3	1.15	1.29					1	1	3860	5939	RNA binding motif, single stranded interactingprotein 2	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes

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SOX9	6662	transcription factor SOX-9	NP_000337.1	1	1	1	1	1.15	1.26					1	1	6427	6662	SRY (sex determining region Y)-box 9 (campomelicdysplasia, autosomal sex-reversal)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG	No
MESDC2	23184	LDLR chaperone MESD precursor	NP_055969.1	1	3	3	4	1.15	1.24	2.57	17.97	5.1	40.1	3	3	12129	23184	mesoderm development candidate 2	Chaperone activity	Endoplasmic reticulum	Chaperone	Cell growth and/or maintenance	SP	Yes
CANX	821	calnexin precursor	NP_001737.1	1	16	16	56	1.15	1.24	3.39	3.51	23	25.7	34	34	252	821	calnexin	Chaperone activity	Endoplasmic reticulum membrane	Chaperone	Protein folding	SP;TM;CC	Yes
NAT10	55226	N-acetyltransferase 10 isoform a	NP_078938.2	3	25	26	64	1.15	1.24	4.27	4.16	28.8	30.4	33	33	10964	55226	None	Acyltransferase activity	Nucleus	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM	Yes
TMEM68	137695	transmembrane protein 68 isoform 1	NP_001273586.1	1	1	1	2	1.15	1.22					1	1	8128	137695	None	Acyltransferase activity	-	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM	No
MRPL39	54148	39S ribosomal protein L39, mitochondrial isoform a	NP_059142.2	2	6	6	11	1.15	1.19	9.55	15.29	25	42.5	5	5	11371	54148	mitochondrial ribosomal protein L39	Structural constituent of ribosome;RNA binding	Mitochondrion	Ribosomal subunit	Biological_process unknown	-	Yes
KIF2A	3796	kinesin-like protein KIF2A isoform 4	NP_001230882.1	4	10	12	23	1.15	1.18	4.63	5.83	16.9	22	10	10	3996	3796	kinesin heavy chain member 2	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	CC;KISC	Yes
RAI14	26064	ankycorbin isoform d	NP_001138997.1	4	19	19	43	1.15	1.18	2.85	4.48	15.8	25.8	23	23	9416	26064	retinoic acid induced 14	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	ANK;CC	No
CD55	1604	complement decay-accelerating factor isoform 5 precursor	NP_001287831.1	5	1	1	1	1.15	1.15					1	1	500	1604	decay accelerating factor for complement (CD55,Cromer blood group system)	Complement activity	Plasma membrane	Complement protein	Immune response	SUSHI;SP;GPI	Yes
ITFG1	81533	T-cell immunomodulatory protein isoform 1 precursor	NP_110417.2	2	2	2	2	1.15	1.15					1	1	16692	81533	None	Molecular function unknown	Plasma membrane	Integral membrane protein	Immune response	TM;SP	Yes
GLS	2744	glutaminase kidney isoform, mitochondrial isoform 2	NP_001243239.1	2	10	10	23	1.15	1.1	4.18	8.56	16.8	33.4	12	12	700	2744	glutaminase	Deaminase activity	Mitochondrion	Enzyme: Deaminase	Metabolism;Energy pathways	ANK	Yes
MGAT4B	11282	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B isoform 2	NP_463459.1	2	1	1	2	1.15	1.1					1	1	5190	11282	mannosyl (alpha-1,3-)-glycoproteinbeta-1,4-N-acetylglucosaminyltransferase, isoenzyme B	Catalase activity	-	Enzyme: Glucosaminyltransferase	Glycoprotein metabolism	TM	No
PSMA3	5684	proteasome subunit alpha type-3 isoform 1	NP_002779.1	2	9	9	34	1.15	1.09	3.28	9.11	17	46.5	20	20	1463	5684	proteasome (prosome, macropain) subunit, alphatype, 3	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
PRUNE	58497	protein prune homolog isoform 1	NP_067045.1	2	1	1	4	1.15	1.09	9.31	4.2	15.2	6.5	2	2	15188	58497	prune homolog (Drosophila)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
RABL6	55684	rab-like protein 6 isoform 1	NP_078994.3	3	7	7	15	1.15	1.07	8.08	9.67	29.9	33.7	10	10									
EIF4A3	9775	eukaryotic initiation factor 4A-III	NP_055555.1	1	14	16	54	1.15	1.07	3.28	7.14	18.7	38.6	24	24	6482	9775	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
RIC8A	60626	synembryn-A isoform 2	NP_001273063.1	3	15	15	30	1.15	1.06	6.12	6	30.6	27.6	18	18	12373	60626	None	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	-	Yes
RPL38	6169	60S ribosomal protein L38	NP_001030335.1	1	3	3	20	1.15	1.05	3.07	3.94	11.1	13.1	10	10	16048	6169	ribosomal protein L38	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	No
SPINT2	10653	kunitz-type protease inhibitor 2 isoform a precursor	NP_066925.1	2	2	2	3	1.15	1.05	6.23	13.06	10.2	19.5	2	2	5495	10653	serine protease inhibitor, Kunitz type, 2	Protease inhibitor activity	Plasma membrane	Protease inhibitor	Protein metabolism	TM;KUNITZ;SP	Yes
FAM96A	84191	MIP18 family protein FAM96A isoform a precursor	NP_115607.1	2	2	2	3	1.15	1.05	3.48	3.69	5.7	5.5	2	2	8010	84191	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes
ASAP1	50807	arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 isoform 1	NP_060952.2	2	3	3	8	1.15	1.04	7.07	1.93	16.4	4	4	4	5809	50807	development and differentiation enhancingfactor 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	BAR;PH;ARFGAP;ANK;SH3	Yes
RASAL2	9462	ras GTPase-activating protein nGAP isoform 2	NP_733793.2	3	8	10	20	1.15	1.04	4.61	3.13	14.1	8.6	7	7	5845	9462	RAS protein activator like 2	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	PH;C2;RASGAP;CC	Yes
ALDH18A1	5832	delta-1-pyrroline-5-carboxylate synthase isoform 1	NP_002851.2	2	18	18	52	1.15	1.04	1.98	6.44	12	36.5	28	28	696	5832	aldehyde dehydrogenase 18 family, member A1	Ligase activity	Mitochondrion	Enzyme: Phosphotransferase;Enzyme: Ligase;Enzyme: Reductase	Metabolism;Energy pathways;Amino acid and derivative metabolism	-	Yes
GOLPH3L	55204	Golgi phosphoprotein 3-like	NP_060648.2	1	2	2	5	1.15	1.04	10.22	10.02	20.5	18.2	3	3	17048	55204	golgi phosphoprotein 3-like	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
FMNL2	114793	formin-like protein 2	NP_443137.2	3	4	4	9	1.15	1.03	5.32	9.62	12.3	20.1	4	4	13545	114793	formin-like 2	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	FH2;CC	No
ELOVL1	64834	elongation of very long chain fatty acids protein 1 isoform 1	NP_073732.1	3	2	2	11	1.15	1.01	7.38	0.35	17	0.7	4	4	10935	64834	elongation of very long chain fatty acids(FEN1/Elo2, SUR4/Elo3, yeast)-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
EMC3	55831	ER membrane protein complex subunit 3	NP_060917.1	1	3	3	6	1.15	1.01	5.43	21.05	10.8	38.2	3	3									
EDC4	23644	enhancer of mRNA-decapping protein 4	NP_055144.3	5	16	16	35	1.15	1.01	6.54	8.76	29.8	35.2	15	15	6911	23644	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	WD40;CC;NLS	Yes

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NFATC2IP	84901	NFATC2-interacting protein	NP_116204.3	1	3	3	7	1.15	1	11.23	16.68	26.3	34.4	4	4	10971	84901	nuclear factor of activated T-cells,cytoplasmic, calcineurin-dependent 2 interacting protein	Molecular function unknown	-	Unclassified	Protein metabolism	UBQ	No
YWHAB	7529	14-3-3 protein beta/alpha	NP_003395.1	1	7	14	147	1.15	0.99	3.86	7.4	24.2	40.4	29	28	3184	7529	tyrosine 3-monooxygenase/tryptophan5-monooxygenase activation protein, beta polypeptide	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Signal transduction	CC	Yes
SMARCA2	6595	probable global transcription activator SNF2L2 isoform a	NP_001276325.1	6	2	5	7	1.15	0.99	29.66	27.72	51.1	40.4	2	2	2483	6595	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 2	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRK;HELIC;BROMO;DEXDc;CC	Yes
GARS	2617	glycine--tRNA ligase precursor	NP_002038.2	1	24	24	101	1.15	0.99	4.6	7.32	38.6	54.6	50	50	2617	2617	glycyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	SP	Yes
CDC5L	988	cell division cycle 5-like protein	NP_001244.1	1	21	21	46	1.15	0.98	4.14	5.25	23.7	25.7	24	24	4184	988	CDC5 cell division cycle 5-like (S. pombe)	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	SANT;CC	Yes
PGAM5	192111	serine/threonine-protein phosphatase PGAM5, mitochondrial isoform 2	NP_001164015.1	1	1	8	13	1.15	0.98					1	1	14681	192111	None	Catalytic activity	Cytosol	Enzyme: Mutase	Metabolism;Energy pathways	SP	No
LSM2	57819	U6 snRNA-associated Sm-like protein LSm2	NP_067000.1	1	4	4	7	1.15	0.97	7.68	12.91	19.9	28.6	5	5	6282	57819	LSM2 homolog, U6 small nuclear RNA associated(S. cerevisiae)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
SLC7A1	6541	high affinity cationic amino acid transporter 1	NP_003036.1	1	1	1	1	1.15	0.97					1	1	91	6541	solute carrier family 7 (cationic amino acidtransporter, y+ system), member 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
SLC25A22	79751	mitochondrial glutamate carrier 1	NP_078974.1	2	8	8	20	1.15	0.96	7.24	9.65	22.3	24.9	7	7	15356	79751	solute carrier family 25 (mitochondrialcarrier: glutamate), member 22	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	TM	Yes
RPS3A	6189	40S ribosomal protein S3a isoform 1	NP_000997.1	2	21	21	102	1.15	0.94	2.54	3.56	21.9	25.2	55	55	1606	6189	ribosomal protein S3A	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	-	Yes
METTL16	79066	methyltransferase-like protein 16	NP_076991.3	1	2	2	2	1.15	0.93					1	1									
NAPG	8774	gamma-soluble NSF attachment protein	NP_003817.1	1	2	2	3	1.15	0.92					1	1	4448	8774	N-ethylmaleimide-sensitive factor attachmentprotein, gamma	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	-	Yes
EPB41L2	2037	band 4.1-like protein 2 isoform a	NP_001422.1	4	10	10	15	1.15	0.92	8.47	9	28	23.6	8	8	9126	2037	erythrocyte membrane protein band 4.1-like 2	Structural constituent of cytoskeleton	Plasma membrane	Cytoskeletal protein	Cell communication;Signal transduction	B41;CC	Yes
PSMB10	5699	proteasome subunit beta type-10 precursor	NP_002792.1	1	1	1	4	1.15	0.91	28.43	4.82	48.9	6.2	2	2	1465	5699	proteasome (prosome, macropain) subunit, betatype, 10	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
KNOP1	400506	lysine-rich nucleolar protein 1	NP_001013009.2	1	2	2	4	1.15	0.91	6.25	3.78	10.2	4.8	2	2									
IQGAP2	10788	ras GTPase-activating-like protein IQGAP2 isoform 1	NP_006624.2	6	2	5	15	1.15	0.9	21.5	0.51	36.1	0.7	2	2	9253	10788	IQ motif containing GTPase activating protein2	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	CC;CH;IQ;RASGAP;WW	Yes
TPX2	22974	targeting protein for Xklp2	NP_036244.2	1	1	1	1	1.15	0.9					1	1	5802	22974	TPX2, microtubule-associated protein homolog(Xenopus laevis)	ATP binding	Nucleus	Cell cycle control protein	Cell growth and/or maintenance;Spindle assembly	CC	Yes
KIFAP3	22920	kinesin-associated protein 3 isoform 1	NP_055785.2	4	4	4	13	1.15	0.89	9.57	15.32	27.4	34.3	6	6	3499	22920	kinesin-associated protein 3	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ARM	Yes
COX15	1355	cytochrome c oxidase assembly protein COX15 homolog isoform 1	NP_510870.1	2	2	2	3	1.15	0.89	13.52	20.19	22.2	25.9	2	2	4707	1355	COX15 homolog, cytochrome c oxidase assemblyprotein (yeast)	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	TM	Yes
CAMLG	819	calcium signal-modulating cyclophilin ligand	NP_001736.1	1	2	2	3	1.15	0.88					1	1	3073	819	calcium modulating ligand	Receptor binding	Endoplasmic reticulum	Membrane bound ligand	Cell communication;Signal transduction	TM	Yes
EXT2	2132	exostosin-2 isoform 1	NP_000392.3	3	2	2	2	1.15	0.86	31.2	64.45	54.2	92.6	2	2	599	2132	exostoses (multiple) 2	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase	Metabolism;Energy pathways;Glycosaminoglycan metabolism	TM	Yes
BAZ1B	9031	tyrosine-protein kinase BAZ1B	NP_115784.1	1	8	8	12	1.15	0.8	8.7	5.74	22.7	10.3	5	5	10416	9031	bromodomain adjacent to zinc finger domain, 1B	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of gene expression, epigenetic	CC;PHD;BROMO;PEST;NLS;DDT;RING	Yes

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SAP18	10284	histone deacetylase complex subunit SAP18	NP_005861.2	1	2	2	3	1.15	0.79	0.64	8.84	1	9.9	2	2	4256	10284	sin3-associated polypeptide, 18kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
NUTF2	10204	nuclear transport factor 2	NP_005787.1	1	1	1	4	1.15	0.7	22.53	66.17	47.2	94.6	3	3	12050	10204	nuclear transport factor 2	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
KDM2A	22992	lysine-specific demethylase 2A isoform a	NP_036440.1	2	3	3	4	1.15	0.68	4.73	60.51	7.7	63.5	2	2	5741	22992	F-box and leucine-rich repeat protein 11	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism;Regulation of gene expression, epigenetic	JMJC;PHD;F_BOX;LRR	Yes
HEATR3	55027	HEAT repeat-containing protein 3	NP_891552.1	1	2	2	3	1.15	0.66	0.59	89.75	1	100.9	2	2	7945	55027	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
AVL9	23080	late secretory pathway protein AVL9 homolog	NP_055875.1	1	1	1	3	1.15	0.62					1	1	13788	23080	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
FLCN	201163	folliculin isoform 1	NP_659434.2	1	1	1	1	1.15	0.61					1	1	6278	201163	folliculin	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	No
STX18	53407	syntaxin-18	NP_058626.1	1	1	1	2	1.15	0.56	16.94	25.72	28	20.7	2	2	6923	53407	syntaxin 18	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	CC;TM	Yes
TBC1D22A	25771	TBC1 domain family member 22A isoform a	NP_055161.1	3	1	1	2	1.15	0.55					1	1	15474	25771	TBC1 domain family, member 22A	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	TBC	Yes
IL18	3606	interleukin-18 isoform 1 proprotein	NP_001553.1	2	5	5	6	1.15	0.53	11.07	27.59	25.8	29.8	4	4	2976	3606	interleukin 18 (interferon-gamma-inducingfactor)	Cytokine activity	Extracellular	Cytokine	Immune response	-	Yes
GSTO1	9446	glutathione S-transferase omega-1 isoform 1	NP_004823.1	3	9	9	28	1.14	1.87	3.87	2.09	15.4	13.6	12	12	10401	9446	glutathione S-transferase omega 1	Glutathione transferase activity	Nucleus	Enzyme: Glutathione transferase	Metabolism;Energy pathways	-	Yes
MADD	8567	MAP kinase-activating death domain protein isoform d	NP_003673.3	10	3	3	4	1.14	1.81	37.2	33.64	65.8	104.9	2	2	4664	8567	MAP-kinase activating death domain	Kinase regulator activity;Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Anti-apoptosis;Cell communication;Signal transduction	NLS	Yes
DUSP12	11266	dual specificity protein phosphatase 12	NP_009171.1	1	1	1	2	1.14	1.64					1	1	5323	11266	dual specificity phosphatase 12	Protein tyrosine/serine/threonine phosphatase activity	Nucleus	Dual specificity phosphatase	Cell communication;Signal transduction	DSPC	Yes
NRBP1	29959	nuclear receptor-binding protein	NP_037524.1	1	6	6	14	1.14	1.59	1.03	9.23	3.1	40.3	7	7	5819	29959	nuclear receptor binding protein	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	S_T_Y_Kinase;NLS	No
RNH1	6050	ribonuclease inhibitor	NP_002930.2	1	23	23	107	1.14	1.55	3.01	3.77	25.5	45.1	54	54	1412	6050	ribonuclease/angiogenin inhibitor 1	Translation regulator activity	Cytoplasm	Translation regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LRR	Yes
ANXA6	309	annexin A6 isoform 1	NP_001146.2	2	50	50	221	1.14	1.53	2.65	3.15	33.3	55	114	114	231	309	annexin A6	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein	Cell communication;Signal transduction	ANX	Yes
RARS2	57038	probable arginine--tRNA ligase, mitochondrial precursor	NP_064716.2	1	2	2	3	1.14	1.48	7.35	24.05	11.9	53.8	2	2	15209	57038	arginyl-tRNA synthetase-like	Catalytic activity	-	Enzyme: Synthase	Metabolism;Energy pathways	-	No
F8A1	8263	factor VIII intron 22 protein	NP_036283.2	1	1	1	2	1.14	1.42					1	1	2374	8263	coagulation factor VIII-associated (intronictranscript) 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
AGRN	375790	agrin isoform 2 precursor	NP_940978.2	2	30	30	57	1.14	1.41	3.27	4.16	20.3	32.4	29	29	10550	375790	agrin	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	KAZAL;EGFLAM;EGF;SEA;EGFCA;LAMG;FOLN	Yes
VCP	7415	transitional endoplasmic reticulum ATPase	NP_009057.1	2	52	52	337	1.14	1.38	2.38	2.78	36	53	166	167	3013	7415	valosin-containing protein	ATPase activity	Cytoplasm;Nucleus;Nucleolus;Perinuclear region	ATPase	Metabolism;Energy pathways	AAA	Yes
PAFAH1B2	5049	platelet-activating factor acetylhydrolase IB subunit beta isoform a	NP_002563.1	4	2	2	16	1.14	1.36	3.77	6.52	11.4	23.8	7	7	3940	5049	platelet-activating factor acetylhydrolase,isoform Ib, beta subunit 30kDa	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Cell communication;Signal transduction	-	No
STRN4	29888	striatin-4 isoform 2	NP_001034966.1	2	6	6	10	1.14	1.35	10.88	8.52	28.4	26.2	5	5	18125	29888	striatin, calmodulin binding protein 4	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	CC;WD40	Yes
IPO11	51194	importin-11 isoform 1	NP_001128251.1	2	6	6	10	1.14	1.34	11.49	8.21	26.7	22.4	4	4	10003	51194	importin 11	Transporter activity	Nucleus	Transport/cargo protein	Cell communication;Signal transduction	IBN_NT	Yes
DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 1	NP_003578.2	2	6	6	15	1.14	1.31	6.35	6	20.7	22.6	8	8	4555	8449	DEAH (Asp-Glu-Ala-His) box polypeptide 16	ATPase activity	Nucleus	ATPase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;DEXDc;CC	Yes
AHSA1	10598	activator of 90 kDa heat shock protein ATPase homolog 1	NP_036243.1	1	12	12	38	1.14	1.29	3.08	5.05	16.1	30.6	21	21	9768	10598	AHA1, activator of heat shock 90kDa proteinATPase homolog 1 (yeast)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
MRPL14	64928	39S ribosomal protein L14, mitochondrial	NP_115487.2	1	4	4	13	1.14	1.28	2.65	6.11	7.4	19.3	6	6	14741	64928	mitochondrial ribosomal protein L14	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
RAVER1	125950	ribonucleoprotein PTB-binding 1	NP_597709.2	1	11	11	30	1.14	1.28	4.63	6.55	20.7	33.5	15	15	11484	125950	None	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein	Biological_process unknown	RRM	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
RRP1	8568	ribosomal RNA processing protein 1 homolog A	NP_003674.1	1	5	5	10	1.14	1.27	2.5	2.41	6.3	6.8	5	5	10857	8568	None	Molecular function unknown	Nucleolus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
SERPINB8	5271	serpin B8 isoform a	NP_002631.3	5	2	4	11	1.14	1.27	4.57	4.1	10.4	10.4	4	4	3412	5271	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 8	Protease inhibitor activity	Nucleus	Protease inhibitor	Protein metabolism	SERPIN	Yes
RUVBL2	10856	ruvB-like 2	NP_006657.1	1	28	28	107	1.14	1.26	3.39	3.14	29	29.6	54	54	16070	10856	RuvB-like 2 (E. coli)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA	Yes
PATL1	219988	protein PAT1 homolog 1	NP_689929.2	1	4	4	9	1.14	1.23	24.27	11.21	68	31.5	5	5	8214	219988	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	Yes
GMPPA	29926	mannose-1-phosphate guanyltransferase alpha	NP_995319.1	1	8	8	15	1.14	1.22	0.92	4.39	2.6	13.2	6	6	13588	29926	GDP-mannose pyrophosphorylase A	Phosphorylase activity	-	Enzyme: Phosphorylase	Carbohydrate mediated signaling;Metabolism	-	No
KRR1	11103	KRR1 small subunit processome component homolog	NP_008974.5	1	5	5	13	1.14	1.22	11.51	2.49	33.1	7.5	6	6	11027	11103	HIV-1 rev binding protein 2	DNA binding	Nucleolus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
KRI1	65095	protein KRI1 homolog	NP_075384.3	1	4	4	10	1.14	1.2	3.12	6.2	8.7	18.4	6	6	10969	65095	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	CC	No
SKIV2L2	23517	superkiller viralicidic activity 2-like 2	NP_056175.3	1	23	23	49	1.14	1.19	2.12	3.35	12.6	20.9	27	27	13777	23517	superkiller viralicidic activity 2-like 2 (S.cerevisiae)	Helicase activity	Nucleus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC	Yes
INTS8	55656	integrator complex subunit 8	NP_060334.2	1	2	2	4	1.14	1.18	38.15	8.19	67.8	13.7	2	2	8626	55656	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NOP14	8602	nucleolar protein 14 isoform 1	NP_001278907.1	2	7	7	15	1.14	1.18	13.44	9.45	38.7	27.9	6	6	12827	8602	chromosome 4 open reading frame 9	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
SFPQ	6421	splicing factor, proline- and glutamine-rich	NP_005057.1	1	21	22	67	1.14	1.17	4.15	2.61	26.3	16.9	30	30	7284	6421	splicing factor proline/glutamine rich(polypyrimidine tract binding protein associated)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
STK10	6793	serine/threonine-protein kinase 10	NP_005981.3	1	16	17	46	1.14	1.17	3.19	6.14	16.4	33.1	20	20	6796	6793	serine/threonine kinase 10	Protein serine/threonine kinase activity	-	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
TRIM21	6737	E3 ubiquitin-protein ligase TRIM21	NP_003132.2	1	12	12	15	1.14	1.16	2.95	17.27	9.6	61.7	8	8	170	6737	tripartite motif-containing 21	Ribonucleoprotein	Plasma membrane	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;SPRY;PRY;BBOX;CC	Yes
SYAP1	94056	synapse-associated protein 1	NP_116185.2	1	5	5	8	1.14	1.16	3.42	1.86	7.8	4.3	4	4	6733	94056	synapse associated protein 1, SAP47 homolog(Drosophila)	Transporter activity	Nucleus;Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	CC	No
RPL29	6159	60S ribosomal protein L29	NP_000983.1	1	2	2	10	1.14	1.16	3	1.3	7.6	3.3	5	5	3495	6159	ribosomal protein L29	Structural constituent of ribosome	Plasma membrane	Ribosomal subunit	Protein metabolism	-	Yes
SRP14	6727	signal recognition particle 14 kDa protein	NP_003125.3	1	7	7	21	1.14	1.15	9.89	2.2	32.9	7.2	8	8	2831	6727	signal recognition particle 14kDa (homologousAlu RNA binding protein)	RNA binding	Cytoplasm	RNA binding protein	Protein metabolism	-	Yes
DNAJC3	5611	dnaJ homolog subfamily C member 3 precursor	NP_006251.1	1	10	10	26	1.14	1.13	1.96	5.75	8.1	23.8	13	13	3114	5611	DnaJ (Hsp40) homolog, subfamily C, member 3	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	TPR;DNAJ	No
OSBPL8	114882	oxysterol-binding protein-related protein 8 isoform a	NP_065892.1	2	7	8	18	1.14	1.13	7.37	3.16	25.7	10.8	9	9	9478	114882	oxysterol binding protein-like 8	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	PH;CC;TM	Yes
PHACTR4	65979	phosphatase and actin regulator 4 isoform 2	NP_076412.3	2	3	3	4	1.14	1.11	3.84	18.83	6.2	30.1	2	2	7816	65979	phosphatase and actin regulator 4	Phosphatase regulator activity	Perinuclear region	Regulatory/other subunit	Signal transduction	-	No
PA2G4	5036	proliferation-associated protein 2G4	NP_006182.2	1	23	23	110	1.14	1.11	4.4	5.48	39.9	49.3	59	59	3685	5036	proliferation-associated 2G4, 38kDa	Transcription regulator activity;DNA binding	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
STK38L	23012	serine/threonine-protein kinase 38-like	NP_055815.1	1	3	3	5	1.14	1.09	3.8	0.37	7.5	0.7	3	3	10256	23012	serine/threonine kinase 38 like	Protein serine/threonine kinase activity	-	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
C7orf50	84310	uncharacterized protein C7orf50	NP_115726.1	1	5	5	7	1.14	1.09	11.32	5.51	26.3	12	4	4	14413	84310	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
RBM12B	389677	RNA-binding protein 12B	NP_976324.2	1	8	8	10	1.14	1.07	6.13	5.15	20	15.6	8	8	14213	389677	None	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
CYCS	54205	cytochrome c	NP_061820.1	1	4	4	15	1.14	1.06	8	6.32	26.3	19	8	8	479	54205	cytochrome c, somatic	Catalytic activity	Mitochondrion	Enzyme: Oxidase	Metabolism;Energy pathways	-	Yes
ADSS	159	adenylosuccinate synthetase isozyme 2	NP_001117.2	1	12	14	45	1.14	1.05	2.03	5.31	11.3	27.9	24	24	50	159	adenylosuccinate synthase	Ligase activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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MAPK13	5603	mitogen-activated protein kinase 13	NP_002745.1	6	4	5	9	1.14	1.04	2.4	5.22	5.5	10.9	4	4	9113	5603	mitogen-activated protein kinase 13	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
RPAP3	79657	RNA polymerase II-associated protein 3 isoform 1	NP_078880.2	3	8	8	16	1.14	1.04	3.17	12.66	9.6	35.8	7	7	7970	79657	None	Molecular function unknown	Cytoplasm	Unclassified	Apoptosis	CC;TPR	No
TSC2	7249	tuberin isoform 1	NP_000539.2	3	3	3	7	1.14	1.03	7.96	6.82	18.3	14.1	4	4	1850	7249	tuberous sclerosis 2	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	-	Yes
ACBD5	91452	acyl-CoA-binding domain-containing protein 5 isoform 1	NP_663736.2	5	4	4	5	1.14	1.03	5.15	13.02	11.8	27.3	4	4	12415	91452	acyl-Coenzyme A binding domain containing 5	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;TM	No
TUBB4B	10383	tubulin beta-4B chain	NP_006079.1	2	4	35	758	1.14	1.03	3.81	6.72	25.3	41.3	33	33									
TMUB1	83590	transmembrane and ubiquitin-like domain-containing protein 1	NP_001129516.1	1	1	1	2	1.14	1.02					1	1	12910	83590	chromosome 7 open reading frame 21	Molecular function unknown	Integral to membrane	Integral membrane protein	Protein metabolism	SP;UBQ;TM	No
RIOK3	8780	serine/threonine-protein kinase RIO3	NP_003822.2	1	3	3	5	1.14	1.01	26.9	33.56	45.4	50.8	2	2	4659	8780	RIO kinase 3 (yeast)	Protein kinase activity	-	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
DDX51	317781	ATP-dependent RNA helicase DDX51	NP_778236.2	1	4	4	8	1.14	1.01	2.07	5.51	5.3	12.5	5	5	10865	317781	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	Helicase activity	Nucleolus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;DEXDc;CC	No
CKAP4	10970	cytoskeleton-associated protein 4	NP_006816.2	6	43	44	177	1.14	1.01	1.38	2.92	14.7	28.3	87	88	16717	10970	cytoskeleton-associated protein 4	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	TM;CC	No
PPFIA1	8500	liprin-alpha-1 isoform b	NP_003617.1	14	7	8	15	1.14	1	11.77	14.1	33.7	35.7	6	6	11451	8500	protein tyrosine phosphatase, receptor type, fpolypeptide (PTPRF), interacting protein (liprin), alpha 1	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein	Cell growth and/or maintenance	SAM;CC	Yes
OTUD6B	51633	OTU domain-containing protein 6B isoform 1	NP_057107.3	2	3	3	4	1.14	0.98	0.04	7.06	0.1	9.8	2	2	13041	51633	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
DUSP3	1845	dual specificity protein phosphatase 3	NP_004081.1	1	4	4	7	1.14	0.98	12.7	6.47	29.5	12.7	4	4	2553	1845	dual specificity phosphatase 3 (vaccinia virusphosphatase VH1-related)	Protein tyrosine/serine/threonine phosphatase activity	Nucleus	Dual specificity phosphatase	Cell communication;Signal transduction	DSPC	Yes
PPP1R12A	4659	protein phosphatase 1 regulatory subunit 12A isoform a	NP_002471.1	4	20	20	45	1.14	0.95	2.75	4.89	15.7	23.5	25	25	3606	4659	protein phosphatase 1, regulatory(inhibitor) subunit 12A	Phosphatase regulator activity	Cytoplasm	Regulatory/other subunit	Metabolism;Energy pathways	ANK;CC	Yes
RFC4	5984	replication factor C subunit 4	NP_002907.1	1	5	5	14	1.14	0.94	12.12	14.95	40.5	41.1	8	8	22	5984	replication factor C (activator 1) 4, 37kDa	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA	Yes
MAP2K1	5604	dual specificity mitogen-activated protein kinase kinase 1	NP_002746.1	1	5	8	39	1.14	0.93	2.26	8.96	8.2	26.7	10	10	1469	5604	mitogen-activated protein kinase kinase 1	Protein threonine/tyrosine kinase activity	Cytoplasm	Dual specificity kinase	Cell communication;Signal transduction	S_T_Y_Kinase;CC	No
RANBP3	8498	ran-binding protein 3 isoform RANBP3-d	NP_015561.1	4	8	8	21	1.14	0.92	8.23	16.29	28.6	47.4	9	9	4508	8498	RAN binding protein 3	Transporter activity	Nucleus	Transport/cargo protein	Cell communication;Signal transduction	-	Yes
RABGGTB	5876	geranylgeranyl transferase type-2 subunit beta	NP_004573.2	1	3	3	8	1.14	0.91	8.62	5.09	19.8	9.3	4	4	1532	5876	Rab geranylgeranyltransferase, beta subunit	Transferase activity	Cytoplasm	Enzyme: Prenyltransferase	Metabolism;Energy pathways	-	Yes
EIF5A	1984	eukaryotic translation initiation factor 5A-1 isoform A	NP_001137232.1	4	9	9	38	1.14	0.89	4.34	8.9	23.6	38.5	22	22	2555	1984	eukaryotic translation initiation factor 5A	Translation factor activity, nucleic acid binding	Cytoplasm	Translation Factor	Protein metabolism	KOW	Yes
ARHGEF28	64283	rho guanine nucleotide exchange factor 28 isoform 1	NP_001073948.2	3	8	8	14	1.14	0.89	6.55	7.32	20	17.4	7	7									
CCNT1	904	cyclin-T1 isoform a	NP_001231.2	2	3	3	6	1.14	0.88	3.63	11.48	8.3	20.3	4	4	3938	904	cyclin T1	Kinase binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CYCLIN;CC	Yes
CCDC91	55297	coiled-coil domain-containing protein 91	NP_060788.3	1	3	3	4	1.14	0.88					1	1	16905	55297	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	Yes
RWDD4	201965	RWD domain-containing protein 4 isoform 1	NP_689895.2	2	2	2	3	1.14	0.86	6.73	16.3	10.9	19.9	2	2									
NT5DC1	221294	5'-nucleotidase domain-containing protein 1	NP_689942.2	1	7	7	19	1.14	0.86	3.89	4.89	14.8	13.9	11	11	14845	221294	5`-nucleotidase, cytosolic II-like 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
WDR70	55100	WD repeat-containing protein 70	NP_060504.1	1	5	5	9	1.14	0.76	8.23	17.49	21.2	30.3	5	5	8542	55100	WD repeat domain 70	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	WD40;CC	No
CHTOP	26097	chromatin target of PRMT1 protein isoform 2	NP_001193541.1	3	4	4	12	1.14	0.76	17.47	37.35	47.1	70.1	5	5									
TRAM1	23471	translocating chain-associated membrane protein 1	NP_055109.1	1	1	1	4	1.14	0.75	2.24	25.48	3.6	27.5	2	2	5545	23471	translocation associated membrane protein 1	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	SP;TM;TLC	Yes
PTPN2	5771	tyrosine-protein phosphatase non-receptor type 2 isoform 1	NP_002819.2	5	1	1	2	1.14	0.75					1	1	6768	5771	protein tyrosine phosphatase, non-receptor type2	Protein tyrosine phosphatase activity	Endoplasmic reticulum;Nucleus	Tyrosine phosphatase	Cell communication;Signal transduction	Tyr_Phos;CC;NLS	No
AMFR	267	E3 ubiquitin-protein ligase AMFR	NP_001135.3	1	1	1	2	1.14	0.74					1	1	9130	267	autocrine motility factor receptor	Ubiquitin-specific protease activity	Endoplasmic reticulum	Ubiquitin proteasome system protein	Protein metabolism	SP;TM;RING;CUE	Yes
MRPL41	64975	39S ribosomal protein L41, mitochondrial	NP_115866.1	1	3	3	13	1.14	0.73	10.22	16.72	26.6	27.8	5	5	14760	64975	mitochondrial ribosomal protein L41	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	No

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CCDC90B	60492	coiled-coil domain-containing protein 90B, mitochondrial isoform 1 precursor	NP_068597.2	5	1	1	4	1.14	0.69	2.58	14.63	4.1	14.4	2	2	14378	60492	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;TM	No
GLTP	51228	glycolipid transfer protein	NP_057517.1	1	2	2	3	1.14	0.67	19.7	10.28	32.6	9.8	2	2	16409	51228	None	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
KIF16B	55614	kinesin-like protein KIF16B isoform 1	NP_001186795.1	6	1	2	5	1.14	0.66					1	1	10731	55614	chromosome 20 open reading frame 23	Auxiliary transport protein activity	-	Membrane transport protein	Transport	KISC;FHA;CC;PX	Yes
CASP6	839	caspase-6 isoform alpha preproprotein	NP_001217.2	1	2	2	3	1.14	0.63	10.98	13.89	21.9	15.3	3	3	3321	839	caspase 6, apoptosis-related cysteine protease	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Apoptosis	CASc	Yes
LRCH3	84859	leucine-rich repeat and calponin homology domain-containing protein 3 precursor	NP_116162.1	1	2	2	2	1.14	0.62					1	1	14308	84859	leucine-rich repeats and calponin homology (CH)domain containing 3	Molecular function unknown	-	Unclassified	Biological_process unknown	LRR	No
PHACTR2	9749	phosphatase and actin regulator 2 isoform 1	NP_001093634.1	4	1	1	2	1.14	0.57					1	1	16378	9749	phosphatase and actin regulator 2	Phosphatase regulator activity	Cytoplasm	Enzyme regulator	Metabolism;Energy pathways	CC	Yes
MYL6	4637	myosin light polypeptide 6 isoform 1	NP_066299.2	5	1	10	68	1.14	0.54	2.7	55.36	4.4	44.1	2	2	17618	4637	myosin, light polypeptide 6, alkali, smoothmuscle and non-muscle	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	EF	Yes
CDH18	1016	cadherin-18 isoform 2 preproprotein	NP_001161139.1	1	1	1	2	1.13	1.9					1	1	4314	1016	cadherin 18, type 2	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;Cadherin;TM	Yes
UBE2J2	118424	ubiquitin-conjugating enzyme E2 J2 isoform 1	NP_919296.1	2	1	1	1	1.13	1.7					1	1	15600	118424	ubiquitin-conjugating enzyme E2, J2 (UBC6homolog, yeast)	Molecular function unknown	Endoplasmic reticulum membrane	Ubiquitin proteasome system protein	Protein metabolism	UBC;TM	Yes
TXNDC5	81567	thioredoxin domain-containing protein 5 isoform 1 precursor	NP_110437.2	2	10	10	22	1.13	1.63	10.3	8.06	43.8	50.2	13	13	18249	81567	thioredoxin domain containing 5	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase	Protein metabolism	SP	Yes
TRA2A	29896	transformer-2 protein homolog alpha isoform 1	NP_037425.1	3	4	6	13	1.13	1.6	10.5	6.66	29.6	26.6	6	6	4096	29896	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
CDK11A	728642	cyclin-dependent kinase 11A isoform 1	NP_076916.2	2	1	8	15	1.13	1.52					1	1									
CC2D1B	200014	coiled-coil and C2 domain-containing protein 1B	NP_115825.1	1	4	4	5	1.13	1.51	4.3	20.81	9.8	69.8	4	4	12393	200014	None	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	C2	No
PRKAR2B	5577	cAMP-dependent protein kinase type II-beta regulatory subunit	NP_002727.2	1	1	5	10	1.13	1.46					1	1	1486	5577	protein kinase, cAMP-dependent, regulatory,type II, beta	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	CNMP	No
IBTK	25998	inhibitor of Bruton tyrosine kinase isoform 1	NP_056340.2	2	1	1	2	1.13	1.46					1	1	12105	25998	inhibitor of Bruton agammaglobulinemia tyrosinekinase	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	ANK;BTB	No
SCD	6319	acyl-CoA desaturase	NP_005054.3	1	3	3	6	1.13	1.44	7.7	17.99	15.2	47.2	3	3	4941	6319	stearoyl-CoA desaturase (delta-9-desaturase)	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	Yes
ALDOB	229	fructose-bisphosphate aldolase B	NP_000026.2	1	4	6	34	1.13	1.42	5.16	10.95	25.9	76.5	19	19	1972	229	aldolase B, fructose-bisphosphate	Lyase activity	Cytoplasm	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
SETD3	84193	histone-lysine N-methyltransferase setd3 isoform a	NP_115609.2	2	9	9	18	1.13	1.36	4.43	2.57	15.1	10.5	9	9	8664	84193	chromosome 14 open reading frame 154	Methyltransferase activity	-	Enzyme: Methyltransferase	Biological_process unknown	SET	No
CAPN5	726	calpain-5	NP_004046.2	1	1	1	1	1.13	1.36					1	1	3963	726	calpain 5	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Protein metabolism	CYSPC;CALPAIN_III;C2	Yes
AIP	9049	AH receptor-interacting protein isoform 1	NP_003968.3	3	4	4	8	1.13	1.35	9.66	12.65	22.2	35.2	4	4	10408	9049	aryl hydrocarbon receptor interacting protein	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TPR	Yes
UBAP2L	9898	ubiquitin-associated protein 2-like isoform b	NP_001120792.1	3	1	26	69	1.13	1.31					1	1	6665	9898	ubiquitin associated protein 2-like	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	UBA	Yes
PTGES3	10728	prostaglandin E synthase 3 isoform e	NP_001269533.1	6	5	5	26	1.13	1.3	2.45	7.01	10	33.7	13	13	6138	10728	None	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
RBMX	27316	RNA-binding motif protein, X chromosome isoform 1	NP_002130.2	4	6	24	90	1.13	1.3	3.61	1.76	10.9	6.1	7	7	2186	27316	RNA binding motif protein, X-linked	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
SARS2	54938	serine--tRNA ligase, mitochondrial isoform b precursor	NP_060297.1	2	9	9	24	1.13	1.27	4.43	3.16	16.7	13.4	11	11	15295	54938	seryl-tRNA synthetase 2	Ligase activity	Mitochondrion	Enzyme: Ligase	Protein metabolism	-	Yes
PSMD6	9861	26S proteasome non-ATPase regulatory subunit 6 isoform 2	NP_055629.1	4	12	12	28	1.13	1.27	5.12	5.63	23.5	29.2	16	16	18370	9861	proteasome (prosome, macropain) 26S subunit,non-ATPase, 6	Ubiquitin-specific protease activity	Peroxisome	Ubiquitin proteasome system protein	Protein metabolism	CC;PINT	Yes
PSMD4	5710	26S proteasome non-ATPase regulatory subunit 4	NP_002801.1	1	16	16	76	1.13	1.25	4.88	4.31	33.9	33.2	36	36	3386	5710	proteasome (prosome, macropain) 26S subunit,non-ATPase, 4	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	VWA;UIM	Yes
CHERP	10523	calcium homeostasis endoplasmic reticulum protein	NP_006378.3	1	7	7	26	1.13	1.25	5.31	4.57	18.2	17.3	9	9	13051	10523	calcium homeostasis endoplasmic reticulumprotein	Molecular function unknown	Endoplasmic reticulum membrane	Unclassified	Regulation of cell proliferation;Homeostasis	SWAP;CC;G_PATCH;TM	Yes

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SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 1	NP_001290377.1	3	8	8	27	1.13	1.21	12.55	12.03	49.9	51.4	11	11	10441	10250	serine/arginine repetitive matrix 1	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PWI	Yes
DDX10	1662	probable ATP-dependent RNA helicase DDX10	NP_004389.2	1	3	3	9	1.13	1.21	5.96	7.12	15.1	19.4	5	5	3138	1662	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;DEXDc;CC	Yes
MAN2B1	4125	lysosomal alpha-mannosidase isoform 1 precursor	NP_000519.2	2	6	6	17	1.13	1.2	3.15	13.32	10.7	50.8	9	9	2007	4125	mannosidase, alpha, class 2B, member 1	Catalytic activity	Lysosome	Enzyme: Glycosidase	Metabolism;Energy pathways	-	Yes
LRRFIP1	9208	leucine-rich repeat flightless-interacting protein 1 isoform 4	NP_004726.2	5	21	21	85	1.13	1.19	4.06	4.72	30.4	37.6	42	42	4460	9208	leucine rich repeat (in FLII) interactingprotein 1	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	NP_057085.2	1	10	10	18	1.13	1.18	5.1	5.68	21	24.4	13	13	10825	51096	WD repeat domain 50	Molecular function unknown	Nucleolus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
SLC44A1	23446	choline transporter-like protein 1 isoform a	NP_536856.2	2	1	1	2	1.13	1.17					1	1	16197	23446	CDW92 antigen	Molecular function unknown	Integral to membrane	Integral membrane protein	Transport	TM	No
TDP1	55775	tyrosyl-DNA phosphodiesterase 1	NP_060789.2	1	1	1	4	1.13	1.17	10.51	23.73	16.9	40.7	2	2	6226	55775	tyrosyl-DNA phosphodiesterase 1	Phosphoric diester hydrolase activity	Nucleus	Enzyme: Phosphodiesterase	DNA repair	HKD	Yes
SQLE	6713	squalene monooxygenase	NP_003120.2	1	7	7	17	1.13	1.16	4.43	6.35	14.3	21.1	8	8	11802	6713	squalene epoxidase	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase	Metabolism;Energy pathways	TM	Yes
POLDIP2	26073	polymerase delta-interacting protein 2 isoform 1	NP_056399.1	2	7	7	11	1.13	1.14	9.62	8.61	31.6	28.3	8	8	17874	26073	polymerase (DNA-directed), delta interactingprotein 2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
DPH2	1802	diphthamide biosynthesis protein 2 isoform a	NP_001375.2	2	2	2	7	1.13	1.13	12.68	36.05	25.3	80.6	3	3	16023	1802	DPH2 homolog (S. cerevisiae)	Catalytic activity	-	Enzyme: Adenosyltransferase	Metabolism;Energy pathways	-	No
QSOX1	5768	sulfhydryl oxidase 1 isoform a precursor	NP_002817.2	2	1	1	1	1.13	1.1					1	1	6785	5768	quiescin Q6	Molecular function unknown	Extracellular	Cell cycle control protein	Regulation of cell cycle	TM;SP	Yes
RPL34	6164	60S ribosomal protein L34	NP_000986.2	1	6	6	17	1.13	1.09	7.72	2.99	25.1	9.2	8	8	17996	6164	ribosomal protein L34	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
GOT1	2805	aspartate aminotransferase, cytoplasmic	NP_002070.1	1	20	20	71	1.13	1.09	3.18	5.19	21.6	34.5	35	35	687	2805	glutamic-oxaloacetic transaminase 1, soluble(aspartate aminotransferase 1)	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase	Metabolism;Energy pathways	-	Yes
CYP4F11	57834	phylloquinone omega-hydroxylase CYP4F11 precursor	NP_067010.3	5	4	4	6	1.13	1.09	6.25	15.28	14.2	34.4	4	4	7101	57834	cytochrome P450, family 4, subfamily F,polypeptide 11	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase	Metabolism;Energy pathways	TM	Yes
ADNP	23394	activity-dependent neuroprotector homeobox protein	NP_001269460.1	1	5	5	11	1.13	1.08	2.82	0.54	7.2	1.3	5	5	9793	23394	activity-dependent neuroprotector	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;HOX;NLS	Yes
TRMT1	55621	tRNA (guanine(26)-N(2))-dimethyltransferase isoform 1	NP_001129507.1	2	13	13	18	1.13	1.07	4.64	0.93	14.9	2.8	8	8	8617	55621	None	RNA methyltransferase activity	-	RNA methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1;SP	Yes
DBN1	1627	drebrin isoform b	NP_543157.1	2	15	15	56	1.13	1.07	4.41	5.23	25.4	28.6	25	25	545	1627	drebrin 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	ADF;CC	Yes
LSM8	51691	LSM8 homolog, U6 small nuclear RNA associated	NP_057284.1	1	1	1	2	1.13	1.07					1	1									
DEK	7913	protein DEK isoform 1	NP_003463.1	2	7	7	30	1.13	1.06	5.04	6.84	23	29.6	16	16	503	7913	DEK oncogene (DNA binding)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;CC	Yes
COIL	8161	coilin	NP_004636.1	1	2	2	8	1.13	1.06	10.64	19.88	24.3	44.2	4	4	2605	8161	coilin	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PSMC1	5700	26S protease regulatory subunit 4	NP_002793.2	1	23	24	76	1.13	1.04	2.3	3.78	16.5	25.2	40	40	4084	5700	proteasome (prosome, macropain) 26S subunit,ATPase, 1	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	AAA;CC	Yes
CSNK1G3	1456	casein kinase I isoform gamma-3 isoform 4	NP_001038188.1	6	1	1	2	1.13	1.03					1	1	5034	1456	casein kinase 1, gamma 3	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Signal transduction	S_T_Y_Kinase;S_T_kinase;Tyr_Kinase	No
OGT	8473	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit isoform 1	NP_858058.1	2	16	16	36	1.13	1.03	3.66	4.14	18.1	18.8	19	19	2222	8473	O-linked N-acetylglucosamine (GlcNAc) transferase(UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Transferase activity	Nucleus	Enzyme: Glucosaminyltransferase	Protein metabolism	TPR	Yes

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DDX46	9879	probable ATP-dependent RNA helicase DDX46 isoform 1	NP_001287789.1	2	17	17	41	1.13	1.03	2.94	3.75	15.7	18.2	22	22	10862	9879	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Helicase activity	Nucleus;Cytoplasm	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;CC;DEXDc	Yes
MTSS1	9788	metastasis suppressor protein 1 isoform 1	NP_001269900.1	3	3	3	6	1.13	1.02	9.54	4.67	18.8	8.3	3	3	12243	9788	metastasis suppressor 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC;WH2	Yes
SURF6	6838	surfeit locus protein 6 isoform 1	NP_006744.2	2	2	2	3	1.13	1.02	6.41	12.81	10.3	18.6	2	2	1714	6838	surfeit 6	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
TM9SF2	9375	transmembrane 9 superfamily member 2 precursor	NP_004791.1	1	7	8	14	1.13	1.01	2.78	15.14	8.3	42	7	7	9198	9375	transmembrane 9 superfamily member 2	Molecular function unknown	Endosome	Integral membrane protein	Transport	TM;SP	No
ST14	6768	suppressor of tumorigenicity 14 protein	NP_068813.1	1	3	3	5	1.13	1	5.39	3.17	12.2	6.3	4	4	6005	6768	suppression of tumorigenicity 14 (coloncarcinoma, matriptase, epithin)	Serine-type peptidase activity	Plasma membrane	Serine protease	Protein metabolism	TM;CUB;LDLA;TRYPSIN	Yes
SSH3	54961	protein phosphatase Slingshot homolog 3	NP_060327.3	1	5	6	8	1.13	1	12.12	8.72	31.4	19.7	5	5	9488	54961	slingshot homolog 3 (Drosophila)	Protein tyrosine/serine/threonine phosphatase activity	Cytoplasm	Dual specificity phosphatase	Cell growth and/or maintenance	DSPC	No
DPH1	1801	diphthamide biosynthesis protein 1	NP_001374.3	1	1	1	3	1.13	0.99					1	1	4634	1801	DPH1 homolog (S. cerevisiae)	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	No
AP2M1	1173	AP-2 complex subunit mu isoform a	NP_004059.2	2	9	9	24	1.13	0.98	2.47	10.85	9.3	36.5	11	11	3014	1173	adaptor-related protein complex 2, mu 1 subunit	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Transport	-	Yes
GOLGA5	9950	Golgin subfamily A member 5	NP_005104.3	1	3	3	6	1.13	0.98	4.9	17.43	9.6	30.3	3	3	6079	9950	golgi autoantigen, golgin subfamily a, 5	Auxiliary transport protein activity	Golgi apparatus;Nucleus;Cytoplasm	Membrane transport protein	Transport	CC;TM	Yes
SOGA1	140710	protein SOGA1 isoform 1	NP_542194.2	2	1	2	2	1.13	0.97					1	1									
BHLHA15	168620	class A basic helix-loop-helix protein 15	NP_803238.1	1	1	1	1	1.13	0.97					1	1	16356	168620	None	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HLH	Yes
CCDC47	57003	coiled-coil domain-containing protein 47 precursor	NP_064583.2	1	8	8	22	1.13	0.96	7.46	8.62	29.8	29.2	12	12	17041	57003	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	SP;CC	No
GLE1	2733	nucleoporin GLE1 isoform 1	NP_001003722.1	2	2	2	2	1.13	0.96	14.26	4.79	23	6.5	2	2	4536	2733	GLE1 RNA export mediator-like (yeast)	Transporter activity	Nuclear membrane	Transport/cargo protein	Transport	CC	No
NT5C3A	51251	cytosolic 5'-nucleotidase 3A isoform 1	NP_001002010.1	3	2	2	3	1.13	0.95					1	1									
AAR2	25980	protein AAR2 homolog	NP_056326.2	1	3	3	4	1.13	0.94	14.74	37.47	23.9	52.8	2	2									
MED16	10025	mediator of RNA polymerase II transcription subunit 16	NP_005472.2	1	2	2	3	1.13	0.94	12.14	26.74	19.6	36.5	2	2	6816	10025	thyroid hormone receptor associated protein 5	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	No
THOC1	9984	THO complex subunit 1	NP_005122.2	1	4	4	5	1.13	0.92	5.67	9.65	9.1	12.7	2	2	9498	9984	THO complex 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEATH	Yes
COG8	84342	conserved oligomeric Golgi complex subunit 8	NP_115758.3	1	4	4	7	1.13	0.92	7.14	7.26	16.2	13.4	4	4	7374	84342	component of oligomeric golgi complex 8	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	Yes
ARMC1	55156	armadillo repeat-containing protein 1 isoform 1	NP_060590.1	2	2	2	4	1.13	0.92	24.42	40.16	40.7	55.9	2	2	16506	55156	armadillo repeat containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	ARM	No
RPS17	6218	40S ribosomal protein S17	NP_001012.1	1	9	9	89	1.13	0.91	5.86	9.24	46.7	61.4	45	45	1600	6218	ribosomal protein S17	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
SBF1	6305	myotubularin-related protein 5	NP_002963.2	1	3	3	8	1.13	0.9	13.01	15.24	30.1	27.9	4	4	6788	6305	SET binding factor 1	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	GRAM;PH	Yes
SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform a	NP_003066.2	3	4	9	27	1.13	0.9	7.16	19.46	24.6	56.6	9	9	3437	6601	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily c, member 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CHROMO;SANT;CC	Yes
PIN4	5303	peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 isoform 1	NP_006214.2	2	1	1	1	1.13	0.89					1	1	2219	5303	protein (peptidyl-prolyl cis/trans isomerase)NIMA-interacting, 4 (parvulin)	Isomerase activity	Nucleus	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
SPC24	147841	kinetochore protein Spc24	NP_872319.1	1	1	1	2	1.13	0.89					1	1	15464	147841	spindle pole body component 24 homolog (S.cerevisiae)	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CC	No
SLC25A16	8034	graves disease carrier protein	NP_689920.1	1	1	1	2	1.13	0.87					1	1	740	8034	solute carrier family 25 (mitochondrialcarrier; Graves disease autoantigen), member 16	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	-	Yes

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ABI2	10152	abl interactor 2 isoform a	NP_001269854.1	5	1	2	3	1.13	0.86					1	1	7338	10152	abl interactor 2	Kinase regulator activity;Protein kinase binding	Cytoplasm	Adapter molecule	Cell communication;Signal transduction;Regulation of cell proliferation	SH3	Yes
PPP1R10	5514	serine/threonine-protein phosphatase 1 regulatory subunit 10	NP_002705.2	1	4	4	7	1.13	0.74	9.26	8.14	21.2	12.2	4	4	4797	5514	protein phosphatase 1, regulatory subunit 10	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase	Cell communication;Signal transduction	TFS	No
NCAPG2	54892	condensin-2 complex subunit G2 isoform b	NP_001268862.1	2	1	1	2	1.13	0.74					1	1	10539	54892	leucine zipper protein 5	Molecular function unknown	-	Unclassified	Cell growth and/or maintenance	-	Yes
POLR1A	25885	DNA-directed RNA polymerase I subunit RPA1	NP_056240.2	1	7	7	14	1.13	0.74	14.07	9.95	40.4	18.3	6	6	10161	25885	polymerase (RNA) I polypeptide A, 194kDa	DNA-directed RNA polymerase activity	Nucleolus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
PRKCA	5578	protein kinase C alpha type	NP_002728.1	1	1	1	5	1.13	0.74	4.42	35.69	7.1	38.8	2	2	1498	5578	protein kinase C, alpha	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	C1;C2;S_T_kinase	Yes
STX8	9482	syntaxin-8	NP_004844.1	1	2	2	5	1.13	0.72	18.01	25.77	29.5	26.9	2	2	5012	9482	syntaxin 8	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM;CC	Yes
CTDSPL2	51496	CTD small phosphatase-like protein 2	NP_057480.2	1	1	1	1	1.13	0.71					1	1	13697	51496	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CPDc	No
COL4A2	1284	collagen alpha-2(IV) chain preproprotein	NP_001837.2	1	1	1	2	1.13	0.67					1	1	355	1284	collagen, type IV, alpha 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	COLL;C4;SP	Yes
KLK3	354	prostate-specific antigen isoform 1 preproprotein	NP_001639.1	3	1	1	1	1.13	0.62					1	1	1461	354	kallikrein 3, (prostate specific antigen)	Serine-type peptidase activity	Extracellular	Serine protease	Proteolysis and peptidolysis;Immune response	TRYPSIN;SP	Yes
FST	10468	follistatin isoform FST344 precursor	NP_037541.1	2	7	7	14	1.12	1.43	5.17	7.08	15.5	27.2	7	7	641	10468	follistatin	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	FOLN;KAZAL;SP	Yes
NHP2L1	4809	NHP2-like protein 1	NP_004999.1	1	2	2	4	1.12	1.43	11.76	18.01	18.7	37.7	2	2	3197	4809	NHP2 non-histone chromosome protein 2-like 1(S. cerevisiae) [Homo sapiens]Other Aliases: HGNC:7819, NHPX, OTK27OtherDesignations: NHP2 non-histone chromosome protein 2-like 1;	RNA binding	Nucleolus	RNA binding protein	RNA metabolism	-	Yes
GGA1	26088	ADP-ribosylation factor-binding protein GGA1 isoform 1	NP_037497.1	6	1	2	5	1.12	1.39	11.39	27.64	18.2	58.6	2	2	12078	26088	golgi associated, gamma adaptin ear containing,ARF binding protein 1	Molecular function unknown;Transporter activity	Golgi membrane	Transport/cargo protein;Unclassified	Biological_process unknown;Transport	VHS	Yes
SAMD4B	55095	protein Smaug homolog 2 isoform a	NP_060498.2	2	4	4	6	1.12	1.39	0.13	17.02	0.2	42.7	3	3	10960	55095	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SAM	Yes
TIGAR	57103	fructose-2,6-bisphosphatase TIGAR	NP_065108.1	1	8	8	24	1.12	1.36	7.57	8.13	27.2	36.1	10	10									
ALDOA	226	fructose-bisphosphate aldolase A isoform 1	NP_000025.1	2	28	32	390	1.12	1.35	2.09	2.94	29.2	51.5	149	149	70	226	aldolase A, fructose-bisphosphate	Lyase activity	Cytoplasm	Enzyme: Lyase;Enzyme: Aldolase	Metabolism;Energy pathways	-	Yes
MRE11A	4361	double-strand break repair protein MRE11A isoform 1	NP_005582.1	2	11	11	26	1.12	1.31	3.23	5.23	14.1	27	15	15	2889	4361	MRE11 meiotic recombination 11 homolog A (S.cerevisiae)	Exonuclease activity	Nucleus;Cytoplasm	DNA repair protein	DNA repair	CC	Yes
PPP1R18	170954	phostensin	NP_001128342.1	1	16	16	35	1.12	1.3	5.19	2.22	25	12	18	17									
RCN2	5955	reticulocalbin-2 isoform b precursor	NP_001258766.1	2	10	10	39	1.12	1.29	7.98	6.22	38	34.1	17	17	3993	5955	reticulocalbin 2, EF-hand calcium binding domain	Calcium ion binding	Endoplasmic reticulum	Calcium binding protein	Cell communication;Signal transduction	SP;EF	No
QRICH1	54870	glutamine-rich protein 1	NP_060200.2	1	2	2	4	1.12	1.27	2.41	24.36	3.8	45.9	2	2	13372	54870	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
SMIM12	113444	small integral membrane protein 12	NP_612437.3	1	1	1	1	1.12	1.26					1	1									
IDE	3416	insulin-degrading enzyme isoform 1	NP_004960.2	2	10	10	23	1.12	1.24	6.89	7.47	26	31.4	11	11	894	3416	insulin-degrading enzyme	Metallopeptidase activity	Cytoplasm	Metallo protease	Protein metabolism	-	Yes
PSMB5	5693	proteasome subunit beta type-5 isoform 1	NP_002788.1	3	14	14	41	1.12	1.19	3.29	4.57	17	25.4	21	21	2629	5693	proteasome (prosome, macropain) subunit, betatype, 5	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism;Proteolysis and peptidolysis	-	Yes
CUL4B	8450	cullin-4B isoform 1	NP_003579.3	2	9	14	28	1.12	1.19	1.54	2.52	4.9	8.5	8	8	2251	8450	cullin 4B	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CULL	Yes
SPAG1	6674	sperm-associated antigen 1	NP_757367.1	1	1	1	2	1.12	1.18					1	1	4548	6674	sperm associated antigen 1	GTPase activity	Cytoplasm	GTPase	Reproduction	TPR;CC	Yes
NAA50	80218	N-alpha-acetyltransferase 50 isoform 1	NP_079422.1	2	2	2	2	1.12	1.18	13.98	1.88	22.4	3.2	2	2	14350	80218	Mak3 homolog (S. cerevisiae)	Acyltransferase activity	-	Enzyme: Acyltransferase	Biological_process unknown	-	No
PRMT3	10196	protein arginine N-methyltransferase 3 isoform 1	NP_005779.1	3	8	8	16	1.12	1.14	5.87	7.89	19.9	27.6	9	9	11934	10196	HMT1 hnRNP methyltransferase-like 3 (S.cerevisiae)	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase	Metabolism;Energy pathways	ZNFC2;CC	Yes
FBXO21	23014	F-box only protein 21 isoform 1	NP_296373.1	2	1	1	2	1.12	1.14					1	1	9948	23014	F-box protein 21	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	F_BOX	No

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RPL23A	6147	60S ribosomal protein L23a	NP_000975.2	1	10	10	49	1.12	1.14	3.97	4.61	24	28.5	28	28	15998	6147	ribosomal protein L23a	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
LUZP1	7798	leucine zipper protein 1	NP_361013.3	1	20	20	34	1.12	1.13	4.39	4.71	21.7	23.5	19	19	3250	7798	leucine zipper protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;LZ;NLS	Yes
OLA1	29789	obg-like ATPase 1 isoform 1	NP_037473.3	2	14	14	60	1.12	1.12	1.59	4.48	10	28.6	31	31	15194	29789	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes
FNDC3B	64778	fibronectin type III domain-containing protein 3B	NP_073600.3	1	6	6	12	1.12	1.11	6.07	6.97	16.7	19.1	6	6	10943	64778	fibronectin type III domain containing 3B	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	FN3;TM	No
TRAP1	10131	heat shock protein 75 kDa, mitochondrial isoform 1 precursor	NP_057376.2	2	21	22	93	1.12	1.11	4.31	6.44	31.5	48.2	41	41	5868	10131	TNF receptor-associated protein 1	Heat shock protein activity	Mitochondrion	Heat shock protein	Protein metabolism	-	Yes
VAPB	9217	vesicle-associated membrane protein-associated protein B/C isoform 1	NP_004729.1	2	12	13	33	1.12	1.1	7.44	4.84	35.5	22.3	17	17	9300	9217	VAMP (vesicle-associated membraneprotein)-associated protein B and C	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	CC;TM	Yes
CKAP5	9793	cytoskeleton-associated protein 5 isoform a	NP_001008938.1	2	30	30	78	1.12	1.07	3.02	2.59	21.8	17.9	41	41	10830	9793	cytoskeleton associated protein 5	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein	Mitosis	-	Yes
PGM1	5236	phosphoglucomutase-1 isoform 1	NP_002624.2	3	23	23	88	1.12	1.07	3.1	4.92	24.2	37.1	47	47	1389	5236	phosphoglucomutase 1	Catalytic activity	Cytoplasm	Enzyme: Mutase	Metabolism;Energy pathways	-	Yes
ERBB2IP	55914	protein LAP2 isoform 8	NP_001240628.1	6	9	9	15	1.12	1.06	5.59	7.04	16.7	19.9	7	7	6090	55914	erbb2 interacting protein	Protein binding;Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Signal transduction;Cell communication	PDZ;LRR	Yes
CNOT7	29883	CCR4-NOT transcription complex subunit 7 isoform 1	NP_037486.2	2	3	3	7	1.12	1.06	11.38	17.51	22.3	33	3	3	5370	29883	CCR4-NOT transcription complex, subunit 7	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ITPK1	3705	inositol-tetrakisphosphate 1-kinase isoform a	NP_055031.2	2	5	5	10	1.12	1.06	4.06	5.41	11.1	14.1	6	6	3501	3705	inositol 1,3,4-triphosphate 5/6 kinase	Catalytic activity	-	Enzyme: Phosphotransferase	Cell communication;Signal transduction	-	Yes
Sep-09	10801	septin-9 isoform a	NP_001106963.1	8	32	32	113	1.12	1.06	2.45	3.9	21	32.1	57	57									
ALDH16A1	126133	aldehyde dehydrogenase family 16 member A1 isoform 1	NP_699160.2	2	10	10	25	1.12	1.05	5.85	8.99	21	30.4	10	10	14394	126133	aldehyde dehydrogenase 16 family, member A1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
SCAMP4	113178	secretory carrier-associated membrane protein 4	NP_524558.1	1	2	2	4	1.12	1.05	6.05	3.98	9.6	5.9	2	2	11536	113178	secretory carrier membrane protein 4	Auxiliary transport protein activity	Cytoplasmic vesicle	Membrane transport protein	Transport	TM	No
QTRTD1	79691	queuine tRNA-ribosyltransferase subunit QTRTD1 isoform 2	NP_001243764.1	4	4	4	13	1.12	1.05	2.28	8.67	6.8	24.3	7	7	17944	79691	queuine tRNA-ribosyltransferase domaincontaining 1	Catalytic activity	-	Enzyme: Ribosyltransferase	Metabolism;Energy pathways	-	Yes
ELP5	23587	elongator complex protein 5 isoform 1	NP_981960.1	1	1	1	2	1.12	1.03					1	1									
RAPH1	65059	ras-associated and pleckstrin homology domains-containing protein 1 isoform 1	NP_998754.1	2	4	4	6	1.12	1.02	16.84	16.11	33.5	29	3	3	12356	65059	Ras association (RalGDS/AF-6) and pleckstrinhomology domains 1	Cytoskeletal protein binding	Cell projection	Cytoskeletal associated protein	Cell growth and/or maintenance	RA;PH;CC	Yes
KPNA6	23633	importin subunit alpha-7	NP_036448.1	2	5	10	33	1.12	1.02	12.36	4.05	37.8	11	7	7	9465	23633	karyopherin alpha 6 (importin alpha 7)	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Transport	ARM	Yes
FAM84B	157638	protein FAM84B	NP_777571.1	1	2	2	3	1.12	1.01	26.52	0.75	43.8	1.1	2	2	11403	157638	None	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	-	No
TMCC3	57458	transmembrane and coiled-coil domains protein 3 isoform 1	NP_065749.2	2	1	1	2	1.12	1.01					1	1	15519	57458	transmembrane and coiled-coil domains 3	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	CC;TM	Yes
FAM98A	25940	protein FAM98A isoform 1	NP_056290.3	2	5	5	9	1.12	1.01	9.56	12.6	24.4	29.1	5	5	16808	25940	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
VPS33B	26276	vacuolar protein sorting-associated protein 33B isoform 1	NP_061138.3	3	3	3	5	1.12	1	2.79	14.64	5.4	25.7	3	3	10541	26276	vacuolar protein sorting 33B (yeast)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
PUM1	9698	pumilio homolog 1 isoform 1	NP_001018494.1	6	5	5	12	1.12	1	2.16	15.61	6.4	43.1	7	7	6230	9698	pumilio homolog 1 (Drosophila)	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of translation	Pumilio	Yes
LPCAT1	79888	lysophosphatidylcholine acyltransferase 1	NP_079106.3	1	7	7	19	1.12	0.98	4.21	9.85	14.2	31.2	9	10	8572	79888	None	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Cell organization and biogenesis	TM	No
CHMP7	91782	charged multivesicular body protein 7	NP_689485.1	1	1	1	2	1.12	0.98					1	1	14534	91782	CHMP family, member 7	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TNFRSF10A	8797	tumor necrosis factor receptor superfamily member 10A	NP_003835.3	1	2	2	2	1.12	0.98					1	1	4679	8797	tumor necrosis factor receptor superfamily,member 10a	Receptor activity	Integral to membrane	Cell surface receptor	Cell communication;Signal transduction	TM;TNFR;DEATH;SP	Yes
SORL1	6653	sortilin-related receptor preproprotein	NP_003096.1	1	3	3	5	1.12	0.98	8.49	0.58	16.6	1	3	3	3595	6653	sortilin-related receptor, L(DLR class) Arepeats-containing	Transmembrane receptor activity	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	SP;LDLRB;LDLA;FN3;TM	Yes
CHMP2A	27243	charged multivesicular body protein 2a	NP_055268.1	1	5	5	9	1.12	0.98	21.43	19.45	50.7	39.6	4	4	12520	27243	chromatin modifying protein 2A	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC	No
PTGR1	22949	prostaglandin reductase 1 isoform 1	NP_036344.2	2	15	15	41	1.12	0.97	3.91	5.44	21.7	25.6	24	23	3173	22949	leukotriene B4 12-hydroxydehydrogenase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes

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C14orf166	51637	UPF0568 protein C14orf166	NP_057123.1	1	10	10	40	1.12	0.97	6.97	9.6	31.1	38.7	15	16	16615	51637	chromosome 14 open reading frame 166	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;CC	Yes
DHX38	9785	pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	NP_054722.2	1	9	9	20	1.12	0.96	9.13	3.58	27.5	9.1	7	7	5720	9785	DEAH (Asp-Glu-Ala-His) box polypeptide 38	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC	Yes
TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 1	NP_001135452.1	3	19	19	55	1.12	0.96	4.03	6.66	22.3	32.1	24	24	5569	7158	tumor protein p53 binding protein, 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRCT	Yes
EIF4A2	1974	eukaryotic initiation factor 4A-II	NP_001958.2	1	9	21	95	1.12	0.92	4.42	13.11	19.3	49.5	15	15	3062	1974	eukaryotic translation initiation factor 4A,isoform 2	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	DEXDc;HELIC	Yes
ATRX	546	transcriptional regulator ATRX isoform 1	NP_000480.3	2	1	2	4	1.12	0.91					1	1	2069	546	alpha thalassemia/mental retardation syndromeX-linked (RAD54 homolog, S. cerevisiae)	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;DEXDc;HELIC;CC	Yes
HCFC1	3054	host cell factor 1	NP_005325.2	1	16	16	38	1.12	0.9	3.64	7.26	18.9	30.7	21	21	2061	3054	host cell factor C1 (VP16-accessory protein)	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;KELCH;FN3	Yes
UHRF2	115426	E3 ubiquitin-protein ligase UHRF2	NP_690856.1	1	1	1	1	1.12	0.9					1	1	18257	115426	ubiquitin-like, containing PHD and RING fingerdomains, 2	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBQ;PHD;RING;NLS	No
ILK	3611	integrin-linked protein kinase isoform 1	NP_004508.1	3	8	8	24	1.12	0.9	8.47	24.04	32.4	82.3	11	11	3842	3611	integrin-linked kinase	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	ANK	Yes
PACS1	55690	phosphofurin acidic cluster sorting protein 1	NP_060496.2	1	5	5	9	1.12	0.89	4.23	7.57	8.2	11.7	3	3	6320	55690	phosphofurin acidic cluster sorting protein 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Transport	-	Yes
TMA16	55319	translation machinery-associated protein 16	NP_060822.2	1	3	3	8	1.12	0.86	8.03	7.52	18.2	13	4	4									
SLC4A7	9497	sodium bicarbonate cotransporter 3 isoform b	NP_001245308.1	3	5	5	13	1.12	0.85	6.03	6.27	17.9	14.2	7	7	4521	9497	solute carrier family 4, sodium bicarbonatecotransporter, member 7	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	Yes
SNX4	8723	sorting nexin-4	NP_003785.1	1	1	1	1	1.12	0.84					1	1	9334	8723	sorting nexin 4	Transporter activity	Integral to membrane	Transport/cargo protein	Transport	PX;CC	Yes
SERPING1	710	plasma protease C1 inhibitor precursor	NP_000053.2	1	1	1	2	1.12	0.77					1	1	6033	710	serine (or cysteine) proteinase inhibitor,clade G (C1 inhibitor), member 1, (angioedema, hereditary)	Protease inhibitor activity	Extracellular matrix	Protease inhibitor	Protein metabolism	SERPIN;SP	Yes
GOLT1B	51026	vesicle transport protein GOT1B	NP_057156.1	1	1	1	3	1.12	0.75	2.13	7.62	3.4	8.1	2	2	13035	51026	golgi transport 1 homolog B (S. cerevisiae)	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	TM	Yes
EEF1D	1936	elongation factor 1-delta isoform 4	NP_001123528.1	1	1	9	46	1.12	0.75					1	1	560	1936	eukaryotic translation elongation factor 1delta (guanine nucleotide exchange protein)	Guanyl-nucleotide exchange factor activity	Endoplasmic reticulum	Guanine nucleotide exchange factor	Cell communication;Signal transduction	CC	Yes
STK26	51765	serine/threonine-protein kinase 26 isoform 1	NP_057626.2	3	4	9	24	1.12	0.74	3.29	11.46	9	20.9	6	6									
SLAIN2	57606	SLAIN motif-containing protein 2	NP_065897.1	1	5	5	8	1.12	0.69	16.04	12.4	37	17.3	4	4	13863	57606	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TCP11	6954	T-complex protein 11 homolog isoform 1	NP_001087197.1	6	1	1	1	1.12	0.6					1	1	1749	6954	t-complex 11 (mouse)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	-	No
C18orf21	83608	UPF0711 protein C18orf21 isoform a	NP_113634.3	2	1	1	1	1.12	0.6					1	1	12688	83608	chromosome 18 open reading frame 21	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
STIP1	10963	stress-induced-phosphoprotein 1 isoform a	NP_001269581.1	3	25	25	65	1.11	1.91	5.12	5.49	35.7	70.8	37	37	5454	10963	stress-induced-phosphoprotein 1(Hsp70/Hsp90-organizing protein)	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	TPR;STI1;NLS	Yes
FBXO2	26232	F-box only protein 2	NP_036300.2	1	5	5	32	1.11	1.53	2.79	4.94	12	29.9	15	15	6171	26232	F-box protein 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	F_BOX	No
ERP44	23071	endoplasmic reticulum resident protein 44 precursor	NP_055866.1	1	13	13	38	1.11	1.51	2.87	2.72	14.6	19	21	21	10290	23071	thioredoxin domain containing 4 (endoplasmicreticulum)	Molecular function unknown	Endoplasmic reticulum	Unclassified	Protein metabolism	SP	Yes
DDX28	55794	probable ATP-dependent RNA helicase DDX28	NP_060850.2	1	4	4	9	1.11	1.41	26.67	40.35	74.4	201.6	5	5	6357	55794	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	RNA binding	Mitochondrion	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;NLS;NES	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
C19orf43	79002	uncharacterized protein C19orf43	NP_076943.1	1	4	4	5	1.11	1.39	4.41	6.97	9.8	19.6	4	4	14528	79002	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
U2AF2	11338	splicing factor U2AF 65 kDa subunit isoform a	NP_009210.1	2	11	11	49	1.11	1.38	2.4	2.96	13.1	20.2	24	24	1872	11338	U2 (RNU2) small nuclear RNA auxiliary factor 2	Spliceosomal catalysis	Nucleus	RNA binding protein	RNA metabolism	RRM	Yes
PGK1	5230	phosphoglycerate kinase 1	NP_000282.1	2	29	29	205	1.11	1.34	2.8	3.3	33.2	48.6	109	109	2412	5230	phosphoglycerate kinase 1	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	PGK	Yes
MTHFD2	10797	bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial precursor	NP_006627.2	1	3	3	5	1.11	1.32	13.81	25.87	27.1	51.1	3	2	5351	10797	methylenetetrahydrofolate dehydrogenase (NADP+dependent) 2, methenyltetrahydrofolate cyclohydrolase	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
WDR3	10885	WD repeat-containing protein 3	NP_006775.1	1	9	9	19	1.11	1.31	3.94	5.03	14.6	22.2	11	11	16066	10885	WD repeat domain 3	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	WD40;NLS	Yes
OSGEP	55644	probable tRNA N6-adenosine threonylcarbamoyltransferase	NP_060277.1	1	1	1	2	1.11	1.31					1	1	10133	55644	O-sialoglycoprotein endopeptidase	Peptidase activity	-	Protease	Protein metabolism	-	Yes
COX1	4512	cytochrome c oxidase subunit I	YP_003024028.1	1	1	1	1	1.11	1.28					1	1									
SMARCC1	6599	SWI/SNF complex subunit SMARCC1	NP_003065.3	1	5	10	19	1.11	1.27	1.34	0.34	3	0.9	4	4	3435	6599	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily c, member 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CHROMO;SANT;CC	Yes
TMX2	51075	thioredoxin-related transmembrane protein 2 isoform 1 precursor	NP_057043.1	2	3	3	5	1.11	1.25	7.91	23.4	17.8	63.7	4	4	7159	51075	None	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM;SP	No
SMPD4	55627	sphingomyelin phosphodiesterase 4 isoform 2	NP_060421.2	3	6	6	10	1.11	1.24	3.13	6.36	8.5	19.5	6	6	13374	55627	None	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Biological_process unknown	TM	Yes
TBC1D4	9882	TBC1 domain family member 4 isoform 3	NP_001273588.1	3	3	3	5	1.11	1.24	0.88	0.81	1.4	1.4	2	2	18164	9882	TBC1 domain family, member 4	GTPase activator activity	Nucleus;Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	CC;PTB;TBC	Yes
TRIM33	51592	E3 ubiquitin-protein ligase TRIM33 isoform alpha	NP_056990.3	2	3	3	7	1.11	1.24	2.9	6.48	5.6	14	3	3	10423	51592	tripartite motif-containing 33	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;BBOX;BBC;CC;PHD;BROMO	Yes
NOL11	25926	nucleolar protein 11 isoform 1	NP_056277.2	5	6	6	18	1.11	1.23	6.28	0.71	21.2	2.5	9	8	10900	25926	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
FAU	2197	ubiquitin-like protein fubi and ribosomal protein S30 precursor	NP_001988.1	1	3	3	13	1.11	1.23	5.7	5.76	19.2	21.4	9	9	2	2197	Finkel-Biskis-Reilly murine sarcoma virus(FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	Ubiquitin-specific protease activity	Ribosome	Ubiquitin proteasome system protein	Protein metabolism	UBQ;NLS	Yes
RPF1	80135	ribosome production factor 1	NP_079341.2	1	2	2	3	1.11	1.21					1	1	15272	80135	brix domain containing 5	Molecular function unknown	Nucleolus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
NUP88	4927	nuclear pore complex protein Nup88	NP_002523.2	1	13	13	27	1.11	1.2	3.7	4.83	15.4	21.9	14	14	3974	4927	nucleoporin 88kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	CC	Yes
TWF2	11344	twinfilin-2	NP_009215.1	1	10	11	31	1.11	1.2	5.85	8.71	26.4	45	16	17	8464	11344	PTK9L protein tyrosine kinase 9-like(A6-related protein)	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase	Cell communication;Signal transduction	ADF;CC	Yes
CDK12	51755	cyclin-dependent kinase 12 isoform 1	NP_057591.2	47	6	7	24	1.11	1.19	12.94	3.29	29.3	7.8	4	4	10849	51755	None	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
CCT3	7203	T-complex protein 1 subunit gamma isoform a	NP_005989.3	3	30	31	195	1.11	1.19	2.53	3.13	26.7	35.8	87	87	8969	7203	chaperonin containing TCP1, subunit 3 (gamma)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
RRP1B	23076	ribosomal RNA processing protein 1 homolog B	NP_055871.1	1	11	11	22	1.11	1.18	3.35	4.85	13	20.8	12	13	10009	23076	KIAA0179	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes
SDC4	6385	syndecan-4 precursor	NP_002990.2	1	5	5	10	1.11	1.17	12.41	7.86	31.7	20.8	5	5	8366	6385	syndecan 4 (amphiglycan, ryudocan)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;TM;Band 4.1	Yes
CD2AP	23607	CD2-associated protein	NP_036252.1	1	15	15	42	1.11	1.17	1.89	2.72	9.9	15	22	22	5026	23607	CD2-associated protein	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	SH3;CC	Yes
PSAT1	29968	phosphoserine aminotransferase isoform 1	NP_478059.1	2	14	14	60	1.11	1.16	3.88	4.25	24.7	28.4	32	32	17918	29968	phosphoserine aminotransferase 1	Transaminase activity	Cytosol	Enzyme: Aminotransferase	Metabolism;Energy pathways	-	Yes
HOOK3	84376	protein Hook homolog 3	NP_115786.1	1	8	8	12	1.11	1.16	3.18	8.23	9.3	25.6	7	7	9699	84376	hook homolog 3 (Drosophila)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
HNRNPM	4670	heterogeneous nuclear ribonucleoprotein M isoform a	NP_005959.2	3	31	31	141	1.11	1.16	2.06	3.99	20	41.9	75	75	1188	4670	heterogeneous nuclear ribonucleoprotein M	Ribonucleoprotein	Nucleolus;Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
PRDX1	5052	peroxiredoxin-1	NP_859048.1	1	12	15	68	1.11	1.14	5.36	5.32	34.8	35.4	32	32	1458	5052	peroxiredoxin 1	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase	Metabolism;Energy pathways	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
EBNA1BP2	10969	probable rRNA-processing protein EBP2 isoform 1	NP_001153408.1	2	7	7	15	1.11	1.13	2.17	4.42	6.8	14.1	8	8	16849	10969	EBNA1 binding protein 2	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes
DDX52	11056	probable ATP-dependent RNA helicase DDX52 isoform 1	NP_008941.3	2	6	6	20	1.11	1.13	17.6	5.14	50.5	15.5	6	7	9911	11056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Helicase activity	Nucleolus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
CHAC2	494143	putative glutathione-specific gamma-glutamylcyclotransferase 2	NP_001008708.1	1	2	2	4	1.11	1.12	17.87	14.78	28.7	23.7	2	2	17418	494143	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NAA15	80155	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NP_476516.1	3	22	27	61	1.11	1.11	2.68	4.62	16.4	28.6	30	30	10471	80155	NMDA receptor regulated 1	Transferase activity	Cytoplasm;Nucleus	Enzyme: Transferase	Metabolism;Energy pathways	CC;TPR	Yes
SMEK1	55671	serine/threonine-protein phosphatase 4 regulatory subunit 3A isoform 1	NP_001271209.1	5	7	7	13	1.11	1.1	4.65	6.64	13.7	19.6	7	7	11176	55671	KIAA2010	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
YTHDF1	54915	YTH domain-containing family protein 1	NP_060268.2	1	3	6	13	1.11	1.1	16.79	6.09	26.8	9.5	2	2	11691	54915	YTH domain family, member 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
NAF1	92345	H/ACA ribonucleoprotein complex non-core subunit NAF1 isoform a	NP_612395.2	2	1	1	2	1.11	1.09					1	1	10054	92345	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
POLR1E	64425	DNA-directed RNA polymerase I subunit RPA49 isoform 1	NP_071935.1	2	3	3	4	1.11	1.08	1.54	6.46	3	12.2	3	3	15096	64425	None	Transcription factor activity	Nucleolus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
KTI12	112970	protein KTI12 homolog	NP_612426.1	1	3	3	5	1.11	1.08	8.96	8.01	17.4	15	3	3	14471	112970	None	ATP binding	-	Unclassified	Biological_process unknown	-	No
EPHA2	1969	ephrin type-A receptor 2 precursor	NP_004422.2	9	12	13	31	1.11	1.06	6.03	5.3	26.3	22.1	15	15	1494	1969	EPH receptor A2	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	FN3;Tyr_Kinase;SAM;TM;SP	Yes
KRT18	3875	keratin, type I cytoskeletal 18	NP_000215.1	4	26	27	172	1.11	1.06	3.42	4.06	35.7	41.1	84	84	1020	3875	keratin 18	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
POU2F1	5451	POU domain, class 2, transcription factor 1 isoform 1	NP_002688.3	5	3	4	7	1.11	1.05	6.92	2.43	13.4	4.4	3	3	1250	5451	POU domain, class 2, transcription factor 1	Transcription factor activity	Nucleus	Transcription factor	Cell growth and/or maintenance	POU;HOX	Yes
GPI	2821	glucose-6-phosphate isomerase isoform 3	NP_001276718.1	5	24	24	162	1.11	1.05	3.29	4.32	32.9	41.6	78	78	1394	2821	glucose phosphate isomerase	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
ZFPL1	7542	zinc finger protein-like 1	NP_006773.2	1	2	2	3	1.11	1.04					1	1	15729	7542	zinc finger protein-like 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;TM;NLS	Yes
SCAF1	58506	splicing factor, arginine/serine-rich 19	NP_067051.2	1	2	2	3	1.11	1.03	20.82	3.67	33.6	5.3	2	2	11604	58506	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
WRNIP1	56897	ATPase WRNIP1 isoform 1	NP_064520.2	2	2	2	3	1.11	1.03	4.38	22.7	6.9	34.1	2	2	10494	56897	Werner helicase interacting protein 1	DNA repair protein	Nucleus;Cytoplasm	ATPase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA	Yes
PPP1R9B	84687	neurabin-2	NP_115984.3	1	3	3	5	1.11	1.02	11.77	4.18	22.8	7.4	3	3	4506	84687	protein phosphatase 1, regulatory subunit 9B,spinophilin	Phosphatase regulator activity	Cytoplasm	Regulatory/other subunit	Cell communication;Signal transduction	PDZ;CC	No
THRAP3	9967	thyroid hormone receptor-associated protein 3	NP_005110.2	1	16	16	34	1.11	1.02	8.49	8.15	41.7	36.6	18	18	7543	9967	thyroid hormone receptor associated protein 3	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
C12orf10	60314	UPF0160 protein MYG1, mitochondrial precursor	NP_067653.3	1	4	4	5	1.11	1.01	13.99	0.96	27.4	1.7	3	3	10705	60314	chromosome 12 open reading frame 10	Molecular function unknown	Cytosol	Unclassified	Biological_process unknown	SP	No
MRPL57	78988	ribosomal protein 63, mitochondrial	NP_076931.1	1	1	1	2	1.11	1.01					1	1									
MRPS33	51650	28S ribosomal protein S33, mitochondrial	NP_057155.1	1	1	1	4	1.11	1.01	2.75	6.12	4.3	8.7	2	2	17598	51650	mitochondrial ribosomal protein S33	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
SNX5	27131	sorting nexin-5 isoform a	NP_689413.1	2	6	7	16	1.11	1.01	5	2.36	15.8	6.7	8	8	10439	27131	sorting nexin 5	Transporter activity	Endosome	Transport/cargo protein	Transport	PX	Yes
RHOG	391	rho-related GTP-binding protein RhoG precursor	NP_001656.2	3	7	8	24	1.11	1	3.23	4.87	12.5	16.9	12	12	1537	391	ras homolog gene family, member G (rho G)	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	RHO	Yes
TRIP11	9321	thyroid receptor-interacting protein 11	NP_004230.2	1	14	14	27	1.11	0.99	6.04	5.5	25.4	20.6	14	14	5143	9321	thyroid hormone receptor interactor 11	Receptor binding	Golgi apparatus	Ligand	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;SP	Yes
MCAM	4162	cell surface glycoprotein MUC18 precursor	NP_006491.2	1	5	5	7	1.11	0.98	7.21	14.29	16.1	28.6	4	4	1120	4162	melanoma cell adhesion molecule	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;IGC2;TM;IG;Ig_LIKE	Yes
WDR12	55759	ribosome biogenesis protein WDR12	NP_060726.3	1	2	2	3	1.11	0.98	0.54	19.94	0.9	28.3	2	2	18295	55759	WD repeat domain 12	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	WD40	Yes
VRK1	7443	serine/threonine-protein kinase VRK1	NP_003375.1	1	5	5	7	1.11	0.97	4.6	7.13	12.6	17	6	6	3701	7443	vaccinia related kinase 1	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
SPRYD7	57213	SPRY domain-containing protein 7 isoform 1	NP_065189.1	2	2	2	2	1.11	0.96					1	1									

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PDCD11	22984	protein RRP5 homolog	NP_055791.1	1	19	19	42	1.11	0.95	3.47	2.98	18.2	13.3	22	22	18752	22984	Programmed cell death 11	Transcription factor binding	Nucleus	Transcription regulatory protein	Apoptosis	S1;CC;HAT	Yes
MRPL2	51069	39S ribosomal protein L2, mitochondrial isoform 1	NP_057034.2	2	5	5	14	1.11	0.94	8.71	11.82	25.9	30.1	7	7	14745	51069	mitochondrial ribosomal protein L2	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	No
SOD3	6649	extracellular superoxide dismutase [Cu-Zn] precursor	NP_003093.2	1	1	1	4	1.11	0.94	14.65	3.29	23.2	4.4	2	2	1708	6649	superoxide dismutase 3, extracellular	Superoxide dismutase activity	Extracellular	Enzyme: Superoxide dismutase	Metabolism;Energy pathways	SP	Yes
ACSL1	2180	long-chain-fatty-acid--CoA ligase 1 isoform a	NP_001986.2	4	1	1	1	1.11	0.94					1	1	1068	2180	acyl-CoA synthetase long-chain family member 1	Ligase activity	Endoplasmic reticulum	Enzyme: Ligase	Metabolism;Energy pathways	TM	Yes
SEC61A1	29927	protein transport protein Sec61 subunit alpha isoform 1	NP_037468.1	4	6	6	13	1.11	0.93	1.4	8.98	3.8	20.7	6	6	15316	29927	Sec61 alpha 1 subunit (S. cerevisiae)	Protein translocase activity;Intracellular transporter activity	Endoplasmic reticulum	Integral membrane protein	Transport	TM	No
MRPL19	9801	39S ribosomal protein L19, mitochondrial	NP_055578.2	1	6	6	13	1.11	0.92	12.37	3.41	37.5	8.4	7	7	11370	9801	mitochondrial ribosomal protein L19	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
CUL2	8453	cullin-2 isoform a	NP_001185707.1	3	14	14	26	1.11	0.91	3.2	5.88	13.8	21	15	15	6786	8453	cullin 2	Ubiquitin binding	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CULL	Yes
WASF1	8936	wiskott-Aldrich syndrome protein family member 1	NP_003922.1	1	1	1	2	1.11	0.9					1	1	5434	8936	WAS protein family, member 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	WH2	Yes
SNRPD3	6634	small nuclear ribonucleoprotein Sm D3	NP_004166.1	1	4	4	25	1.11	0.89	9.02	28.11	30.7	87.1	9	9	3039	6634	small nuclear ribonucleoprotein D3 polypeptide18kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
ARFIP1	27236	arfaptin-1 isoform 1	NP_001274360.1	2	9	10	21	1.11	0.87	3.96	13.63	14	38.8	10	10	9331	27236	ADP-ribosylation factor interacting protein 1(arfaptin 1)	Regulator of G-protein signaling activity	Cytoplasm	Unclassified	Signal transduction	CC	Yes
FXR1	8087	fragile X mental retardation syndrome-related protein 1 isoform a	NP_005078.2	3	13	15	34	1.11	0.86	3.98	4.1	18.4	14.7	17	17	2892	8087	fragile X mental retardation, autosomal homolog1	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of translation	NES;KH	Yes
LARS2	23395	probable leucine--tRNA ligase, mitochondrial	NP_056155.1	3	8	8	16	1.11	0.86	3.42	3.63	10.1	8.2	7	7	5178	23395	leucyl-tRNA synthetase 2, mitochondrial	Transferase activity	Mitochondrion	Enzyme: Transferase	Metabolism;Energy pathways	SP	Yes
UQCRFS1	7386	cytochrome b-c1 complex subunit Rieske, mitochondrial	NP_005994.2	1	9	9	23	1.11	0.83	6.37	17.97	25.9	57.8	13	13	1874	7386	ubiquinol-cytochrome c reductase, Rieskeiron-sulfur polypeptide 1	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	TM	No
HMGN4	10473	high mobility group nucleosome-binding domain-containing protein 4	NP_006344.1	1	4	4	5	1.11	0.82	21.17	31.42	49.9	55.1	4	4	17111	10473	high mobility group nucleosomal binding domain4	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
RAB5A	5868	ras-related protein Rab-5A isoform 1	NP_004153.2	2	5	8	53	1.11	0.81	11.56	8.31	44.6	22.7	11	11	1542	5868	RAB5A, member RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAB	Yes
PUF60	22827	poly(U)-binding-splicing factor PUF60 isoform a	NP_510965.1	4	1	14	64	1.11	0.81					1	1	18051	22827	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
LSM3	27258	U6 snRNA-associated Sm-like protein LSm3	NP_055278.1	1	2	2	3	1.11	0.7	19.86	7.38	32.1	7.3	2	2	6283	27258	LSM3 homolog, U6 small nuclear RNA associated(S. cerevisiae)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
SCAMP2	10066	secretory carrier-associated membrane protein 2	NP_005688.2	1	3	3	7	1.11	0.65	9.8	18.38	22.1	24.3	4	4	6073	10066	secretory carrier membrane protein 2	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM;CC	No
WASL	8976	neural Wiskott-Aldrich syndrome protein	NP_003932.3	1	3	3	7	1.11	0.64	34.16	55.28	73.2	68	3	3	5448	8976	Wiskott-Aldrich syndrome-like	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	WH1;PBD;WH2	Yes
RALA	5898	ras-related protein Ral-A precursor	NP_005393.2	1	4	5	24	1.11	0.58	10.76	7.18	43.4	14.6	12	12	1549	5898	v-ral simian leukemia viral oncogene homolog A(ras related)	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	Yes
HTRA1	5654	serine protease HTRA1 precursor	NP_002766.1	1	17	17	40	1.1	1.42	6.43	4.43	31.6	28	19	19	3725	5654	protease, serine, 11 (IGF binding)	Serine-type peptidase activity	Extracellular	Serine protease	Protein metabolism	IB;KAZAL;TRYPSIN;PDZ;SP	Yes
OGFOD3	79701	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3 isoform 2	NP_787098.3	2	1	1	2	1.1	1.4					1	1									
GCA	25801	grancalcin	NP_036330.1	1	1	1	2	1.1	1.38					1	1	6122	25801	grancalcin, EF-hand calcium binding protein	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	SP;EF	Yes
HSPD1	3329	60 kDa heat shock protein, mitochondrial	NP_002147.2	1	37	37	257	1.1	1.38	2.16	2.56	27.1	41.8	127	128	318	3329	heat shock 60kDa protein 1 (chaperonin)	Heat shock protein activity	Mitochondrial matrix	Heat shock protein	Protein metabolism;Protein folding;Apoptosis;Regulation of immune response;Signal transduction	CC	Yes

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PSMD7	5713	26S proteasome non-ATPase regulatory subunit 7	NP_002802.2	1	11	11	34	1.1	1.37	3.38	5.12	15.9	32.2	18	20	1147	5713	proteasome (prosome, macropain) 26S subunit,non-ATPase, 7 (Mov34 homolog)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	JAB	Yes
EIF2S1	1965	eukaryotic translation initiation factor 2 subunit 1	NP_004085.1	1	22	22	80	1.1	1.36	3.75	3.62	27	32.4	41	41	4881	1965	eukaryotic translation initiation factor 2,subunit 1 alpha, 35kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	S1;CC	Yes
CSNK2A2	1459	casein kinase II subunit alpha'	NP_001887.1	1	8	10	19	1.1	1.36	7.93	9.21	26.6	39	9	9	279	1459	casein kinase 2, alpha prime polypeptide	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
DDX41	51428	probable ATP-dependent RNA helicase DDX41	NP_057306.2	1	3	3	7	1.1	1.35	8.21	4.84	18.2	13.1	4	4	10490	51428	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	Helicase activity	Nucleolus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;ZNFC2;CC	Yes
GADD45GIP1	90480	growth arrest and DNA damage-inducible proteins-interacting protein 1	NP_443082.2	1	6	6	17	1.1	1.31	9.29	6.18	29.4	23.2	8	8	5519	90480	growth arrest and DNA-damage-inducible,gamma interacting protein 1	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CC	No
SLC3A2	6520	4F2 cell-surface antigen heavy chain isoform b	NP_001012680.1	4	26	26	150	1.1	1.28	2.56	1.8	24.9	20.4	77	77	1148	6520	solute carrier family 3 (activators of dibasicand neutral amino acid transport), member 2	Auxiliary transport protein activity	Plasma membrane;Nucleus;Cytoplasm	Membrane transport protein	Transport	TM;AMY	Yes
ELAVL1	1994	ELAV-like protein 1	NP_001410.2	9	10	10	42	1.1	1.28	4.48	4.71	22.9	28.1	21	21	16025	1994	ELAV (embryonic lethal, abnormal vision,Drosophila)-like 1 (Hu antigen R)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
C3orf38	285237	uncharacterized protein C3orf38	NP_776185.2	1	1	1	2	1.1	1.27					1	1	14509	285237	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PSME2	5721	proteasome activator complex subunit 2	NP_002809.2	1	8	8	48	1.1	1.26	3.67	5.67	18.6	33.7	21	21	3697	5721	proteasome (prosome, macropain) activatorsubunit 2 (PA28 beta)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
KHDRBS1	10657	KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 1	NP_006550.1	6	9	9	32	1.1	1.25	4.86	3.3	22.2	17.1	17	17	3926	10657	KH domain containing, RNA binding, signaltransduction associated 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
PSMC2	5701	26S protease regulatory subunit 7 isoform 1	NP_002794.1	2	22	22	79	1.1	1.23	2.62	3.8	18	29.7	39	39	1105	5701	proteasome (prosome, macropain) 26S subunit,ATPase, 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	AAA;CC	Yes
UBA2	10054	SUMO-activating enzyme subunit 2	NP_005490.1	1	17	17	46	1.1	1.23	3.59	5.03	18.2	29	21	21	11658	10054	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
AP2A1	160	AP-2 complex subunit alpha-1 isoform 1	NP_055018.2	2	15	23	68	1.1	1.21	3.33	5.82	18	35.5	24	24	3016	160	adaptor-related protein complex 2, alpha 1subunit	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	CC	Yes
DNAJC19	131118	mitochondrial import inner membrane translocase subunit TIM14 isoform 1	NP_660304.1	2	2	2	7	1.1	1.19	7.53	6.55	16.7	15.7	4	4	12349	131118	None	Protein translocase activity	Mitochondrial membrane	Enzyme: Translocase	Mitochondrial transport	TM;DNAJ	No
NOL7	51406	nucleolar protein 7	NP_057251.2	1	5	5	9	1.1	1.19	4.5	9.6	12.2	28.4	6	6	17641	51406	nucleolar protein 7, 27kDa	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	No
ECHS1	1892	enoyl-CoA hydratase, mitochondrial	NP_004083.3	1	5	5	11	1.1	1.18	7.37	11.47	21.7	36.8	7	7	3799	1892	enoyl Coenzyme A hydratase, short chain, 1,mitochondrial	Catalytic activity	Mitochondrion	Enzyme: Hydratase	Metabolism;Energy pathways	SP	Yes
PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	NP_002799.3	3	30	30	86	1.1	1.17	3.62	4.15	29	35.6	51	51	5870	5708	proteasome (prosome, macropain) 26S subunit,non-ATPase, 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
MATR3	9782	matrin-3 isoform a	NP_954659.1	3	22	23	116	1.1	1.16	3.27	2.81	27.4	25	56	57	5270	9782	matrin 3	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
DNAJC8	22826	dnaJ homolog subfamily C member 8	NP_055095.2	1	10	10	16	1.1	1.15	8.91	8.61	33.2	33.6	11	11	13236	22826	DnaJ (Hsp40) homolog, subfamily C, member 8	Chaperone activity	Nucleolus	Chaperone	Protein metabolism	DNAJ;CC	Yes
IDI1	3422	isopentenyl-diphosphate Delta-isomerase 1	NP_004499.2	2	8	8	38	1.1	1.15	5.38	9.15	27	49.8	20	20	7235	3422	isopentenyl-diphosphate delta isomerase	Isomerase activity	Peroxisome	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
PABPC1	26986	polyadenylate-binding protein 1	NP_002559.2	4	21	31	132	1.1	1.15	3.41	2.85	21.5	18.7	32	32	5247	26986	poly(A) binding protein, cytoplasmic 1	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
VPRBP	9730	protein VPRBP isoform 1	NP_055518.1	2	5	5	6	1.1	1.14	3.26	0.47	6.2	0.9	3	3	11674	9730	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	LISH;CC	Yes

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ILF2	3608	interleukin enhancer-binding factor 2 isoform 1	NP_004506.2	2	17	17	103	1.1	1.14	3.67	4.95	30.1	42.6	53	52	4419	3608	interleukin enhancer binding factor 2, 45kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PFKP	5214	ATP-dependent 6-phosphofructokinase, platelet type isoform 1	NP_002618.1	2	38	40	248	1.1	1.13	2.61	3.17	31.1	39.3	112	111	1384	5214	phosphofructokinase, platelet	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
SBDS	51119	ribosome maturation protein SBDS	NP_057122.2	1	13	13	27	1.1	1.13	4.52	8.28	18.1	34.8	13	13	7393	51119	Shwachman-Bodian-Diamond syndrome	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes
METAP2	10988	methionine aminopeptidase 2	NP_006829.1	1	10	10	21	1.1	1.13	9.14	7.81	37.6	32.5	13	13	3522	10988	methionyl aminopeptidase 2	Translation regulator activity	-	Translation regulatory protein	Protein metabolism	-	Yes
MBD2	8932	methyl-CpG-binding domain protein 2 isoform 1	NP_003918.1	2	4	4	6	1.1	1.12	5.31	0.91	11.7	2	4	4	4647	8932	methyl-CpG binding domain protein 2	DNA binding	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MBD;CC	Yes
NOM1	64434	nucleolar MIF4G domain-containing protein 1	NP_612409.1	1	7	7	12	1.1	1.12	14.02	5.36	39.1	14.8	6	6	18485	64434	nucleolar protein with MIF4G domain 1	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	MIF4G;MA3;CC	No
MTHFS	10588	5-formyltetrahydrofolate cyclo-ligase isoform a	NP_006432.1	3	1	1	2	1.1	1.11					1	1	9174	10588	5,10-methenyltetrahydrofolate synthetase(5-formyltetrahydrofolate cyclo-ligase)	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
MRPL30	51263	39S ribosomal protein L30, mitochondrial precursor	NP_660213.1	1	2	2	2	1.1	1.11	3.62	8.49	5.6	13.3	2	2	14751	51263	mitochondrial ribosomal protein L30	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
EIF4H	7458	eukaryotic translation initiation factor 4H isoform 1	NP_071496.1	2	5	5	8	1.1	1.11	3	12.16	6.6	27.5	4	4	11940	7458	Williams-Beuren syndrome chromosome region 1	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	RRM	Yes
COPG1	22820	coatomer subunit gamma-1	NP_057212.1	1	29	31	130	1.1	1.1	2.75	4.67	23.4	41.1	58	59									
RNF213	57674	E3 ubiquitin-protein ligase RNF213 isoform 3	NP_001243000.2	2	21	21	33	1.1	1.09	3.85	3.4	19.1	16.7	20	20	10716	57674	chromosome 17 open reading frame 27	Molecular function unknown	-	Unclassified	Biological_process unknown	RING;AAA;A2M	Yes
PELP1	27043	proline-, glutamic acid- and leucine-rich protein 1 isoform 1	NP_055204.3	2	10	10	18	1.1	1.08	8.91	11.68	31.6	41.5	10	10	10144	27043	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	No
CCT7	10574	T-complex protein 1 subunit eta isoform a	NP_006420.1	4	35	35	205	1.1	1.07	2.9	4	32.2	44.1	97	97	6896	10574	chaperonin containing TCP1, subunit 7 (eta)	Chaperone activity	Cytoplasm	Chaperone	Protein folding	-	Yes
THOC6	79228	THO complex subunit 6 homolog isoform 1	NP_077315.2	2	2	2	9	1.1	1.06	13.14	3.62	29.5	7.7	4	4	14504	79228	WD repeat domain 58	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	No
SRSF1	6426	serine/arginine-rich splicing factor 1 isoform 1	NP_008855.1	2	13	13	54	1.1	1.05	2.11	3.02	12.6	17.3	29	29									
ATP6V0A1	535	V-type proton ATPase 116 kDa subunit a isoform 1 isoform a	NP_001123492.1	3	7	7	15	1.1	1.05	4.58	4.19	14.3	12.5	8	8	1886	535	ATPase, H+ transporting, lysosomal V0subunit a isoform 1	Ion channel activity	Brush border	Ion channel	Transport	SP;TM;CC	Yes
CCT5	22948	T-complex protein 1 subunit epsilon isoform a	NP_036205.1	5	30	31	145	1.1	1.04	3.78	5.42	34.5	47.2	65	63	6468	22948	chaperonin containing TCP1, subunit 5 (epsilon)	Chaperone activity	Centrosome	Chaperone	Protein metabolism	-	Yes
SARNP	84324	SAP domain-containing ribonucleoprotein	NP_149073.1	1	5	5	13	1.1	1.02	4.41	10.42	13.8	30.7	8	8	16716	84324	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	SAP;NLS	Yes
LIMA1	51474	LIM domain and actin-binding protein 1 isoform 1	NP_001107018.1	2	1	37	100	1.1	1.01					1	1	9755	51474	None	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	LIM	Yes
SCCPDH	51097	saccharopine dehydrogenase-like oxidoreductase	NP_057086.2	1	5	5	12	1.1	1	8.48	0.47	23.1	1.2	6	6	13038	51097	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	TM	No
SERBP1	26135	plasminogen activator inhibitor 1 RNA-binding protein isoform 1	NP_001018077.1	4	17	17	67	1.1	1	3.47	5.25	21.9	30.3	32	32	9570	26135	None	RNA binding	Cytoplasm;Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
KIAA1468	57614	lisH domain and HEAT repeat-containing protein KIAA1468	NP_065905.2	1	5	5	9	1.1	0.99	14.75	15.04	37.4	34.3	5	5	13866	57614	KIAA1468	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC;LISH	Yes
ORC3	23595	origin recognition complex subunit 3 isoform 1	NP_862820.1	3	2	2	2	1.1	0.98	16.79	15.78	26.5	22.1	2	2									
ZFR	51663	zinc finger RNA-binding protein	NP_057191.2	1	10	10	20	1.1	0.97	4.54	5.33	16.7	17.2	11	11	15730	51663	zinc finger RNA binding protein	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	No
RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 1	NP_689876.2	2	2	2	2	1.1	0.95					1	1	15206	55103	Ral GEF with PH domain and SH3 binding motif2	Guanyl-nucleotide exchange factor activity	Nucleus	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RasGEF;PH	No
OASL	8638	2'-5'-oligoadenylate synthase-like protein isoform a	NP_003724.1	3	3	3	5	1.1	0.94	14.56	13.67	22.9	18.3	2	2	4473	8638	2`-5`-oligoadenylate synthetase-like	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBQ	Yes
ARGLU1	55082	arginine and glutamate-rich protein 1	NP_060481.3	1	6	6	8	1.1	0.92	4.03	9.87	8.9	18.3	4	4	7648	55082	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 1	NP_004759.1	2	4	4	14	1.1	0.9	5.75	9.72	18	25.2	8	8									

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PRRC2A	7916	protein PRRC2A	NP_004629.3	1	19	22	34	1.1	0.89	3.86	9.08	18.7	36.1	19	19									
SREK1	140890	splicing regulatory glutamine/lysine-rich protein 1 isoform a	NP_001070667.1	4	7	7	14	1.1	0.89	7.12	7.18	20.9	17.1	7	7									
TOM1	10043	target of Myb protein 1 isoform 2	NP_001129204.1	4	4	4	10	1.1	0.89	7.8	6.8	19.3	13.5	5	5	5265	10043	target of myb1 (chicken)	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	VHS;CC	Yes
CRAT	1384	carnitine O-acetyltransferase isoform 1 precursor	NP_000746.2	2	4	4	7	1.1	0.88	2.38	19.05	5.3	34.7	4	4	8971	1384	carnitine acetyltransferase	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
NUDT5	11164	ADP-sugar pyrophosphatase	NP_054861.2	1	8	8	30	1.1	0.86	5.47	7.69	25.9	28.8	18	18	14851	11164	nudix (nucleoside diphosphate linked moietyX)-type motif 5	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
RPL27A	6157	60S ribosomal protein L27a	NP_000981.1	1	9	9	24	1.1	0.86	9.79	8.78	40.5	27.9	13	13	4701	6157	ribosomal protein L27a	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
MAP2K2	5605	dual specificity mitogen-activated protein kinase kinase 2	NP_109587.1	1	4	7	19	1.1	0.85	2.23	5.45	4.9	9.3	4	4	3164	5605	mitogen-activated protein kinase kinase 2	Protein threonine/tyrosine kinase activity	Cytoplasm	Dual specificity kinase	Cell communication;Signal transduction	S_T_Y_Kinase;CC	Yes
SRGAP3	9901	SLIT-ROBO Rho GTPase-activating protein 3 isoform a	NP_055665.1	2	2	3	5	1.1	0.84	10.41	0.75	20.1	1.1	3	3	12108	9901	SLIT-ROBO Rho GTPase activating protein 3	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	FCH;CC;RHOGAP;SH3	Yes
WDR61	80349	WD repeat-containing protein 61 isoform a	NP_079510.1	2	3	3	11	1.1	0.84	15.51	9.71	39.5	18.5	5	5	15236	80349	WD repeat domain 61	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
TIMM23	100287932	mitochondrial import inner membrane translocase subunit Tim23	NP_006318.1	3	4	4	7	1.1	0.84	1.17	20.16	2.2	30	3	3	16089	10431	translocase of inner mitochondrial membrane 23homolog (yeast)	Catalytic activity	Mitochondrial membrane	Enzyme: Translocase	Protein metabolism	TM	No
MMGT1	93380	membrane magnesium transporter 1 precursor	NP_775741.1	1	1	1	4	1.1	0.83	14.8	8.69	23.3	10.2	2	2	6626	93380	transmembrane protein 32	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM	No
MB21D2	151963	protein MB21D2	NP_848591.2	1	5	5	9	1.1	0.81	5.31	2.41	13.1	4.4	5	5									
NFXL1	152518	NF-X1-type zinc finger protein NFXL1	NP_694540.3	1	1	1	2	1.1	0.8					1	1	11025	152518	nuclear transcription factor, X-boxbinding-like 1	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;TM	No
PSMA5	5686	proteasome subunit alpha type-5 isoform 1	NP_002781.2	2	9	9	26	1.1	0.79	4.66	10.91	19.4	33	14	14	1464	5686	proteasome (prosome, macropain) subunit, alphatype, 5	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
B4GALT7	11285	beta-1,4-galactosyltransferase 7	NP_009186.1	1	1	1	2	1.1	0.79					1	1	5060	11285	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase	Metabolism;Energy pathways	TM	Yes
ATAD1	84896	ATPase family AAA domain-containing protein 1	NP_116199.2	1	5	5	11	1.1	0.78	16.52	67.44	37.6	141.1	4	4	12499	84896	ATPase family, AAA domain containing 1	ATPase activity	Mitochondrion;Nucleus	ATPase	Metabolism;Energy pathways	AAA;CC	No
NOL9	79707	polynucleotide 5'-hydroxyl-kinase NOL9	NP_078930.3	1	4	4	13	1.1	0.77	1.87	9.06	5.5	18.7	7	7	8667	79707	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
MRPS18B	28973	28S ribosomal protein S18b, mitochondrial	NP_054765.1	1	4	4	10	1.1	0.77	2.52	2.77	6.8	5.3	6	6	14781	28973	mitochondrial ribosomal protein S18B	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
ATG9A	79065	autophagy-related protein 9A	NP_001070666.1	1	6	6	12	1.1	0.76	9.86	5.92	27.1	11.1	6	6	7979	79065	APG9 autophagy 9-like 1 (S. cerevisiae)	Molecular function unknown	Cytosol;Nucleus	Integral membrane protein	Biological_process unknown	TM	No
COMMD5	28991	COMM domain-containing protein 5	NP_001274166.1	1	1	1	3	1.1	0.66					1	1	16301	28991	COMM domain containing 5	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
TNKS	8658	tankyrase-1	NP_003738.2	1	1	1	1	1.1	0.57					1	1	4490	8658	tankyrase, TRF1-interacting ankyrin-relatedADP-ribose polymerase	Catalytic activity	Cytoplasm	Enzyme: Ribosyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ANK;SAM	Yes
ABCB6	10058	ATP-binding cassette sub-family B member 6, mitochondrial	NP_005680.1	1	1	1	2	1.09	1.93					1	1	9261	10058	ATP-binding cassette, sub-family B (MDR/TAP),member 6	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	TM;AAA	Yes
THYN1	29087	thymocyte nuclear protein 1 isoform 1	NP_054893.1	2	5	5	6	1.09	1.82	15.41	2.08	34.6	7.6	4	4	18183	29087	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	NLS	No
ATP6AP2	10159	renin receptor precursor	NP_005756.2	1	1	1	2	1.09	1.44					1	1	6454	10159	ATPase, H+ transporting, lysosomal accessoryprotein 2	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;TM	Yes
PSMA1	5682	proteasome subunit alpha type-1 isoform 1	NP_683877.1	3	16	16	44	1.09	1.43	3.07	4.65	16.5	33.5	24	24	4170	5682	proteasome (prosome, macropain) subunit, alphatype, 1	Peptidase activity	Cytoplasm	Protease	Protein metabolism	TM	Yes
APTX	54840	aprataxin isoform e	NP_001182177.1	7	2	2	6	1.09	1.42	9.81	0.79	18.7	1.9	3	3	5892	54840	aprataxin	Protein binding;Hydrolase activity	Nucleoplasm	DNA repair protein	DNA repair	ZNFC2;FHA	Yes
TXN	7295	thioredoxin isoform 1	NP_003320.2	2	6	6	35	1.09	1.33	6.06	6.34	30.1	39	20	20	1761	7295	thioredoxin	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	CAAX	Yes
PSMD9	5715	26S proteasome non-ATPase regulatory subunit 9 isoform 1	NP_002804.2	1	2	2	3	1.09	1.32	1.45	8.42	2.2	15.8	2	2	4394	5715	proteasome (prosome, macropain) 26S subunit,non-ATPase, 9	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	PDZ;CC	Yes

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THOP1	7064	thimet oligopeptidase	NP_003240.1	1	14	14	29	1.09	1.3	3.24	6.36	13.7	33	15	15	3072	7064	thimet oligopeptidase 1	Metallopeptidase activity	Cytoplasm	Metallo protease	Protein metabolism	-	Yes
DRAP1	10589	dr1-associated corepressor	NP_006433.2	1	3	3	5	1.09	1.3	10.13	7.32	19.2	16.6	3	3	3796	10589	DR1-associated protein 1 (negative cofactor 2alpha)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ISOC1	51015	isochorismatase domain-containing protein 1	NP_057132.2	1	5	5	19	1.09	1.28	5.44	4.52	18	17.6	9	9	13030	51015	isochorismatase domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TRAPPC5	126003	trafficking protein particle complex subunit 5	NP_001035926.1	1	2	2	3	1.09	1.27	2.72	7.78	4.2	14.1	2	2	15547	126003	trafficking protein particle complex 5	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
SAFB2	9667	scaffold attachment factor B2	NP_055464.1	1	3	11	21	1.09	1.25	0.32	11.2	0.5	20	2	2	6424	9667	scaffold attachment factor B2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	SAP;RRM;CC;NLS	Yes
FUBP3	8939	far upstream element-binding protein 3	NP_003925.1	1	11	12	17	1.09	1.24	6.46	8.16	23.7	34.6	11	11	4640	8939	far upstream element (FUSE) binding protein 3	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
CD44	960	CD44 antigen isoform 1 precursor	NP_000601.3	8	14	14	72	1.09	1.22	3.26	6.54	22.7	53.7	40	40	115	960	CD44 antigen (homing function and Indian bloodgroup system)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	LINK;TM;SP	Yes
CCT2	10576	T-complex protein 1 subunit beta isoform 1	NP_006422.1	2	35	35	170	1.09	1.21	2.26	3.88	23.2	45.5	86	85	6895	10576	chaperonin containing TCP1, subunit 2 (beta)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
PES1	23481	pescadillo homolog isoform 1	NP_055118.1	3	10	10	17	1.09	1.21	4.18	3.91	13.8	14.3	9	9	5783	23481	pescadillo homolog 1, containing BRCT domain(zebrafish)	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	BRCT;CC	Yes
PDE12	201626	2',5'-phosphodiesterase 12	NP_808881.3	1	6	6	15	1.09	1.19	3.47	7.96	11.4	29.1	9	9	11842	201626	None	Phosphoric diester hydrolase activity	-	Enzyme: Phosphodiesterase	Metabolism;Energy pathways	-	No
PMPCA	23203	mitochondrial-processing peptidase subunit alpha isoform 1 precursor	NP_055975.1	3	15	15	39	1.09	1.18	3.16	8.51	15.1	44.8	19	18	7500	23203	peptidase (mitochondrial processing) alpha	Peptidase activity	Mitochondrion	Protease	Protein metabolism	SP	Yes
RPN2	6185	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 isoform 1 precursor	NP_002942.2	2	19	19	90	1.09	1.17	4.9	4.22	35.8	32.4	42	41	1609	6185	ribophorin II	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase	Protein metabolism	SP;TM	Yes
APP	351	amyloid beta A4 protein isoform a precursor	NP_000475.1	10	6	6	14	1.09	1.17	7.57	11.12	23.5	38	8	8	100	351	amyloid beta (A4) precursor protein (proteasenexin-II, Alzheimer disease)	Receptor activity	Cell surface;Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	KUNITZ;TM;SP;CC	Yes
MAPK8	5599	mitogen-activated protein kinase 8 isoform alpha2	NP_620637.1	11	1	3	5	1.09	1.17					1	1	3100	5599	mitogen-activated protein kinase 8	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Signal transduction	S_T_kinase	Yes
RPS19	6223	40S ribosomal protein S19	NP_001013.1	1	14	14	68	1.09	1.14	2.57	2.44	16.9	16.9	36	36	4591	6223	ribosomal protein S19	Structural constituent of ribosome	Nucleolus	Ribosomal subunit	Protein metabolism	-	Yes
PSMB2	5690	proteasome subunit beta type-2 isoform 1	NP_002785.1	3	6	6	19	1.09	1.12	4.63	15.06	16.9	60.4	11	11	3708	5690	proteasome (prosome, macropain) subunit, betatype, 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
UBE2R2	54926	ubiquitin-conjugating enzyme E2 R2	NP_060281.2	1	1	2	3	1.09	1.12					1	1	15602	54926	ubiquitin-conjugating enzyme E2R 2	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBC	No
PPP1R12C	54776	protein phosphatase 1 regulatory subunit 12C isoform a	NP_060077.1	2	4	4	6	1.09	1.11	6.49	2.28	12.3	4.4	3	3	11452	54776	protein phosphatase 1, regulatory(inhibitor) subunit 12C	Protein binding	Cytoplasm	Regulatory/other subunit	Metabolism;Energy pathways	CC;ANK	No
PSMD14	10213	26S proteasome non-ATPase regulatory subunit 14	NP_005796.1	1	6	6	28	1.09	1.1	3.22	10.31	12.7	40.9	13	12	6208	10213	proteasome (prosome, macropain) 26S subunit,non-ATPase, 14	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	JAB	Yes
TRAPPC12	51112	trafficking protein particle complex subunit 12	NP_057114.5	1	4	4	6	1.09	1.09	2.41	4.61	5.3	10.1	4	4									
LSM14A	26065	protein LSM14 homolog A isoform b	NP_056393.2	2	5	5	19	1.09	1.08	8.77	5.08	19.2	11.1	4	4	12697	26065	family with sequence similarity 61, member A	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RBM27	54439	RNA-binding protein 27	NP_061862.1	1	5	7	14	1.09	1.08	7.38	5.48	18.1	13.3	5	5	19614	54439	RNA binding motif protein 27	RNA binding	-	RNA binding protein	Transcription	-	Yes
KIAA0368	23392	proteasome-associated protein ECM29 homolog	NP_001073867.1	1	27	27	81	1.09	1.07	3.04	5.22	21.5	36.8	41	41	11078	23392	KIAA0368	Translation regulator activity	Centrosome	Translation regulatory protein	Protein metabolism	VHS;NLS;HEAT	Yes
DDX50	79009	ATP-dependent RNA helicase DDX50	NP_076950.1	1	7	9	29	1.09	1.07	2.11	8.8	6.1	25.3	7	7	9910	79009	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
C10orf76	79591	UPF0668 protein C10orf76	NP_078817.2	1	4	4	8	1.09	1.07	9.46	5.62	20.9	12.1	4	4	12588	79591	chromosome 10 open reading frame 76	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
SHMT2	6472	serine hydroxymethyltransferase, mitochondrial isoform 1 precursor	NP_005403.2	3	18	19	106	1.09	1.06	4.55	4.17	34.2	30.8	45	46	717	6472	serine hydroxymethyltransferase 2(mitochondrial)	Methyltransferase activity	Mitochondrion	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	Yes
OTUB1	55611	ubiquitin thioesterase OTUB1	NP_060140.2	1	10	10	31	1.09	1.05	4.46	7.03	20.2	31.2	17	17	8493	55611	OTU domain, ubiquitin aldehyde binding 1	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	-	Yes

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YTHDC1	91746	YTH domain-containing protein 1 isoform 1	NP_001026902.1	2	4	4	7	1.09	1.04	3.05	5.62	6.6	11.7	4	4	11689	91746	None	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
DIS3	22894	exosome complex exonuclease RRP44 isoform a	NP_055768.3	2	17	17	38	1.09	1.03	6.66	3.82	32.3	17.3	19	19	6338	22894	KIAA1008	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PINc	Yes
SUPT16H	11198	FACT complex subunit SPT16	NP_009123.1	1	25	25	60	1.09	1.03	3.06	3.45	19.6	21	34	34	16088	11198	suppressor of Ty 16 homolog (S. cerevisiae)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
TPST1	8460	protein-tyrosine sulfotransferase 1	NP_003587.1	1	1	1	1	1.09	1.02					1	1	7216	8460	tyrosylprotein sulfotransferase 1	Sulfotransferase activity	Golgi apparatus	Enzyme: Sulphotransferase	Metabolism;Energy pathways	TM	Yes
MAPK9	5601	mitogen-activated protein kinase 9 isoform alpha2	NP_002743.3	15	3	5	9	1.09	1.02	16.44	11.51	31.8	20.5	3	3	4206	5601	mitogen-activated protein kinase 9	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Regulation of cell cycle;Apoptosis;Signal transduction	S_T_kinase	Yes
MRPS31	10240	28S ribosomal protein S31, mitochondrial	NP_005821.2	1	11	11	31	1.09	1.02	7.1	10.82	30.7	44.9	15	15	10098	10240	mitochondrial ribosomal protein S31	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	CC	Yes
POLR2A	5430	DNA-directed RNA polymerase II subunit RPB1	NP_000928.1	1	13	13	28	1.09	1	2.71	4.78	11.5	18.7	15	15	8916	5430	polymerase (RNA) II (DNA directed) polypeptideA, 220kDa	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
FBL	2091	rRNA 2'-O-methyltransferase fibrillarin	NP_001427.2	1	14	14	47	1.09	1	2.24	4.37	13	23.4	28	28	617	2091	fibrillarin	Ribonucleoprotein	Nucleolus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
DDX6	1656	probable ATP-dependent RNA helicase DDX6	NP_004388.2	7	11	12	56	1.09	0.99	3.34	6.1	16.7	28.2	21	21	2638	1656	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
GGNBP2	79893	gametogenetin-binding protein 2	NP_079111.1	1	1	1	1	1.09	0.99					1	1	18337	79893	zinc finger protein 403	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
PSMD1	5707	26S proteasome non-ATPase regulatory subunit 1 isoform 1	NP_002798.2	2	30	30	115	1.09	0.99	5.25	7.3	45.3	59.8	57	58	10169	5707	proteasome (prosome, macropain) 26S subunit,non-ATPase, 1	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism;Proteolysis and peptidolysis	CC	Yes
GEMIN4	50628	gem-associated protein 4	NP_056536.2	2	8	8	17	1.09	0.98	3.68	8.29	10.6	21.7	7	7	7370	50628	gem (nuclear organelle) associated protein 4	Molecular function unknown	Nucleus	Unclassified	Reproductive behavior	-	Yes
DHX30	22907	putative ATP-dependent RNA helicase DHX30 isoform 1	NP_619520.1	2	14	14	25	1.09	0.98	4.46	8.93	17.7	32.4	13	13	13142	22907	DEAH (Asp-Glu-Ala-His) box polypeptide 30	RNA binding	Nucleus	RNA binding protein	RNA metabolism	DSRM;DEXDc;HELIC	No
PPP1CC	5501	serine/threonine-protein phosphatase PP1-gamma catalytic subunit isoform 2	NP_001231903.1	2	1	13	49	1.09	0.98					1	1	8911	5501	protein phosphatase 1, catalytic subunit,gamma isoform	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2A	Yes
BMS1	9790	ribosome biogenesis protein BMS1 homolog	NP_055568.3	1	6	6	11	1.09	0.98	4.51	4.94	12.1	10.8	6	5	10689	9790	BMS1-like, ribosome assembly protein (yeast)	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC;GTP_EFTU	Yes
CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform c	NP_001234926.1	3	15	16	40	1.09	0.97	4.16	4.62	20.4	20.3	20	20	1568	6249	restin (Reed-Steinberg cell-expressedintermediate filament-associated protein)	Structural molecule activity	Microtubule;Cytoplasm	Structural protein	Cell growth and/or maintenance;Mitosis	ZnF_C2HC;CC	Yes
PNPLA6	10908	neuropathy target esterase isoform a	NP_001159583.1	4	7	7	17	1.09	0.97	15.76	7.54	51.7	21	8	8	4432	10908	None	Hydrolase activity	Endoplasmic reticulum	Enzyme: Esterase	Metabolism;Energy pathways	TM	Yes
N4BP1	9683	NEDD4-binding protein 1	NP_694574.3	1	3	3	4	1.09	0.97					1	1									
RPL24	6152	60S ribosomal protein L24	NP_000977.1	1	8	8	69	1.09	0.96	5	5.34	34.9	32.9	39	39	10365	6152	ribosomal protein L24	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	CC;TRASH	Yes
NPM1	4869	nucleophosmin isoform 1	NP_002511.1	4	2	17	164	1.09	0.96	12.24	16.84	63.2	80.2	19	19	1246	4869	nucleophosmin (nucleolar phosphoprotein B23,numatrin)	Chaperone activity	Nucleolus;Nucleus;Cytoplasm	Chaperone	Protein metabolism	-	Yes
CBX3	11335	chromobox protein homolog 3	NP_057671.2	1	6	7	24	1.09	0.95	6.55	3.86	19	9.7	7	7	5130	11335	chromobox homolog 3 (HP1 gamma homolog,Drosophila)	DNA binding	Nucleus	DNA binding protein	Regulation of gene expression, epigenetic	CHROMO	Yes
AHCYL1	10768	putative adenosylhomocysteinase 2 isoform a	NP_006612.2	6	7	9	17	1.09	0.95	10.56	10.07	31.2	25.7	7	7	7613	10768	S-adenosylhomocysteine hydrolase-like 1	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	CC	Yes
ACBD3	64746	Golgi resident protein GCP60	NP_073572.2	1	12	12	38	1.09	0.95	4.63	12.36	21.1	51.3	17	17	8432	64746	acyl-Coenzyme A binding domain containing 3	Transporter activity	Golgi apparatus	Transport/cargo protein	Cell communication;Signal transduction	CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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MSH2	4436	DNA mismatch repair protein Msh2 isoform 1	NP_000242.1	3	12	12	18	1.09	0.93	4.69	5.52	15.4	15.5	9	9	389	4436	mutS homolog 2, colon cancer, nonpolyposis type1 (E. coli)	DNA repair protein	Nucleus	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;MUTSd;MUTSac	Yes
TFAM	7019	transcription factor A, mitochondrial isoform 1 precursor	NP_003192.1	2	7	7	12	1.09	0.93	3.89	6.06	11.3	14.9	7	7	2702	7019	transcription factor A, mitochondrial	Transcription factor activity	Mitochondrion	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;SP	No
PIGK	10026	GPI-anchor transamidase precursor	NP_005473.1	1	3	3	9	1.09	0.92	4.45	6.21	11.9	14.1	6	6	5474	10026	phosphatidylinositol glycan, class K	Cysteine-type peptidase activity	Endoplasmic reticulum	Cysteine protease	Protein metabolism	SP;TM	No
COPS3	8533	COP9 signalosome complex subunit 3 isoform 1	NP_003644.2	2	7	7	20	1.09	0.92	9.14	18.98	32.2	59.4	10	10	7262	8533	COP9 constitutive photomorphogenic homologsubunit 3 (Arabidopsis)	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Cell communication;Signal transduction	PINT	No
DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 1	NP_001104792.1	2	3	3	3	1.09	0.91	0.16	6.02	0.3	9.5	3	3	13129	79039	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	RNA binding	Nucleolus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;NLS	Yes
NBN	4683	nibrin	NP_002476.2	2	3	3	6	1.09	0.9	2.09	5.95	3.9	9.3	3	3	4050	4683	nibrin	DNA binding	Nucleus	DNA repair protein	DNA repair	FHA;CC;BRCT	Yes
CLPTM1L	81037	cleft lip and palate transmembrane protein 1-like protein	NP_110409.2	1	3	3	5	1.09	0.88	1.13	4.54	2.1	6.9	3	3	7480	81037	None	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
RPTOR	57521	regulatory-associated protein of mTOR isoform 1	NP_065812.1	2	3	3	5	1.09	0.87	15.47	10.24	29.8	15.5	3	3	6184	57521	None	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	WD40	Yes
PTBP1	5725	polypyrimidine tract-binding protein 1 isoform c	NP_114368.1	3	19	22	246	1.09	0.82	3.52	5.69	38.9	48.2	95	95	2823	5725	polypyrimidine tract binding protein 1	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
CC2D1A	54862	coiled-coil and C2 domain-containing protein 1A	NP_060191.3	1	9	9	20	1.09	0.81	4.65	10.5	15.3	25.9	9	9	8616	54862	None	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Cell communication;Signal transduction	C2;CC	Yes
SCO1	6341	protein SCO1 homolog, mitochondrial	NP_004580.1	1	3	3	5	1.09	0.79	5.87	19.7	11.1	27.4	3	3	4705	6341	SCO cytochrome oxidase deficient homolog 1(yeast)	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	-	No
RBM19	9904	probable RNA-binding protein 19	NP_057280.2	1	1	1	1	1.09	0.78					1	1	15225	9904	RNA binding motif protein 19	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
GHITM	27069	growth hormone-inducible transmembrane protein	NP_055209.2	1	3	3	3	1.09	0.77	4.44	17.5	6.8	19.1	2	2	17038	27069	growth hormone inducible transmembrane protein	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
HDHD1	8226	pseudouridine-5'-phosphatase isoform a	NP_001129037.1	3	1	1	2	1.09	0.74					1	1									
HDAC7	51564	histone deacetylase 7 isoform a	NP_056216.2	3	1	1	1	1.09	0.74					1	1	9133	51564	histone deacetylase 7A	Deacetylase activity	Nucleus	Enzyme: Deacetylase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of gene expression, epigenetic	NES;NLS	Yes
LAPTM4A	9741	lysosomal-associated transmembrane protein 4A	NP_055528.1	1	1	1	1	1.09	0.72					1	1	13959	9741	lysosomal-associated protein transmembrane 4alpha	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	TM	No
SYNJ2	8871	synaptojanin-2 isoform 1	NP_003889.1	2	1	1	1	1.09	0.71					1	1	10259	8871	synaptojanin 2	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase	Metabolism;Energy pathways	I_Phosphatase	Yes
C12orf57	113246	protein C10 isoform 1	NP_612434.1	4	2	2	5	1.09	0.71	16.96	12.02	33	14.8	3	3	13609	113246	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
RAP1B	5908	ras-related protein Rap-1b isoform 1 precursor	NP_056461.1	4	3	10	26	1.09	0.7	3.29	17.46	8	27.8	5	5	1546	5908	RAP1B, member of RAS oncogene family	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	RAS	Yes
DVL3	1857	segment polarity protein dishevelled homolog DVL-3	NP_004414.3	1	1	2	3	1.09	0.61					1	1	3222	1857	dishevelled, dsh homolog 3 (Drosophila)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	DSH;PDZ	Yes
FLII	2314	protein flightless-1 homolog isoform 1	NP_002009.1	3	1	35	94	1.09	0.54					1	1	2647	2314	flightless I homolog (Drosophila)	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	GEL;CC;LRR	Yes
AFF4	27125	AF4/FMR2 family member 4	NP_055238.1	1	2	2	6	1.08	1.63	26.62	1.26	53.3	3.6	3	3	9187	27125	None	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
NTMT1	28989	N-terminal Xaa-Pro-Lys N-methyltransferase 1 isoform a	NP_001273725.1	3	5	5	10	1.08	1.62	10.19	6.11	22.3	20	4	4									
CALM2	805	calmodulin isoform 1	NP_001292553.1	3	7	7	187	1.08	1.62	8.94	5.18	75.6	60.9	48	45	242	805	calmodulin 2 (phosphorylase kinase, delta)	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes

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KHSRP	8570	far upstream element-binding protein 2	NP_003676.2	1	16	17	40	1.08	1.58	4.67	4.08	24	30.9	22	22	10350	8570	KH-type splicing regulatory protein (FUSEbinding protein 2)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
ERCC2	2068	TFIIH basal transcription factor complex helicase XPD subunit isoform 1	NP_000391.1	2	2	2	6	1.08	1.56	25.02	27.45	49.6	85.6	3	3	530	2068	excision repair cross-complementing rodentrepair deficiency, complementation group 2 (xeroderma pigmentosum D)	DNA repair protein	Nucleus	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
RBM4	5936	RNA-binding protein 4 isoform 1	NP_002887.2	4	4	4	7	1.08	1.5	4.2	15.67	7.9	42.5	3	3	3982	5936	RNA binding motif protein 4	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;ZnF_C2HC	No
PDHX	8050	pyruvate dehydrogenase protein X component, mitochondrial isoform 1 precursor	NP_003468.2	3	6	6	10	1.08	1.49	7.28	8.82	17.7	29.9	5	5	2002	8050	pyruvate dehydrogenase complex, component X	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
PPP6R3	55291	serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform 4	NP_001157632.1	6	11	11	17	1.08	1.48	8.71	3.37	30.4	15.9	10	10									
RPS6KB2	6199	ribosomal protein S6 kinase beta-2	NP_003943.2	6	1	2	2	1.08	1.46					1	1	10203	6199	ribosomal protein S6 kinase, 70kDa,polypeptide 2	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Protein metabolism;Signal transduction	S_T_kinase;NES;NLS;S_T_Y_Kinase	Yes
ATP5SL	55101	ATP synthase subunit s-like protein isoform 1	NP_001161339.1	3	2	2	5	1.08	1.46	4.13	14.23	6.3	30	2	2	7655	55101	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
FGFBP1	9982	fibroblast growth factor-binding protein 1 precursor	NP_005121.1	1	7	7	11	1.08	1.44	10.27	4.83	32.1	19.8	8	8	6371	9982	fibroblast growth factor binding protein 1	Chaperone activity	Extracellular	Chaperone	Cell communication;Signal transduction	SP	No
WDR26	80232	WD repeat-containing protein 26 isoform a	NP_079436.4	2	6	6	10	1.08	1.4	6.45	10.67	15.7	34.4	5	5	18298	80232	WD repeat domain 26	Molecular function unknown	-	Unclassified	Biological_process unknown	CTLH;WD40	Yes
PSAP	5660	prosaposin isoform b preproprotein	NP_001035930.1	3	14	14	44	1.08	1.38	3.96	9.62	19.8	67	21	21	1460	5660	prosaposin (variant Gaucher disease and variantmetachromatic leukodystrophy)	Lipid binding	Lysosome	Integral membrane protein	Cell communication;Signal transduction	SAPA;SAPB;SP	Yes
TUBA3C	7278	tubulin alpha-3C/D chain	NP_005992.1	2	1	24	444	1.08	1.34					1	1	3958	7278	tubulin, alpha 2	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	TUBULIN;CC	Yes
TUSC3	7991	tumor suppressor candidate 3 isoform a precursor	NP_006756.2	2	1	1	2	1.08	1.34					1	1	3228	7991	tumor suppressor candidate 3	Molecular function unknown	Integral to membrane	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
BUB3	9184	mitotic checkpoint protein BUB3 isoform a	NP_004716.1	2	9	9	24	1.08	1.33	6.36	5.11	23	22.9	11	11	4761	9184	BUB3 budding uninhibited by benzimidazoles 3homolog (yeast)	Protein transporter activity	Cytoplasm	Cell cycle control protein	Regulation of cell cycle;Signal transduction	WD40	Yes
NLE1	54475	notchless protein homolog 1 isoform a	NP_060566.2	2	4	4	9	1.08	1.25	2.35	9.23	5.7	26.2	5	5	16903	54475	notchless homolog 1 (Drosophila)	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	WD40	Yes
ERI1	90459	3'-5' exoribonuclease 1	NP_699163.2	1	1	1	1	1.08	1.23					1	1	11784	90459	three prime histone mRNA exonuclease 1	Ribonuclease activity	-	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;EXOIII	No
IBA57	200205	putative transferase CAF17, mitochondrial precursor	NP_001010867.1	1	2	2	4	1.08	1.22	8.6	21.98	13.2	39.3	2	2									
MPP6	51678	MAGUK p55 subfamily member 6	NP_057531.2	4	5	6	14	1.08	1.22	3.51	6.29	9.3	19	6	6	9509	51678	membrane protein, palmitoylated 6 (MAGUK p55subfamily member 6)	Molecular function unknown	Plasma membrane	Unclassified	Cell communication;Signal transduction	PDZ;SH3;GuKinase	Yes
DNAJC10	54431	dnaJ homolog subfamily C member 10 isoform 1 precursor	NP_061854.1	2	10	10	18	1.08	1.22	10.27	7.49	36.2	29.4	10	10	9722	54431	DnaJ (Hsp40) homolog, subfamily C, member 10	Molecular function unknown	Endoplasmic reticulum	Unclassified	Protein metabolism	DNAJ	No
EXOSC2	23404	exosome complex component RRP4 isoform 1	NP_055100.2	3	4	4	14	1.08	1.22	2.04	9.87	5.8	32.6	7	7	3758	23404	exosome component 2	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S1	Yes
TARS	6897	threonine--tRNA ligase, cytoplasmic isoform 1	NP_689508.3	3	30	30	119	1.08	1.21	2.96	3.48	25.7	34.3	63	63	1762	6897	threonyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
MMP14	4323	matrix metalloproteinase-14 preproprotein	NP_004986.1	1	5	5	7	1.08	1.21	3.79	6.93	9.2	18.9	5	5	2856	4323	matrix metalloproteinase 14 (membrane-inserted)	Metallopeptidase activity	Extracellular	Metallo protease	Protein metabolism	TM;ZnMc;HX;SP	Yes
SGTB	54557	small glutamine-rich tetratricopeptide repeat-containing protein beta	NP_061945.1	1	1	1	2	1.08	1.2					1	1	18049	54557	small glutamine-rich tetratricopeptide repeat(TPR)-containing, beta	Molecular function unknown	-	Unclassified	Biological_process unknown	TPR	Yes
RPS25	6230	40S ribosomal protein S25	NP_001019.1	1	5	5	28	1.08	1.2	3.6	4.76	14.6	21.6	14	14	1593	6230	ribosomal protein S25	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PCYT2	5833	ethanolamine-phosphate cytidylyltransferase isoform 1	NP_001171846.1	6	1	1	1	1.08	1.2					1	1	4059	5833	phosphate cytidylyltransferase 2, ethanolamine	Nucleotidyltransferase activity	Cytoplasm	Enzyme: Nucleotidyltransferase	Metabolism;Energy pathways	-	Yes

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Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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UBE2O	63893	ubiquitin-conjugating enzyme E2 O	NP_071349.3	1	9	9	17	1.08	1.19	7.47	3.67	27.2	14.6	11	11	10928	63893	None	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CC;UBC	No
PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	NP_055706.1	1	5	5	11	1.08	1.19	4.88	3.75	12.9	11	6	6	6149	11333	PDGFA associated protein 1	Growth factor binding	Extracellular	Secreted polypeptide	Cell communication;Signal transduction	CC	Yes
LAMB1	3912	laminin subunit beta-1 precursor	NP_002282.2	1	21	21	47	1.08	1.18	4.22	4.45	23.2	26.7	25	25	1029	3912	laminin, beta 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	LAMNT;EGFLAM;SP;CC	Yes
TNRC6B	23112	trinucleotide repeat-containing gene 6B protein isoform 1	NP_001155973.1	2	1	1	2	1.08	1.17					1	1	10021	23112	trinucleotide repeat containing 6B	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;RRM	Yes
PLEKHF2	79666	pleckstrin homology domain-containing family F member 2	NP_078889.1	1	2	3	6	1.08	1.17	13.06	5.01	20.2	8.3	2	2	15147	79666	pleckstrin homology domain containing, familyF (with FYVE domain) member 2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	PH;FYVE	No
CWF19L1	55280	CWF19-like protein 1 isoform 1	NP_060764.3	3	4	4	9	1.08	1.17	2.53	5.6	5.5	13.1	4	4	13101	55280	CWF19-like 1, cell cycle control (S. pombe)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ACTL6A	86	actin-like protein 6A isoform 1	NP_004292.1	3	4	4	8	1.08	1.17	3.62	13.38	7.8	32.1	4	4	5389	86	actin-like 6A	Chromatin binding	Cytoplasm;Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ACTIN;NLS	Yes
ERCC6	2074	DNA excision repair protein ERCC-6	NP_000115.1	2	1	1	1	1.08	1.16					1	1	596	2074	excision repair cross-complementing rodentrepair deficiency, complementation group 6	DNA repair protein	Nucleus	DNA repair protein	DNA repair	DEXDc;HELIC;CC	Yes
FYTTD1	84248	UAP56-interacting factor isoform 1	NP_115664.2	2	3	3	7	1.08	1.15	2.73	3.48	5.9	8	4	4	10909	84248	forty-two-three domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
RBBP5	5929	retinoblastoma-binding protein 5 isoform 1	NP_005048.2	3	8	8	18	1.08	1.15	4.83	3.37	13.9	10.3	7	7	2826	5929	retinoblastoma binding protein 5	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
VWA9	81556	von Willebrand factor A domain-containing protein 9 isoform 4	NP_001193987.1	3	5	5	9	1.08	1.14	17.21	13.32	43.4	34.8	5	5									
RBMXL1	494115	RNA binding motif protein, X-linked-like-1	NP_062556.2	2	3	21	77	1.08	1.14	16.61	0.59	31.7	1.2	3	3	17417	494115	RNA binding motif protein, X-linked-like 1	-	-	-	-	-	No
SIRT3	23410	NAD-dependent protein deacetylase sirtuin-3, mitochondrial isoform a	NP_036371.1	2	2	2	6	1.08	1.13	2.23	5.4	4.2	10.6	3	3	6836	23410	sirtuin (silent mating type informationregulation 2 homolog) 3 (S. cerevisiae)	Deacetylase activity	Mitochondrion	Enzyme: Deacetylase	Gene silencing	SP	Yes
ARIH2	10425	E3 ubiquitin-protein ligase ARIH2	NP_006312.1	1	5	5	8	1.08	1.13	4.58	10.01	11.1	25.8	5	5	9286	10425	ariadne homolog 2 (Drosophila)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	RING;IBR;CC	Yes
PAPOLA	10914	poly(A) polymerase alpha isoform 1	NP_116021.2	10	8	8	14	1.08	1.11	6.46	4.9	15.7	12.2	5	5	10407	10914	poly(A) polymerase alpha	RNA binding	-	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
EFTUD2	9343	116 kDa U5 small nuclear ribonucleoprotein component isoform a	NP_004238.3	3	30	31	93	1.08	1.11	2.43	3.71	17.7	28.2	45	45	4869	9343	None	GTPase activity	Nucleus	Unclassified	Protein metabolism	GTP_EFTU_D2; GTP_EFTU	Yes
ACADM	34	medium-chain specific acyl-CoA dehydrogenase, mitochondrial isoform d precursor	NP_001272972.1	5	8	8	16	1.08	1.1	3.66	2.85	11.2	8.9	8	8	8447	34	acyl-Coenzyme A dehydrogenase, C-4 to C-12straight chain	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
NUP93	9688	nuclear pore complex protein Nup93 isoform 1	NP_055484.3	2	23	23	45	1.08	1.1	3.54	3.38	19.6	19.2	26	26	14854	9688	nucleoporin 93kDa	Auxiliary transport protein activity	Nucleus	Membrane transport protein	Transport	-	Yes
TINAGL1	64129	tubulointerstitial nephritis antigen-like isoform 1 precursor	NP_071447.1	3	3	3	6	1.08	1.09	1.12	13.63	2.1	26.1	3	3	7122	64129	lipocalin 7	Transporter activity	Extracellular	Transport/cargo protein	Transport	SP;SOM;PPTC1	No
COPE	11316	coatomer subunit epsilon isoform a	NP_009194.2	3	11	11	28	1.08	1.09	6.73	6.9	27.7	27.7	14	13	6089	11316	coatomer protein complex, subunit epsilon	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	No
PSMA7	5688	proteasome subunit alpha type-7	NP_002783.1	5	16	16	84	1.08	1.09	1.72	2.92	12.2	21.1	43	43	5967	5688	proteasome (prosome, macropain) subunit, alphatype, 7	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
DHX9	1660	ATP-dependent RNA helicase A	NP_001348.2	1	40	40	162	1.08	1.08	2.39	2.68	23.8	27.1	83	84	4386	1660	DEAH (Asp-Glu-Ala-His) box polypeptide 9	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DSRM;DEXDc;HELIC	Yes
CSNK2A1	1457	casein kinase II subunit alpha isoform a	NP_808227.1	3	8	10	26	1.08	1.07	3.58	5.05	13.4	18.9	12	12	277	1457	casein kinase 2, alpha 1 polypeptide	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Signal transduction;Protein modification	S_T_kinase	No
GNL1	2794	guanine nucleotide-binding protein-like 1	NP_005266.2	1	14	14	31	1.08	1.07	3.63	3.83	16.7	17.5	18	18	879	2794	guanine nucleotide binding protein-like 1	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
HNRNPR	10236	heterogeneous nuclear ribonucleoprotein R isoform 2	NP_005817.1	7	17	26	115	1.08	1.06	3.9	1.89	28.9	13.5	45	45	6228	10236	heterogeneous nuclear ribonucleoprotein R	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
NADK2	133686	NAD kinase 2, mitochondrial isoform 1	NP_001078880.1	3	5	5	8	1.08	1.05	5.09	5.27	11.1	11.1	4	4									

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HMGB1	3146	high mobility group protein B1	NP_002119.1	1	6	7	24	1.08	1.04	4.95	6.59	17.1	22	10	10	1228	3146	high-mobility group box 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	Yes
REEP4	80346	receptor expression-enhancing protein 4 precursor	NP_079508.2	1	1	1	2	1.08	1.03					1	1	9864	80346	chromosome 8 open reading frame 20	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	SP;TM	No
WDR18	57418	WD repeat-containing protein 18	NP_077005.2	1	4	4	7	1.08	1.03	10.72	1.93	23.4	4	4	4	18296	57418	WD repeat domain 18	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	WD40	Yes
TMEM160	54958	transmembrane protein 160 precursor	NP_060324.1	1	1	1	2	1.08	1.02					1	1	7920	54958	None	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM	No
GART	2618	trifunctional purine biosynthetic protein adenosine-3 isoform 1	NP_001129477.1	2	38	38	140	1.08	1.02	2.28	3.48	21.5	31.4	75	75	716	2618	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	Ligase activity	Cytosol	Enzyme: Transferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MIF4GD	57409	MIF4G domain-containing protein isoform 4	NP_001229430.1	1	1	1	1	1.08	1.02					1	1	10629	57409	None	Molecular function unknown	-	Unclassified	Biological_process unknown	MIF4G	No
C9orf89	84270	bcl10-interacting CARD protein	NP_115686.3	1	1	1	1	1.08	1.02					1	1	12985	84270	chromosome 9 open reading frame 89	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	CARD;TM	No
SCYL2	55681	SCY1-like protein 2	NP_060458.3	1	3	3	4	1.08	1.01	7.33	5.72	11.2	8.2	2	2	7642	55681	SCY1-like 2 (S. cerevisiae)	Kinase activity	Perinuclear region	Serine/threonine kinase	Regulation of endocytosis	CC;Tyr_Kinase	No
CDK7	1022	cyclin-dependent kinase 7	NP_001790.1	3	3	3	8	1.08	1.01	2.59	8.25	4.9	14.6	3	3	15993	1022	cyclin-dependent kinase 7 (MO15 homolog, Xenopuslaevis, cdk-activating kinase)	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_kinase	Yes
HSD17B4	3295	peroxisomal multifunctional enzyme type 2 isoform 2	NP_000405.1	5	31	31	128	1.08	1.01	2.22	3.52	19.9	29.8	67	67	3514	3295	hydroxysteroid (17-beta) dehydrogenase 4	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
CSRP2	1466	cysteine and glycine-rich protein 2	NP_001312.1	1	1	1	2	1.08	1					1	1	3523	1466	cysteine and glycine-rich protein 2	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	LIM;NLS	Yes
EMC1	23065	ER membrane protein complex subunit 1 isoform 1 precursor	NP_055862.1	4	15	15	41	1.08	0.99	3.02	6.04	15.8	29.4	23	23									
TKT	7086	transketolase isoform 2	NP_001244957.1	2	30	30	275	1.08	0.99	1.71	2.57	20.8	29	124	124	6001	7086	transketolase (Wernicke-Korsakoff syndrome)	Transferase activity, transferring aldehyde or ketonic groups	Cytoplasm	Enzyme: Transketolase	Metabolism;Energy pathways	-	Yes
XAB2	56949	pre-mRNA-splicing factor SYF1	NP_064581.2	1	9	9	16	1.08	0.99	1.42	3.22	4.9	10.1	10	10	18306	56949	XPA binding protein 2	DNA repair protein	Nucleus	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TPR	Yes
ATP6V1D	51382	V-type proton ATPase subunit D	NP_057078.1	1	4	4	9	1.08	0.99	4.17	3.3	10.1	7.3	5	5	16524	51382	ATPase, H+ transporting, lysosomal 34kDa, V1subunit D	ATPase activity	Integral to membrane	ATPase	Metabolism;Energy pathways	CC	Yes
NFS1	9054	cysteine desulfurase, mitochondrial isoform a precursor	NP_066923.3	2	11	11	18	1.08	0.98	7.44	6.53	25.8	20.5	10	10	4597	9054	NFS1 nitrogen fixation 1 (S. cerevisiae)	Sulfotransferase activity	Mitochondrion	Enzyme: Sulphotransferase	Metabolism;Energy pathways	NLS	Yes
NUP214	8021	nuclear pore complex protein Nup214	NP_005076.3	1	21	21	34	1.08	0.97	5.35	3.62	25.6	15.4	19	19	258	8021	nucleoporin 214kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	WD40	Yes
RAPGEF2	9693	rap guanine nucleotide exchange factor 2	NP_055062.1	1	1	1	2	1.08	0.97					1	1	19358	9693	Rap guanine nucleotide exchange factor (GEF) 2	Guanyl-nucleotide exchange factor activity	Synapse	Guanine nucleotide exchange factor	Signal transduction;Cell communication	CNMP;RasGEFN;PDZ;RA;RasGEF	Yes
TIMM44	10469	mitochondrial import inner membrane translocase subunit TIM44	NP_006342.2	1	10	10	23	1.08	0.96	6.7	5.12	26.6	17.9	13	13	5450	10469	translocase of inner mitochondrial membrane 44homolog (yeast)	Catalytic activity	Mitochondrion	Enzyme: Translocase	Transport	CC	Yes
PTRH1	138428	probable peptidyl-tRNA hydrolase	NP_001002913.1	1	1	1	2	1.08	0.96					1	1	12936	138428	chromosome 9 open reading frame 115	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
SMARCA4	6597	transcription activator BRG1 isoform A	NP_001122321.1	9	9	12	22	1.08	0.96	3.81	5.43	13.7	17.4	11	11	4459	6597	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 4	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRK;DEXDc;HELIC;BROMO;CC	Yes
HNRNPU	3192	heterogeneous nuclear ribonucleoprotein U isoform b	NP_004492.2	2	26	26	197	1.08	0.95	2.64	4.11	30.2	41.9	106	106	4185	3192	heterogeneous nuclear ribonucleoprotein U(scaffold attachment factor A)	RNA binding	Nucleus;Cytoplasm	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;SPRY;CC;NLS	Yes
ARHGAP12	94134	rho GTPase-activating protein 12 isoform 1	NP_060757.4	6	1	1	2	1.08	0.95					1	1	6446	94134	Rho GTPase activating protein 12	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	SH3;WW;PH;RHOGAP	Yes
MRPS12	6183	28S ribosomal protein S12, mitochondrial precursor	NP_066930.1	1	3	3	6	1.08	0.95	5.3	1.19	9.9	1.9	3	3	4316	6183	mitochondrial ribosomal protein S12	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism;Ribosome biogenesis and assembly	SP	Yes
YME1L1	10730	ATP-dependent zinc metalloprotease YME1L1 isoform 1	NP_647473.1	3	9	9	20	1.08	0.95	4.11	7.28	14.8	23.2	11	11	6981	10730	YME1-like 1 (S. cerevisiae)	Metallopeptidase activity	Mitochondrion	Metallo protease	Protein metabolism	AAA	Yes

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GDI1	2664	rab GDP dissociation inhibitor alpha	NP_001484.1	1	15	22	86	1.08	0.94	5.27	10.1	24.6	43	18	19	2114	2664	GDP dissociation inhibitor 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	-	Yes
TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	NP_203754.2	1	64	64	206	1.08	0.94	1.53	2.9	16.3	26.9	95	94	6164	85456	tankyrase 1 binding protein 1, 182kDa	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
NUPL1	9818	nucleoporin p58/p45 isoform a	NP_054808.1	2	3	3	5	1.08	0.93	16.51	2.17	31.5	3.5	3	3	6355	9818	nucleoporin like 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
UBE3C	9690	ubiquitin-protein ligase E3C	NP_055486.2	1	6	6	10	1.08	0.92	8.89	17.28	19.4	32.4	4	4	15604	9690	ubiquitin protein ligase E3C	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	IQ;HECT	Yes
ZNF638	27332	zinc finger protein 638 isoform 1	NP_055312.2	2	12	12	24	1.08	0.91	2.71	6.83	10.2	21.8	12	12	11736	27332	zinc finger protein 638	DNA binding	Nuclear matrix;Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;RRM	Yes
PLEKHM2	23207	pleckstrin homology domain-containing family M member 2	NP_055979.2	1	1	1	2	1.08	0.91					1	1	11440	23207	pleckstrin homology domain containing, familyM (with RUN domain) member 2	Molecular function unknown	Cytosol	Unclassified	Biological_process unknown	PH	Yes
ARPC1A	10552	actin-related protein 2/3 complex subunit 1A isoform 1	NP_006400.2	2	3	3	5	1.08	0.91	4.7	1.6	8.8	2.5	3	3	7252	10552	actin related protein 2/3 complex, subunit 1A,41kDa	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	WD40	Yes
BBX	56987	HMG box transcription factor BBX isoform 1	NP_001136040.1	2	1	1	2	1.08	0.9					1	1	10688	56987	bobby sox homolog (Drosophila)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	Yes
GOSR2	9570	Golgi SNAP receptor complex member 2 isoform B	NP_473363.1	3	3	3	5	1.08	0.9	5.94	21.3	11.1	34.2	3	3	4937	9570	golgi SNAP receptor complex member 2	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	CC;TM	No
STX16	8675	syntaxin-16 isoform b	NP_003754.2	5	2	2	7	1.08	0.87	13.46	22.42	29.6	40.5	4	4	4718	8675	syntaxin 16	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	TM;t_SNARE;SynN	Yes
CCDC51	79714	coiled-coil domain-containing protein 51 isoform 1	NP_001243893.1	2	5	5	8	1.08	0.87	9.09	4.88	19.8	8.5	4	4	8571	79714	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;TM	No
HMGCR	3156	3-hydroxy-3-methylglutaryl-Coenzyme A reductase isoform 1	NP_000850.1	2	2	2	4	1.08	0.87	1.95	30.15	3	38.5	2	2	836	3156	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase	Metabolism;Energy pathways	TM;SP	Yes
CLN6	54982	ceroid-lipofuscinosis neuronal protein 6	NP_060352.1	1	1	1	5	1.08	0.86	9.1	14.03	13.9	17.3	2	2	5991	54982	ceroid-lipofuscinosis, neuronal 6, lateinfantile, variant	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM	Yes
WDR54	84058	WD repeat-containing protein 54	NP_115494.1	1	1	1	2	1.08	0.84					1	1	8577	84058	WD repeat domain 54	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	No
SERINC1	57515	serine incorporator 1 precursor	NP_065806.1	1	2	2	3	1.08	0.82	13.43	7.86	20.7	9.1	2	2	15480	57515	tumor differentially expressed 2	Protein binding	Plasma membrane	Integral membrane protein	Biological_process unknown	SP;TM	Yes
MAN1B1	11253	endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	NP_057303.2	1	3	3	4	1.08	0.82	6.73	3.23	12.6	4.6	3	3	5068	11253	mannosidase, alpha, class 1B, member 1	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase	Metabolism;Energy pathways	TM	Yes
PRPS2	5634	ribose-phosphate pyrophosphokinase 2 isoform 2	NP_002756.1	2	3	10	24	1.08	0.81	7.82	5.21	14.8	7.3	3	3	2414	5634	phosphoribosyl pyrophosphate synthetase 2	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
NSFL1C	55968	NSFL1 cofactor p47 isoform d	NP_001193665.1	3	7	7	22	1.08	0.79	6.17	8.13	22.3	21.5	11	11	9425	55968	NSFL1 (p97) cofactor (p47)	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Cell growth and/or maintenance	UBX;NLS;UBA	Yes
GNA13	10672	guanine nucleotide-binding protein subunit alpha-13 isoform 1	NP_006563.2	9	3	4	35	1.08	0.79	5.07	6.73	9.5	9.3	3	3	5100	10672	guanine nucleotide binding protein (G protein),alpha 13	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	-	Yes
MIEN1	84299	migration and invasion enhancer 1	NP_115715.3	1	1	1	2	1.08	0.78					1	1									
PMVK	10654	phosphomevalonate kinase	NP_006547.1	1	1	1	1	1.08	0.73					1	1	7404	10654	phosphomevalonate kinase	Lipid kinase activity	Peroxisome	Lipid Kinase	Metabolism;Energy pathways	-	Yes
LSM4	25804	U6 snRNA-associated Sm-like protein LSm4 isoform 1	NP_036453.1	2	3	3	6	1.08	0.63	15.28	32.64	33.9	42.6	4	4	6284	25804	LSM4 homolog, U6 small nuclear RNA associated(S. cerevisiae)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
MEMO1	51072	protein MEMO1 isoform 1	NP_057039.1	3	1	1	2	1.07	1.91					1	1	12814	51072	chromosome 2 open reading frame 4	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
TAF15	8148	TATA-binding protein-associated factor 2N isoform 1	NP_631961.1	2	12	14	51	1.07	1.6	14.47	5.27	60.7	29.9	13	12	9031	8148	TAF15 RNA polymerase II, TATA box bindingprotein (TBP)-associated factor, 68kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;ZnF_RBZ	Yes
GANAB	23193	neutral alpha-glucosidase AB isoform 2 precursor	NP_938148.1	3	1	36	143	1.07	1.55	2.13	5.93	3.9	16	3	3	3516	23193	glucosidase, alpha; neutral AB	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase	Carbohydrate metabolism	SP	Yes

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PAF1	54623	RNA polymerase II-associated factor 1 homolog isoform 1	NP_061961.2	2	7	7	17	1.07	1.5	11.98	9.06	40	42.4	9	9	10140	54623	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown;Cell homeostasis;Transcription;Cell development;Cell differentiation;Regulation of metabolism;Drug metabolism	CC;NLS	No
GOLPH3	64083	Golgi phosphoprotein 3	NP_071413.1	1	4	4	8	1.07	1.39	6.81	4.75	16.4	14.8	5	5	11007	64083	golgi phosphoprotein 3 (coat-protein)	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	Yes
HSPA9	3313	stress-70 protein, mitochondrial precursor	NP_004125.3	1	43	43	264	1.07	1.37	2.33	3.12	30.7	53.9	146	139	2770	3313	heat shock 70kDa protein 9B (mortalin-2)	Chaperone activity	Mitochondrion	Chaperone	Protein metabolism	-	Yes
NPLOC4	55666	nuclear protein localization protein 4 homolog	NP_060391.2	1	14	14	31	1.07	1.36	2.02	2.86	8.7	16.1	16	17	6975	55666	None	Transporter activity	Nucleus	Transport/cargo protein	Transport	ZnF_RBZ	Yes
RBM3	5935	RNA-binding protein 3	NP_006734.1	1	1	1	1	1.07	1.33					1	1	2067	5935	RNA binding motif (RNP1, RRM) protein 3	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
SMNDC1	10285	survival of motor neuron-related-splicing factor 30	NP_005862.1	1	3	3	12	1.07	1.32	9.09	6.36	24.2	20.7	6	6	4627	10285	survival motor neuron domain containing 1	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	TUDOR;CC	Yes
ANP32E	81611	acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 1	NP_112182.1	5	6	6	25	1.07	1.3	13.24	5.09	50	22.1	11	11	16493	81611	acidic (leucine-rich) nuclear phosphoprotein32 family, member E	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;LRR	Yes
GSR	2936	glutathione reductase, mitochondrial isoform 1 precursor	NP_000628.2	4	8	8	27	1.07	1.29	4.42	8.46	18.4	44.1	15	15	704	2936	glutathione reductase	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	SP	Yes
HDHD2	84064	haloacid dehalogenase-like hydrolase domain-containing protein 2	NP_115500.1	1	2	2	4	1.07	1.28	11.88	17.66	18	32.9	2	2	13640	84064	haloacid dehalogenase-like hydrolase domaincontaining 2	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
RNF214	257160	RING finger protein 214 isoform 1	NP_997226.2	2	3	3	6	1.07	1.27	2.14	14.28	3.2	26.2	2	2	16815	257160	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	RING;CC	Yes
UBXN7	26043	UBX domain-containing protein 7	NP_056377.1	1	6	7	24	1.07	1.27	6.06	2.63	21.7	11.1	11	11	19396	26043	UBX domain containing 7	Molecular function unknown	-	Unclassified	Biological_process unknown	UBA;UBX	Yes
HSD17B12	51144	very-long-chain 3-oxoacyl-CoA reductase	NP_057226.1	1	12	12	43	1.07	1.26	2.86	6.21	14.4	38	22	22	9989	51144	hydroxysteroid (17-beta) dehydrogenase 12	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM	No
SEL1L	6400	protein sel-1 homolog 1 isoform 1 precursor	NP_005056.3	2	4	4	6	1.07	1.25	6	2.38	11.2	5.2	3	3	7532	6400	sel-1 suppressor of lin-12-like (C. elegans)	Binding	Cytoplasmic vesicle	Integral membrane protein	Biological_process unknown	SP;FN2;TM;SEL1	Yes
CES2	8824	cocaine esterase isoform 1	NP_003860.2	2	3	3	5	1.07	1.24	6.88	2.56	12.8	5.5	3	3	7062	8824	carboxylesterase 2 (intestine, liver)	Hydrolase activity	Microsome	Enzyme: Esterase	Metabolism	-	Yes
P4HA1	5033	prolyl 4-hydroxylase subunit alpha-1 isoform 1 precursor	NP_000908.2	3	13	13	25	1.07	1.24	7.63	4.53	31.4	21.2	14	14	8901	5033	procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Metabolism;Energy pathways;Protein metabolism	P4HC;SP;TPR	Yes
RPSA	3921	40S ribosomal protein SA isoform 2	NP_001291217.1	3	13	14	102	1.07	1.23	3.06	4.14	23	36.5	48	48	1038	3921	ribosomal protein SA	Structural constituent of ribosome;Cell adhesion molecule activity	Cytoplasm	Cell surface receptor;Ribosomal subunit	Cell communication;Signal transduction;Cell adhesion	-	Yes
LDHB	3945	L-lactate dehydrogenase B chain	NP_001167568.1	2	19	22	158	1.07	1.22	2.63	4.82	23.5	51.6	68	68	1026	3945	lactate dehydrogenase B	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
COPB1	1315	coatomer subunit beta	NP_057535.1	1	37	37	142	1.07	1.21	3.52	2.81	34.7	31	80	80	2981	1315	coatomer protein complex, subunit beta	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ADAP	Yes
PPP4R1	9989	serine/threonine-protein phosphatase 4 regulatory subunit 1 isoform a	NP_001035847.1	2	18	18	42	1.07	1.21	4.53	4.28	22	22.8	20	19	5366	9989	protein phosphatase 4, regulatory subunit 1	Enzyme regulator activity	Centrosome	Enzyme regulator	Cell communication;Signal transduction	HEAT	Yes
TRMT11	60487	tRNA (guanine(10)-N2)-methyltransferase homolog	NP_001026882.2	1	3	3	6	1.07	1.18	8.7	29.05	16.2	65.1	3	3	12898	60487	chromosome 6 open reading frame 75	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
GPHN	10243	gephyrin isoform 1	NP_065857.1	2	3	3	3	1.07	1.18	1.69	5.3	3.2	10.8	3	3	4893	10243	gephyrin	Molecular function unknown;Receptor binding	Cytosol	Anchor protein;Unclassified	Cell communication;Signal transduction;Synapse organization and biogenesis	-	Yes
BCAR3	8412	breast cancer anti-estrogen resistance protein 3 isoform 1	NP_001248337.1	3	7	7	14	1.07	1.17	6.42	10.92	20.8	39.9	9	9	5268	8412	breast cancer anti-estrogen resistance 3	Guanyl-nucleotide exchange factor activity	Nucleus	Guanine nucleotide exchange factor	Cell communication;Signal transduction	SH2;RasGEF	Yes
SNX2	6643	sorting nexin-2 isoform 1	NP_003091.2	2	14	16	40	1.07	1.17	2.69	4.82	12.9	25.7	20	20	9332	6643	sorting nexin 2	Transporter activity	Endosome	Transport/cargo protein	Transport	PX;CC	Yes
MCCC2	64087	methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	NP_071415.1	1	14	14	48	1.07	1.17	5.02	6.44	26.2	37.3	23	23	1952	64087	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Ligase activity	Mitochondrion	Enzyme: Carboxylase	Metabolism;Energy pathways	SP	Yes
PAWR	5074	PRKC apoptosis WT1 regulator protein	NP_002574.2	1	6	6	10	1.07	1.16	6.72	2.35	16.2	6.1	5	5	9051	5074	PRKC, apoptosis, WT1, regulator	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
GCC1	79571	GRIP and coiled-coil domain-containing protein 1	NP_078799.2	1	5	5	8	1.07	1.14	19.05	2.55	36.3	5	3	3	7599	79571	GRIP and coiled-coil domain containing 1	Structural molecule activity	Golgi apparatus	Structural protein	Cell growth and/or maintenance	CC	Yes

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MRTO4	51154	mRNA turnover protein 4 homolog	NP_057267.2	1	5	5	7	1.07	1.14	6.21	11.15	14.9	28.9	5	5	12725	51154	chromosome 1 open reading frame 33	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
PKN2	5586	serine/threonine-protein kinase N2	NP_006247.1	1	5	5	9	1.07	1.14	18.02	20.33	45.4	55.6	5	5	3972	5586	protein kinase N2	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	HR1;C2;S_T_kinase;CC	Yes
CTPS1	1503	CTP synthase 1 isoform a	NP_001896.2	2	17	19	49	1.07	1.14	3.5	3.75	18.4	21.2	24	24									
PAK4	10298	serine/threonine-protein kinase PAK 4 isoform 1	NP_005875.1	2	5	5	7	1.07	1.13	6.71	7.07	16.2	18.1	5	5	5675	10298	p21(CDKN1A)-activated kinase 4	Cytoskeletal protein binding	Golgi membrane;Nucleus;Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance;Cell motility	PBD;S_T_kinase	Yes
NCAPD2	9918	condensin complex subunit 1	NP_055680.3	1	11	11	25	1.07	1.13	4.02	12	14.3	47.6	11	11	6472	9918	None	DNA binding	Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
JMJD6	23210	bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 isoform 1	NP_001074930.1	2	4	4	9	1.07	1.13	7.74	16.8	18.7	44.4	5	5	5371	23210	phosphatidylserine receptor	Molecular function unknown	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	TM;NLS	No
FPGS	2356	folylpolyglutamate synthase, mitochondrial isoform a precursor	NP_004948.4	3	3	3	4	1.07	1.12	7.81	14.9	14.6	29.5	3	3	642	2356	folylpolyglutamate synthase	Ligase activity	Cytosol;Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways;Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP	Yes
HDLBP	3069	vigilin isoform a	NP_005327.1	2	46	46	132	1.07	1.11	2.38	2.81	21.7	26.8	71	71	813	3069	high density lipoprotein binding protein(vigilin)	Transporter activity	Cytoplasm;Plasma membrane	Transport/cargo protein;RNA binding protein	Transport	CC;KH;NLS	Yes
NIPSNAP3A	25934	protein NipSnap homolog 3A	NP_056284.1	1	3	3	13	1.07	1.11	2.87	5.94	6.9	14.8	5	5	16399	25934	nipsnap homolog 3A (C. elegans)	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	SP	Yes
USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 1	NP_001259004.1	2	16	16	39	1.07	1.1	2.35	3.41	11.8	17.7	22	22	7029	9100	ubiquitin specific protease 10	Ubiquitin-specific protease activity	Nucleus;Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UCH	Yes
NGDN	25983	neuroguidin isoform 1	NP_001036100.1	2	3	3	6	1.07	1.1	12.33	6.91	23.1	13.2	3	3	10708	25983	chromosome 14 open reading frame 120	Molecular function unknown	Nucleolus;Nucleus	Unclassified	Biological_process unknown	CC	Yes
STAU2	27067	double-stranded RNA-binding protein Staufen homolog 2 isoform a	NP_001157852.1	6	2	3	9	1.07	1.1	4.62	12.19	7	19.1	2	2	9328	27067	staufen, RNA binding protein, homolog 2(Drosophila)	RNA binding	Ribosome	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DSRM	No
PEX14	5195	peroxisomal membrane protein PEX14	NP_004556.1	1	4	4	10	1.07	1.09	4.29	3.05	9.2	6.6	4	4	3477	5195	peroxisomal biogenesis factor 14	Protein binding	Peroxisome	Integral membrane protein	Cell communication;Signal transduction	CC	Yes
MRPL40	64976	39S ribosomal protein L40, mitochondrial	NP_003767.2	1	5	5	13	1.07	1.09	1.95	1.9	5.9	5.8	8	8	5476	64976	mitochondrial ribosomal protein L40	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	CC;LZ	Yes
ERCC3	2071	TFIIH basal transcription factor complex helicase XPB subunit isoform a	NP_000113.1	2	4	4	10	1.07	1.08	5.63	5.36	13.5	12.9	5	5	593	2071	excision repair cross-complementing rodentrepair deficiency, complementation group 3 (xeroderma pigmentosum group Bcomplementing)	DNA repair protein	Nucleus	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
KHNYN	23351	protein KHNYN isoform 2	NP_001277185.1	2	2	2	3	1.07	1.07	14.13	16.92	21.7	25.9	2	2	11076	23351	KIAA0323	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
DFFA	1676	DNA fragmentation factor subunit alpha isoform 1	NP_004392.1	2	8	8	24	1.07	1.06	10.11	5.06	39	18.8	12	12	3531	1676	DNA fragmentation factor, 45kDa, alphapolypeptide	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
TMEM165	55858	transmembrane protein 165 precursor	NP_060945.2	1	3	3	10	1.07	1.06	1.07	15.85	2.6	39.1	5	5	18216	55858	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM;CC	No
ATP2C1	27032	calcium-transporting ATPase type 2C member 1 isoform 2b	NP_001186110.1	9	7	7	11	1.07	1.04	3.06	4.87	7.3	11.4	5	5	5089	27032	ATPase, Ca++ transporting, type 2C, member 1	ATPase activity	Golgi apparatus	ATPase	Ion transport	TM	Yes
SYNJ2BP-COX16	100529257	SYNJ2BP-COX16 protein isoform 1	NP_001189476.1	4	3	3	5	1.07	1.04	3.45	9.17	7.4	19.3	4	4									
MGEA5	10724	protein O-GlcNAcase isoform a	NP_036347.1	2	10	10	49	1.07	1.04	3.69	4.6	19.1	23.1	23	23	4949	10724	meningioma expressed antigen 5 (hyaluronidase)	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
PNN	5411	pinin	NP_002678.2	1	10	10	18	1.07	1.04	5.96	7.69	19.4	24.3	9	9	4401	5411	pinin, desmosome associated protein	Cell adhesion molecule activity	Plasma membrane;Nucleus	Adhesion molecule	Cell communication;Signal transduction	CC	Yes
WDR36	134430	WD repeat-containing protein 36	NP_644810.1	1	12	12	24	1.07	1.03	10.12	9.73	40.6	37.2	13	13	10305	134430	WD repeat domain 36	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	WD40	Yes
CMAS	55907	N-acylneuraminate cytidylyltransferase	NP_061156.1	1	8	8	18	1.07	1.02	2.37	3.37	8	11	10	10	4501	55907	cytidine monophosphate N-acetylneuraminic acidsynthetase	Ligase activity	Nucleus	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
BICD2	23299	protein bicaudal D homolog 2 isoform 1	NP_001003800.1	2	18	18	36	1.07	1.02	3.38	4.36	16.3	20.1	20	20	9826	23299	bicaudal D homolog 2 (Drosophila)	Protein binding	Golgi apparatus;Nucleus;Cytoplasm	Structural protein	Vesicle-mediated transport	CC	Yes
FKBP9	11328	peptidyl-prolyl cis-trans isomerase FKBP9 isoform 1 precursor	NP_009201.2	3	4	4	6	1.07	1.02	5.67	8.58	12.2	17.6	4	4	6510	11328	FK506 binding protein 9, 63 kDa	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP;EF	Yes

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Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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EIF4G3	8672	eukaryotic translation initiation factor 4 gamma 3 isoform 1	NP_001185730.1	3	5	9	13	1.07	1.01	6.8	8.19	16.4	18.6	5	5	6802	8672	eukaryotic translation initiation factor 4gamma, 3	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	MIF4G;CC	Yes
INTS1	26173	integrator complex subunit 1	NP_001073922.2	1	6	6	13	1.07	1.01	12.24	14.82	35.8	41.4	7	7	10899	26173	None	Molecular function unknown	Nucleus	Unclassified	RNA metabolism;Transcription	CC	No
WDR1	9948	WD repeat-containing protein 1 isoform 1	NP_059830.1	2	23	23	91	1.07	1	1.98	2.06	15.2	14.8	51	51	9199	9948	WD repeat domain 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	WD40	Yes
GOLGB1	2804	Golgin subfamily B member 1 isoform 1	NP_001243415.1	7	36	37	71	1.07	0.99	2.55	3.12	16.9	19.2	38	38	3933	2804	golgi autoantigen, golgin subfamily b,macrogolgin (with transmembrane signal), 1	Structural molecule activity	Golgi apparatus	Structural protein	Cell growth and/or maintenance	CC;TM	Yes
PCYT1A	5130	choline-phosphate cytidylyltransferase A	NP_005008.2	4	5	5	9	1.07	0.99	4.38	7.24	10.5	16.2	5	5	438	5130	phosphate cytidylyltransferase 1, choline,alpha isoform	Nucleotidyltransferase activity	Nucleus	Enzyme: Nucleotidyltransferase	Metabolism;Energy pathways	CC	Yes
PPP2R1A	5518	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	NP_055040.2	1	20	27	140	1.07	0.99	4.76	8.55	37.5	67.3	51	52	16184	5518	protein phosphatase 2 (formerly 2A),regulatory subunit A (PR 65), alpha isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	HEAT	Yes
ACAA1	30	3-ketoacyl-CoA thiolase, peroxisomal isoform a	NP_001598.1	2	9	9	31	1.07	0.99	10.9	18.33	49.2	83.1	16	16	6815	30	acetyl-Coenzyme A acyltransferase 1(peroxisomal 3-oxoacyl-Coenzyme A thiolase)	Acyltransferase activity	Peroxisome	Enzyme: Acyltransferase	Metabolism;Energy pathways	SP	Yes
FBXO3	26273	F-box only protein 3 isoform 1	NP_036307.2	2	3	3	6	1.07	0.99	0.8	2.28	1.5	3.9	3	3	16433	26273	F-box protein 3	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	F_BOX	Yes
PPIL4	85313	peptidyl-prolyl cis-trans isomerase-like 4	NP_624311.1	1	5	5	7	1.07	0.98	1.62	2.04	3.9	4.5	5	5	7606	85313	peptidylprolyl isomerase (cyclophilin)-like 4	Chaperone activity	Nucleus	Chaperone	Protein metabolism	RRM;NLS	No
CDK1	983	cyclin-dependent kinase 1 isoform 1	NP_001777.1	48	9	11	45	1.07	0.98	7.62	2.43	30.1	8.6	13	13	302	983	cell division cycle 2, G1 to S and G2 to M	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;Tyr_Kinase	Yes
UBQLN1	29979	ubiquilin-1 isoform 1	NP_038466.2	4	7	8	22	1.07	0.97	5.32	13.38	14	32.5	6	6	5440	29979	ubiquilin 1	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBQ;UBA;STI1	Yes
KIF1C	10749	kinesin-like protein KIF1C	NP_006603.2	3	4	5	11	1.07	0.97	6.02	10.53	12.9	20.7	4	4	4342	10749	kinesin family member 1C	Motor activity	Golgi apparatus	Motor protein	Cell growth and/or maintenance	KISC;FHA;CC	Yes
MRPS35	60488	28S ribosomal protein S35, mitochondrial isoform 1 precursor	NP_068593.2	2	8	8	27	1.07	0.97	8.66	9.23	38.2	37.1	16	16	11373	60488	mitochondrial ribosomal protein S35	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP;CC	No
QARS	5859	glutamine--tRNA ligase isoform a	NP_005042.1	2	25	25	53	1.07	0.97	3.64	6.24	21.5	33.6	30	29	7223	5859	glutaminyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	NP_056417.2	2	14	15	39	1.07	0.97	3.37	4.52	16.2	19.8	20	20	13958	26092	torsin A interacting protein 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	TM	Yes
SSR4	6748	translocon-associated protein subunit delta isoform 1 precursor	NP_001191455.1	3	5	5	19	1.07	0.96	5.44	8.41	18.6	25.9	10	10	2101	6748	signal sequence receptor, delta(translocon-associated protein delta)	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	SP	Yes
ZNF800	168850	zinc finger protein 800	NP_789784.2	1	1	1	1	1.07	0.96					1	1	14112	168850	None	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	No
SEC23A	10484	protein transport protein Sec23A	NP_006355.2	1	17	19	73	1.07	0.95	4.12	7.08	25.7	39.6	33	32	6714	10484	Sec23 homolog A (S. cerevisiae)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	GEL	Yes
IKBIP	121457	inhibitor of nuclear factor kappa-B kinase-interacting protein isoform 2	NP_963906.1	2	11	15	28	1.07	0.94	3.62	4.24	14	14.5	13	13	8092	121457	None	Molecular function unknown	Endoplasmic reticulum	Unclassified	Apoptosis	CC;LZ	No
CYC1	1537	cytochrome c1, heme protein, mitochondrial precursor	NP_001907.2	1	7	7	25	1.07	0.94	3.33	5.97	13.5	21.3	14	14	480	1537	cytochrome c-1	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	-	Yes
CYP51A1	1595	lanosterol 14-alpha demethylase isoform 1 precursor	NP_000777.1	2	10	10	19	1.07	0.93	5.94	14.27	22.4	48.6	12	12	3381	1595	cytochrome P450, family 51, subfamily A,polypeptide 1	Molecular function unknown	Endoplasmic reticulum	Unclassified	Metabolism;Energy pathways	SP;TM	Yes
WASF2	10163	wiskott-Aldrich syndrome protein family member 2 isoform 1	NP_008921.1	2	6	6	14	1.07	0.93	4.99	4.56	14.1	12.1	7	8	5796	10163	WAS protein family, member 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	WH2	Yes
DCUN1D1	54165	DCN1-like protein 1 isoform 1	NP_065691.2	2	2	2	16	1.07	0.92	2.21	6.4	5.3	13.3	5	5	12067	54165	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
AP3M2	10947	AP-3 complex subunit mu-2	NP_006794.1	1	2	3	6	1.07	0.92	1.4	41.36	2.1	58.1	2	2	9801	10947	adaptor-related protein complex 3, mu 2 subunit	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	Yes
RAB1A	5861	ras-related protein Rab-1A isoform 1	NP_004152.1	13	6	14	132	1.07	0.91	12	28.81	60.8	155.8	19	18	1538	5861	RAB1A, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB;Small_GTPase	Yes
RPS23	6228	40S ribosomal protein S23	NP_001016.1	3	7	7	41	1.07	0.9	2.19	3.85	10.5	15.5	20	20	4729	6228	ribosomal protein S23	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
APOL2	23780	apolipoprotein L2	NP_663612.2	1	8	8	12	1.07	0.86	8.27	7.19	25.5	17.7	8	8	6263	23780	apolipoprotein L, 2	Transporter activity;Molecular function unknown	-	Integral membrane protein;Transport/cargo protein	Metabolism;Energy pathways;Biological_process unknown	CC;TM	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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MRPL22	29093	39S ribosomal protein L22, mitochondrial isoform a	NP_054899.2	2	6	6	13	1.07	0.85	9.41	7.95	29.1	19.4	8	8	14748	29093	mitochondrial ribosomal protein L22	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
INTS3	65123	integrator complex subunit 3	NP_075391.3	1	5	5	7	1.07	0.84	6.99	14.3	16.9	27.3	5	5	8644	65123	chromosome 1 open reading frame 60	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NRP1	8829	neuropilin-1 isoform a precursor	NP_003864.4	5	1	1	3	1.07	0.84					1	1	3642	8829	neuropilin 1	Receptor activity	Plasma membrane	Cell surface receptor	Signal transduction;Cell migration;Morphogenesis;Immune response	TM;CUB;F58C;MAM;SP	Yes
CCDC22	28952	coiled-coil domain-containing protein 22	NP_054727.1	1	3	3	16	1.07	0.84	6.64	6.43	19	14.3	7	7	6594	28952	chromosome X open reading frame 37	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
FBXO22	26263	F-box only protein 22 isoform a	NP_671717.1	2	5	5	12	1.07	0.83	6.34	12.1	18.1	27	7	7	16437	26263	F-box protein 22	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	F_BOX	Yes
ADGRG1	9289	G-protein coupled receptor 56 isoform a precursor	NP_005673.3	5	1	1	1	1.07	0.81					1	1									
SLC27A3	11000	long-chain fatty acid transport protein 3	NP_077306.1	1	1	1	1	1.07	0.81					1	1	11967	11000	solute carrier family 27 (fatty acidtransporter), member 3	Auxiliary transport protein activity	Integral to membrane	Membrane transport protein	Transport	TM	No
RALGAPB	57148	ral GTPase-activating protein subunit beta isoform 1	NP_001269846.1	2	5	5	12	1.07	0.81	8.08	18.74	21.4	38.4	6	6	11133	57148	None	GTPase activator activity	Smooth microsome	GTPase activating protein	Cell communication;Signal transduction	-	Yes
L3MBTL3	84456	lethal(3)malignant brain tumor-like protein 3 isoform a	NP_115814.1	2	1	1	1	1.07	0.76					1	1	11222	84456	l(3)mbt-like 3 (Drosophila)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAM;MBT	No
DVL2	1856	segment polarity protein dishevelled homolog DVL-2	NP_004413.1	1	5	6	10	1.07	0.75	14.6	19.36	31.9	29.8	4	4	3690	1856	dishevelled, dsh homolog 2 (Drosophila)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	DSH;PDZ	Yes
KIF14	9928	kinesin-like protein KIF14 isoform 1	NP_055690.1	2	2	2	4	1.07	0.72	20.52	13.89	31.8	14.3	2	2	6605	9928	kinesin family member 14	Motor activity	Microtubule;Nucleus	Motor protein	Cell growth and/or maintenance	CC;KISC;FHA	Yes
GMPR	2766	GMP reductase 1	NP_006868.3	1	1	2	4	1.07	0.72					1	1	754	2766	guanosine monophosphate reductase	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	-	Yes
CNOT2	4848	CCR4-NOT transcription complex subunit 2	NP_055330.1	1	2	2	4	1.07	0.66	4.65	2.06	7	1.9	2	2	5367	4848	CCR4-NOT transcription complex, subunit 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
TCEB1	6921	transcription elongation factor B polypeptide 1 isoform a	NP_005639.1	2	5	5	14	1.07	0.6	5.98	15.2	17	24.6	7	7	2875	6921	transcription elongation factor B (SIII),polypeptide 1 (15kDa, elongin C)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SKP1	Yes
ARHGDIB	397	rho GDP-dissociation inhibitor 2	NP_001166.3	1	3	3	4	1.07	0.59	1.31	3.97	2.4	4.1	3	3	4162	397	Rho GDP dissociation inhibitor (GDI) beta	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
IDH3B	3420	isocitrate dehydrogenase [NAD] subunit beta, mitochondrial isoform a precursor	NP_008830.2	3	7	7	14	1.07	0.53	6.8	50.18	22.1	93.7	9	9	5163	3420	isocitrate dehydrogenase 3 (NAD+) beta	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
PTPN14	5784	tyrosine-protein phosphatase non-receptor type 14	NP_005392.2	1	1	1	2	1.06	1.67					1	1	4402	5784	protein tyrosine phosphatase, non-receptortype 14	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	B41;Tyr_Phos	Yes
PSPC1	55269	paraspeckle component 1	NP_001035879.1	1	6	6	16	1.06	1.47	5.62	7.79	19.1	37.5	10	10	10172	55269	paraspeckle component 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;RRM	Yes
PPID	5481	peptidyl-prolyl cis-trans isomerase D	NP_005029.1	7	10	11	24	1.06	1.45	9.33	3.87	36.6	20.5	13	13	11875	5481	peptidylprolyl isomerase D (cyclophilin D)	Isomerase activity	Nucleolus	Enzyme: Isomerase	Metabolism;Energy pathways	TPR	Yes
PCMT1	5110	protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 2	NP_001238978.1	5	5	5	13	1.06	1.45	3.26	8.58	9.2	33.9	7	7	8908	5110	protein-L-isoaspartate (D-aspartate)O-methyltransferase	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase	Protein metabolism	-	Yes
DAZAP1	26528	DAZ-associated protein 1 isoform b	NP_061832.2	2	2	2	7	1.06	1.37	8.25	6.22	17.6	17.1	4	4	8462	26528	DAZ associated protein 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
CRELD2	79174	cysteine-rich with EGF-like domain protein 2 isoform a precursor	NP_001128573.1	4	3	3	6	1.06	1.34	0.07	8.25	0.1	19.4	3	3	8455	79174	None	Calcium ion binding	Extracellular	Calcium binding protein	Cell communication;Signal transduction	SP;EGFL;EGFCA;EGF;FU	No
TAF6L	10629	TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L	NP_006464.1	1	3	3	5	1.06	1.34	28.09	9.37	44.1	17.8	2	2	4253	10629	TAF6-like RNA polymerase II,p300/CBP-associated factor (PCAF)-associated factor, 65kDa	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
HDGF	3068	hepatoma-derived growth factor isoform a	NP_004485.1	3	14	15	59	1.06	1.32	7.06	8	45.6	68	34	34	2079	3068	hepatoma-derived growth factor (high-mobilitygroup protein 1-like)	Growth factor activity	Nucleus	Growth factor	Cell communication;Signal transduction	PWWP;NLS	Yes
COMMD9	29099	COMM domain-containing protein 9 isoform 1	NP_054905.2	3	2	2	3	1.06	1.31	19.22	12.85	29.4	24.2	2	2	13087	29099	COMM domain containing 9	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes

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MTMR12	54545	myotubularin-related protein 12 isoform 1	NP_001035536.1	3	4	4	8	1.06	1.3	4.82	12	10.3	32	4	4	5933	54545	myotubularin related protein 12	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
RTCA	8634	RNA 3'-terminal phosphate cyclase isoform b	NP_003720.1	2	4	4	12	1.06	1.3	5.33	5.97	15	20.8	7	7									
HERC6	55008	probable E3 ubiquitin-protein ligase HERC6 isoform 1	NP_060382.3	2	1	1	1	1.06	1.29					1	1	13647	55008	hect domain and RLD 6	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	HECT	No
STAT1	6772	signal transducer and activator of transcription 1-alpha/beta isoform beta	NP_644671.1	1	1	34	103	1.06	1.28	5.98	19.6	9	36.6	2	2	2777	6772	signal transducer and activator oftranscription 1, 91kDa	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SH2;CC	Yes
TES	26136	testin isoform 1	NP_056456.1	2	14	14	28	1.06	1.26	5.04	7.74	22.3	41.9	17	17	5833	26136	testis derived transcript (3 LIM domains)	Molecular function unknown	Extracellular	Secreted polypeptide	Cell growth and/or maintenance	LIM	No
PREP	5550	prolyl endopeptidase	NP_002717.3	1	36	36	110	1.06	1.26	2.95	3.49	23.7	33.8	56	56	2673	5550	prolyl endopeptidase	Serine-type peptidase activity	Cytoplasm	Serine protease	Protein metabolism	-	Yes
DLST	1743	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial isoform 1 precursor	NP_001924.2	2	13	13	47	1.06	1.24	5.36	3.04	24.4	16	18	18	520	1743	dihydrolipoamide S-succinyltransferase (E2component of 2-oxo-glutarate complex)	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	CC	Yes
SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	NP_001124000.1	6	19	19	48	1.06	1.24	4.89	4.93	25.8	30.7	24	24	10398	9043	sperm associated antigen 9	Molecular function unknown	Cytoplasm;Plasma membrane	Integral membrane protein	Cell growth and/or maintenance	CC;LZ;TM;SP	Yes
TRMT112	51504	multifunctional methyltransferase subunit TRM112-like protein isoform 1	NP_057488.1	3	3	3	5	1.06	1.24	23.62	24.46	36.7	44.8	2	2	13705	51504	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
PPP5C	5536	serine/threonine-protein phosphatase 5 isoform 1	NP_006238.1	2	13	13	51	1.06	1.22	5.39	5.13	30.3	33.4	27	27	2805	5536	protein phosphatase 5, catalytic subunit	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase	Cell communication;Signal transduction	TPR;PP2A	Yes
RAD17	5884	cell cycle checkpoint protein RAD17 isoform 2	NP_579917.1	4	1	1	2	1.06	1.22					1	1	9124	5884	RAD17 homolog (S. pombe)	Molecular function unknown	Nucleus	Cell cycle control protein	Signal transduction;Cell communication;Regulation of cell cycle	AAA	Yes
ZGPAT	84619	zinc finger CCCH-type with G patch domain-containing protein isoform a	NP_115916.3	3	1	1	2	1.06	1.21					1	1	15736	84619	zinc finger, CCCH-type with G patch domain	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1;G_PATCH;CC	Yes
CIRH1A	84916	cirhin	NP_116219.2	1	9	9	20	1.06	1.21	4.84	4.34	16.3	16.7	10	10	8468	84916	cirrhosis, autosomal recessive 1A (cirhin)	Molecular function unknown	Mitochondrion	Unclassified	Cell communication;Signal transduction	WD40	No
IPO5	3843	importin-5	NP_002262.3	1	30	32	135	1.06	1.2	4.49	4.99	39.5	50.8	64	64	3597	3843	RAN binding protein 5	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	HEAT;IBN_NT	Yes
TXNDC9	10190	thioredoxin domain-containing protein 9	NP_005774.2	1	3	3	10	1.06	1.2	1.28	6.81	3	18.5	5	5	15592	10190	thioredoxin domain containing 9	Molecular function unknown	Cytoplasm	Unclassified;Cell cycle control protein	Biological_process unknown;Cell growth and/or maintenance	CC	No
NUDC	10726	nuclear migration protein nudC	NP_006591.1	1	15	15	32	1.06	1.18	4.04	7.79	18.9	41.7	19	19	10122	10726	nuclear distribution gene C homolog (A.nidulans)	Protein binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	No
ACP2	53	lysosomal acid phosphatase isoform 1 precursor	NP_001601.1	5	2	2	4	1.06	1.18	11.18	18.39	16.9	31.6	2	2	1375	53	acid phosphatase 2, lysosomal	Acid phosphatase activity	Lysosome	Enzyme: Acid phosphatase	Metabolism;Energy pathways	SP;TM	Yes
P3H1	64175	prolyl 3-hydroxylase 1 isoform 1 precursor	NP_071751.3	3	10	10	22	1.06	1.16	2.52	5.19	9.7	22	13	13									
HMBS	3145	porphobilinogen deaminase isoform 1	NP_000181.2	4	5	5	7	1.06	1.16	7.86	12.7	14.5	25.9	3	3	1440	3145	hydroxymethylbilane synthase	Transferase activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
SPIN1	10927	spindlin-1	NP_006708.2	2	3	3	7	1.06	1.14	16.17	10.19	35.4	23.6	4	4	18096	10927	spindlin	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
RBM25	58517	RNA-binding protein 25	NP_067062.1	1	12	12	21	1.06	1.14	5.53	5.99	19.6	23	11	11	15229	58517	RNA binding motif protein 25	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;PWI	Yes
STOML2	30968	stomatin-like protein 2, mitochondrial isoform a	NP_038470.1	4	12	12	81	1.06	1.14	3.83	4.3	22.6	27.3	30	30	16310	30968	stomatin (EPB72)-like 2	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	SP;PHB;CC	Yes
PTPRF	5792	receptor-type tyrosine-protein phosphatase F isoform 1 precursor	NP_002831.2	2	2	2	2	1.06	1.13					1	1	1552	5792	protein tyrosine phosphatase, receptor type, F	Receptor signaling protein tyrosine phosphatase activity	Plasma membrane	Receptor tyrosine phosphatase	Cell communication;Signal transduction	FN3;Tyr_Phos;SP;CC;TM;IGC2	Yes
PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	NP_004148.1	1	14	18	42	1.06	1.12	3.87	9.45	17.5	47.4	18	18	1484	5576	protein kinase, cAMP-dependent, regulatory,type II, alpha	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	CNMP	Yes
LONP1	9361	lon protease homolog, mitochondrial isoform 1 precursor	NP_004784.2	3	25	26	70	1.06	1.12	3.49	3.57	23.4	25.1	39	38	5689	9361	protease, serine, 15	Serine-type peptidase activity	Mitochondrion	Serine protease	Protein metabolism	AAA	Yes
SNX7	51375	sorting nexin-7 isoform a	NP_057060.2	2	1	1	2	1.06	1.11					1	1	15416	51375	sorting nexin 7	Molecular function unknown	-	Unclassified	Biological_process unknown	PX	Yes
SF3B3	23450	splicing factor 3B subunit 3	NP_036558.3	1	32	32	98	1.06	1.1	2.79	3.16	21.1	24.9	50	50	12027	23450	splicing factor 3b, subunit 3, 130kDa	Ribonucleoprotein	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
POFUT1	23509	GDP-fucose protein O-fucosyltransferase 1 isoform 1 precursor	NP_056167.1	2	8	8	19	1.06	1.1	13.51	11.19	47.7	40.4	10	10	6319	23509	protein O-fucosyltransferase 1	Transferase activity	Golgi membrane	Enzyme: Transferase	Metabolism	TM	Yes
MME	4311	neprilysin	NP_000893.2	1	1	1	2	1.06	1.1					1	1	392	4311	membrane metallo-endopeptidase (neutralendopeptidase, enkephalinase, CALLA, CD10)	Metallopeptidase activity	Plasma membrane	Metallo protease	Protein metabolism;Peptide metabolism	CC;TM;NLS	Yes
DDX20	11218	probable ATP-dependent RNA helicase DDX20	NP_009135.4	1	10	10	21	1.06	1.09	2.62	5.24	9.2	19	11	11	5859	11218	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	ATPase activity	Nucleus	ATPase	Metabolism;Energy pathways	DEXDc;HELIC	Yes
RTF1	23168	RNA polymerase-associated protein RTF1 homolog	NP_055953.3	1	4	4	7	1.06	1.09	2.6	7.56	5.5	16.6	4	4	11071	23168	KIAA0252	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
KARS	3735	lysine--tRNA ligase isoform 1	NP_001123561.1	2	23	23	90	1.06	1.08	2.69	6.37	18.9	47.4	43	43	3249	3735	lysyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	TRNA aminoacylation	CC;TRNAA	Yes
CPSF1	29894	cleavage and polyadenylation specificity factor subunit 1	NP_037423.2	1	11	11	19	1.06	1.07	2.87	8.77	8.7	27.1	8	8	5823	29894	cleavage and polyadenylation specific factor 1,160kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
BRD4	23476	bromodomain-containing protein 4 isoform long	NP_490597.1	2	8	10	16	1.06	1.06	3.36	4.93	10.1	14.8	8	8	10574	23476	bromodomain containing 4	Chromatin binding	Nucleus;Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	CC;BROMO;NLS	Yes
FKBP3	2287	peptidyl-prolyl cis-trans isomerase FKBP3	NP_002004.1	1	5	5	8	1.06	1.06	11.47	4.72	24.6	10	4	4	1743	2287	FK506 binding protein 3, 25kDa	Isomerase activity	Nucleus	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
PRKCI	5584	protein kinase C iota type	NP_002731.4	1	3	3	8	1.06	1.05	2.97	4.49	6.3	9.4	4	4	2105	5584	protein kinase C, iota	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	PB1;C1;S_T_kinase	Yes
CLINT1	9685	clathrin interactor 1 isoform 2	NP_055481.1	1	1	11	29	1.06	1.05	36	82.12	58.3	186.1	2	2	6273	9685	None	Transporter activity	Golgi apparatus;Nucleus;Cytoplasm	Transport/cargo protein	Transport	CC	Yes
DCTN3	11258	dynactin subunit 3 isoform 1	NP_009165.1	5	4	4	5	1.06	1.05	1.25	17.26	2.3	32.1	3	3	6303	11258	dynactin 3 (p22)	Cytoskeletal protein binding	Centrosome	Cell cycle control protein	Cell communication;Signal transduction;Cell cycle	-	Yes
FAR1	84188	fatty acyl-CoA reductase 1	NP_115604.1	1	2	2	2	1.06	1.04	5	17.71	7.5	26.5	2	2	14724	84188	male sterility domain containing 2	Catalytic activity	-	Enzyme: Reductase	Metabolism;Energy pathways	TM	No
NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NP_073568.2	1	5	5	11	1.06	1.03	9.01	5.58	23.8	14.2	6	6	11406	64710	None	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
GSTM3	2947	glutathione S-transferase Mu 3	NP_000840.2	2	5	6	9	1.06	1.03	5.37	11.99	12.7	28.1	5	5	712	2947	glutathione S-transferase M3 (brain)	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase	Metabolism;Energy pathways	-	Yes
DDX23	9416	probable ATP-dependent RNA helicase DDX23	NP_004809.2	1	15	15	36	1.06	1.02	3.27	2.47	15.6	11.3	20	20	9908	9416	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	RNA binding	Nucleus	RNA binding protein	Protein metabolism	DEXDc;HELIC;CC	Yes
RPL28	6158	60S ribosomal protein L28 isoform 2	NP_000982.2	5	7	8	36	1.06	1.02	6.61	7.63	29.5	33.1	17	17	4702	6158	ribosomal protein L28	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
HSPBP1	23640	hsp70-binding protein 1 isoform 1	NP_001284529.1	2	10	10	29	1.06	1.02	5.02	7.26	21.4	31.1	16	17	9991	23640	None	Molecular function unknown	-	Unclassified	Protein metabolism	CC	No
SMARCA5	8467	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	NP_003592.3	1	11	18	33	1.06	1.01	4.14	3.83	15.9	14	13	13	4538	8467	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 5	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;SANT;CC	Yes
TCP1	6950	T-complex protein 1 subunit alpha isoform a	NP_110379.2	2	31	31	166	1.06	1.01	2.5	3.65	24.5	34.6	83	83	1748	6950	t-complex 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
CCT8	10694	T-complex protein 1 subunit theta isoform 1	NP_006576.2	4	41	41	193	1.06	1.01	2.89	3.18	31.5	33.4	102	102	10816	10694	chaperonin containing TCP1, subunit 8 (theta)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
ANAPC1	64682	anaphase-promoting complex subunit 1	NP_073153.1	4	6	6	9	1.06	1.01	1.51	4.58	3.6	10.4	5	5	9769	64682	anaphase promoting complex subunit 1	Protein binding	Chromosome	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
GPC1	2817	glypican-1 precursor	NP_002072.2	2	10	10	27	1.06	1.01	8.02	10.88	31.3	41.3	13	13	2671	2817	glypican 1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP	Yes
USO1	8615	general vesicular transport factor p115 isoform 1	NP_001276978.1	2	26	26	65	1.06	1	3.53	4.52	20.7	25.2	30	30	9135	8615	None	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	CC	Yes
CREB1	1385	cyclic AMP-responsive element-binding protein 1 isoform B	NP_604391.1	10	4	4	6	1.06	1	2.53	20.38	5.4	42.5	4	4	442	1385	cAMP responsive element binding protein 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
DDX17	10521	probable ATP-dependent RNA helicase DDX17 isoform 3	NP_001091974.1	2	24	34	108	1.06	1	2.68	4.97	17.8	31.7	39	39	10532	10521	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	ATPase activity	Nucleus	RNA helicase;ATPase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
AP3M1	26985	AP-3 complex subunit mu-1	NP_996895.1	1	9	10	24	1.06	1	3.26	4.98	12	17.3	12	12	16496	26985	adaptor-related protein complex 3, mu 1 subunit	Protein transporter activity	Golgi apparatus	Transport/cargo protein	Protein targeting	-	No
ME2	4200	NAD-dependent malic enzyme, mitochondrial isoform 1 precursor	NP_002387.1	2	14	14	35	1.06	0.99	3	4.63	12.8	18.4	16	16	1103	4200	malic enzyme 2, NAD(+)-dependent, mitochondrial	Carboxy-lyase activity	Mitochondrion	Enzyme: Decarboxylase	Metabolism;Energy pathways	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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USP39	10713	U4/U6.U5 tri-snRNP-associated protein 2 isoform 1	NP_006581.2	4	11	11	28	1.06	0.98	5.78	6.49	23.2	24	14	14	7165	10713	ubiquitin specific protease 39	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	ZNFC2	Yes
CSTF2T	23283	cleavage stimulation factor subunit 2 tau variant	NP_056050.1	1	3	6	17	1.06	0.98	12.26	0.69	18.5	1	2	2	9900	23283	cleavage stimulation factor, 3` pre-RNA,subunit 2, 64kDa, tau variant	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	No
EHD4	30844	EH domain-containing protein 4	NP_644670.1	1	19	20	66	1.06	0.97	2.97	3.92	19.3	23.5	37	37	10435	30844	EH-domain containing 4	Calcium ion binding	Extracellular	Calcium binding protein	Cell communication;Signal transduction	EH	Yes
XPO5	57510	exportin-5	NP_065801.1	1	8	8	10	1.06	0.97	5.47	20.97	11.6	42.3	4	4	6385	57510	exportin 5	Transporter activity	Nucleus	Transport/cargo protein	Transport	CC	No
ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	NP_001020262.1	2	22	23	45	1.06	0.96	5.05	9.09	27.9	47	26	26	9139	23	ATP-binding cassette, sub-family F (GCN20),member 1	Translation regulator activity	Ribosome;Nucleus	Translation regulatory protein	Protein metabolism	CC;AAA;NLS	Yes
ILKAP	80895	integrin-linked kinase-associated serine/threonine phosphatase 2C	NP_110395.1	1	4	4	6	1.06	0.96	2.99	5.48	6.4	10.5	4	4	17147	80895	integrin-linked kinase-associatedserine/threonine phosphatase 2C	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell death	PP2C	No
MEAF6	64769	chromatin modification-related protein MEAF6 isoform 1	NP_073593.2	3	2	2	4	1.06	0.95	2.89	16.27	4.4	22.1	2	2	13347	64769	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
BRK1	55845	protein BRICK1	NP_060932.2	1	1	1	1	1.06	0.95					1	1									
CCAR2	57805	cell cycle and apoptosis regulator protein 2	NP_066997.3	1	25	25	85	1.06	0.94	2.34	4.42	16.5	27.9	44	43									
ATAD3A	55210	ATPase family AAA domain-containing protein 3A isoform 2	NP_001164006.1	3	8	21	38	1.06	0.93	4.74	16.76	13.3	43.2	7	7	12500	55210	ATPase family, AAA domain containing 3A	ATPase activity	-	ATPase	Metabolism;Energy pathways	CC;AAA	No
PARP1	142	poly [ADP-ribose] polymerase 1	NP_001609.2	1	32	32	102	1.06	0.93	2.51	3.25	20.8	23.7	60	60	1435	142	poly (ADP-ribose) polymerase family, member 1	Catalytic activity	Nucleus	Enzyme: Ribosyltransferase	Protein metabolism	BRCT;NLS	Yes
CSK	1445	tyrosine-protein kinase CSK	NP_004374.1	1	9	9	14	1.06	0.92	7.02	9.17	21.3	24.1	8	8	496	1445	c-src tyrosine kinase	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase	Cell communication;Signal transduction	SH3;SH2;Tyr_Kinase	Yes
ACOT7	11332	cytosolic acyl coenzyme A thioester hydrolase isoform hBACHb	NP_863654.1	4	16	16	61	1.06	0.92	2.81	6.37	18.3	36.7	37	37	12517	11332	None	Hydrolase activity	Cytoplasm;Mitochondrion;Cytosol	Enzyme: Hydrolase	Lipid metabolism;Metabolism;Energy pathways	NLS	Yes
C1orf174	339448	UPF0688 protein C1orf174	NP_997239.2	1	1	1	2	1.06	0.91					1	1	17353	339448	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PPFIBP1	8496	liprin-beta-1 isoform 2	NP_803193.2	7	11	11	18	1.06	0.9	6.07	10.87	22.6	34.7	12	12	4390	8496	PTPRF interacting protein, binding protein 1(liprin beta 1)	Cytoskeletal anchoring activity	Plasma membrane	Anchor protein	Cell communication;Signal transduction	SAM;CC	Yes
SEC61B	10952	protein transport protein Sec61 subunit beta	NP_006799.1	1	3	3	5	1.06	0.89	16.07	52.91	24.4	74.2	2	2	6715	10952	Sec61 beta subunit	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	TM	No
MPI	4351	mannose-6-phosphate isomerase isoform 1	NP_002426.1	4	6	6	11	1.06	0.87	3.87	9.57	9.2	18.7	5	5	1108	4351	mannose phosphate isomerase	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
C11orf73	51501	protein Hikeshi	NP_057485.2	1	1	1	1	1.06	0.87					1	1	13701	51501	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
HIP1	3092	huntingtin-interacting protein 1 isoform 1	NP_005329.3	2	2	3	3	1.06	0.86					1	1	3461	3092	huntingtin interacting protein 1	Structural molecule activity	Integral to membrane	Structural protein	Cell death	CC	Yes
HEXA	3073	beta-hexosaminidase subunit alpha preproprotein	NP_000511.2	1	9	10	13	1.06	0.85	11.26	10.59	36.9	27.5	9	9	6040	3073	hexosaminidase A (alpha polypeptide)	Hydrolase activity	Lysosome	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
ANAPC5	51433	anaphase-promoting complex subunit 5 isoform a	NP_057321.2	2	1	1	2	1.06	0.85					1	1	10453	51433	anaphase promoting complex subunit 5	Ubiquitin-specific protease activity	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CC	Yes
C7orf55-LUC7L2	100996928	C7orf55-LUC7L2 protein	NP_001231513.1	4	10	10	36	1.06	0.84	5.64	14.94	25.1	55.6	17	17									
CCDC43	124808	coiled-coil domain-containing protein 43 isoform 1	NP_653210.2	2	2	2	4	1.06	0.83	18.99	16.29	29	19.3	2	2	8107	124808	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
PFKFB2	5208	6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 isoform a	NP_006203.2	2	3	3	5	1.06	0.83	4.26	15.58	6.4	18.5	2	2	1383	5208	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
BIVM-ERCC5	100533467	BIVM-ERCC5 protein	NP_001191354.1	2	1	1	2	1.06	0.82					1	1									
RYBP	23429	RING1 and YY1-binding protein	NP_036366.3	1	1	1	1	1.06	0.79					1	1	9607	23429	RING1 and YY1 binding protein	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_RBZ	No
MYDGF	56005	UPF0556 protein C19orf10 precursor	NP_061980.1	1	2	2	2	1.06	0.78	18.69	9.65	28.7	10.6	2	2									
KPNA1	3836	importin subunit alpha-5	NP_002255.3	1	5	10	31	1.06	0.75	3.61	10.14	9.4	18.8	6	6	2819	3836	karyopherin alpha 1 (importin alpha 5)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ARM	Yes
CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 1	NP_001264.2	6	19	19	62	1.06	0.73	6.39	12.1	39.2	52.1	31	31	4472	1108	chromodomain helicase DNA binding protein 4	DNA binding	Nucleus;Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PHD;CHROMO;DEXDc;HELIC;RING	Yes
TBCA	6902	tubulin-specific chaperone A isoform 2	NP_004598.1	3	4	4	10	1.06	0.72	5.98	16.5	15.7	29.7	6	6	18166	6902	tubulin-specific chaperone a	Chaperone activity	Cytoskeleton	Chaperone	Protein metabolism	CC	Yes
FAM169A	26049	soluble lamin-associated protein of 75 kDa	NP_056381.1	1	4	4	8	1.06	0.69	7.1	13.16	15.1	18.4	4	4	19525	26049	family with sequence similarity 169, member A	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
RPL3	6122	60S ribosomal protein L3 isoform a	NP_000958.1	3	21	21	109	1.06	0.68	4.24	8.91	32.8	44.7	51	50	16042	6122	ribosomal protein L3	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	-	Yes
PDCD10	11235	programmed cell death protein 10	NP_009148.2	1	4	4	8	1.06	0.67	2.93	10.28	7	15.4	5	5	10141	11235	programmed cell death 10	Molecular function unknown	-	Unclassified	Apoptosis	-	No
RAB13	5872	ras-related protein Rab-13 isoform 1	NP_002861.1	2	3	4	21	1.06	0.63	2.55	26	4.7	29	3	3	4053	5872	RAB13, member RAS oncogene family	GTPase activity	Cytoplasmic vesicle	GTPase	Cell communication;Signal transduction	RAB	Yes
PIGS	94005	GPI transamidase component PIG-S	NP_149975.1	1	2	2	9	1.05	1.67	4.12	12.21	8.7	42.5	4	4	15135	94005	phosphatidylinositol glycan, class S	Cytoskeletal anchoring activity	Microsome	Anchor protein	Cell growth and/or maintenance	TM	Yes
TFB1M	51106	dimethyladenosine transferase 1, mitochondrial	NP_057104.2	1	4	4	5	1.05	1.46	2.35	8.64	4.3	22.1	3	3	9515	51106	transcription factor B1, mitochondrial	Transcription factor activity	Mitochondrion	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
C18orf25	147339	uncharacterized protein C18orf25 isoform a	NP_659492.1	2	1	1	3	1.05	1.4	29.97	12.01	46.8	24.2	2	2	12690	147339	chromosome 18 open reading frame 25	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	No
TBCB	1155	tubulin-folding cofactor B isoform 1	NP_001272.2	2	7	7	11	1.05	1.36	2	1.73	4.2	4.7	4	4	3196	1155	cytoskeleton associated protein 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
RPP14	11102	ribonuclease P protein subunit p14	NP_008973.1	1	1	1	2	1.05	1.34					1	1	18001	11102	ribonuclease P 14kDa subunit	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CPSF3	51692	cleavage and polyadenylation specificity factor subunit 3	NP_057291.1	1	3	3	8	1.05	1.33	0.98	3.54	1.8	8.2	3	3	5825	51692	cleavage and polyadenylation specific factor 3,73kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
GAR1	54433	H/ACA ribonucleoprotein complex subunit 1	NP_061856.1	1	6	6	11	1.05	1.32	4.15	5.38	12.4	20.2	8	8	7569	54433	nucleolar protein family A, member 1 (H/ACAsmall nucleolar RNPs)	Ribonucleoprotein	Nucleolus	Enzyme: Reductase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
UBE2E2	7325	ubiquitin-conjugating enzyme E2 E2	NP_689866.1	1	1	1	1	1.05	1.31					1	1	6779	7325	ubiquitin-conjugating enzyme E2E 2 (UBC4/5homolog, yeast)	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
MXRA7	439921	matrix-remodeling-associated protein 7 isoform 1 precursor	NP_001008528.1	3	2	2	12	1.05	1.26	2.33	2.97	6	9.2	6	6	18199	439921	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
PARK7	11315	protein DJ-1	NP_009193.2	1	6	6	17	1.05	1.25	5.16	3.66	15.4	13	8	8	3961	11315	Parkinson disease (autosomal recessive, earlyonset) 7	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
TBC1D23	55773	TBC1 domain family member 23 isoform 1	NP_001186127.1	2	3	3	5	1.05	1.23	6.31	13.82	11.5	30.2	3	3	7727	55773	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TBC	No
PLS1	5357	plastin-1	NP_001165783.1	1	4	7	31	1.05	1.22	13.17	5.53	43.4	20.4	9	9	4110	5357	plastin 1 (I isoform)	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	EF;CH	Yes
ARMC10	83787	armadillo repeat-containing protein 10 isoform a	NP_114111.2	6	2	2	3	1.05	1.22					1	1	18133	83787	None	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Biological_process unknown	TM	No
RTCB	51493	tRNA-splicing ligase RtcB homolog	NP_055121.1	1	18	18	42	1.05	1.22	2.71	5.59	14	34.4	24	24									
HSPA4	3308	heat shock 70 kDa protein 4	NP_002145.3	1	52	56	272	1.05	1.22	3.1	3.48	37.2	49.9	123	123	9025	3308	heat shock 70kDa protein 4	Chaperone activity	Golgi apparatus;Cytoplasm	Chaperone	Protein metabolism	SP;CC	Yes
HPRT1	3251	hypoxanthine-guanine phosphoribosyltransferase	NP_000185.1	3	9	9	40	1.05	1.22	4.53	4.35	22.6	24.1	22	20	2388	3251	hypoxanthine phosphoribosyltransferase 1(Lesch-Nyhan syndrome)	Catalytic activity	Cytoplasm	Enzyme: Ribosyltransferase	Metabolism;Energy pathways	-	Yes
DCPS	28960	m7GpppX diphosphatase	NP_054745.1	1	9	9	18	1.05	1.21	5.06	1.15	16.9	4.4	10	10	16787	28960	decapping enzyme, scavenger	Hydrolase activity	Nucleus	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
ARHGAP18	93663	rho GTPase-activating protein 18	NP_277050.2	1	5	5	10	1.05	1.21	3.71	1.67	8.7	4.5	5	5	12474	93663	Rho GTPase activating protein 18	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	RHOGAP	Yes
BRD7	29117	bromodomain-containing protein 7 isoform 1	NP_001167455.1	2	1	1	2	1.05	1.2					1	1	12531	29117	bromodomain containing 7	Transcription regulator activity	Nucleus	Transcription factor	Regulation of cell cycle;Signal transduction	BROMO;CC	Yes
HARS2	23438	probable histidine--tRNA ligase, mitochondrial isoform 1 precursor	NP_036340.1	3	1	6	18	1.05	1.2					1	1	2871	23438	histidyl-tRNA synthetase-like	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
PSME4	23198	proteasome activator complex subunit 4	NP_055429.2	2	9	9	20	1.05	1.2	8.36	6.9	26.8	23.7	9	8	9652	23198	proteasome (prosome, macropain) activatorsubunit 4	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC;HEAT;NLS	No
OTUD4	54726	OTU domain-containing protein 4 isoform 3	NP_001096123.1	1	7	7	12	1.05	1.19	2.53	1.06	6.5	3.1	6	6	11033	54726	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
EXOC7	23265	exocyst complex component 7 isoform 4	NP_001138769.1	7	4	4	6	1.05	1.19	5.21	18.1	11	45	4	4	16292	23265	exocyst complex component 7	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	No
P4HA2	8974	prolyl 4-hydroxylase subunit alpha-2 isoform 2 precursor	NP_001136070.1	2	13	13	28	1.05	1.18	4.7	2.86	18.7	12.7	14	14	11862	8974	procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Metabolism;Energy pathways;Peptide metabolism	P4HC;SP	Yes

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BCL10	8915	B-cell lymphoma/leukemia 10	NP_003912.1	1	3	3	3	1.05	1.15	8.91	15.36	16.3	31.3	3	3	4625	8915	B-cell CLL/lymphoma 10	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	CARD	Yes
UMPS	7372	uridine 5'-monophosphate synthase	NP_000364.1	1	10	10	36	1.05	1.14	2.92	6.04	13.1	29.9	18	18	2022	7372	uridine monophosphate synthetase (orotatephosphoribosyl transferase and orotidine-5`-decarboxylase)	Transferase activity	Nucleus	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
EIF4B	1975	eukaryotic translation initiation factor 4B isoform 1	NP_001287750.1	2	19	19	39	1.05	1.14	8.03	6.66	41.1	36.6	22	22	4892	1975	eukaryotic translation initiation factor 4B	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	RRM;CC	Yes
ZC3H14	79882	zinc finger CCCH domain-containing protein 14 isoform 1	NP_079100.2	5	8	8	14	1.05	1.14	5.58	6.41	16.7	20.9	8	8	13348	79882	None	RNA binding	Nucleus	RNA binding protein	Biological_process unknown	ZnF_C3H1	No
CAT	847	catalase	NP_001743.1	1	11	11	20	1.05	1.14	2.43	4.56	8.5	17.3	11	11	282	847	catalase	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
EPS15L1	58513	epidermal growth factor receptor substrate 15-like 1 isoform 1	NP_001245303.1	4	10	10	15	1.05	1.13	7.89	14.43	25.3	52	9	9	9445	58513	epidermal growth factor receptor pathwaysubstrate 15-like 1	Calcium ion binding	Nucleus	Calcium binding protein	Cell communication;Signal transduction	EH;CC	Yes
STXBP5	134957	syntaxin-binding protein 5 isoform b	NP_001121187.1	2	1	1	2	1.05	1.13					1	1	6845	134957	syntaxin binding protein 5 (tomosyn)	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	WD40	No
RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 1	NP_002865.1	3	11	13	45	1.05	1.13	7.76	10.07	32.3	46.4	15	15	6772	5887	RAD23 homolog B (S. cerevisiae)	DNA binding	Nucleus	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBQ;UBA;STI1	Yes
DNAJC5	80331	dnaJ homolog subfamily C member 5	NP_079495.1	1	3	3	5	1.05	1.13	16.33	4.4	30.4	8.6	3	3	8539	80331	DnaJ (Hsp40) homolog, subfamily C, member 5	Chaperone activity	Cytoplasmic vesicle	Chaperone	Protein metabolism	DNAJ;TM	No
SRP72	6731	signal recognition particle subunit SRP72 isoform 1	NP_008878.3	2	26	26	60	1.05	1.12	3.16	3.37	19.3	22	33	33	3671	6731	signal recognition particle 72kDa	RNA binding	Nucleolus	RNA binding protein	Protein metabolism	TPR;CC	Yes
DNAJC9	23234	dnaJ homolog subfamily C member 9	NP_056005.1	1	9	9	33	1.05	1.11	2.49	6.63	10.1	29	15	15	13237	23234	DnaJ (Hsp40) homolog, subfamily C, member 9	Chaperone activity	-	Chaperone	Protein metabolism	DNAJ;CC	Yes
WDR6	11180	WD repeat-containing protein 6	NP_060501.3	1	4	4	11	1.05	1.1	7.08	7.83	18.3	21.4	6	6	6912	11180	WD repeat domain 6	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	WD40;TM	Yes
TTC1	7265	tetratricopeptide repeat protein 1	NP_001269429.1	1	8	8	12	1.05	1.1	2.62	5.44	7.8	17.1	8	8	11881	7265	tetratricopeptide repeat domain 1	Receptor signaling complex scaffold activity	-	Adapter molecule	Cell communication;Signal transduction	TPR;CC	Yes
COPS2	9318	COP9 signalosome complex subunit 2 isoform 2	NP_001137359.1	2	13	13	32	1.05	1.1	5.17	9.2	22.6	43.5	17	17	5146	9318	COP9 constitutive photomorphogenic homologsubunit 2 (Arabidopsis)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PINT	Yes
PHLDA3	23612	pleckstrin homology-like domain family A member 3	NP_036528.1	1	1	1	2	1.05	1.1					1	1	9519	23612	pleckstrin homology-like domain, family A,member 3	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	PH	No
ARHGAP17	55114	rho GTPase-activating protein 17 isoform 1	NP_001006635.1	2	5	5	9	1.05	1.09	1.1	3.29	2.3	7.2	4	4	12207	55114	Rho GTPase activating protein 17	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	BAR;RHOGAP;CC	Yes
ETHE1	23474	persulfide dioxygenase ETHE1, mitochondrial	NP_055112.2	1	9	9	27	1.05	1.09	8.6	10.5	34.9	45	14	14	9764	23474	ethylmalonic encephalopathy 1 [Homosapiens]Other Aliases: HGNC:23287, HSCO, YF13H12Other Designations: ETHE1protein; YF13H12 (interim symbol); hepatoma subtracted clone one; homology to aplant EST:RICS2753A	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	-	No
PDIA4	9601	protein disulfide-isomerase A4 precursor	NP_004902.1	1	39	39	202	1.05	1.08	2.83	3.23	30.6	36.4	101	102	6501	9601	protein disulfide isomerase-associated 4	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	CC;SP	Yes
SNRNP40	9410	U5 small nuclear ribonucleoprotein 40 kDa protein	NP_004805.2	1	6	6	11	1.05	1.08	6.73	9.79	18.9	28.6	7	7	8481	9410	WD repeat domain 57 (U5 snRNP specific)	Ribonucleoprotein	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
HK2	3099	hexokinase-2	NP_000180.2	2	15	18	38	1.05	1.08	2.93	4.61	12.3	20.1	16	16	3080	3099	hexokinase 2	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
SRGAP1	57522	SLIT-ROBO Rho GTPase-activating protein 1	NP_065813.1	1	2	4	9	1.05	1.08					1	1	9406	57522	SLIT-ROBO Rho GTPase activating protein 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	FCH;CC;RHOGAP;SH3	Yes
PTPN12	5782	tyrosine-protein phosphatase non-receptor type 12 isoform 1	NP_002826.3	3	11	11	26	1.05	1.08	4.34	3.82	16.5	15	13	13	2513	5782	protein tyrosine phosphatase, non-receptortype 12	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	Tyr_Phos	Yes
AGO2	27161	protein argonaute-2 isoform 1	NP_036286.2	2	3	3	5	1.05	1.07	0.52	8.03	0.9	15	3	3									

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TGFBR2	7048	TGF-beta receptor type-2 isoform A precursor	NP_001020018.1	2	2	2	4	1.05	1.07	5.2	1.46	7.8	2.2	2	2	1823	7048	transforming growth factor, beta receptor II(70/80kDa)	Receptor signaling protein serine/threonine kinase activity	Extracellular matrix;Nucleus	Receptor serine/threonine kinase	Signal transduction;Regulation of cell proliferation;Regulation of immune response	S_T_kinase;TM;SP;S_T_Y_Kinase	Yes
RPS6	6194	40S ribosomal protein S6	NP_001001.2	1	15	15	77	1.05	1.07	4.93	5.58	34.9	40.8	43	43	1592	6194	ribosomal protein S6	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	CC	Yes
SLTM	79811	SAFB-like transcription modulator isoform a	NP_079031.2	2	8	8	14	1.05	1.06	2.38	4.19	6.6	11.8	7	7	7819	79811	None	Nucleic acid binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;SAP;RRM	Yes
SART3	9733	squamous cell carcinoma antigen recognized by T-cells 3	NP_055521.1	1	10	10	17	1.05	1.06	6.06	6.3	20.3	21.4	10	10	11532	9733	squamous cell carcinoma antigen recognised by Tcells 3	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HAT;CC;RRM	Yes
EEF1E1	9521	eukaryotic translation elongation factor 1 epsilon-1 isoform 1	NP_004271.1	2	5	5	26	1.05	1.06	3.13	3.36	10.5	11.3	10	10	10931	9521	eukaryotic translation elongation factor 1epsilon 1	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
GSPT1	2935	eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 1	NP_002085.2	4	19	19	52	1.05	1.06	4.19	4.99	22.8	27.6	26	26	753	2935	G1 to S phase transition 1	GTPase activity	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
TRIP4	9325	activating signal cointegrator 1	NP_057297.2	1	8	8	13	1.05	1.06	2.64	6.25	7.8	18.8	8	8	5140	9325	thyroid hormone receptor interactor 4	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
HNRNPAB	3182	heterogeneous nuclear ribonucleoprotein A/B isoform b	NP_004490.2	2	11	12	42	1.05	1.04	3.82	9.87	16.6	44.5	17	17	4067	3182	heterogeneous nuclear ribonucleoprotein A/B	MRNA binding	Nucleolus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
SND1	27044	staphylococcal nuclease domain-containing protein 1	NP_055205.2	1	47	47	196	1.05	1.04	2.73	3.24	29.2	34.4	100	98	3714	27044	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TUDOR;NLS	Yes
DNMBP	23268	dynamin-binding protein	NP_056036.1	1	7	7	12	1.05	1.03	12.2	2.42	29.1	5.6	5	5	10918	23268	dynamin binding protein	Guanyl-nucleotide exchange factor activity	Extracellular	Guanine nucleotide exchange factor	Cell communication;Signal transduction	SH3;CC;RHOGEF;BAR	Yes
PNKP	11284	bifunctional polynucleotide phosphatase/kinase	NP_009185.2	1	3	3	4	1.05	1.03					1	1	9284	11284	polynucleotide kinase 3`-phosphatase	DNA repair protein	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	FHA;NLS	Yes
DERL2	51009	derlin-2 isoform a	NP_057125.2	2	1	1	6	1.05	1.03					1	1	16796	51009	Der1-like domain family, member 2	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Biological_process unknown	TM	No
FAM20B	9917	glycosaminoglycan xylosylkinase	NP_055679.1	1	3	3	5	1.05	1.03	16.45	8.62	30.7	15.5	3	3	13297	9917	family with sequence similarity 20, member B	Molecular function unknown	Extracellular	Secreted polypeptide	Biological_process unknown	SP	Yes
ABCE1	6059	ATP-binding cassette sub-family E member 1	NP_002931.2	1	20	20	71	1.05	0.99	3.12	3.18	21.2	20.5	41	41	3132	6059	ATP-binding cassette, sub-family E (OABP),member 1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	AAA	Yes
NCOR2	9612	nuclear receptor corepressor 2 isoform 1	NP_006303.4	3	3	3	4	1.05	0.99	0.99	3.62	1.8	6.2	3	3	2910	9612	nuclear receptor co-repressor 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT;CC	Yes
DIEXF	27042	digestive organ expansion factor homolog	NP_055203.4	1	6	6	11	1.05	0.98	4.56	2.86	10.7	6.3	5	5									
NSF	4905	vesicle-fusing ATPase	NP_006169.2	1	9	9	19	1.05	0.98	3.03	3.59	9.5	10.6	9	9	3380	4905	N-ethylmaleimide-sensitive factor	ATPase activity	Cytoplasm	ATPase	Metabolism;Energy pathways	AAA	Yes
ARFGAP2	84364	ADP-ribosylation factor GTPase-activating protein 2 isoform 1	NP_115765.2	2	10	10	25	1.05	0.98	4.59	5.87	16.9	20.1	12	12	6069	84364	zinc finger protein 289, ID1 regulated	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	ARFGAP;CC	No
FARSA	2193	phenylalanine--tRNA ligase alpha subunit	NP_004452.1	1	15	15	35	1.05	0.98	3.69	9.62	17	42.8	19	19	4227	2193	phenylalanine-tRNA synthetase-like, alphasubunit	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
ITGA2	3673	integrin alpha-2 precursor	NP_002194.2	1	29	29	143	1.05	0.98	2.28	2.99	19.8	24.4	67	67	1893	3673	integrin, alpha 2 (CD49B, alpha 2 subunit ofVLA-2 receptor)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;INTA;VWA;SP	Yes
GSDMD	79792	gasdermin-D	NP_079012.3	1	2	2	3	1.05	0.97	1.99	24.77	3	34.9	2	2	11014	79792	gasdermin domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
YTHDF3	253943	YTH domain-containing family protein 3 isoform b	NP_001264743.1	3	6	10	19	1.05	0.96	5.35	12.29	13.8	29.4	6	6	8106	253943	YTH domain family, member 3	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
AIDA	64853	axin interactor, dorsalization-associated protein	NP_073742.2	1	6	6	12	1.05	0.96	3.19	17.67	8.3	47.3	6	7	7798	64853	chromosome 1 open reading frame 80	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
OCIAD1	54940	OCIA domain-containing protein 1 isoform 4	NP_001161726.1	4	6	6	27	1.05	0.96	8.81	13.63	37.2	54.1	15	15	17654	54940	OCIA domain containing 1	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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MAPK14	1432	mitogen-activated protein kinase 14 isoform 2	NP_620581.1	9	9	10	23	1.05	0.96	6.29	5.24	19.9	15.2	9	9	2619	1432	mitogen-activated protein kinase 14	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
CNOT10	25904	CCR4-NOT transcription complex subunit 10 isoform 3	NP_001243671.1	3	3	3	5	1.05	0.95	1.33	11.18	2.4	18.6	3	3	16731	25904	CCR4-NOT transcription complex, subunit 10	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;TPR	No
SP100	6672	nuclear autoantigen Sp-100 isoform 1	NP_001073860.1	9	9	9	24	1.05	0.95	2.11	3.18	7.4	10	11	11	6844	6672	nuclear antigen Sp100	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SPECTRIN;SAND;HMG;CC;PHD;BROMO	Yes
UBE2V2	7336	ubiquitin-conjugating enzyme E2 variant 2	NP_003341.1	2	2	6	21	1.05	0.95	2.85	25.33	4.2	34.9	2	2	4300	7336	ubiquitin-conjugating enzyme E2 variant 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBC	Yes
HNRNPH1	3187	heterogeneous nuclear ribonucleoprotein H	NP_005511.1	1	9	15	79	1.05	0.94	5.33	7.74	21.9	28.6	15	15	3021	3187	heterogeneous nuclear ribonucleoprotein H1 (H)	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
LARP1	23367	la-related protein 1	NP_056130.2	2	19	19	43	1.05	0.94	3.1	3.43	17	16.6	27	26	11225	23367	None	Molecular function unknown;Ribonucleoprotein	Nucleus;Cytoplasm	Unclassified;Ribonucleoprotein	Biological_process unknown;Transport	LA	Yes
PDCD6	10016	programmed cell death protein 6 isoform 1	NP_037364.1	5	5	5	37	1.05	0.94	4.21	3.24	18.3	12.7	17	17	3035	10016	programmed cell death 6	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
BABAM1	29086	BRISC and BRCA1-A complex member 1 isoform 1	NP_001028721.1	2	3	3	5	1.05	0.94	22.88	19.04	43.4	31.8	3	3									
CHMP4A	29082	charged multivesicular body protein 4a	NP_054888.2	1	6	6	10	1.05	0.92	3.44	6.26	8.8	14.2	6	6	16597	29082	chromatin modifying protein 4A	Molecular function unknown	Cytoplasmic vesicle	Unclassified	Cell growth and/or maintenance	CC	Yes
SPECC1L	23384	cytospin-A isoform 1	NP_056145.4	2	4	4	6	1.05	0.92	7.11	8.6	15	15.9	4	4									
SCAF11	9169	protein SCAF11	NP_004710.2	1	6	6	10	1.05	0.91	4.13	8.75	10.6	19.8	6	6									
LOC105375810	105375810	uncharacterized protein LOC105375810	XP_011515795.1	1	1	1	2	1.05	0.91					1	1									
LRRC8A	56262	volume-regulated anion channel subunit LRRC8A	NP_001120716.1	1	8	9	22	1.05	0.91	4.97	4.97	14.8	12.8	8	8	9754	56262	leucine rich repeat containing 8	Molecular function unknown	Integral to membrane	Unclassified;Integral membrane protein	Biological_process unknown;Immune response	TM;LRR	Yes
SRRM2	23524	serine/arginine repetitive matrix protein 2	NP_057417.3	1	25	25	61	1.05	0.88	4.08	5.77	25.3	30.2	34	34	6913	23524	serine/arginine repetitive matrix 2	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RBD	Yes
TAP2	6891	antigen peptide transporter 2 isoform 1	NP_000535.3	3	10	10	29	1.05	0.87	4.67	6.98	19.1	24	15	15	1360	6891	transporter 2, ATP-binding cassette, sub-familyB (MDR/TAP)	Transporter activity	Endoplasmic reticulum;Integral to membrane	Transport/cargo protein	Transport	TM;AAA	Yes
PANK4	55229	pantothenate kinase 4	NP_060686.2	1	8	8	14	1.05	0.84	7	5.99	21.1	14.3	8	8	7313	55229	pantothenate kinase 4	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
LMAN2	10960	vesicular integral-membrane protein VIP36 precursor	NP_006807.1	1	12	12	35	1.05	0.84	11.63	7.88	59.1	30.3	20	20	17285	10960	lectin, mannose-binding 2	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	SP;TM	Yes
FAM3C	10447	protein FAM3C precursor	NP_055703.1	1	7	7	25	1.05	0.82	4.04	14.94	16	48.4	14	14	12270	10447	family with sequence similarity 3, member C	Cytokine activity	Extracellular	Cytokine	Cell communication;Signal transduction	SP	Yes
ALAD	210	delta-aminolevulinic acid dehydratase	NP_000022.3	1	2	2	4	1.05	0.81	49.06	8.15	83.4	9.3	2	2	504	210	aminolevulinate, delta-, dehydratase	Hydro-lyase activity	Cytoplasm	Enzyme: Dehydratase	Metabolism;Energy pathways	SP	Yes
SRCAP	10847	helicase SRCAP	NP_006653.2	1	1	1	1	1.05	0.81					1	1	18103	10847	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;DEXDc;HELIC;AT_hook	No
PITHD1	57095	PITH domain-containing protein 1	NP_065095.2	1	4	4	8	1.05	0.8	14.45	26.17	35.1	49.7	5	5									
MAP4K4	9448	mitogen-activated protein kinase kinase kinase kinase 4 isoform 4	NP_001229488.1	15	8	12	20	1.05	0.79	5.15	15.55	16.3	38.3	9	9	5235	9448	mitogen-activated protein kinase kinase kinasekinase 4	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Signal transduction	S_T_kinase;CNH;CC	Yes
FIG4	9896	polyphosphoinositide phosphatase	NP_055660.1	1	1	1	1	1.05	0.79					1	1	11073	9896	KIAA0274	Phospholipase activity	-	Enzyme: Phospholipase	Metabolism;Energy pathways	-	Yes
ACAA2	10449	3-ketoacyl-CoA thiolase, mitochondrial	NP_006102.2	1	6	6	17	1.05	0.77	8.43	12.1	27.1	28.5	9	9	10380	10449	acetyl-Coenzyme A acyltransferase 2(mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
TPD52	7163	tumor protein D52 isoform 4	NP_001274069.1	7	3	3	7	1.05	0.76	16.59	15.88	35.8	24.4	4	4	4963	7163	tumor protein D52	Molecular function unknown	-	Unclassified	Cell proliferation	PEST;CC	Yes
RBFA	79863	putative ribosome-binding factor A, mitochondrial isoform 1 precursor	NP_079081.2	1	3	3	4	1.05	0.75	32.78	8.89	65.5	11.6	3	3									
MED14	9282	mediator of RNA polymerase II transcription subunit 14	NP_004220.2	1	2	3	4	1.05	0.74					1	1	2172	9282	cofactor required for Sp1 transcriptionalactivation, subunit 2, 150kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
RAB8B	51762	ras-related protein Rab-8B	NP_057614.1	12	2	6	69	1.05	0.71	2.9	18.66	5.3	23.1	3	3	11476	51762	RAB8B, member RAS oncogene family	GTPase activity	Cytoplasmic vesicle	GTPase	Cell communication;Signal transduction	RAB	Yes
ND1	4535	NADH dehydrogenase subunit 1	YP_003024026.1	1	2	2	3	1.05	0.69	25.18	6.3	38.6	6.2	2	2									

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TUBGCP5	114791	gamma-tubulin complex component 5 isoform a	NP_443135.3	2	2	2	4	1.05	0.69	13.14	38.22	19.6	38.7	2	2	12177	114791	tubulin, gamma complex associated protein 5	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein	Cell growth and/or maintenance	-	Yes
DYNLT1	6993	dynein light chain Tctex-type 1 isoform 1	NP_006510.1	3	2	2	3	1.05	0.55					1	1	15987	6993	t-complex-associated-testis-expressed 1-like 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
H2AFX	3014	histone H2AX	NP_002096.1	2	3	9	36	1.04	1.82	21.86	15.65	33.1	42.1	2	2	3465	3014	H2A histone family, member X	DNA binding	Nucleus	DNA binding protein	DNA repair	-	Yes
CDCP1	64866	CUB domain-containing protein 1 isoform 1 precursor	NP_073753.3	2	8	8	21	1.04	1.46	5.53	2.44	19.3	11.8	11	11	16696	64866	CUB domain containing protein 1	Molecular function unknown;Cell adhesion molecule activity	Plasma membrane	Adhesion molecule;Unclassified	Cell communication;Signal transduction;Cell adhesion;Cell-cell adhesion	SP;CUB;TM	No
SMYD5	10322	SET and MYND domain-containing protein 5	NP_006053.2	1	2	2	3	1.04	1.43					1	1	18080	10322	SMYD family member 5	Methyltransferase activity	-	Enzyme: Methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SET	No
HPCAL1	3241	hippocalcin-like protein 1	NP_002140.2	2	6	6	10	1.04	1.42	3.28	0.98	7.7	3.1	5	5	2564	3241	hippocalcin-like 1	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
SRP54	6729	signal recognition particle 54 kDa protein isoform 1	NP_003127.1	2	13	13	30	1.04	1.32	11.33	16.16	49.9	103.8	16	16	5330	6729	signal recognition particle 54kDa	RNA binding	Cytoplasm	RNA binding protein	Protein metabolism	AAA	Yes
PPP2R5B	5526	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit beta isoform	NP_006235.1	1	1	2	2	1.04	1.31					1	1	9038	5526	protein phosphatase 2, regulatory subunit B(B56), beta isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	-	Yes
G3BP2	9908	ras GTPase-activating protein-binding protein 2 isoform b	NP_987100.1	2	13	13	38	1.04	1.3	6.21	6.28	29.6	37.7	20	20	6570	9908	None	Molecular function unknown	Cytoplasm;Nucleus	Unclassified	Cell communication;Signal transduction	RRM	Yes
PFAS	5198	phosphoribosylformylglycinamidine synthase	NP_036525.1	1	19	19	38	1.04	1.29	5.51	5.12	26.6	31	21	21	9072	5198	phosphoribosylformylglycinamidine synthase (FGARamidotransferase)	Ligase activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
TUSC1	286319	tumor suppressor candidate gene 1 protein	NP_001004125.1	1	1	1	2	1.04	1.28					1	1	18247	286319	tumor suppressor candidate 1	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	CC	No
DDX1	1653	ATP-dependent RNA helicase DDX1	NP_004930.1	1	19	19	53	1.04	1.28	4.11	5.26	23.7	38.2	30	30	3158	1653	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
RPL23	9349	60S ribosomal protein L23	NP_000969.1	1	8	8	79	1.04	1.23	5.75	5.74	38.2	45.8	38	38	4716	9349	ribosomal protein L23	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PSMD11	5717	26S proteasome non-ATPase regulatory subunit 11	NP_001257411.1	1	23	23	86	1.04	1.23	3.43	3.44	25.1	29.6	48	47	5119	5717	proteasome (prosome, macropain) 26S subunit,non-ATPase, 11	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	PINT	Yes
RQCD1	9125	cell differentiation protein RCD1 homolog isoform 2	NP_005435.1	3	4	4	9	1.04	1.23	6.78	8.72	14.1	21.8	4	4	8828	9125	RCD1 required for cell differentiation1 homolog(S. pombe)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
RRP7A	27341	ribosomal RNA-processing protein 7 homolog A	NP_056518.2	1	3	3	6	1.04	1.2	4.58	1.53	9.5	3.7	4	4	13043	27341	None	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 1	NP_001281269.1	2	9	9	12	1.04	1.19	6.82	3.39	18.9	10.7	7	7	11232	124245	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;ZnF_C3H1	Yes
TSR1	55720	pre-rRNA-processing protein TSR1 homolog	NP_060598.3	1	10	10	19	1.04	1.17	6.27	22.46	19.7	93.1	9	9	7681	55720	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
DNM1L	10059	dynamin-1-like protein isoform 1	NP_036192.2	6	1	27	108	1.04	1.17					1	1	4833	10059	dynamin 1-like	GTPase activity	Cytoplasm	GTPase	Mitochondrion organization and biogenesis	DYNC;GED	Yes
PRDX4	10549	peroxiredoxin-4 precursor	NP_006397.1	1	4	6	16	1.04	1.17	9.57	20.17	20.1	50	4	4	5935	10549	peroxiredoxin 4	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase	Metabolism;Energy pathways	SP	Yes
LASP1	3927	LIM and SH3 domain protein 1 isoform a	NP_006139.1	2	8	8	14	1.04	1.17	8.34	7.61	23.2	24	7	7	4229	3927	LIM and SH3 protein 1	Cytoskeletal protein binding	Focal adhesion	Cytoskeletal associated protein	Signal transduction;Regulation of signal transduction;Cytoskeleton organization and biogenesis	LIM;NEBULIN;SH3	Yes
RRAS2	22800	ras-related protein R-Ras2 isoform a	NP_036382.2	3	4	6	25	1.04	1.15	0.83	9.63	1.9	25.2	5	5	2518	22800	related RAS viral (r-ras) oncogene homolog 2	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS;CAAX;Small_GTPase	No
U2SURP	23350	U2 snRNP-associated SURP motif-containing protein	NP_001073884.1	1	8	8	16	1.04	1.15	6.92	14.24	19.2	45.4	7	7									
SLC27A4	10999	long-chain fatty acid transport protein 4	NP_005085.2	1	6	6	11	1.04	1.14	4.12	2.7	11.4	8.2	7	7	9172	10999	solute carrier family 27 (fatty acidtransporter), member 4	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	No
SYNCRIP	10492	heterogeneous nuclear ribonucleoprotein Q isoform 1	NP_006363.4	7	23	32	140	1.04	1.14	4.64	3.22	37.2	28.1	56	56	6734	10492	synaptotagmin binding, cytoplasmic RNAinteracting protein	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes

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MLEC	9761	malectin isoform1 precursor	NP_055545.1	3	8	8	16	1.04	1.13	6.11	12.44	18.2	41.2	8	8	13781	9761	KIAA0152	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	SP;CC;TM	Yes
RPL11	6135	60S ribosomal protein L11 isoform 1	NP_000966.2	2	4	4	25	1.04	1.13	9.19	2.86	32.4	10.7	11	11	10364	6135	ribosomal protein L11	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
SNF8	11267	vacuolar-sorting protein SNF8	NP_009172.2	1	3	3	4	1.04	1.11	2.68	8.91	4.8	17.3	3	3	16847	11267	None	Transcription regulator activity	-	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
TRIM3	10612	tripartite motif-containing protein 3 isoform 1	NP_006449.2	2	1	1	2	1.04	1.11					1	1	5690	10612	tripartite motif-containing 3	Metal ion binding	Cytoplasm	Anchor protein	Cell growth and/or maintenance	RING;BBOX;BBC;IGFLMN;CC	Yes
RPS14	6208	40S ribosomal protein S14	NP_005608.1	1	8	8	37	1.04	1.1	8.87	6.68	44.2	34.5	21	21	562	6208	ribosomal protein S14	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PAK2	5062	serine/threonine-protein kinase PAK 2	NP_002568.2	6	14	18	59	1.04	1.1	3.34	6.41	18.5	38.8	28	28	5428	5062	p21 (CDKN1A)-activated kinase 2	Protein serine/threonine kinase activity	Endoplasmic reticulum	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;PBD	Yes
APEH	327	acylamino-acid-releasing enzyme	NP_001631.3	1	17	17	69	1.04	1.09	5.18	2.73	31.8	17.1	33	33	34	327	N-acylaminoacyl-peptide hydrolase	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
BRD3	8019	bromodomain-containing protein 3	NP_031397.1	1	8	9	14	1.04	1.09	4.85	8.69	14.3	27.2	8	8	3327	8019	bromodomain containing 3	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BROMO;CC	Yes
LRPPRC	10128	leucine-rich PPR motif-containing protein, mitochondrial precursor	NP_573566.2	1	69	69	231	1.04	1.09	2.14	3.13	24.8	38.8	120	120	6343	10128	leucine-rich PPR-motif containing	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
WDR44	54521	WD repeat-containing protein 44 isoform 1	NP_061918.3	3	7	7	9	1.04	1.08	5.53	6.51	14.2	17.4	6	6	11682	54521	WD repeat domain 44	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	WD40	Yes
EIF4G2	1982	eukaryotic translation initiation factor 4 gamma 2 isoform 1	NP_001409.3	2	25	25	64	1.04	1.07	6.33	5.97	40.7	39.2	35	35	9084	1982	eukaryotic translation initiation factor 4gamma, 2	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	MIF4G;MA3	Yes
IPO4	79711	importin-4	NP_078934.3	1	13	13	31	1.04	1.06	5.49	9.31	21.7	38.1	14	14	7022	79711	importin 4	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	IBN_NT	Yes
ABCF2	10061	ATP-binding cassette sub-family F member 2 isoform b	NP_005683.2	2	12	12	29	1.04	1.04	5.4	6.11	21.9	25	15	15	12403	10061	ATP-binding cassette, sub-family F (GCN20),member 2	Molecular function unknown	Mitochondrion	Unclassified	Immune response	CC;AAA	Yes
STK4	6789	serine/threonine-protein kinase 4	NP_006273.1	1	4	6	10	1.04	1.03	8.66	2.7	15.7	4.8	3	3	5395	6789	serine/threonine kinase 4	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NES	Yes
ATP6V0D1	9114	V-type proton ATPase subunit d 1	NP_004682.2	1	12	12	24	1.04	1.03	5.01	6.26	18.2	22.7	12	12	6121	9114	ATPase, H+ transporting, lysosomal 38kDa, V0subunit d isoform 1	ATPase activity	-	ATPase	Transport	-	Yes
RPL4	6124	60S ribosomal protein L4	NP_000959.2	1	19	19	131	1.04	1.03	2.71	4.46	23.8	39.5	69	68	1607	6124	ribosomal protein L4	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
CLIC1	1192	chloride intracellular channel protein 1	NP_001279.2	2	17	18	132	1.04	1.03	3.05	2.19	26	18.4	65	65	4188	1192	chloride intracellular channel 1	Intracellular ligand-gated ion channel activity	Nucleus	Intracellular ligand gated channel	Transport	-	Yes
FKBP15	23307	FK506-binding protein 15	NP_056073.1	1	14	14	31	1.04	1.03	3.48	5.37	15.8	24.4	19	19	19414	23307	FK506 binding protein 15, 133kDa	Isomerase activity	Axon	Enzyme: Isomerase	Cell growth and/or maintenance	WH1;CC	No
STX3	6809	syntaxin-3 isoform 1	NP_004168.1	2	3	3	5	1.04	1.03	8.92	6.63	16.1	11.8	3	3	15985	6809	syntaxin 3A	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	SynN;t_SNARE;TM;CC	No
FAM114A1	92689	protein NOXP20	NP_612398.2	1	11	11	39	1.04	1.02	4.24	9.91	14.7	34.4	11	11	11282	92689	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	No
UBA3	9039	NEDD8-activating enzyme E1 catalytic subunit isoform 1	NP_003959.3	2	12	12	33	1.04	1.02	6.02	4.21	26.3	17.8	17	17	4413	9039	ubiquitin-activating enzyme E1C (UBA3 homolog,yeast)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
PPCDC	60490	phosphopantothenoylcysteine decarboxylase isoform a	NP_068595.3	2	1	1	1	1.04	1.02					1	1	14377	60490	None	Catalytic activity	-	Enzyme: Decarboxylase	Coenzyme and prosthetic group metabolism	-	No
PLCD1	5333	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 isoform 1	NP_001124436.1	2	1	1	4	1.04	1.02	26.69	1.17	40.9	1.7	2	2	9073	5333	phospholipase C, delta 1	Phospholipase activity	Plasma membrane	Enzyme: Phospholipase	Metabolism;Energy pathways	PH;EF;C2;PLCXc;PLCYc	Yes
TRAPPC6B	122553	trafficking protein particle complex subunit 6B isoform 1	NP_001073005.1	2	2	2	7	1.04	1.01	10.4	15.91	22	32.9	4	4	18221	122553	trafficking protein particle complex 6B	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
ATP6V1B2	526	V-type proton ATPase subunit B, brain isoform	NP_001684.2	2	18	18	64	1.04	1	3.29	4.78	20.8	29.3	36	36	6088	526	ATPase, H+ transporting, lysosomal 56/58kDa,V1 subunit B, isoform 2	Transporter activity	Endosome	Transport/cargo protein	Transport	-	Yes
DDX47	51202	probable ATP-dependent RNA helicase DDX47 isoform 1	NP_057439.2	2	9	9	22	1.04	1	9.25	13.69	32.7	48.1	11	11	10863	51202	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	Molecular function unknown	Nucleus	Unclassified;RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Ribosome biogenesis and assembly	DEXDc;HELIC;DEAD	Yes
AP2A2	161	AP-2 complex subunit alpha-2 isoform 2	NP_036437.1	2	15	23	73	1.04	1	4.25	6.02	21	28.9	22	22	6256	161	adaptor-related protein complex 2, alpha 2subunit	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	ADAP;CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
PPP6R2	9701	serine/threonine-protein phosphatase 6 regulatory subunit 2 isoform 1	NP_001229827.1	4	5	5	8	1.04	0.99	1.47	8.21	3.4	18.4	5	5									
HS2ST1	9653	heparan sulfate 2-O-sulfotransferase 1 isoform 1	NP_036394.1	2	1	1	1	1.04	0.99					1	1	9215	9653	heparan sulfate 2-O-sulfotransferase 1	Sulfotransferase activity	-	Enzyme: Sulphotransferase	Metabolism;Energy pathways	CC;SP	No
TMX3	54495	protein disulfide-isomerase TMX3 precursor	NP_061895.3	1	5	5	11	1.04	0.99	5.79	17.68	12.1	36.2	4	4	15591	54495	thioredoxin domain containing 10	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
RAB21	23011	ras-related protein Rab-21	NP_055814.1	1	8	8	23	1.04	0.98	5.13	6.79	19.4	24.4	13	13	6695	23011	RAB21, member RAS oncogene family	GTPase activity	Endoplasmic reticulum	GTPase	Cell communication;Signal transduction	RAB	Yes
TRABD	80305	traB domain-containing protein	NP_079480.2	1	3	3	5	1.04	0.97	8.14	1.29	14.7	2.2	3	3	11450	80305	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
YIPF4	84272	protein YIPF4	NP_115688.1	1	1	1	1	1.04	0.96					1	1	14410	84272	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
ASMTL	8623	N-acetylserotonin O-methyltransferase-like protein isoform 1	NP_004183.2	3	1	1	2	1.04	0.96					1	1	2156	8623	acetylserotonin O-methyltransferase-like	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
CPD	1362	carboxypeptidase D isoform 1 precursor	NP_001295.2	2	15	15	29	1.04	0.95	6.07	10	26.4	40.5	17	17	4375	1362	carboxypeptidase D	Carboxypeptidase activity	Plasma membrane	Carboxypeptidase	Protein metabolism	SP;Zn_pept;TM	Yes
MRPL13	28998	39S ribosomal protein L13, mitochondrial	NP_054797.2	1	6	6	13	1.04	0.95	3.01	3.01	8.9	8.1	8	8	14740	28998	mitochondrial ribosomal protein L13	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
LANCL1	10314	lanC-like protein 1	NP_006046.1	1	6	6	13	1.04	0.95	5.89	5.17	16.3	13.1	7	7	16040	10314	LanC lantibiotic synthetase component C-like 1(bacterial)	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Immune response	TM	Yes
KIF5B	3799	kinesin-1 heavy chain	NP_004512.1	3	40	40	107	1.04	0.94	2.46	2.65	19.8	19.3	59	59	7214	3799	kinesin family member 5B	Motor activity	Mitochondrion	Motor protein	Cell growth and/or maintenance	KISC;CC	Yes
MRPL47	57129	39S ribosomal protein L47, mitochondrial isoform a	NP_065142.2	2	5	5	8	1.04	0.93	10.14	4.25	21.2	7.9	4	4	14766	57129	mitochondrial ribosomal protein L47	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP;CC	Yes
VDR	7421	vitamin D3 receptor isoform VDRB1	NP_001017536.1	2	1	1	2	1.04	0.92					1	1	3463	7421	vitamin D (1,25-dihydroxyvitamin D3) receptor	Transcription factor activity	Nucleus	Transcription factor	Regulation of gene expression, epigenetic	ZnF_C4;HOLI;NLS;NES	Yes
ELP4	26610	elongator complex protein 4 isoform 3	NP_001275655.1	3	2	2	4	1.04	0.91	4.88	43.8	7.2	61	2	2	7377	26610	elongation protein 4 homolog (S. cerevisiae)	Acyltransferase activity	Nucleus	Enzyme: Acyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
PLEKHA5	54477	pleckstrin homology domain-containing family A member 5 isoform 4	NP_001243399.1	5	10	10	22	1.04	0.89	4.82	4.27	15.9	12	10	10	9684	54477	pleckstrin homology domain containing, familyA member 5	Receptor signaling complex scaffold activity	Nucleus;Cytoplasm	Adapter molecule	Cell communication;Signal transduction	WW;PH;CC	Yes
AIFM1	9131	apoptosis-inducing factor 1, mitochondrial isoform 1 precursor	NP_004199.1	5	15	15	41	1.04	0.89	6.77	9.58	34.6	42.6	23	23	2161	9131	programmed cell death 8 (apoptosis-inducingfactor)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Cell communication;Signal transduction	TM	Yes
WFS1	7466	wolframin	NP_005996.2	1	2	2	4	1.04	0.89	5.8	5.04	8.6	6.4	2	2	5864	7466	Wolfram syndrome 1 (wolframin)	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
RBM33	155435	RNA-binding protein 33	NP_444271.2	1	2	2	3	1.04	0.87	15.34	7.62	22.8	9.3	2	2	17310	155435	RNA binding motif protein 33	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	No
CCAR1	55749	cell division cycle and apoptosis regulator protein 1 isoform a	NP_060707.2	2	10	10	22	1.04	0.86	5.39	11.03	19.6	33.8	12	12	10811	55749	cell division cycle and apoptosis regulator 1	Molecular function unknown	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction;Regulation of cell cycle	SAP;CC	Yes
ISG15	9636	ubiquitin-like protein ISG15 precursor	NP_005092.1	1	4	4	8	1.04	0.85	25.47	28.97	57.1	52.5	4	4	958	9636	interferon, alpha-inducible protein (cloneIFI-15K)	Cytokine activity	Extracellular	Cytokine	Immune response	UBQ;SP	Yes
COA3	28958	cytochrome c oxidase assembly factor 3 homolog, mitochondrial	NP_001035521.1	1	3	3	10	1.04	0.85	6.04	9.62	14	18.5	5	5									
DNAJB12	54788	dnaJ homolog subfamily B member 12	NP_001002762.2	1	2	2	4	1.04	0.84	5.43	2.5	8	3	2	2	7086	54788	DnaJ (Hsp40) homolog, subfamily B, member 12	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	DNAJ;TM	Yes
STK38	11329	serine/threonine-protein kinase 38	NP_009202.1	1	3	3	7	1.04	0.84	0.88	8.03	1.8	13.5	4	4	9511	11329	serine/threonine kinase 38	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NLS	No
NAA30	122830	N-alpha-acetyltransferase 30	NP_001011713.2	1	1	1	2	1.04	0.82					1	1	16619	122830	chromosome 14 open reading frame 35	Transferase activity	-	Enzyme: Transferase	Metabolism;Energy pathways	-	No
MYH11	4629	myosin-11 isoform SM1B	NP_001035203.1	13	6	27	691	1.04	0.77	2.14	2.8	32.7	31.4	204	204	1174	4629	myosin, heavy polypeptide 11, smooth muscle	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	MYOSIN;IQ;CC	Yes
LONP2	83752	lon protease homolog 2, peroxisomal isoform 1	NP_113678.2	2	1	1	2	1.04	0.75					1	1	7491	83752	None	Aminopeptidase activity	-	Aminopeptidase	Protein metabolism	AAA	No
PDCD5	9141	programmed cell death protein 5	NP_004699.1	1	4	4	10	1.04	0.74	2.53	5.12	5.9	8.4	5	5	6843	9141	programmed cell death 5	Molecular function unknown	Cytoplasm	Unclassified	Apoptosis	-	Yes
CCDC12	151903	coiled-coil domain-containing protein 12 1	NP_653317.2	2	2	2	3	1.04	0.74	0.91	9.52	1.3	10	2	2	13007	151903	coiled-coil domain containing 12	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TIPRL	261726	TIP41-like protein isoform 1	NP_690866.1	2	10	10	19	1.04	0.72	14	8.05	56.1	21.1	13	13	14608	261726	TIP41, TOR signalling pathway regulator-like(S. cerevisiae)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
DDX49	54555	probable ATP-dependent RNA helicase DDX49	NP_061943.2	1	1	1	2	1.03	1.8					1	1	10864	54555	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	Helicase activity	Nucleus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC	No
DHX8	1659	ATP-dependent RNA helicase DHX8 isoform 1	NP_004932.1	2	2	2	5	1.03	1.79	0.58	26.1	1	96.1	3	3	2672	1659	DEAH (Asp-Glu-Ala-His) box polypeptide 8	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;S1;CC	Yes
HNRNPA2B1	3181	heterogeneous nuclear ribonucleoproteins A2/B1 isoform B1	NP_112533.1	2	19	22	96	1.03	1.74	3.26	5.11	21.4	61.2	40	40	2526	3181	heterogeneous nuclear ribonucleoprotein A2/B1	Transcription factor binding;RNA binding	Nucleus	Ribonucleoprotein;RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
KLC2	64837	kinesin light chain 2 isoform 1	NP_073733.1	3	8	13	21	1.03	1.61	3.77	3.33	10.3	14.3	7	7	13917	64837	None	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	CC;TPR	Yes
FBXO4	26272	F-box only protein 4 isoform 1	NP_036308.1	3	2	2	3	1.03	1.58					1	1	9949	26272	F-box protein 4	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	F_BOX	Yes
RPUSD2	27079	RNA pseudouridylate synthase domain-containing protein 2 isoform 1	NP_689473.1	1	1	1	2	1.03	1.48					1	1	12668	27079	RNA pseudouridylate synthase domain containing2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
COX4I1	1327	cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	NP_001852.1	1	6	6	21	1.03	1.46	7.53	5.88	24.9	27.7	10	10	466	1327	cytochrome c oxidase subunit IV isoform 1	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM;SP	Yes
MPST	4357	3-mercaptopyruvate sulfurtransferase isoform 1	NP_066949.2	2	7	7	27	1.03	1.42	5.15	7.08	19.3	37.4	13	13	11896	4357	mercaptopyruvate sulfurtransferase	Sulfotransferase activity	Mitochondrion	Enzyme: Sulphotransferase	Metabolism;Energy pathways	RHOD	Yes
ARMC6	93436	armadillo repeat-containing protein 6 isoform 1	NP_001186125.1	2	3	3	6	1.03	1.39	2.37	0.22	4.2	0.5	3	3	12488	93436	armadillo repeat containing 6	Molecular function unknown	-	Unclassified	Signal transduction	ARM	No
KIAA0391	9692	mitochondrial ribonuclease P protein 3 isoform 1 precursor	NP_055487.2	4	3	3	6	1.03	1.35	7.21	2.52	10.5	4.8	2	2	18711	9692	KIAA0391	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	Yes
UTP3	57050	something about silencing protein 10	NP_065101.1	1	4	4	4	1.03	1.31	4.54	0.92	8.1	2.1	3	3	18016	57050	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	Yes
RANBP9	10048	ran-binding protein 9	NP_005484.2	1	2	2	3	1.03	1.29	5.83	11.48	8.5	21.2	2	2	4835	10048	RAN binding protein 9	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	SPRY;LISH;CTLH	No
MAPK3	5595	mitogen-activated protein kinase 3 isoform 1	NP_002737.2	4	5	8	20	1.03	1.28	7.65	15.67	11.2	29	2	2	3479	5595	mitogen-activated protein kinase 3	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Signal transduction	S_T_kinase	Yes
PURA	5813	transcriptional activator protein Pur-alpha	NP_005850.1	1	7	7	29	1.03	1.27	7.12	11.29	29.1	60.3	15	15	2721	5813	purine-rich element binding protein A	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PPP2R4	5524	serine/threonine-protein phosphatase 2A activator isoform a	NP_821068.1	5	10	10	26	1.03	1.27	5.99	5.65	23.5	27.3	14	14	2858	5524	protein phosphatase 2A, regulatory subunit B`(PR 53)	Phosphatase regulator activity	Cytoplasm	Enzyme regulator;Cell cycle control protein	Cell communication;Signal transduction;Regulation of cell cycle	-	Yes
DNAAF5	54919	dynein assembly factor 5, axonemal	NP_060272.3	1	13	13	25	1.03	1.27	3.92	8.87	15.2	44.3	14	14									
CTH	1491	cystathionine gamma-lyase isoform 1	NP_001893.2	3	2	2	3	1.03	1.26					1	1	9633	1491	cystathionase (cystathionine gamma-lyase)	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Protein metabolism	-	Yes
MRPL50	54534	39S ribosomal protein L50, mitochondrial	NP_061924.1	1	2	2	3	1.03	1.23	23.88	5.61	35.9	9.8	2	2	14768	54534	mitochondrial ribosomal protein L50	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
WARS	7453	tryptophan--tRNA ligase, cytoplasmic isoform a	NP_004175.2	2	20	20	65	1.03	1.21	5.07	8.12	30.4	60.3	32	32	1845	7453	tryptophanyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
TCERG1	10915	transcription elongation regulator 1 isoform 1	NP_006697.2	2	10	10	22	1.03	1.21	5.64	3.17	20.3	13.4	12	12	10393	10915	transcription elongation regulator 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WW;CC;FF	Yes
TAF7	6879	transcription initiation factor TFIID subunit 7	NP_005633.2	1	3	3	5	1.03	1.2	0.7	4.63	1.3	9.7	3	3	7196	6879	TAF7 RNA polymerase II, TATA box binding protein(TBP)-associated factor, 55kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
LYPLAL1	127018	lysophospholipase-like protein 1 isoform a	NP_620149.2	4	3	3	6	1.03	1.18	1.25	2.38	2.2	4.9	3	3	14335	127018	lysophospholipase-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
HSPG2	3339	basement membrane-specific heparan sulfate proteoglycan core protein isoform a precursor	NP_001278789.1	2	15	15	40	1.03	1.18	5.69	5.77	26.7	31.3	20	20	804	3339	heparan sulfate proteoglycan 2 (perlecan)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	SP;SEA;LDLA;IGC2;LAMB;EGFLAM;LAMG;EGF	Yes
USP8	9101	ubiquitin carboxyl-terminal hydrolase 8 isoform a	NP_005145.3	2	2	2	3	1.03	1.17	5.82	8.62	8.5	14.4	2	2	4405	9101	ubiquitin specific protease 8	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC;RHOD;UCH	Yes
PLAA	9373	phospholipase A-2-activating protein	NP_001026859.1	1	26	26	51	1.03	1.16	3.14	2.13	17	12.8	27	27	4850	9373	phospholipase A2-activating protein	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	WD40	Yes
RC3H2	54542	roquin-2 isoform 1	NP_001094058.1	6	1	1	4	1.03	1.15	9.88	9.77	14.5	16.1	2	2	14726	54542	membrane associated DNA binding protein	DNA binding	Endoplasmic reticulum	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1;RING	No

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DLD	1738	dihydrolipoyl dehydrogenase, mitochondrial isoform 1 precursor	NP_000099.2	4	15	15	38	1.03	1.15	5.28	3.88	25.8	21.2	22	22	2006	1738	dihydrolipoamide dehydrogenase (E3 component ofpyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain ketoacid dehydrogenase complex)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
TAOK3	51347	serine/threonine-protein kinase TAO3	NP_057365.3	4	5	7	11	1.03	1.14	9.4	4.54	16.8	9	3	3	11620	51347	TAO kinase 3	Protein serine/threonine kinase activity	-	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
COPB2	9276	coatomer subunit beta'	NP_004757.1	1	33	33	112	1.03	1.14	3.25	2.92	27.2	27.2	64	64	6103	9276	coatomer protein complex, subunit beta 2 (betaprime)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	WD40	Yes
DDI2	84301	protein DDI1 homolog 2	NP_115717.3	1	1	1	2	1.03	1.14					1	1	18702	84301	None	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBQ	Yes
MRPS9	64965	28S ribosomal protein S9, mitochondrial	NP_872578.1	1	9	9	23	1.03	1.14	10.93	6.25	38.5	24	11	11	17602	64965	mitochondrial ribosomal protein S9	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	Yes
TOR1A	1861	torsin-1A precursor	NP_000104.1	1	4	4	5	1.03	1.13	8.11	4.36	14.5	8.6	3	3	6897	1861	torsin family 1, member A (torsin A)	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP	Yes
GNPNAT1	64841	glucosamine 6-phosphate N-acetyltransferase	NP_932332.1	1	6	6	15	1.03	1.13	9.25	43.55	23.6	182.3	6	6	17046	64841	glucosamine-phosphate N-acetyltransferase 1	Acyltransferase activity	-	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
PLOD2	5352	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 isoform 1 precursor	NP_891988.1	2	16	16	45	1.03	1.13	3.44	5.09	16.8	27.6	22	22	3519	5352	procollagen-lysine, 2-oxoglutarate5-dioxygenase 2	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Metabolism;Energy pathways	SP;P4HC	Yes
SOAT1	6646	sterol O-acyltransferase 1 isoform 1	NP_003092.4	3	1	1	1	1.03	1.13					1	1	33	6646	sterol O-acyltransferase (acyl-Coenzyme A:cholesterol acyltransferase) 1	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM	Yes
AP2B1	163	AP-2 complex subunit beta isoform a	NP_001025177.1	2	19	32	127	1.03	1.1	4.41	4.24	26.9	27.7	34	34	3015	163	adaptor-related protein complex 2, beta 1subunit	Molecular function unknown;Transporter activity	Plasma membrane	Unclassified;Transport/cargo protein	Biological_process unknown;Transport	ADAP	No
TRMT10C	54931	mitochondrial ribonuclease P protein 1 precursor	NP_060289.2	1	13	13	30	1.03	1.1	4.79	5.78	21.2	27.4	18	18									
FARSB	10056	phenylalanine--tRNA ligase beta subunit	NP_005678.3	1	21	22	66	1.03	1.09	3.04	3.07	18.2	19.4	33	33	9947	10056	phenylalanine-tRNA synthetase-like, betasubunit	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
RDX	5962	radixin isoform 1	NP_001247422.1	5	17	29	131	1.03	1.09	3.26	2.53	18.2	15	29	29	1534	5962	radixin	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	B41;CC;ERM	Yes
PAN3	255967	PAB-dependent poly(A)-specific ribonuclease subunit PAN3	NP_787050.6	1	1	1	2	1.03	1.09					1	1	17818	255967	None	Ribonuclease activity	Cytoplasm	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_Y_Kinase	No
RBM39	9584	RNA-binding protein 39 isoform a	NP_909122.1	7	12	12	44	1.03	1.09	3.11	5.93	15.5	31.6	23	23	9201	9584	RNA-binding region (RNP1, RRM) containing 2	RNA binding;Transcription regulator activity	Nucleus	RNA binding protein;Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
MECP2	4204	methyl-CpG-binding protein 2 isoform 2	NP_001104262.1	2	4	4	7	1.03	1.08	3.04	7.82	6.3	17	4	4	2050	4204	methyl CpG binding protein 2 (Rett syndrome)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MBD	Yes
CFAP20	29105	cilia- and flagella-associated protein 20	NP_037374.1	1	3	3	7	1.03	1.08	8.87	0.01	16	0	3	3									
RAF1	5894	RAF proto-oncogene serine/threonine-protein kinase	NP_002871.1	1	1	2	3	1.03	1.07					1	1	1265	5894	v-raf-1 murine leukemia viral oncogene homolog 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	RBD;C1;S_T_kinase	Yes
WDR43	23160	WD repeat-containing protein 43	NP_055946.1	1	6	6	9	1.03	1.07	11.69	16.4	30.1	45.2	6	6	19518	23160	WD repeat domain 43	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
ZC3H13	23091	zinc finger CCCH domain-containing protein 13	NP_055885.3	1	1	1	2	1.03	1.07					1	1	8307	23091	KIAA0853	Transcription regulator activity	-	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;ZnF_C3H1	Yes
AKAP8L	26993	A-kinase anchor protein 8-like isoform 1	NP_055186.3	2	4	4	10	1.03	1.07	6.62	10.41	15.3	25.3	5	5	10641	26993	A kinase (PRKA) anchor protein 8-like	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;ZNFC2	Yes
ANAPC4	29945	anaphase-promoting complex subunit 4 isoform 1	NP_001273685.1	2	2	2	4	1.03	1.06	12.78	13.68	18.7	20.6	2	2	9505	29945	anaphase promoting complex subunit 4	Molecular function unknown	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
BPNT1	10380	3'(2'),5'-bisphosphate nucleotidase 1 isoform 1	NP_006076.4	3	12	12	34	1.03	1.05	4.65	5.51	21	25.7	19	19	6814	10380	3`(2`), 5`-bisphosphate nucleotidase 1	Hydrolase activity	-	Enzyme: Esterase	Cell communication;Signal transduction	I_Phosphatase	No

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DHX15	1665	pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	NP_001349.2	1	31	31	105	1.03	1.05	3.02	3.9	23.6	31.6	56	56	4553	1665	DEAH (Asp-Glu-Ala-His) box polypeptide 15	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;DEXDc	Yes
FMR1	2332	fragile X mental retardation protein 1 isoform ISO1	NP_002015.1	5	4	6	11	1.03	1.05	2.49	5.05	5.8	11.9	5	5	2398	2332	fragile X mental retardation 1	RNA binding	Cytoplasm;Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
NOP58	51602	nucleolar protein 58	NP_057018.1	1	18	18	58	1.03	1.04	3.5	4.17	20.3	24.4	31	31	11036	51602	None	Ribonucleoprotein	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
GFM1	85476	elongation factor G, mitochondrial isoform 2	NP_079272.4	3	9	9	18	1.03	1.04	5.48	4.59	18	15.2	10	10	7365	85476	G elongation factor, mitochondrial 1	Translation regulator activity	Mitochondrion	Translation regulatory protein	Protein metabolism	SP;GTP_EFTU;GTP_EFTU_D2	Yes
SF3A2	8175	splicing factor 3A subunit 2	NP_009096.2	1	3	3	7	1.03	1.04	7.58	2.94	15.8	6.1	4	4	2877	8175	splicing factor 3a, subunit 2, 66kDa	RNA binding	Nucleus	RNA binding protein	Protein metabolism	-	Yes
RPL19	6143	60S ribosomal protein L19	NP_000972.1	1	7	7	27	1.03	1.02	3.9	4.92	14	17.5	12	12	1594	6143	ribosomal protein L19	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	CC	Yes
SH3BP1	23616	SH3 domain-binding protein 1	NP_061830.3	1	8	8	19	1.03	1.02	4.03	2.18	13.2	6.7	10	9	10227	23616	SH3-domain binding protein 1	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	CC;RHOGAP;BAR	Yes
SOWAHC	65124	ankyrin repeat domain-containing protein SOWAHC	NP_075392.2	1	7	7	14	1.03	1.01	6.81	2.67	20.1	7.6	8	8									
MAP4	4134	microtubule-associated protein 4 isoform 1	NP_002366.2	3	47	47	126	1.03	0.99	3.35	5.69	30.4	50.9	74	73	1141	4134	microtubule-associated protein 4	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
UQCRC1	7384	cytochrome b-c1 complex subunit 1, mitochondrial precursor	NP_003356.2	1	16	16	58	1.03	0.98	8.44	6.71	47.5	35.3	27	27	1875	7384	ubiquinol-cytochrome c reductase core proteinI	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	-	Yes
ZDHHC13	54503	palmitoyltransferase ZDHHC13 isoform 1	NP_061901.2	2	2	2	5	1.03	0.98	2.24	3.67	4.6	7.2	4	4	15710	54503	zinc finger, DHHC-type containing 13	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	ANK;TM	Yes
TWF1	5756	twinfilin-1 isoform 2	NP_002813.3	2	7	8	20	1.03	0.97	3.52	6.67	11.5	18.4	10	8	10174	5756	PTK9 protein tyrosine kinase 9	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase	Cell communication;Signal transduction	ADF	Yes
VCAN	1462	versican core protein isoform 1 precursor	NP_004376.2	4	6	6	11	1.03	0.97	14.57	29.85	38.1	81	6	6	340	1462	chondroitin sulfate proteoglycan 2 (versican)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	IG;LINK;EGFL;EGFCA;LECTIN_C;SUSHI;SP;EGF	Yes
KCTD12	115207	BTB/POZ domain-containing protein KCTD12	NP_612453.1	1	15	15	43	1.03	0.97	4.56	3.32	22.4	15.5	22	23	11060	115207	potassium channel tetramerisation domaincontaining 12	Ion channel activity	-	Ion channel	Transport	BTB	Yes
Sep-02	4735	septin-2 isoform b	NP_001269901.1	3	15	15	62	1.03	0.96	3.19	2.83	17.8	14.7	29	29									
RPP25L	138716	ribonuclease P protein subunit p25-like protein	NP_680544.1	1	2	2	3	1.03	0.96					1	1									
CAPNS1	826	calpain small subunit 1 isoform 1	NP_001740.1	3	11	11	82	1.03	0.95	7.35	14.06	49.2	98	38	38	240	826	calpain, small subunit 1	Peptide binding	Cytoplasm	Regulatory/other subunit	Protein folding	EF	Yes
NOL10	79954	nucleolar protein 10 isoform 1	NP_079170.2	3	3	3	3	1.03	0.95	1.71	14.57	3.1	24.4	3	3	7849	79954	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	No
ACTR2	10097	actin-related protein 2 isoform b	NP_005713.1	2	17	18	70	1.03	0.95	4.97	10.61	30.1	62.8	33	33	5023	10097	ARP2 actin-related protein 2 homolog (yeast)	Structural constituent of cytoskeleton	Actin cytoskeleton	Cytoskeletal protein	Cell motility;Cell growth and/or maintenance	ACTIN	Yes
MBOAT7	79143	lysophospholipid acyltransferase 7 isoform 1	NP_077274.3	3	5	5	12	1.03	0.94	3.06	3	8.3	7.4	7	7	6925	79143	leukocyte receptor cluster (LRC) member 4	Receptor activity	Plasma membrane	Integral membrane protein	Biological_process unknown	TM	No
MFN2	9927	mitofusin-2	NP_055689.1	1	5	6	12	1.03	0.94	5.04	3.5	13.8	8.7	7	7	8495	9927	mitofusin 2	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	CC;TM	Yes
NDRG1	10397	protein NDRG1 isoform 1	NP_006087.2	3	9	9	29	1.03	0.94	7.34	9.85	31	38.5	16	16	5586	10397	N-myc downstream regulated gene 1	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	ABH	Yes
TLN1	7094	talin-1	NP_006280.3	2	120	120	551	1.03	0.93	1.48	2.07	25.2	32	262	261	1726	7094	talin 1	Cytoskeletal protein binding	Extracellular	Cytoskeletal associated protein	Cell growth and/or maintenance	B41;CC	Yes
NOP56	10528	nucleolar protein 56	NP_006383.2	1	27	27	88	1.03	0.93	1.84	4.13	13.2	27.2	48	48	10119	10528	nucleolar protein 5A (56kDa with KKE/D repeat)	Molecular function unknown	Nucleolus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
AGAP3	116988	arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 isoform a	NP_114152.3	5	2	2	4	1.03	0.92	9.05	5.59	13.2	7.3	2	2	16707	116988	centaurin, gamma 3	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	Small_GTPase;PH;ARFGAP;ANK	Yes
RABGEF1	27342	rab5 GDP/GTP exchange factor isoform b	NP_001273990.1	2	1	1	1	1.03	0.92					1	1	11477	27342	RAB guanine nucleotide exchange factor (GEF)1	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	ZnFA20;VPS9;CC;C-C	Yes
UBR4	23352	E3 ubiquitin-protein ligase UBR4	NP_065816.2	1	40	40	91	1.03	0.92	3.18	2.92	23	18.8	48	48	10184	23352	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
AAGAB	79719	alpha- and gamma-adaptin-binding protein p34 isoform 1	NP_078942.3	1	2	2	6	1.03	0.91	8.99	12.39	16.1	19.7	3	3	7754	79719	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
CNIH4	29097	protein cornichon homolog 4 isoform 1	NP_054903.1	3	1	1	3	1.03	0.9	1.07	48.73	1.6	68.5	2	2	13709	29097	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No

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PARD3	56288	partitioning defective 3 homolog isoform 3	NP_001171715.1	11	7	7	13	1.03	0.9	15.36	6.98	50.2	19	9	9	5994	56288	par-3 partitioning defective 3 homolog (C.elegans)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PDZ;CC	Yes
MED20	9477	mediator of RNA polymerase II transcription subunit 20 isoform 1	NP_004266.2	3	3	3	5	1.03	0.9	6.79	11.16	12.1	17.6	3	3	15638	9477	Trf (TATA binding protein-relatedfactor)-proximal homolog (Drosophila)	Transcription regulator activity	-	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	NP_005487.3	2	12	12	21	1.03	0.9	6.23	8.01	23.4	26.6	13	13	9276	10051	SMC4 structural maintenance of chromosomes4-like 1 (yeast)	Structural constituent of chromatin	Nucleus	Structural protein	Chromosome organization and biogenesis (sensu Eukarya)	CC	Yes
NAE1	8883	NEDD8-activating enzyme E1 regulatory subunit isoform d	NP_001273429.1	4	11	11	25	1.03	0.89	4.47	9.43	17.4	32.2	14	14	4545	8883	amyloid beta precursor protein binding protein1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
MED19	219541	mediator of RNA polymerase II transcription subunit 19	NP_703151.1	1	1	1	2	1.03	0.87					1	1	17477	219541	mediator of RNA polymerase II transcription,subunit 19 homolog (yeast)	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	-	No
SEC62	7095	translocation protein SEC62	NP_003253.1	1	4	4	7	1.03	0.85	11.75	5.07	27.5	9.6	5	5	3706	7095	translocation protein 1	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Protein metabolism	CC;TM	No
GNL2	29889	nucleolar GTP-binding protein 2	NP_037417.1	1	3	3	4	1.03	0.84	0.07	0.98	0.1	1.4	3	3	11006	29889	guanine nucleotide binding protein-like 2(nucleolar)	GTPase activity	Nucleolus	GTPase	Cell communication;Signal transduction	CC	Yes
FCF1	51077	rRNA-processing protein FCF1 homolog	NP_057046.1	1	1	1	2	1.03	0.83					1	1	12633	51077	chromosome 14 open reading frame 111	Ribonuclease activity	Nucleolus	Ribonuclease	Biological_process unknown	PINc	No
TANC2	26115	protein TANC2	NP_079461.2	1	3	3	5	1.03	0.82	3.93	8.27	7	11.8	3	3	10894	26115	None	Molecular function unknown	-	Unclassified	Biological_process unknown	ANK;TPR	No
NIPSNAP1	8508	protein NipSnap homolog 1 isoform 1	NP_003625.2	2	3	3	7	1.03	0.8	1.77	3.04	3.7	4.9	4	4	10342	8508	nipsnap homolog 1 (C. elegans)	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	Yes
NDUFV3	4731	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial isoform a precursor	NP_066553.3	1	2	2	2	1.03	0.78	17.55	13.69	25.9	15.1	2	2	3716	4731	NADH dehydrogenase (ubiquinone) flavoprotein3, 10kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
TRMT2A	27037	tRNA (uracil-5-)-methyltransferase homolog A isoform a	NP_892029.2	2	2	2	3	1.03	0.73					1	1	13719	27037	None	Molecular function unknown	-	Unclassified	Biological_process unknown	RRM	Yes
AGPAT5	55326	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	NP_060831.2	1	5	5	11	1.03	0.72	15.3	22.55	40.2	41.3	6	6	12438	55326	1-acylglycerol-3-phosphate O-acyltransferase 5(lysophosphatidic acid acyltransferase, epsilon)	Transferase activity	Integral to membrane	Enzyme: Transferase	Metabolism;Energy pathways	TM;PISC	Yes
TEFM	79736	transcription elongation factor, mitochondrial	NP_078959.3	1	2	2	3	1.03	0.51					1	1									
GTF2F2	2963	general transcription factor IIF subunit 2	NP_004119.1	1	3	3	3	1.02	1.85	2.45	23.43	4.3	87.1	3	3	1804	2963	general transcription factor IIF, polypeptide2, 30kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SF1	7536	splicing factor 1 isoform 6	NP_001171501.1	6	8	8	16	1.02	1.78	6.63	8.48	19.3	44.8	8	8	3306	7536	splicing factor 1	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH;ZnF_C2HC;NLS	Yes
PSMA6	5687	proteasome subunit alpha type-6 isoform a	NP_002782.1	3	9	9	25	1.02	1.57	3.35	4.37	11.9	24.1	12	12	4171	5687	proteasome (prosome, macropain) subunit, alphatype, 6	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
GON4L	54856	GON-4-like protein isoform c	NP_001269785.1	2	1	1	2	1.02	1.55					1	1	13370	54856	None	DNA binding	Nucleus	DNA binding protein	Biological_process unknown	SANT	Yes
RABGAP1L	9910	rab GTPase-activating protein 1-like isoform A	NP_055672.3	1	1	1	1	1.02	1.49					1	1	16464	9910	RAB GTPase activating protein 1-like	GTPase activator activity	-	GTPase activating protein	Biological_process unknown	PTB;TBC	No
DHFR	1719	dihydrofolate reductase isoform 1	NP_000782.1	2	1	1	2	1.02	1.4					1	1	519	1719	dihydrofolate reductase	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
HMGCS1	3157	hydroxymethylglutaryl-CoA synthase, cytoplasmic	NP_001091742.1	3	15	15	54	1.02	1.38	5.69	3.51	32.1	26.5	29	29	7515	3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase1 (soluble)	CoA-ligase activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
RRM1	6240	ribonucleoside-diphosphate reductase large subunit	NP_001024.1	1	16	16	41	1.02	1.37	5.03	5.46	21.4	31.7	17	17	1588	6240	ribonucleotide reductase M1 polypeptide	Oxidoreductase activity	Cytoplasm	Cell cycle control protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 1	NP_976225.1	2	5	5	7	1.02	1.34	2.68	10.94	6.1	33.7	5	5	9185	9406	zinc finger protein 265	RNA binding	Nucleus;Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_RBZ;NLS	Yes
CELF1	10658	CUGBP Elav-like family member 1 isoform 4	NP_001166110.1	9	5	5	7	1.02	1.34	18.81	24.99	39.8	75.1	4	4									
SPTBN2	6712	spectrin beta chain, non-erythrocytic 2	NP_008877.1	1	5	9	20	1.02	1.32	4.89	13.13	11.2	40.2	5	5	5404	6712	spectrin, beta, non-erythrocytic 2	Cytoskeletal protein binding	Golgi apparatus	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;SPECTRIN;PH;CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
ASCC1	51008	activating signal cointegrator 1 complex subunit 1 isoform a	NP_001185728.1	2	1	1	2	1.02	1.31					1	1	12497	51008	activating signal cointegrator 1 complexsubunit 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
ENO2	2026	gamma-enolase	NP_001966.1	1	6	8	53	1.02	1.29	7.96	6.06	26	25.1	10	10	573	2026	enolase 2 (gamma, neuronal)	Catalytic activity	Cytoplasm	Enzyme: Hydratase	Metabolism;Energy pathways	-	Yes
PSMC6	5706	26S protease regulatory subunit 10B	NP_002797.3	1	16	16	66	1.02	1.26	4.35	4.3	26.7	32.8	35	35	4086	5706	proteasome (prosome, macropain) 26S subunit,ATPase, 6	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	AAA;CC	Yes
CTR9	9646	RNA polymerase-associated protein CTR9 homolog	NP_055448.1	1	3	3	5	1.02	1.26	1.27	0.72	2.2	1.6	3	3	6717	9646	SH2 domain binding protein 1(tetratricopeptide repeat containing)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TPR;CC	No
TNPO1	3842	transportin-1 isoform 1	NP_002261.3	2	18	22	80	1.02	1.25	6.08	5.66	36.8	42.4	33	33	4210	3842	transportin 1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	IBN_NT;ARM;HEAT	Yes
PSMD13	5719	26S proteasome non-ATPase regulatory subunit 13 isoform 1	NP_002808.3	2	20	20	85	1.02	1.24	3.21	3.5	21.9	29.3	44	44	4595	5719	proteasome (prosome, macropain) 26S subunit,non-ATPase, 13	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	PCI	Yes
ATXN2L	11273	ataxin-2-like protein isoform C	NP_680780.1	7	14	15	24	1.02	1.22	3.75	2.13	15.8	10.8	17	17	6394	11273	ataxin 2-like	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	Yes
SYS1	90196	protein SYS1 homolog isoform a	NP_291020.1	1	1	1	1	1.02	1.22					1	1									
CHM	1121	rab proteins geranylgeranyltransferase component A 1 isoform a	NP_000381.1	1	1	1	1	1.02	1.21					1	1	2312	1121	choroideremia (Rab escort protein 1)	Transaminase activity	Cytoplasm	Enzyme: Prenyltransferase	Metabolism;Energy pathways	-	Yes
KIF3A	11127	kinesin-like protein KIF3A isoform 1	NP_001287720.1	6	6	8	15	1.02	1.21	5.29	8.99	12.1	24.7	5	5	5250	11127	kinesin family member 3A	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	KISC;CC	Yes
TARDBP	23435	TAR DNA-binding protein 43	NP_031401.1	1	6	6	29	1.02	1.2	1.89	5.67	7.2	25.8	14	14	5466	23435	TAR DNA binding protein	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
SNRPD2	6633	small nuclear ribonucleoprotein Sm D2 isoform 1	NP_004588.1	2	9	9	35	1.02	1.19	13.59	8.05	60	39.7	16	16	3038	6633	small nuclear ribonucleoprotein D2 polypeptide16.5kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
MRPS30	10884	28S ribosomal protein S30, mitochondrial	NP_057724.2	1	2	2	11	1.02	1.19	10.04	12.31	25.6	33.6	6	5	17597	10884	mitochondrial ribosomal protein S30	Structural molecule activity	Mitochondrion	Structural protein	Protein metabolism	-	Yes
YEATS4	8089	YEATS domain-containing protein 4 isoform 1	NP_006521.1	2	1	1	1	1.02	1.19					1	1	3666	8089	YEATS domain containing 4	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform a	NP_115593.3	3	7	14	39	1.02	1.18	6.57	4.9	16.5	14.2	6	6	10648	26057	ankyrin repeat domain 17	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;ANK;KH	Yes
ABCB1	5243	multidrug resistance protein 1	NP_000918.2	1	1	1	1	1.02	1.18					1	1	1370	5243	ATP-binding cassette, sub-family B (MDR/TAP),member 1	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM;AAA;CC	Yes
PPIP5K2	23262	inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 isoform 3	NP_001268400.1	3	3	4	11	1.02	1.18	19.56	11.38	41.6	27.4	4	4	13802	23262	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
DPYSL3	1809	dihydropyrimidinase-related protein 3 isoform 1	NP_001184223.1	2	14	17	45	1.02	1.17	6.72	2.43	28.1	11.4	16	16	3104	1809	dihydropyrimidinase-like 3	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
THUMPD1	55623	THUMP domain-containing protein 1	NP_060206.2	1	7	7	19	1.02	1.17	3.54	4.22	10.2	14	8	8	8619	55623	THUMP domain containing 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
DDX3X	1654	ATP-dependent RNA helicase DDX3X isoform 1	NP_001347.3	5	21	24	73	1.02	1.16	3.96	3.35	22.9	21.8	31	31	2154	1654	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3,X-linked	RNA binding	Nucleus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
RBM10	8241	RNA-binding protein 10 isoform 5	NP_001191397.1	5	11	12	21	1.02	1.16	6.18	3.44	20.2	12.7	10	10	2095	8241	RNA binding motif protein 10	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;ZnF_RBZ;G_PATCH;CC;ZNFC2	Yes
TMEM41A	90407	transmembrane protein 41A precursor	NP_542383.1	1	2	2	4	1.02	1.16	0.23	5.08	0.4	10.2	3	3	15539	90407	transmembrane protein 41A	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM;SP	No
SRRT	51593	serrate RNA effector molecule homolog isoform a	NP_056992.4	4	19	19	58	1.02	1.15	3.64	2.6	19.9	15.9	28	28	10665	51593	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;RRM	Yes
DNAAF2	55172	protein kintoun isoform 1	NP_060609.2	2	1	1	2	1.02	1.14					1	1									
SMAD5	4090	mothers against decapentaplegic homolog 5	NP_005894.3	2	2	3	6	1.02	1.13	16.95	38.26	24.7	67.1	2	2	4381	4090	SMAD, mothers against DPP homolog 5(Drosophila)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MH2;MH1;CC	No
LLPH	84298	protein LLP homolog	NP_115714.1	1	1	1	4	1.02	1.13	7.07	7.34	10.2	11.8	2	2	11308	84298	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RAB6A	5870	ras-related protein Rab-6A isoform a	NP_002860.2	15	1	10	79	1.02	1.13	13.19	14.73	19.1	24	2	2	1543	5870	RAB6A, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB	No

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KIF21A	55605	kinesin-like protein KIF21A isoform 1	NP_001166935.1	9	3	4	9	1.02	1.12	3.85	5.24	5.6	8.3	2	2	10506	55605	kinesin family member 21A	Motor activity	Cytoplasm;Nucleus	Motor protein	Cell growth and/or maintenance	WD40;CC;KISC	Yes
EXOSC4	54512	exosome complex component RRP41	NP_061910.1	1	2	2	4	1.02	1.12	7.66	14.18	11.1	22.7	2	2	16221	54512	exosome component 4	Ribonuclease activity	Nucleolus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
FLAD1	80308	FAD synthase isoform 1	NP_079483.3	4	5	5	8	1.02	1.1	1.69	12.5	3.8	31.5	5	5	17887	80308	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
GIPC1	10755	PDZ domain-containing protein GIPC1 isoform 1	NP_005707.1	2	3	3	5	1.02	1.09	15.81	6.02	28.5	11.4	3	3	5462	10755	regulator of G-protein signalling 19interacting protein 1	Binding	Cytoplasm	Unclassified	Signal transduction	PDZ	Yes
UHRF1	29128	E3 ubiquitin-protein ligase UHRF1 isoform 2	NP_037414.3	2	1	1	2	1.02	1.09					1	1	6992	29128	ubiquitin-like, containing PHD and RING fingerdomains, 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBQ;NLS;RING;PHD;LZ	No
RPN1	6184	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor	NP_002941.1	1	38	38	135	1.02	1.09	3.79	2.93	33.7	27.6	72	72	1598	6184	ribophorin I	Ubiquitin-specific protease activity	Endoplasmic reticulum;Nucleus;Cytosol	Ubiquitin proteasome system protein	Protein metabolism	SP;CC;TM	Yes
RAD21	5885	double-strand-break repair protein rad21 homolog	NP_006256.1	2	8	8	16	1.02	1.08	13.25	3.95	39.8	11.3	8	7	5924	5885	RAD21 homolog (S. pombe)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MRM1	79922	rRNA methyltransferase 1, mitochondrial precursor	NP_079140.2	1	1	1	2	1.02	1.08					1	1	8656	79922	None	Methyltransferase activity	-	RNA methyltransferase	Biological_process unknown	-	No
COG3	83548	conserved oligomeric Golgi complex subunit 3	NP_113619.2	1	7	7	13	1.02	1.07	17.13	9.41	48.7	27.2	7	7	8443	83548	component of oligomeric golgi complex 3	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	CC;LZ	Yes
RPA1	6117	replication protein A 70 kDa DNA-binding subunit	NP_002936.1	1	13	13	29	1.02	1.06	2.85	4.99	12	22.1	17	17	1565	6117	replication protein A1, 70kDa	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TRNAA	Yes
GLMN	11146	glomulin	NP_444504.1	1	5	5	8	1.02	1.06	12.51	0.42	29.2	1	5	5	3451	11146	glomulin, FKBP associated protein	Receptor binding;Protein domain specific binding	Cytoplasm	Unclassified;Ligand	Cell communication;Signal transduction;Regulation of cell proliferation	-	Yes
ZNFX1	57169	NFX1-type zinc finger-containing protein 1	NP_066363.1	1	6	6	8	1.02	1.05	0.09	3.67	0.2	7.7	4	4	11142	57169	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
UFSP2	55325	ufm1-specific protease 2	NP_060829.2	1	2	2	6	1.02	1.05	0.29	0.98	0.5	1.8	3	3	7741	55325	None	Peptidase activity	-	Protease	Protein metabolism	-	Yes
CLPX	10845	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial precursor	NP_006651.2	1	12	12	32	1.02	1.04	3.09	5.49	11.4	20.9	13	13	7478	10845	ClpX caseinolytic protease X homolog (E. coli)	Peptidase activity	Mitochondrion	Protease	Protein metabolism	AAA;SP	Yes
MRPL15	29088	39S ribosomal protein L15, mitochondrial	NP_054894.1	1	7	7	18	1.02	1.03	8.74	5.13	28.8	16.9	10	10	14742	29088	mitochondrial ribosomal protein L15	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	No
LNPEP	4012	leucyl-cystinyl aminopeptidase isoform 1	NP_005566.2	2	11	11	21	1.02	1.03	2.13	13.58	7.6	51.2	12	12	1041	4012	leucyl/cystinyl aminopeptidase	Aminopeptidase activity	Plasma membrane	Aminopeptidase	Protein metabolism	TM	Yes
CLCC1	23155	chloride channel CLIC-like protein 1 isoform 1 precursor	NP_001041675.1	4	2	2	4	1.02	1.02	2.27	1.89	3.3	2.7	2	2	17471	23155	None	Ion channel activity	Endoplasmic reticulum	Ion channel	Transport	TM;SP	No
SMCHD1	23347	structural maintenance of chromosomes flexible hinge domain-containing protein 1	NP_056110.2	1	8	8	12	1.02	1.02	6.75	4.65	16.9	11.6	6	6	19413	23347	structural maintenance of chromosomes flexible hinge domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 6	NP_001181875.1	7	37	41	160	1.02	1.02	2.66	3.23	21.1	26	59	60	6774	1981	eukaryotic translation initiation factor 4gamma, 1	Translation regulator activity	Nucleus;Cytoplasm	Translation regulatory protein	Protein metabolism	CC;MIF4G;NLS;MA3	Yes
XRN2	22803	5'-3' exoribonuclease 2	NP_036387.2	1	17	17	38	1.02	1.02	6.27	3.67	30.6	17.7	22	22	10309	22803	5`-3` exoribonuclease 2	Ribonuclease activity	Nucleolus;Nucleus;Cytoplasm	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C2HC	Yes
STAM2	10254	signal transducing adapter molecule 2	NP_005834.4	1	2	2	10	1.02	1.02	4.18	3.48	9.6	7.9	5	5	5876	10254	signal transducing adaptor molecule (SH3 domainand ITAM motif) 2	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	VHS;UIM;SH3;ITAM;CC	No
STK24	8428	serine/threonine-protein kinase 24 isoform a precursor	NP_003567.2	3	9	14	38	1.02	1.01	8.38	11.85	29.1	41.1	11	11	10385	8428	serine/threonine kinase 24 (STE20 homolog,yeast)	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Signal transduction	S_T_kinase;CC;NLS	Yes
KDM3B	51780	lysine-specific demethylase 3B	NP_057688.2	1	8	8	17	1.02	1	7.03	8.65	20.5	23.1	8	7	11055	51780	jumonji domain containing 1B	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	JMJC	Yes
KDM1A	23028	lysine-specific histone demethylase 1A isoform a	NP_001009999.1	2	8	8	19	1.02	1	2.71	9.95	9.6	35.6	12	12	9800	23028	amine oxidase (flavin containing) domain 2	Transcription regulator activity;Deacetylase activity	Nucleus;Cytoplasm	Enzyme: Deacetylase;Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
C12orf29	91298	uncharacterized protein C12orf29	NP_001009894.2	1	1	1	2	1.02	1					1	1	13199	91298	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
GNAS	2778	protein GNAS isoform XLas	NP_536350.2	12	8	9	53	1.02	0.99	4.59	6.19	17.7	23.1	14	14	761	2778	GNAS complex locus	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	CC;SP;ARF	No
LRRC59	55379	leucine-rich repeat-containing protein 59	NP_060979.2	1	12	12	59	1.02	0.99	5.36	4.58	30.6	25.2	30	30	15181	55379	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	LRR;CC;TM	No
ANXA7	310	annexin A7 isoform 2	NP_004025.1	2	17	17	64	1.02	0.99	4.31	4.14	23	21.6	27	27	1720	310	annexin A7	Calcium ion binding	Nucleus	Calcium binding protein	Transport	ANX	Yes
FAHD1	81889	acylpyruvase FAHD1, mitochondrial isoform 1	NP_001018114.1	3	6	6	24	1.02	0.99	10.85	10.37	38	35	11	11	13286	81889	fumarylacetoacetate hydrolase domain containing1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
DIAPH1	1729	protein diaphanous homolog 1 isoform 1	NP_005210.3	2	32	32	157	1.02	0.98	1.95	2.52	17.1	21.3	73	73	3670	1729	diaphanous homolog 1 (Drosophila)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	FH2;CC	Yes
SLC25A24	29957	calcium-binding mitochondrial carrier protein SCaMC-1 isoform 1	NP_037518.3	2	17	17	56	1.02	0.98	6.12	8.62	34.7	47.1	29	28	12290	29957	solute carrier family 25 (mitochondrialcarrier; phosphate carrier), member 24	Transporter activity	Mitochondrial membrane	Transport/cargo protein	Transport	EF;TM	No
TBC1D9B	23061	TBC1 domain family member 9B isoform a	NP_942568.2	2	7	7	10	1.02	0.97	13.43	10.34	34.6	25	6	6	10015	23061	None	Molecular function unknown	-	Unclassified	Biological_process unknown	GRAM;EF	Yes
BID	637	BH3-interacting domain death agonist isoform 1	NP_932070.1	3	5	5	20	1.02	0.96	14.24	14.7	48.5	49.6	10	11	3590	637	BH3 interacting domain death agonist	Receptor binding	Mitochondrion	Ligand	Apoptosis	SP	Yes
MARS	4141	methionine--tRNA ligase, cytoplasmic	NP_004981.2	1	22	22	86	1.02	0.95	3.71	4.83	25.1	30.6	43	42	8864	4141	methionine-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
UXS1	80146	UDP-glucuronic acid decarboxylase 1 isoform 1	NP_001240804.1	3	3	3	4	1.02	0.94	4.49	34.23	6.4	48.1	2	2	15642	80146	UDP-glucuronate decarboxylase 1	Carboxy-lyase activity	Golgi apparatus	Enzyme: Decarboxylase	Metabolism;Energy pathways	TM	No
EXOSC10	5394	exosome component 10 isoform 1	NP_001001998.1	2	15	15	25	1.02	0.94	3.36	8.36	12.9	30.1	14	14	16180	5394	exosome component 10	Protein serine/threonine kinase activity	Nucleolus	Unclassified	Biological_process unknown	35EXO;HRDC	Yes
LBR	3930	lamin-B receptor	NP_919424.1	1	4	4	8	1.02	0.93	5.36	4.26	11	7.9	4	4	2488	3930	lamin B receptor	Chromatin binding	Nuclear membrane	Integral membrane protein	Cytoskeletal anchoring	TUDOR;TM	Yes
KIAA1279	26128	KIF1-binding protein	NP_056449.1	1	3	3	5	1.02	0.93	16.19	37.83	23.7	53.2	2	2	13848	26128	KIAA1279	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
PFKM	5213	ATP-dependent 6-phosphofructokinase, muscle type isoform 1	NP_001160158.1	2	19	21	64	1.02	0.93	4.52	5.09	25.7	26.4	30	30	1988	5213	phosphofructokinase, muscle	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	SP	Yes
RPL7L1	285855	60S ribosomal protein L7-like 1	NP_940888.2	1	4	4	6	1.02	0.92	4.1	6.71	8.4	12.4	4	4	18000	285855	ribosomal protein L7-like 1	Structural constituent of ribosome	-	Ribosomal subunit	Protein metabolism	-	Yes
FIBP	9158	acidic fibroblast growth factor intracellular-binding protein isoform a	NP_942600.1	2	2	2	3	1.02	0.92	5.62	12.11	8.1	15.8	2	2	8492	9158	fibroblast growth factor (acidic) intracellularbinding protein	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	-	Yes
ATXN2	6311	ataxin-2	NP_002964.3	1	1	1	2	1.02	0.91					1	1	3307	6311	ataxin 2	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
HIST1H2BL	8340	histone H2B type 1-L	NP_003510.1	15	3	10	548	1.02	0.9	3.68	2.66	12	7.6	10	10	11898	8340	histone 1, H2bl	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H2B	Yes
SEC24C	9632	protein transport protein Sec24C	NP_004913.2	1	16	16	55	1.02	0.9	3.78	5.18	19.5	23.7	25	25	6217	9632	SEC24 related gene family, member C (S.cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	GEL	Yes
MICALL1	85377	MICAL-like protein 1	NP_203744.1	1	15	16	37	1.02	0.89	2.8	11.55	13.1	49.9	21	21	11363	85377	None	Structural constituent of cytoskeleton	-	Cytoskeletal protein	Cell communication;Signal transduction	CH;LIM;CC	Yes
TMOD3	29766	tropomodulin-3	NP_055362.1	1	8	10	28	1.02	0.89	4.24	3.28	15.7	10.5	13	13	10389	29766	tropomodulin 3 (ubiquitous)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
NGFR	4804	tumor necrosis factor receptor superfamily member 16 precursor	NP_002498.1	1	1	1	2	1.02	0.88					1	1	1197	4804	nerve growth factor receptor (TNFR superfamily,member 16)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;TNFR;TM;DEATH	Yes
SRP68	6730	signal recognition particle subunit SRP68 isoform 1	NP_055045.2	3	22	22	64	1.02	0.87	4.31	3.97	26	20.5	34	34	5331	6730	signal recognition particle 68kDa	RNA binding	Nucleolus	RNA binding protein	Protein metabolism	-	Yes
PCCA	5095	propionyl-CoA carboxylase alpha chain, mitochondrial isoform a precursor	NP_000273.2	3	3	3	4	1.02	0.87	15.44	17.51	22.5	21.9	2	2	1981	5095	propionyl Coenzyme A carboxylase, alphapolypeptide	Ligase activity	Mitochondrion	Enzyme: Carboxylase	Metabolism;Energy pathways	SP	Yes
SOD1	6647	superoxide dismutase [Cu-Zn]	NP_000445.1	1	3	3	4	1.02	0.86	22.3	14.22	40.8	21.5	3	3	937	6647	superoxide dismutase 1, soluble (amyotrophiclateral sclerosis 1 (adult))	Superoxide dismutase activity	Cytoplasm	Enzyme: Superoxide dismutase	Metabolism;Energy pathways	-	Yes
OPLAH	26873	5-oxoprolinase	NP_060040.1	1	9	9	17	1.02	0.85	3.67	9.76	11.3	25.3	9	9	14880	26873	5-oxoprolinase (ATP-hydrolysing)	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
CUL3	8452	cullin-3 isoform 3	NP_001244127.1	3	12	12	25	1.02	0.84	7.7	8.05	32.3	27.5	16	16	9123	8452	cullin 3	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CULL	Yes
EIF2AK4	440275	eukaryotic translation initiation factor 2-alpha kinase 4	NP_001013725.2	1	1	1	1	1.02	0.84					1	1	18447	440275	eukaryotic translation initiation factor 2alpha kinase 4	Transmembrane receptor protein tyrosine kinase activity	Cytoplasm	Receptor tyrosine kinase	Cell communication;Signal transduction	RWD;S_T_Y_Kinase;CC	No
MICU1	10367	calcium uptake protein 1, mitochondrial isoform 1	NP_006068.2	3	2	2	4	1.02	0.83	4.99	1.24	7.2	1.5	2	2									

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YWHAH	7533	14-3-3 protein eta	NP_003396.1	1	12	15	110	1.02	0.83	7.07	11.75	37.3	51.5	25	25	215	7533	tyrosine 3-monooxygenase/tryptophan5-monooxygenase activation protein, eta polypeptide	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
DSC2	1824	desmocollin-2 isoform Dsc2a preproprotein	NP_077740.1	2	3	3	6	1.02	0.8	19.94	13.44	42.3	21.7	4	4	512	1824	desmocollin 2	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	SP;Cadherin;TM	Yes
CARS2	79587	probable cysteine--tRNA ligase, mitochondrial	NP_078813.1	1	9	9	19	1.02	0.79	4.96	6.14	16	15.5	10	10	7763	79587	None	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism	-	Yes
RBM34	23029	RNA-binding protein 34 isoform 1	NP_055829.2	2	2	2	4	1.02	0.79	5.74	15.39	8.3	17.4	2	2	11065	23029	RNA binding motif protein 34	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
DERL1	79139	derlin-1 isoform a	NP_077271.1	2	1	1	2	1.02	0.79					1	1	12302	79139	Der1-like domain family, member 1	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	TM	Yes
KIF2C	11004	kinesin-like protein KIF2C isoform 1	NP_006836.2	4	2	4	6	1.02	0.78					1	1	5172	11004	kinesin family member 2C	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	CC;NLS	Yes
LEMD3	23592	inner nuclear membrane protein Man1 isoform 1	NP_055134.2	2	10	10	19	1.02	0.77	6.54	14.68	22.3	38.7	11	11	9704	23592	LEM domain containing 3	Nucleotide binding	Nucleus	Integral membrane protein	Immune response	TM	Yes
YIPF6	286451	protein YIPF6 isoform A	NP_776195.2	1	1	1	2	1.02	0.77					1	1	6639	286451	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
PCNP	57092	PEST proteolytic signal-containing nuclear protein	NP_065090.1	1	4	4	7	1.02	0.76	8.46	42.19	19.5	81.6	5	5	17826	57092	None	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	-	No
BRCC3	79184	lys-63-specific deubiquitinase BRCC36 isoform 3	NP_001229569.1	3	3	3	4	1.02	0.74					1	1	6465	79184	chromosome X open reading frame 53	Ligase activity	-	Ubiquitin proteasome system protein	Protein metabolism	JAB;CC	Yes
EIF3H	8667	eukaryotic translation initiation factor 3 subunit H	NP_003747.1	1	12	12	33	1.02	0.73	3.02	11.18	12.4	33.7	16	16	4885	8667	eukaryotic translation initiation factor 3,subunit 3 gamma, 40kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism;Translation	JAB	Yes
AKAP9	10142	A-kinase anchor protein 9 isoform 2	NP_005742.4	2	5	5	9	1.02	0.7	12.63	7.84	22.6	9.6	3	3	4921	10142	A kinase (PRKA) anchor protein (yotiao) 9	Receptor signaling complex scaffold activity	Centrosome	Adapter molecule	Cell communication;Signal transduction	CC	Yes
PLEKHO2	80301	pleckstrin homology domain-containing family O member 2 isoform 1	NP_079477.2	2	4	4	12	1.02	0.69	12.43	10.22	31.8	17.4	6	6	15910	80301	None	Molecular function unknown	-	Unclassified	Biological_process unknown	PH	No
TFG	10342	protein TFG isoform 1	NP_006061.2	2	7	7	31	1.02	0.67	7.94	12.45	35.3	36.4	18	18	3932	10342	TRK-fused gene	Receptor regulator activity	Cytoplasm	Enzyme regulator	Signal transduction	PB1;CC	Yes
IDH3G	3421	isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial isoform a precursor	NP_004126.1	2	3	3	8	1.02	0.65	4.35	13.97	8.9	18.4	4	4	2100	3421	isocitrate dehydrogenase 3 (NAD+) gamma	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
ARFRP1	10139	ADP-ribosylation factor-related protein 1 isoform a	NP_003215.1	5	2	2	3	1.01	1.5	18.77	8.45	27.3	18.1	2	2	5264	10139	ADP-ribosylation factor related protein 1	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	ARF	Yes
GRN	2896	granulins precursor	NP_002078.1	1	4	4	5	1.01	1.43	9.33	4.45	19.1	12.8	4	4	733	2896	granulin	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	GRAN;SP	Yes
ANXA11	311	annexin A11 isoform 1	NP_001148.1	4	13	13	49	1.01	1.42	4.01	3.39	19.2	22.9	22	22	3983	311	annexin A11	Calcium ion binding	Cytoplasm	Calcium binding protein	Signal transduction;Cell communication	ANX	Yes
PSMA2	5683	proteasome subunit alpha type-2	NP_002778.1	1	13	13	40	1.01	1.36	4.93	6.55	23.7	43.6	22	22	8907	5683	proteasome (prosome, macropain) subunit, alphatype, 2	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
SF3A1	10291	splicing factor 3A subunit 1	NP_005868.1	1	21	21	51	1.01	1.34	5.2	6.85	27.2	48.3	26	25	6903	10291	splicing factor 3a, subunit 1, 120kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBQ;SWAP	Yes
TUBB6	84617	tubulin beta-6 chain isoform 1	NP_115914.1	6	14	27	337	1.01	1.33	5.53	5.44	54.5	73.5	83	83	11349	84617	tubulin, beta 6	Structural constituent of cytoskeleton	-	Cytoskeletal protein	Cell growth and/or maintenance	TUBULIN	Yes
SH3GLB2	56904	endophilin-B2 isoform b	NP_064530.1	2	3	4	6	1.01	1.28	4.05	15.55	5.8	28.6	2	2	15334	56904	SH3-domain GRB2-like endophilin B2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	BAR;SH3	Yes
VTI1B	10490	vesicle transport through interaction with t-SNAREs homolog 1B	NP_006361.1	1	2	2	7	1.01	1.25	12.73	6.73	22.6	14.6	3	3	4440	10490	vesicle transport through interaction witht-SNAREs homolog 1B (yeast)	Molecular function unknown	Cytoplasmic vesicle	Unclassified	Transport	TM;CC;t_SNARE	No
PRPF4	9128	U4/U6 small nuclear ribonucleoprotein Prp4 isoform 1	NP_004688.2	2	10	10	18	1.01	1.25	4.44	3.77	15	15.7	11	11	8479	9128	PRP4 pre-mRNA processing factor 4 homolog(yeast)	Ribonucleoprotein	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
TCEA1	6917	transcription elongation factor A protein 1 isoform 1	NP_006747.1	2	5	5	9	1.01	1.24	9.09	2.36	20.8	6.5	5	5	3252	6917	transcription elongation factor A (SII), 1	Transcription regulator activity	Nucleus;Cytoplasm	Transcription factor	Transcription	TFS;TFS2M;ZnF_C2C2	Yes
PFDN6	10471	prefoldin subunit 6	NP_001172110.1	1	1	1	2	1.01	1.23					1	1	16135	10471	HLA class II region expressed gene KE2	Chaperone activity	-	Chaperone	Protein metabolism	CC	Yes
CHID1	66005	chitinase domain-containing protein 1 isoform b precursor	NP_001136148.1	3	7	7	15	1.01	1.22	6.77	3.88	19.5	13.4	8	8	14550	66005	None	Transporter activity	Lysosome	Transport/cargo protein	Transport;Cell proliferation;Cell activation;Cell differentiation	SP	No

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IMP3	55272	U3 small nucleolar ribonucleoprotein protein IMP3	NP_060755.1	1	2	2	6	1.01	1.21	4.55	4.67	8	9.8	3	3	12664	55272	chromosome 15 open reading frame 12	Ribonucleoprotein	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S4	Yes
POP1	10940	ribonucleases P/MRP protein subunit POP1	NP_055844.2	1	9	9	17	1.01	1.2	8.54	4.55	26.4	16.5	9	9	3923	10940	processing of precursor 1, ribonuclease P/MRPsubunit (S. cerevisiae)	Ribonuclease activity	Nucleolus	Regulatory/other subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
KPNA3	3839	importin subunit alpha-4	NP_002258.2	1	8	12	47	1.01	1.19	2.07	4.23	7.6	18.3	13	13	3536	3839	karyopherin alpha 3 (importin alpha 4)	Transporter activity	Nucleus	Transport/cargo protein	Transport	ARM	Yes
TTI1	9675	TELO2-interacting protein 1 homolog	NP_055472.1	1	2	2	4	1.01	1.18	10.51	15.25	15.1	25.9	2	2									
ZFYVE9	9372	zinc finger FYVE domain-containing protein 9 isoform 3	NP_004790.2	2	1	1	1	1.01	1.18					1	1	4782	9372	zinc finger, FYVE domain containing 9	Molecular function unknown	Cytoplasm	Anchor protein	Cell growth and/or maintenance	FYVE	Yes
RETSAT	54884	all-trans-retinol 13,14-reductase precursor	NP_060220.3	1	7	7	12	1.01	1.14	7.93	12.86	21.5	40.1	7	7	7893	54884	None	Catalytic activity	Endoplasmic reticulum membrane	Enzyme: Reductase	Vitamin metabolism	SP	No
IST1	9798	IST1 homolog isoform c	NP_001257905.1	5	6	6	12	1.01	1.14	7.91	10.91	21.5	31.3	7	6									
USP7	7874	ubiquitin carboxyl-terminal hydrolase 7 isoform 1	NP_003461.2	3	16	16	32	1.01	1.14	6.76	6.35	31.3	33.2	20	20	3950	7874	ubiquitin specific protease 7 (herpesvirus-associated)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	MATH	Yes
PGM2L1	283209	glucose 1,6-bisphosphate synthase	NP_775853.2	1	3	3	6	1.01	1.13	1.3	24.3	2.3	50.4	3	3	11427	283209	phosphoglucomutase 2-like 1	Catalytic activity	Cytoplasm	Enzyme: Mutase	Metabolism;Energy pathways	-	No
DHTKD1	55526	probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	NP_061176.3	1	5	5	8	1.01	1.13	13.07	16.64	30.1	44.2	5	5	9917	55526	dehydrogenase E1 and transketolase domaincontaining 1	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
SLC2A1	6513	solute carrier family 2, facilitated glucose transporter member 1	NP_006507.2	1	5	5	12	1.01	1.13	9.42	18.12	29.1	67.7	9	9	683	6513	solute carrier family 2 (facilitated glucosetransporter), member 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
TNPO3	23534	transportin-3 isoform 1	NP_036602.1	2	9	9	22	1.01	1.12	13.46	12.37	45.1	45.8	10	10	18209	23534	transportin 3	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor	Cell communication;Signal transduction	ADAP	Yes
PSMD5	5711	26S proteasome non-ATPase regulatory subunit 5 isoform 1	NP_005038.1	2	17	17	69	1.01	1.12	3.77	4.45	22.8	30.3	35	35	5121	5711	proteasome (prosome, macropain) 26S subunit,non-ATPase, 5	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	NPXY	Yes
CUL4A	8451	cullin-4A isoform 1	NP_001008895.1	3	2	7	17	1.01	1.1	10.97	4.37	15.7	6.8	2	2	7218	8451	cullin 4A	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CULL	Yes
SNX6	58533	sorting nexin-6 isoform b	NP_689419.2	2	11	11	33	1.01	1.09	7.43	6.22	30.8	27.7	16	16	12086	58533	sorting nexin 6	Transporter activity	Cytoplasm	Transport/cargo protein	Cell communication;Signal transduction	PX;CC	Yes
TTC26	79989	intraflagellar transport protein 56 isoform 1	NP_079202.2	5	1	1	2	1.01	1.08					1	1	7776	79989	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TPR	No
AK4	205	adenylate kinase 4, mitochondrial	NP_982289.1	1	5	5	11	1.01	1.05	6.89	15.11	18.5	43.7	7	7									
UBE2K	3093	ubiquitin-conjugating enzyme E2 K isoform 1	NP_005330.1	3	7	7	20	1.01	1.04	3.57	5.82	12	20.3	11	11	4165	3093	huntingtin interacting protein 2	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBC;UBA	Yes
NUP85	79902	nuclear pore complex protein Nup85 isoform 1	NP_079120.1	2	5	5	10	1.01	1.03	10.67	14.33	29	40.7	7	7	1363	79902	pericentrin 1	Cytoskeletal anchoring activity	Centrosome	Anchor protein	Cell growth and/or maintenance	-	No
TMEM30A	55754	cell cycle control protein 50A isoform 1	NP_060717.1	2	1	1	1	1.01	1.03					1	1	15535	55754	transmembrane protein 30A	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
MRPS5	64969	28S ribosomal protein S5, mitochondrial	NP_114108.1	1	5	5	7	1.01	1.02	12.35	8.6	25.4	17.7	4	4	10099	64969	mitochondrial ribosomal protein S5	Ribonucleoprotein	Mitochondrion	RNA binding protein	Protein metabolism	SP	Yes
SEC31A	22872	protein transport protein Sec31A isoform 1	NP_001070675.1	8	22	22	62	1.01	1.02	3.84	3.46	21.9	19.9	31	31	15314	22872	SEC31-like 1 (S. cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	WD40	Yes
ARL2	402	ADP-ribosylation factor-like protein 2 isoform 1	NP_001658.2	2	5	5	12	1.01	1.01	4.98	15.93	12.4	41	6	6	11869	402	ADP-ribosylation factor-like 2	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	ARF	Yes
GOPC	57120	Golgi-associated PDZ and coiled-coil motif-containing protein isoform a	NP_065132.1	2	6	6	13	1.01	1.01	6.08	5.85	16.3	15.7	7	7	6024	57120	golgi associated PDZ and coiled-coil motifcontaining	Receptor signaling complex scaffold activity	Golgi apparatus	Unclassified	Biological_process unknown	CC;PDZ	No
MRPL44	65080	39S ribosomal protein L44, mitochondrial	NP_075066.1	1	9	9	31	1.01	1.01	3.42	6.75	13	25.9	14	14	14763	65080	mitochondrial ribosomal protein L44	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	DSRM	Yes
DOHH	83475	deoxyhypusine hydroxylase	NP_112594.1	1	7	7	11	1.01	1.01	5.68	12.47	15.3	34.3	7	7	14627	83475	None	Oxidoreductase activity	-	Enzyme: Hydroxylase	Protein modification	-	No
PLXNA2	5362	plexin-A2 precursor	NP_079455.3	2	4	4	7	1.01	1	6.66	4.18	13.4	8.4	4	4	3033	5362	plexin A2	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;SEMA;PSI;IPT;TM;CC	No
RFC3	5983	replication factor C subunit 3 isoform 1	NP_002906.1	2	5	5	9	1.01	1	1.7	8.73	4.2	21.6	6	6	2676	5983	replication factor C (activator 1) 3, 38kDa	DNA binding	Nucleolus	DNA binding protein	DNA replication	AAA	Yes
CDH3	1001	cadherin-3 preproprotein	NP_001784.2	1	7	10	17	1.01	1	3.64	12.1	10.5	35.1	8	8	227	1001	cadherin 3, type 1, P-cadherin (placental)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	TM;Cadherin;SP	Yes
CYTH2	9266	cytohesin-2 isoform 1	NP_059431.1	6	2	2	6	1.01	0.99	4.79	8.37	8.4	14.5	3	3	3925	9266	pleckstrin homology, Sec7 and coiled-coildomains 2 (cytohesin-2)	Guanyl-nucleotide exchange factor activity	Cytosol	Guanine nucleotide exchange factor	Signal transduction;Regulation of gene expression, epigenetic	CC;Sec7;PH	Yes
SCFD1	23256	sec1 family domain-containing protein 1 isoform a	NP_057190.2	5	14	14	47	1.01	0.99	6.93	3.6	33.9	16.9	22	22	10210	23256	sec1 family domain containing 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
DPF2	5977	zinc finger protein ubi-d4	NP_006259.1	1	5	5	8	1.01	0.99	21.15	7.78	50.6	17.3	5	5	3394	5977	D4, zinc and double PHD fingers family 2	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;PHD	Yes
PAICS	10606	multifunctional protein ADE2 isoform 1	NP_001072993.1	2	19	19	72	1.01	0.99	3.04	7.34	20.7	50.3	44	43	1401	10606	phosphoribosylaminoimidazole carboxylase,phosphoribosylaminoimidazole succinocarboxamide synthetase	Ligase activity	Nucleus	Enzyme: Carboxylase	Metabolism;Energy pathways	-	Yes
PITRM1	10531	presequence protease, mitochondrial isoform 1 precursor	NP_001229236.1	3	23	23	42	1.01	0.99	3.92	4.09	20.4	20.8	26	26	7142	10531	pitrilysin metalloproteinase 1	Metallopeptidase activity	Extracellular	Metallo protease	Protein metabolism	-	Yes
SMG8	55181	protein SMG8	NP_060619.4	1	4	5	7	1.01	0.98	6.79	14.28	12	24.7	3	3									
RBM14	10432	RNA-binding protein 14 isoform 1	NP_006319.1	4	21	21	49	1.01	0.98	5.78	8.88	29.8	46.7	25	26	11485	10432	RNA binding motif protein 14	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
STRN3	29966	striatin-3 isoform 1	NP_001077362.1	2	4	4	8	1.01	0.98	4.7	20.66	9.5	42.3	4	4	11613	29966	striatin, calmodulin binding protein 3	Calcium ion binding	Nucleus	Calcium binding protein	Cell communication;Signal transduction	CC;WD40;NLS	Yes
NDNL2	56160	melanoma-associated antigen G1	NP_619649.1	1	3	3	4	1.01	0.98	0.05	2.5	0.1	3.5	2	2	10503	56160	necdin-like 2	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	MAGE	Yes
Sep-07	989	septin-7 isoform 1	NP_001779.3	4	24	25	84	1.01	0.97	3.51	5.5	20.6	31.5	33	33									
CERS2	29956	ceramide synthase 2	NP_859530.1	1	2	2	3	1.01	0.97	9.76	26.21	14	37.2	2	2									
MRRF	92399	ribosome-recycling factor, mitochondrial isoform 1 precursor	NP_620132.1	3	6	6	17	1.01	0.96	11.88	10.32	39.5	32	10	10	6856	92399	mitochondrial ribosome recycling factor	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	CC	Yes
TIMM21	29090	mitochondrial import inner membrane translocase subunit Tim21 precursor	NP_054896.2	1	2	2	4	1.01	0.96	0.68	11.24	1	15.3	2	2									
RAB34	83871	ras-related protein Rab-34 isoform 5	NP_001138415.1	7	3	3	5	1.01	0.95	3.28	2.39	4.7	3.2	2	2	6701	83871	RAB34, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB;Small_GTPase	Yes
MORF4L1	10933	mortality factor 4-like protein 1 isoform 2	NP_996670.1	2	2	2	2	1.01	0.95	13.79	5.68	19.9	7.7	2	2	9532	10933	mortality factor 4 like 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of gene expression, epigenetic	CHROMO	Yes
NUMA1	4926	nuclear mitotic apparatus protein 1 isoform 1	NP_006176.2	2	69	69	156	1.01	0.95	2.14	2.9	19.9	25.7	83	83	1236	4926	nuclear mitotic apparatus protein 1	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	CC	Yes
PARG	8505	poly(ADP-ribose) glycohydrolase isoform a	NP_003622.2	3	2	2	3	1.01	0.94	12.92	15.98	18.6	21.5	2	2	4611	8505	poly (ADP-ribose) glycohydrolase	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
EIF3E	3646	eukaryotic translation initiation factor 3 subunit E	NP_001559.1	1	14	14	59	1.01	0.94	3.28	4.65	16.6	22.1	25	25	3734	3646	eukaryotic translation initiation factor 3,subunit 6 48kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
SLC38A2	54407	sodium-coupled neutral amino acid transporter 2 isoform 1	NP_061849.2	2	3	3	12	1.01	0.93	7.46	5.02	18.7	11.4	6	6	5535	54407	solute carrier family 38, member 2	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	No
SMC1A	8243	structural maintenance of chromosomes protein 1A isoform 1	NP_006297.2	2	19	19	38	1.01	0.93	4.29	4.99	20.5	22	22	22	2077	8243	SMC1 structural maintenance of chromosomes1-like 1 (yeast)	Chromatin binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CC	Yes
PHLDB2	90102	pleckstrin homology-like domain family B member 2 isoform b	NP_001127909.1	3	8	8	11	1.01	0.93	5.97	2.83	16.1	6.9	7	7	6611	90102	pleckstrin homology-like domain, family B,member 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell communication;Signal transduction	CC;PH	No
PLA2G15	23659	group XV phospholipase A2 precursor	NP_036452.1	1	3	3	5	1.01	0.93	11.38	0.97	23.4	1.8	4	4	7128	23659	lysophospholipase 3 (lysosomal phospholipaseA2)	Phospholipase activity	Extracellular	Enzyme: Phospholipase	Metabolism;Energy pathways	SP	Yes
AJUBA	84962	LIM domain-containing protein ajuba isoform 1	NP_116265.1	2	3	3	5	1.01	0.93	2.36	5.45	3.4	7.2	2	2									
CHURC1-FNTB	100529261	CHURC1-FNTB protein isoform 1	NP_001189488.1	3	1	1	2	1.01	0.93	10.36	1.7	14.9	2.2	2	2									
CIAPIN1	57019	anamorsin isoform 1	NP_064709.2	3	4	4	7	1.01	0.93	8.38	7.6	19.1	16	5	5	12338	57019	cytokine induced apoptosis inhibitor 1	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	-	Yes
EIF4E	1977	eukaryotic translation initiation factor 4E isoform 2	NP_001124151.1	4	3	4	15	1.01	0.92	12.17	7.92	35.9	20.8	8	8	591	1977	eukaryotic translation initiation factor 4E	Translation regulator activity	Nucleus	Translation regulatory protein	Protein metabolism	NLS	Yes
RFC2	5982	replication factor C subunit 2 isoform 1	NP_852136.1	5	5	5	8	1.01	0.92	1.88	7.19	3.8	13.2	4	4	2675	5982	replication factor C (activator 1) 2, 40kDa	DNA binding	Nucleolus	DNA binding protein	DNA replication	AAA	Yes
IPO13	9670	importin-13	NP_055467.3	1	2	2	3	1.01	0.91					1	1	13742	9670	importin 13	Ligand-dependent nuclear receptor activity	Cytoplasm	Nuclear receptor	Cell communication;Signal transduction	-	Yes
EPM2AIP1	9852	EPM2A-interacting protein 1	NP_055620.1	1	2	2	4	1.01	0.91	7.26	4.5	10.4	5.8	2	2	7445	9852	EPM2A (laforin) interacting protein 1	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	CC	Yes
RPL13A	23521	60S ribosomal protein L13a isoform 1	NP_036555.1	2	13	13	45	1.01	0.9	3.04	3.62	14.4	15.3	22	22	11775	23521	ribosomal protein L13a	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	CC	Yes
REPS1	85021	ralBP1-associated Eps domain-containing protein 1 isoform c	NP_001273540.1	4	7	7	12	1.01	0.89	6.98	23.52	18.9	59.9	7	7	9687	85021	RALBP1 associated Eps domain containing 1	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EH;SP;CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
CDK5	1020	cyclin-dependent-like kinase 5 isoform 1	NP_004926.1	47	3	4	22	1.01	0.89	2.8	1.96	4.9	3	3	3	449	1020	cyclin-dependent kinase 5	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
METAP1	23173	methionine aminopeptidase 1	NP_055958.2	1	4	4	8	1.01	0.87	24.44	23.51	52.6	42.8	4	4	10071	23173	methionyl aminopeptidase 1	Aminopeptidase activity	Nucleolus	Aminopeptidase	Protein metabolism	-	Yes
RPS27	6232	40S ribosomal protein S27	NP_001021.1	1	2	4	25	1.01	0.87	3.88	7.91	6.8	12	3	3	4744	6232	ribosomal protein S27 (metallopanstimulin 1)	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CNDP2	55748	cytosolic non-specific dipeptidase isoform 1	NP_060705.2	2	18	18	88	1.01	0.87	3.3	3.91	22.9	23.1	46	45	9893	55748	CNDP dipeptidase 2 (metallopeptidase M20family)	Metallopeptidase activity	Cytoplasm	Metallo protease	Protein metabolism	-	Yes
MBD1	4152	methyl-CpG-binding domain protein 1 isoform 6	NP_001191065.1	13	3	3	7	1.01	0.86	11.03	2.57	19.5	3.8	3	3	1133	4152	methyl-CpG binding domain protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MBD	Yes
CD276	80381	CD276 antigen isoform a precursor	NP_001019907.1	1	2	2	7	1.01	0.86	2.8	4.67	5.7	8.1	4	4	5756	80381	CD276 antigen	Receptor binding	Plasma membrane	Ligand	Immune response	SP;IG;TM;IGV;IGC	Yes
TMEM126A	84233	transmembrane protein 126A isoform 1	NP_115649.1	1	1	1	2	1.01	0.86					1	1	13216	84233	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
HEATR1	55127	HEAT repeat-containing protein 1	NP_060542.4	1	10	10	20	1.01	0.86	7.31	8.99	26.1	27.3	12	12	10962	55127	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
BMP2K	55589	BMP-2-inducible protein kinase isoform a	NP_942595.1	2	2	2	4	1.01	0.85	1.84	1.84	2.6	2.2	2	2	9828	55589	BMP2 inducible kinase	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NLS	Yes
CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	NP_006026.3	8	11	13	26	1.01	0.85	2.97	4.6	10.4	13.6	12	12	8516	9578	CDC42 binding protein kinase beta(DMPK-like)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC;C1;PH;CNH;PBD	No
ATP5F1	515	ATP synthase F(0) complex subunit B1, mitochondrial precursor	NP_001679.2	1	11	11	23	1.01	0.82	6.02	14.15	23.1	45.4	14	14	4467	515	ATP synthase, H+ transporting, mitochondrialF0 complex, subunit b, isoform 1	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	SP;CC	Yes
COPS7A	50813	COP9 signalosome complex subunit 7a	NP_057403.1	1	5	5	9	1.01	0.81	12.53	20.2	28.9	37.6	5	5	16736	50813	COP9 constitutive photomorphogenic homologsubunit 7A (Arabidopsis)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PINT;CC	Yes
MDC1	9656	mediator of DNA damage checkpoint protein 1	NP_055456.2	1	11	11	18	1.01	0.8	2.8	7.92	9	20.2	10	10	16252	9656	mediator of DNA damage checkpoint 1	DNA repair protein	Nucleus;Cytoplasm	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRCT;FHA	No
UBAP2L	9898	ubiquitin-associated protein 2-like isoform a	NP_055662.3	2	1	26	69	1.01	0.8					1	1	6665	9898	ubiquitin associated protein 2-like	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	UBA	Yes
RAB2A	5862	ras-related protein Rab-2A isoform a	NP_002856.1	2	4	11	63	1.01	0.79	1.73	7.25	7.2	24	17	17	1539	5862	RAB2, member RAS oncogene family	GTPase activity	Endoplasmic reticulum	GTPase	Cell communication;Signal transduction	RAB	Yes
THEM6	51337	protein THEM6 precursor	NP_057731.1	1	1	1	1	1.01	0.77					1	1									
TUBA1C	84790	tubulin alpha-1C chain isoform a	NP_001290043.1	5	4	31	488	1.01	0.75	3.34	7.62	23.2	40.5	46	46	6747	84790	None	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC;TUBULIN	Yes
RMDN1	51115	regulator of microtubule dynamics protein 1 isoform 1	NP_057117.2	3	2	2	3	1.01	0.75	0.94	34	1.3	37.1	2	2									
SLA2	84174	src-like-adapter 2 isoform a	NP_115590.1	2	1	1	1	1.01	0.69					1	1	5955	84174	Src-like-adaptor 2	Molecular function unknown	Endosome	Adapter molecule	Regulation of immune response;Signal transduction	SH3;SH2;SP	Yes
PCNXL2	80003	pecanex-like protein 2	NP_055616.3	1	1	1	1	1.01	0.58					1	1	15108	80003	pecanex-like 2 (Drosophila)	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
EXOSC8	11340	exosome complex component RRP43	NP_852480.1	1	3	3	8	1	1.72	5.1	17.41	8.9	55.6	3	3	9351	11340	exosome component 8	Ribonuclease activity	Nucleolus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SETD1A	9739	histone-lysine N-methyltransferase SETD1A	NP_055527.1	1	1	1	2	1	1.42					1	1	13795	9739	None	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Cell differentiation;Cell proliferation	RRM;SET;PSET	No
ADH1A	124	alcohol dehydrogenase 1A	NP_000658.1	2	1	1	7	1	1.36	2.2	3.11	4.9	9.4	5	5	63	124	alcohol dehydrogenase 1A (class I), alphapolypeptide	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
ICT1	3396	peptidyl-tRNA hydrolase ICT1, mitochondrial isoform 2 precursor	NP_001290194.1	2	4	4	10	1	1.33	5.34	4.1	12	12.2	5	5	4299	3396	immature colon carcinoma transcript 1	Molecular function unknown	-	Unclassified	Immune response	-	Yes
TAB3	257397	TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	NP_690000.3	1	1	1	2	1	1.29					1	1									
RPL37A	6168	60S ribosomal protein L37a	NP_000989.1	1	5	5	29	1	1.24	5.94	6.57	23.4	32.4	15	15	17997	6168	ribosomal protein L37a	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	No
GABPA	2551	GA-binding protein alpha chain	NP_001184226.1	1	6	6	11	1	1.24	7.31	8.17	19.5	27.3	7	7	11793	2551	GA binding protein transcription factor, alphasubunit 60kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAM_PNT;ETS	Yes

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UTP20	27340	small subunit processome component 20 homolog	NP_055318.2	1	6	6	7	1	1.23	11.53	27.59	20.1	64	3	3	9928	27340	None	Molecular function unknown	Nucleolus	Unclassified	Cell communication;Signal transduction	-	No
PPP2R5A	5525	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform isoform 1	NP_006234.1	2	3	3	10	1	1.23	3.64	6.41	9	19.5	6	6	3384	5525	protein phosphatase 2, regulatory subunit B(B56), alpha isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	CC	Yes
HNRNPL	3191	heterogeneous nuclear ribonucleoprotein L isoform a	NP_001524.2	2	23	24	114	1	1.22	5.19	6.8	40.2	68.2	56	56	4360	3191	heterogeneous nuclear ribonucleoprotein L	RNA binding	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
LAP3	51056	cytosol aminopeptidase	NP_056991.2	1	22	22	77	1	1.2	2.4	4.38	14.9	33.3	38	38	7516	51056	leucine aminopeptidase 3	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	-	Yes
COPS4	51138	COP9 signalosome complex subunit 4 isoform 1	NP_057213.2	2	11	11	22	1	1.19	5.98	7.17	21	30.2	12	12	9888	51138	COP9 constitutive photomorphogenic homologsubunit 4 (Arabidopsis)	Molecular function unknown	-	Unclassified	Protein metabolism	PINT	No
C5orf51	285636	UPF0600 protein C5orf51	NP_787117.3	1	1	1	7	1	1.18	17.53	21.66	31.2	46.5	3	3	11258	285636	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	NP_003742.2	1	29	29	88	1	1.18	3.89	3.95	27.7	33.7	49	50	6795	8662	eukaryotic translation initiation factor 3,subunit 9 eta, 116kDa	Translation regulator activity	Ribosome	Translation regulatory protein	Protein metabolism	RRM	Yes
GSS	2937	glutathione synthetase	NP_000169.1	1	20	20	59	1	1.18	3.04	2.14	17	13.9	31	30	3000	2937	glutathione synthetase	Ligase activity	-	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
PQBP1	10084	polyglutamine-binding protein 1 isoform 1	NP_005701.1	5	1	1	1	1	1.17					1	1	2354	10084	polyglutamine binding protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WW;NLS	No
WBSCR16	81554	Williams-Beuren syndrome chromosomal region 16 protein isoform 1	NP_110425.2	3	3	3	4	1	1.17	3.38	6.61	5.9	13.5	3	3	15654	81554	Williams-Beuren syndrome chromosome region 16	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	-	Yes
RFTN1	23180	raftlin	NP_055965.1	1	3	3	10	1	1.16	11.41	4.66	28.5	13.3	6	6	17950	23180	None	Molecular function unknown	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	-	Yes
PPP2R2A	5520	serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform isoform 2	NP_001171062.1	15	8	8	34	1	1.15	3.25	4.61	13.5	22.2	17	17	9223	5520	protein phosphatase 2 (formerly 2A),regulatory subunit B (PR 52), alpha isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	-	No
SPATA5	166378	spermatogenesis-associated protein 5	NP_660208.2	1	5	6	9	1	1.14	7.49	10.92	16.9	28.4	5	5	11595	166378	spermatogenesis associated 5	ATPase activity	Mitochondrion	ATPase	Metabolism;Energy pathways	AAA	No
EIF2S3	1968	eukaryotic translation initiation factor 2 subunit 3	NP_001406.1	1	16	16	55	1	1.14	3.48	3.81	19.3	24.2	30	30	2155	1968	eukaryotic translation initiation factor 2,subunit 3 gamma, 52kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
UTP15	84135	U3 small nucleolar RNA-associated protein 15 homolog isoform 1	NP_115551.2	3	4	4	8	1	1.13	23.78	4.03	50.2	9.1	4	4	7796	84135	None	Molecular function unknown	-	Unclassified	Cell communication	WD40	Yes
RSL1D1	26156	ribosomal L1 domain-containing protein 1	NP_056474.2	1	19	19	49	1	1.13	4.87	4.02	25.7	23.9	27	27	10897	26156	ribosomal L1 domain containing 1	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	No
PTP4A1	7803	protein tyrosine phosphatase type IVA 1	NP_003454.1	4	2	2	3	1	1.13	4.52	8.55	6.4	13.7	2	2	3349	7803	protein tyrosine phosphatase type IVA, member1	Protein tyrosine phosphatase activity	Nucleus	Tyrosine phosphatase	Cell communication;Signal transduction	Tyr_Phos	No
NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 1	NP_057404.2	4	16	16	29	1	1.13	4.77	4.07	19.9	19.1	17	17	3012	4928	nucleoporin 98kDa	Transporter activity	Nucleus;Nuclear membrane;Cytoplasm	Transport/cargo protein	Transport	-	Yes
CTBP1	1487	C-terminal-binding protein 1 isoform 1	NP_001319.1	2	6	9	16	1	1.13	5.87	9.72	15.6	29.8	7	7	4015	1487	C-terminal binding protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	2HD	Yes
MRPL24	79590	39S ribosomal protein L24, mitochondrial	NP_663781.1	1	1	1	2	1	1.12					1	1	14749	79590	mitochondrial ribosomal protein L24	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	KOW	No
UPF3A	65110	regulator of nonsense transcripts 3A isoform hUpf3p	NP_075387.1	2	2	2	4	1	1.11	2.58	15.95	3.7	25.5	2	2	9274	65110	UPF3 regulator of nonsense transcripts homologA (yeast)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS;NES	Yes
TMEM209	84928	transmembrane protein 209 isoform 1	NP_116231.2	2	2	2	2	1	1.11	39.28	49.77	60.4	91.7	2	2	7871	84928	None	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
PHB	5245	prohibitin isoform 1	NP_001268644.1	2	18	18	96	1	1.1	2.59	2	17.8	15	46	46	1454	5245	prohibitin	Receptor signaling complex scaffold activity	Mitochondrion	Adapter molecule	Cell communication;Signal transduction	CC;PHB	Yes
CMSS1	84319	protein CMSS1 isoform 1	NP_115735.2	2	4	4	5	1	1.1	9.69	15.16	13.8	23.9	2	2									
GMPR2	51292	GMP reductase 2 isoform 4	NP_001269951.1	5	7	8	14	1	1.1	9.55	11.38	25.6	34	7	7	13590	51292	guanosine monophosphate reductase 2	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism	-	Yes
NOL6	65083	nucleolar protein 6 alpha isoform	NP_075068.2	2	11	11	17	1	1.09	8.74	5.97	29.7	21.8	11	11	14832	65083	nucleolar protein family 6 (RNA-associated)	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No

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LGALS8	3964	galectin-8 isoform a	NP_963839.1	2	3	3	5	1	1.09	2.18	2.33	3.8	4.4	3	3	9356	3964	lectin, galactoside-binding, soluble, 8(galectin 8)	Carbohydrate binding	Cytoplasm	Extracellular matrix protein	Signal transduction	GLECT	Yes
PTDSS1	9791	phosphatidylserine synthase 1 isoform 1	NP_055569.1	2	3	3	7	1	1.09	12.03	10.8	24.4	24	4	4	17926	9791	phosphatidylserine synthase 1	Transferase activity	Mitochondrion	Enzyme: Synthase	Metabolism;Energy pathways	TM	Yes
ATIC	471	bifunctional purine biosynthesis protein PURH	NP_004035.2	1	39	39	149	1	1.09	2.68	4.27	23	41.2	72	72	3434	471	5-aminoimidazole-4-carboxamide ribonucleotideformyltransferase/IMP cyclohydrolase	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
BRD2	6046	bromodomain-containing protein 2 isoform 2	NP_001186384.1	4	3	4	4	1	1.09	0.53	4.84	0.9	9.2	3	3	3326	6046	bromodomain containing 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BROMO;CC;NLS	Yes
MTFR1L	56181	mitochondrial fission regulator 1-like isoform a	NP_062457.3	2	1	1	1	1	1.08					1	1									
IGF2BP2	10644	insulin-like growth factor 2 mRNA-binding protein 2 isoform c	NP_001278798.1	7	19	21	83	1	1.08	2.51	3.15	14.4	19.5	32	32	10507	10644	None	RNA binding;Translation regulator activity	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of translation	RRM;KH	Yes
PXN	5829	paxillin isoform 3	NP_001230685.1	4	9	9	22	1	1.08	4.49	10.61	15	39.4	11	11	3937	5829	paxillin	Cell adhesion molecule activity	Focal adhesion	Cytoskeletal associated protein	Signal transduction	LIM	No
GPS1	2873	COP9 signalosome complex subunit 1 isoform 1	NP_997657.1	2	12	12	31	1	1.07	9.27	2.39	38.5	10.2	16	16	15991	2873	G protein pathway suppressor 1	Signal transducer activity	Nucleus	Unclassified	Cell communication;Signal transduction	PINT	Yes
MRPS27	23107	28S ribosomal protein S27, mitochondrial isoform 1	NP_001273677.1	3	9	9	25	1	1.06	6.88	6.05	26.3	24.3	14	14	17596	23107	mitochondrial ribosomal protein S27	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	CC	Yes
ACOX1	51	peroxisomal acyl-coenzyme A oxidase 1 isoform a	NP_004026.2	3	5	5	10	1	1.05	15.03	9.09	34.6	21.7	5	5	2030	51	acyl-Coenzyme A oxidase 1, palmitoyl	Catalytic activity	Peroxisome;Nucleus	Enzyme: Oxidase	Metabolism;Energy pathways	-	Yes
FNBP1L	54874	formin-binding protein 1-like isoform 3	NP_001157945.1	3	1	1	2	1	1.05					1	1	12317	54874	formin binding protein 1-like	Cytoskeletal protein binding	Microtubule	Cytoskeletal protein	Signal transduction	FCH;CC;SH3	No
PBXIP1	57326	pre-B-cell leukemia transcription factor-interacting protein 1	NP_065385.2	1	8	8	12	1	1.04	7.65	16.58	19	44.3	6	6	17823	57326	pre-B-cell leukemia transcription factorinteracting protein 1	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	No
AAAS	8086	aladin isoform 1	NP_056480.1	2	7	7	16	1	1.04	5.89	12.51	17.8	40.4	9	9	5646	8086	achalasia, adrenocortical insufficiency,alacrimia (Allgrove, triple-A)	Molecular function unknown	Peroxisome	Unclassified	Cell communication;Signal transduction	WD40;SP	No
PDE4DIP	9659	myomegalin isoform 8	NP_001185761.2	7	3	3	5	1	1.03	7.52	2.88	13.1	5.1	3	3	10482	9659	phosphodiesterase 4D interacting protein(myomegalin)	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	DSH;CC	Yes
MSH6	2956	DNA mismatch repair protein Msh6 isoform 1	NP_000170.1	3	12	12	19	1	1.03	3	13.08	10	46.8	11	11	7202	2956	mutS homolog 6 (E. coli)	DNA binding	Nucleus	DNA repair protein	DNA repair	PWWP;MUTSd;MUTSac	Yes
RPL6	6128	60S ribosomal protein L6	NP_000961.2	1	16	16	88	1	1.02	2.24	4	14.4	27	41	42	4745	6128	ribosomal protein L6	Structural constituent of ribosome	Nucleolus	Ribosomal subunit	Protein metabolism	-	Yes
RAD50	10111	DNA repair protein RAD50	NP_005723.2	1	18	18	41	1	1.02	4.82	5.8	21.9	26.9	20	20	4950	10111	RAD50 homolog (S. cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
HNRNPF	3185	heterogeneous nuclear ribonucleoprotein F	NP_004957.1	1	6	8	51	1	1.01	4.38	5.61	14.7	19	11	11	3023	3185	heterogeneous nuclear ribonucleoprotein F	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
GTPBP10	85865	GTP-binding protein 10 isoform 2	NP_149098.2	2	3	3	5	1	1.01	10.82	15.45	22	31.8	4	4	14262	85865	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
ELAC2	60528	zinc phosphodiesterase ELAC protein 2 isoform 1	NP_060597.4	3	13	13	26	1	1.01	9.06	5.56	33.5	20.5	13	13	5641	60528	elaC homolog 2 (E. coli)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
LMO7	4008	LIM domain only protein 7 isoform 3	NP_001293009.1	3	2	2	3	1	1					1	1	5078	4008	LIM domain 7	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CH;CC;PDZ;LIM	Yes
MTHFD1L	25902	monofunctional C1-tetrahydrofolate synthase, mitochondrial isoform 1 precursor	NP_001229696.1	10	15	15	29	1	1	3.88	6.43	16	27	17	17	9967	25902	methylenetetrahydrofolate dehydrogenase(NADP+ dependent) 1-like	Catalytic activity	Mitochondrion	Enzyme: Ligase	Metabolism	SP	No
BAIAP2	10458	brain-specific angiogenesis inhibitor 1-associated protein 2 isoform 2	NP_059345.1	4	7	7	15	1	1	17.36	8.17	55.7	24.9	9	9	5686	10458	BAI1-associated protein 2	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	CC;SH3	Yes
RANBP2	5903	E3 SUMO-protein ligase RanBP2	NP_006258.3	14	52	54	112	1	0.99	1.63	2.3	12.7	17.8	60	60	3111	5903	RAN binding protein 2	Transporter activity	Nucleus	Transport/cargo protein	Cell communication;Signal transduction	TPR;ZnF_RBZ;CC	Yes

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WDR48	57599	WD repeat-containing protein 48 isoform 1	NP_065890.1	1	2	2	3	1	0.98					1	1	11146	57599	WD repeat domain 48	Molecular function unknown	Endosome	Unclassified	Cell communication;Signal transduction	WD40	Yes
AP5Z1	9907	AP-5 complex subunit zeta-1	NP_055670.1	1	2	2	3	1	0.98					1	1									
HERPUD2	64224	homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 2 protein	NP_071768.3	1	1	1	1	1	0.97					1	1	7984	64224	None	Molecular function unknown	-	Unclassified	Biological_process unknown	UBQ;TM	No
URB2	9816	unhealthy ribosome biogenesis protein 2 homolog	NP_055592.2	1	3	3	5	1	0.97	14.64	6.12	21	8.4	2	2	17178	9816	KIAA0133	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
ASPH	444	aspartyl/asparaginyl beta-hydroxylase isoform a	NP_004309.2	12	23	24	83	1	0.97	4.26	4.18	26.6	25.3	38	38	8996	444	aspartate beta-hydroxylase	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Protein metabolism	TM;CC	Yes
PSMD8	5714	26S proteasome non-ATPase regulatory subunit 8	NP_002803.2	1	7	7	31	1	0.95	2.31	6.76	7.7	21.4	11	11	10171	5714	proteasome (prosome, macropain) 26S subunit,non-ATPase, 8	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
MRPL20	55052	39S ribosomal protein L20, mitochondrial	NP_060441.2	1	3	3	8	1	0.95	3.46	4.52	6.9	8.6	4	4	14746	55052	mitochondrial ribosomal protein L20	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
PPP2CB	5516	serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	NP_001009552.1	1	1	12	43	1	0.94					1	1	1487	5516	protein phosphatase 2 (formerly 2A), catalyticsubunit, beta isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	CC;PP2A	Yes
ANAPC7	51434	anaphase-promoting complex subunit 7 isoform a	NP_057322.2	2	3	3	4	1	0.94	0.62	2.99	0.9	4	2	2	16233	51434	anaphase promoting complex subunit 7	Protein binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	TPR	Yes
PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	NP_003904.3	1	11	11	20	1	0.94	6.75	6.61	21.5	19.8	10	10	9087	8899	PRP4 pre-mRNA processing factor 4 homolog B(yeast)	Transcription regulator activity;Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Signal transduction	CC;S_T_kinase	Yes
THOC2	57187	THO complex subunit 2	NP_001075019.1	1	6	6	9	1	0.94	11.3	8.26	25.7	17.5	5	5	2317	57187	THO complex 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
OSBPL9	114883	oxysterol-binding protein-related protein 9 isoform f	NP_683707.3	6	5	5	10	1	0.93	6.31	4.12	16.8	10.1	7	7	9479	114883	oxysterol binding protein-like 9	Transporter activity	Cytoplasm;Nucleus	Transport/cargo protein	Transport	PH;CC	Yes
RPL5	6125	60S ribosomal protein L5	NP_000960.2	1	21	21	97	1	0.92	4.29	5.55	31	37.4	50	50	4699	6125	ribosomal protein L5	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	NLS;NES	Yes
COLGALT1	79709	procollagen galactosyltransferase 1 precursor	NP_078932.2	4	19	19	48	1	0.91	3.78	6.14	19.5	29	26	26									
FRMD8	83786	FERM domain-containing protein 8 isoform 1	NP_114110.1	3	3	3	5	1	0.91	18.36	15.84	32.5	25.3	3	3	13326	83786	None	Cytoskeletal protein binding	-	Cytoskeletal associated protein	Cell growth and/or maintenance	B41	No
DHX36	170506	ATP-dependent RNA helicase DHX36 isoform 1	NP_065916.2	2	7	8	21	1	0.9	8.73	8.6	28.1	24.8	10	10	9918	170506	DEAH (Asp-Glu-Ala-His) box polypeptide 36	RNA binding	Plasma membrane	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;TM	No
ZAK	51776	mitogen-activated protein kinase kinase kinase MLT isoform 2	NP_598407.1	1	1	4	7	1	0.9					1	1									
PIP4K2C	79837	phosphatidylinositol 5-phosphate 4-kinase type-2 gamma isoform a	NP_079055.3	3	8	8	14	1	0.9	9.33	5.58	27	14.2	8	8	15138	79837	phosphatidylinositol-4-phosphate 5-kinase,type II, gamma	Lipid kinase activity	-	Lipid Kinase	Cell communication;Signal transduction	PIPKc	No
HDAC3	8841	histone deacetylase 3	NP_003874.2	1	1	2	3	1	0.9					1	1	8950	8841	histone deacetylase 3	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NES;NLS	Yes
AMPD2	271	AMP deaminase 2 isoform 1	NP_004028.3	5	5	5	9	1	0.89	7.84	7.49	19.3	16.4	6	6	11808	271	adenosine monophosphate deaminase 2 (isoform L)	Deaminase activity	Cytoplasm;Nucleus	Enzyme: Deaminase	Metabolism;Energy pathways	SP	Yes
CCDC167	154467	coiled-coil domain-containing protein 167	NP_612502.1	1	1	1	1	1	0.88					1	1									
MCU	90550	calcium uniporter protein, mitochondrial isoform 1 precursor	NP_612366.1	3	4	4	10	1	0.88	3.68	11.62	9	25.4	6	6									
RER1	11079	protein RER1	NP_008964.3	1	1	1	2	1	0.88					1	1	17967	11079	RER1 retention in endoplasmic reticulum 1homolog (S. cerevisiae)	Molecular function unknown	Golgi apparatus	Integral membrane protein	Biological_process unknown	TM	No
PTRH2	51651	peptidyl-tRNA hydrolase 2, mitochondrial isoform a	NP_001015509.1	2	5	5	12	1	0.87	12.54	8.74	34.2	20.4	7	7	12273	51651	None	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase	Apoptosis	TM	Yes
MRPS17	51373	28S ribosomal protein S17, mitochondrial	NP_057053.1	1	5	5	10	1	0.87	11.37	5.63	28.5	12	6	6	14779	51373	mitochondrial ribosomal protein S17	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
FAM120A	23196	constitutive coactivator of PPAR-gamma-like protein 1 isoform a	NP_055427.2	7	29	29	70	1	0.87	3.16	3.02	20.2	16.8	40	40	12928	23196	chromosome 9 open reading frame 10	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
KTN1	3895	kinectin isoform a	NP_001072989.1	4	43	43	115	1	0.87	2.05	3.15	16.7	22.4	65	65	2661	3895	kinectin 1 (kinesin receptor)	Cytoskeletal anchoring activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Anchor protein	Cell growth and/or maintenance	TM;CC	Yes
POLR1B	84172	DNA-directed RNA polymerase I subunit RPA2 isoform 3	NP_001269701.1	3	1	1	2	1	0.86					1	1	6852	84172	polymerase (RNA) I polypeptide B, 128kDa	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PHD	Yes

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SIRT6	51548	NAD-dependent protein deacetylase sirtuin-6 isoform 1	NP_057623.2	2	1	1	1	1	0.86					1	1	12093	51548	sirtuin (silent mating type informationregulation 2 homolog) 6 (S. cerevisiae)	Deacetylase activity	Nucleus	Enzyme: Deacetylase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
SAR1A	56681	GTP-binding protein SAR1a	NP_064535.1	1	5	9	51	1	0.84	11.84	17.33	38.7	46.1	10	9	7608	56681	SAR1a gene homolog 1 (S. cerevisiae)	GTPase activity	Endoplasmic reticulum	GTPase	Cell communication;Signal transduction	-	Yes
PUF60	22827	poly(U)-binding-splicing factor PUF60 isoform b	NP_055096.2	4	1	14	64	1	0.84					1	1	18051	22827	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
PRKACA	5566	cAMP-dependent protein kinase catalytic subunit alpha isoform 3	NP_001291278.1	5	1	6	8	1	0.84					1	1	3382	5566	protein kinase, cAMP-dependent, catalytic,alpha	Protein serine/threonine kinase activity	Golgi apparatus;Nucleus;Cytoplasm	Serine/threonine kinase	Signal transduction	S_T_kinase	Yes
MUT	4594	methylmalonyl-CoA mutase, mitochondrial precursor	NP_000246.2	1	10	10	23	1	0.8	5.59	3.51	17.9	8.9	10	10	2014	4594	methylmalonyl Coenzyme A mutase	Catalytic activity	Mitochondrion	Enzyme: Mutase	Metabolism;Energy pathways	-	Yes
LACTB	114294	serine beta-lactamase-like protein LACTB, mitochondrial isoform a precursor	NP_116246.2	3	5	5	8	1	0.8	11.88	3.59	26.9	6.4	5	5	7466	114294	lactamase, beta	Structural constituent of ribosome	Mitochondrion;Cytoplasm	Ribosomal subunit	Protein metabolism	TM	Yes
TRMT61B	55006	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial precursor	NP_060380.3	1	2	2	3	1	0.79	16.94	52.9	24.2	64.5	2	2	7935	55006	None	Methyltransferase activity	-	Enzyme: Methyltransferase	Metabolism;Energy pathways	SP	No
XPC	7508	DNA repair protein complementing XP-C cells	NP_004619.3	1	2	2	3	1	0.79	0.8	23.17	1.1	26.4	2	2	2046	7508	xeroderma pigmentosum, complementation group C	DNA repair protein	Nucleus	DNA binding protein	DNA repair	-	Yes
EMD	2010	emerin	NP_000108.1	1	8	8	21	1	0.77	6.11	9.42	23.2	27.5	14	14	2309	2010	emerin (Emery-Dreifuss muscular dystrophy)	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	TM	No
BLVRB	645	flavin reductase (NADPH)	NP_000704.1	1	4	4	7	1	0.76	8.56	25.68	17.3	40.5	4	4	2967	645	biliverdin reductase B (flavin reductase(NADPH))	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
HIST1H4B	8366	histone H4	NP_003535.1	1	12	12	365	1	0.76	3.29	2.57	48.2	27.6	194	194	11920	8366	histone 1, H4b	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
DAG1	1605	dystroglycan preproprotein	NP_001171114.1	1	2	2	3	1	0.75					1	1	546	1605	dystroglycan 1 (dystrophin-associatedglycoprotein 1)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	TM;SP	Yes
TRMT1L	81627	TRMT1-like protein isoform 1	NP_112196.3	2	5	5	10	1	0.72	10.96	4.88	24.9	7.9	5	5									
PPIL1	51645	peptidyl-prolyl cis-trans isomerase-like 1	NP_057143.1	1	4	4	7	1	0.67	9.4	27.18	23.3	46.7	6	6	3194	51645	peptidylprolyl isomerase (cyclophilin)-like 1	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
ERC2	26059	ERC protein 2	NP_056391.1	1	1	2	3	1	0.65					1	1	10810	26059	None	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
ACTN3	89	alpha-actinin-3 isoform 1	NP_001095.2	2	2	12	65	1	0.62					1	1	2148	89	actinin, alpha 3	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;SPECTRIN;EF;CC	Yes
CERS6	253782	ceramide synthase 6 isoform 1	NP_001243055.1	2	1	1	1	1	0.55					1	1									
ERCC6L	54821	DNA excision repair protein ERCC-6-like	NP_060139.2	1	3	3	3	0.99	1.9					1	1	10974	54821	None	Molecular function unknown	-	Unclassified	Biological_process unknown	DEXDc;HELIC	No
TSNAX	7257	translin-associated protein X	NP_005990.1	1	4	4	7	0.99	1.72	3.62	2.34	6.2	7	3	3	4270	7257	translin-associated factor X	Transporter activity	Cytoplasm	Transport/cargo protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
NUDT9	53343	ADP-ribose pyrophosphatase, mitochondrial isoform a precursor	NP_076952.1	3	1	1	1	0.99	1.68					1	1	9353	53343	nudix (nucleoside diphosphate linked moietyX)-type motif 9	Catalytic activity	Mitochondrion;Cytoplasm	Enzyme: Phosphatase	Ion transport	SP	Yes
LRPAP1	4043	alpha-2-macroglobulin receptor-associated protein precursor	NP_002328.1	1	5	5	9	0.99	1.56	7.7	4.43	17.1	15.5	5	5	82	4043	low density lipoprotein receptor-relatedprotein associated protein 1	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	CC;SP	Yes
CDKAL1	54901	threonylcarbamoyladenosine tRNA methylthiotransferase	NP_060244.2	1	2	2	2	0.99	1.54	27	4.71	39.3	10.3	2	2	13022	54901	CDK5 regulatory subunit associated protein1-like 1	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	Yes
SSB	6741	lupus La protein	NP_003133.1	1	21	21	66	0.99	1.51	5.32	4.3	30	37.5	31	31	168	6741	Sjogren syndrome antigen B (autoantigen La)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;RRM	No
PLAU	5328	urokinase-type plasminogen activator isoform 1 preproprotein	NP_002649.1	2	3	3	8	0.99	1.49	2.24	4.31	4.4	12.9	4	4	1883	5328	plasminogen activator, urokinase	Serine-type peptidase activity	Plasma membrane	Serine protease	Protein metabolism	KRINGLE;TRYPSIN;SP	Yes
SFSWAP	6433	splicing factor, suppressor of white-apricot homolog isoform 1	NP_001248340.1	2	2	2	4	0.99	1.46	0.64	22.28	0.9	48.7	2	2									
HSPA8	3312	heat shock cognate 71 kDa protein isoform 1	NP_006588.1	2	24	36	442	0.99	1.43	4.13	5.31	56.6	125.1	167	164	7205	3312	heat shock 70kDa protein 8	Heat shock protein activity	Nucleolus;Cytoplasm	Heat shock protein	Protein metabolism	CC;NLS;NES	Yes

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H1F0	3005	histone H1.0	NP_005309.1	1	9	9	41	0.99	1.4	10.24	13.15	49.4	102.3	21	21	819	3005	H1 histone family, member 0	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H15;NLS	Yes
SEMA4B	10509	semaphorin-4B precursor	NP_064595.2	1	1	1	1	0.99	1.38					1	1	10217	10509	sema domain, immunoglobulin domain (Ig),transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	SP;SEMA;PSI;TM	Yes
EIF4A1	1973	eukaryotic initiation factor 4A-I isoform 1	NP_001407.1	2	11	23	203	0.99	1.36	6.3	8.23	53.9	111.1	65	64	4030	1973	eukaryotic translation initiation factor 4A,isoform 1	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	HELIC;DEXDc	Yes
XPOT	11260	exportin-T	NP_009166.2	1	8	8	15	0.99	1.35	9.49	7.59	28.8	31.5	9	9	4418	11260	exportin, tRNA (nuclear export receptor fortRNAs)	Transporter activity	Nucleus	Transport/cargo protein	Transport	IBN_NT	Yes
NAA10	8260	N-alpha-acetyltransferase 10 isoform 1	NP_003482.1	4	13	13	19	0.99	1.31	8.41	7.46	29.5	34.9	12	12	2056	8260	ARD1 homolog A, N-acetyltransferase (S.cerevisiae)	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
WDR37	22884	WD repeat-containing protein 37	NP_054742.2	1	2	2	4	0.99	1.28	31.04	55.11	45.7	130	2	2	15668	22884	WD repeat domain 37	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;WD40	Yes
SNRPB	6628	small nuclear ribonucleoprotein-associated proteins B and B' isoform B'	NP_937859.1	3	6	6	20	0.99	1.27	7.42	16.5	23.5	74.2	10	10	1655	6628	small nuclear ribonucleoprotein polypeptides Band B1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
LRSAM1	90678	E3 ubiquitin-protein ligase LRSAM1 isoform 1	NP_001005373.1	2	7	7	13	0.99	1.27	14.76	10.91	37	34.9	6	6	14325	90678	leucine rich repeat and sterile alpha motifcontaining 1	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Cell communication;Signal transduction	LRR;CC;SAM;RING;NLS;LZ	Yes
PUS1	80324	tRNA pseudouridine synthase A, mitochondrial isoform 1	NP_079491.2	2	4	4	8	0.99	1.26	1.53	6.51	3	16.5	4	4	10481	80324	pseudouridylate synthase 1	Catalytic activity	Nucleus	Enzyme: Synthase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CHCHD3	54927	MICOS complex subunit MIC19	NP_060282.1	1	11	11	21	0.99	1.25	4.97	4.1	18	18.6	13	13	13044	54927	coiled-coil-helix-coiled-coil-helix domaincontaining 3	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;CHCH	Yes
PLEC	5339	plectin isoform 1	NP_958782.1	16	4	348	1371	0.99	1.24	1.16	13.18	2.3	33.5	4	4									
GSTP1	2950	glutathione S-transferase P	NP_000843.1	1	11	11	300	0.99	1.23	2.33	4.03	22.8	51.2	95	95	614	2950	glutathione S-transferase pi	Glutathione transferase activity	Cytoplasm	Enzyme: Glutathione transferase	Metabolism;Energy pathways	-	Yes
EDEM3	80267	ER degradation-enhancing alpha-mannosidase-like protein 3 precursor	NP_079467.3	1	1	1	2	0.99	1.22					1	1	10724	80267	chromosome 1 open reading frame 22	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
HSPH1	10808	heat shock protein 105 kDa isoform 1	NP_006635.2	4	37	42	143	0.99	1.22	3.47	3.15	28.8	32.2	67	67	9990	10808	heat shock 105kDa/110kDa protein 1	Heat shock protein activity;Chaperone activity	Cytoplasm	Heat shock protein;Chaperone	Protein metabolism	-	Yes
IMPDH2	3615	inosine-5'-monophosphate dehydrogenase 2	NP_000875.2	1	16	17	46	0.99	1.22	4.61	4.39	22.1	26.1	23	23	895	3615	IMP (inosine monophosphate) dehydrogenase 2	Catalytic activity	Cytosol;Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	CBS	Yes
TRNT1	51095	CCA tRNA nucleotidyltransferase 1, mitochondrial isoform 1	NP_886552.2	2	8	8	17	0.99	1.21	6.56	5.6	20.9	21.8	10	10	18227	51095	tRNA nucleotidyl transferase, CCA-adding, 1	Nucleotidyltransferase activity	Mitochondrion	Enzyme: Nucleotidyltransferase	Metabolism	SP	Yes
RANGAP1	5905	ran GTPase-activating protein 1	NP_002874.1	1	22	22	64	0.99	1.21	3.84	5.08	23.1	38.3	36	36	3839	5905	Ran GTPase activating protein 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	LRR;CC	Yes
NDUFAF2	91942	mimitin, mitochondrial	NP_777549.1	1	5	5	15	0.99	1.21	14.71	5.44	40.1	17.6	7	7	14288	91942	None	Molecular function unknown	Mitochondrion	Unclassified	Cell proliferation	-	No
EXOSC7	23016	exosome complex component RRP42	NP_055819.2	1	5	5	12	0.99	1.2	5.24	2.12	12.8	6.2	6	6	9401	23016	exosome component 7	Ribonuclease activity	Nucleolus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CTSA	5476	lysosomal protective protein isoform a precursor	NP_000299.2	3	2	2	6	0.99	1.19	10.23	8.74	17.7	18.1	3	3	2020	5476	protective protein for beta-galactosidase(galactosialidosis)	Serine-type peptidase activity	Lysosome	Serine protease	Protein metabolism	SP	Yes
CORO7-PAM16	100529144	CORO7-PAM16 protein	NP_001188408.1	5	9	9	33	0.99	1.19	4.48	2.87	13.4	10.8	9	10									
C9orf114	51490	putative methyltransferase C9orf114	NP_057474.2	1	1	1	3	0.99	1.15	1.88	9.18	2.6	15	2	2	12935	51490	chromosome 9 open reading frame 114	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	No
EDF1	8721	endothelial differentiation-related factor 1 isoform alpha	NP_003783.1	5	2	2	4	0.99	1.13	2.52	13.1	4.3	26.1	3	3	9235	8721	endothelial differentiation-related factor 1	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
FASTKD5	60493	FAST kinase domain-containing protein 5	NP_068598.1	1	5	5	8	0.99	1.12	8.14	11.2	16.3	25.6	4	4	7813	60493	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
DAP3	7818	28S ribosomal protein S29, mitochondrial isoform 1	NP_387506.1	3	11	11	36	0.99	1.12	6.95	11.68	30.6	61.9	19	19	3646	7818	death associated protein 3	Ribonucleoprotein	Mitochondrion	Ribosomal subunit	Apoptosis	-	Yes
TGM2	7052	protein-glutamine gamma-glutamyltransferase 2 isoform a	NP_004604.2	2	23	23	110	0.99	1.12	3.01	2.12	22.2	17.5	54	54	1825	7052	transglutaminase 2 (C polypeptide,protein-glutamine-gamma-glutamyltransferase)	Transaminase activity	Cytoplasm	Enzyme: Aminotransferase	Metabolism;Energy pathways	TGC;TRANSGLUT	Yes

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ATP6V1E1	529	V-type proton ATPase subunit E 1 isoform a	NP_001687.1	7	7	7	15	0.99	1.11	13.17	15.48	38.3	51.4	8	8	163	529	ATPase, H+ transporting, lysosomal 31kDa, V1subunit E isoform 1	ATPase activity	Lysosome	ATPase	Transport	-	Yes
IGF2R	3482	cation-independent mannose-6-phosphate receptor precursor	NP_000867.2	1	19	19	35	0.99	1.11	2.66	4.4	11.5	21.5	19	19	928	3482	insulin-like growth factor 2 receptor	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;FN2;SP	Yes
APRT	353	adenine phosphoribosyltransferase isoform a	NP_000476.1	2	7	7	24	0.99	1.1	2.2	3.87	7.9	15.5	13	13	29	353	adenine phosphoribosyltransferase	Transferase activity	-	Enzyme: Ribosyltransferase	Purine salvage	-	Yes
SDCBP	6386	syntenin-1 isoform 1	NP_005616.2	3	4	4	15	0.99	1.08	8.52	11.34	22.7	33.4	7	7	3741	6386	syndecan binding protein (syntenin)	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Cell communication;Signal transduction	PDZ	Yes
GNL3L	54552	guanine nucleotide-binding protein-like 3-like protein	NP_061940.1	1	1	1	4	0.99	1.08	14.34	22.08	20.2	34.7	2	2	6514	54552	guanine nucleotide binding protein-like 3(nucleolar)-like	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
TMPO	7112	thymopoietin isoform alpha	NP_003267.1	1	7	14	38	0.99	1.08	8.48	10.98	25.5	36.9	9	9	1777	7112	thymopoietin	Molecular function unknown	Nucleus;Nuclear membrane;Mitochondrion;Cytoplasm	Peptide hormone	Nuclear organization and biogenesis;Regulation of cell cycle	TM	Yes
SUGP2	10147	SURP and G-patch domain-containing protein 2	NP_055699.2	1	3	3	5	0.99	1.07	0.55	21.68	0.9	41.8	3	3									
EIF3D	8664	eukaryotic translation initiation factor 3 subunit D	NP_003744.1	1	19	19	78	0.99	1.07	5.86	6.43	38.4	46.9	41	42	4888	8664	eukaryotic translation initiation factor 3,subunit 7 zeta, 66/67kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
XRCC6	2547	X-ray repair cross-complementing protein 6 isoform 1	NP_001460.1	3	30	30	168	0.99	1.06	2.95	3.48	27.7	35.4	87	87	1071	2547	X-ray repair complementing defective repair inChinese hamster cells 6 (Ku autoantigen, 70kDa)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	Ku78;SAP;VWA	Yes
PACSIN2	11252	protein kinase C and casein kinase substrate in neurons protein 2 isoform A	NP_009160.2	2	13	13	22	0.99	1.05	2.4	8.05	8.2	29.9	12	12	5390	11252	protein kinase C and casein kinase substratein neurons 2	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	FCH;CC;SH3	Yes
TIAL1	7073	nucleolysin TIAR isoform 2	NP_001029097.1	4	3	3	8	0.99	1.05	1.18	9.04	2.3	19.2	4	4	4563	7073	TIA1 cytotoxic granule-associated RNA bindingprotein-like 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	NP_003012.1	1	8	8	18	0.99	1.04	8.44	6.76	26.9	22.6	10	10	4568	6449	small glutamine-rich tetratricopeptide repeat(TPR)-containing, alpha	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	TPR	Yes
TOP3B	8940	DNA topoisomerase 3-beta-1	NP_001269041.1	1	1	1	2	0.99	1.04					1	1	4662	8940	topoisomerase (DNA) III beta	DNA topoisomerase activity	Nucleus	Enzyme: Topoisomerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
LETM1	3954	LETM1 and EF-hand domain-containing protein 1, mitochondrial precursor	NP_036450.1	1	16	16	64	0.99	1.02	7.04	6.32	41.7	38.9	33	34	5101	3954	leucine zipper-EF-hand containing transmembraneprotein 1	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	TM;CC	No
ABCC1	4363	multidrug resistance-associated protein 1	NP_004987.2	1	8	8	22	0.99	1.02	12.61	5.14	41.1	16.7	10	10	1153	4363	ATP-binding cassette, sub-family C (CFTR/MRP),member 1	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM;AAA	Yes
UBA1	7317	ubiquitin-like modifier-activating enzyme 1	NP_695012.1	1	42	42	231	0.99	1.01	2.25	2.86	23.9	31.3	113	112	2440	7317	ubiquitin-activating enzyme E1 (A1S9T and BN75temperature sensitivity complementing)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Proteolysis and peptidolysis	-	Yes
TJP2	9414	tight junction protein ZO-2 isoform 3	NP_001163887.1	6	24	24	43	0.99	1.01	3.75	5.72	19	30.2	26	26	6369	9414	tight junction protein 2 (zona occludens 2)	Cell adhesion molecule activity	Cytoplasm	Cell junction protein	Cell communication;Signal transduction	PDZ;SH3;GuKinase;CC;LZ	Yes
PDS5A	23244	sister chromatid cohesion protein PDS5 homolog A isoform 1	NP_001093869.1	2	13	14	33	0.99	1.01	5.66	4.46	22.8	18.1	16	16	11537	23244	None	Molecular function unknown	Nucleus	Unclassified	Apoptosis	-	Yes
WIZ	58525	protein Wiz	NP_067064.2	1	3	3	5	0.99	1	22.61	2.18	40.4	3.8	3	3	11686	58525	None	Transcription regulator activity	Nucleus	Adapter molecule;Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
RPS3	6188	40S ribosomal protein S3 isoform 1	NP_001243731.1	3	22	22	116	0.99	1	3.99	3.88	31.1	30.4	59	59	10941	6188	ribosomal protein S3	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	NLS;KH	Yes
MRPS15	64960	28S ribosomal protein S15, mitochondrial	NP_112570.2	1	6	6	10	0.99	0.99	7.71	19.55	17.2	45.5	5	5	11372	64960	mitochondrial ribosomal protein S15	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	CC	Yes
HDAC2	3066	histone deacetylase 2	NP_001518.3	1	5	8	19	0.99	0.99	3.44	26.34	8.3	71.3	6	6	5521	3066	histone deacetylase 2	Transcription regulator activity;DNA binding	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;SP	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
MRPL23	6150	39S ribosomal protein L23, mitochondrial	NP_066957.3	2	3	3	6	0.99	0.98	0.34	9.38	0.6	16.1	3	3	2876	6150	mitochondrial ribosomal protein L23	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	No
EIF3A	8661	eukaryotic translation initiation factor 3 subunit A	NP_003741.1	1	61	61	174	0.99	0.98	2.02	2.64	19.6	25.3	93	93	3618	8661	eukaryotic translation initiation factor 3,subunit 10 theta, 150/170kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC	Yes
TIMMDC1	51300	complex I assembly factor TIMMDC1, mitochondrial precursor	NP_057673.2	1	4	4	5	0.99	0.97	8.36	15.07	14.4	25.7	3	3									
TGFBI	7045	transforming growth factor-beta-induced protein ig-h3 precursor	NP_000349.1	1	22	22	75	0.99	0.96	4.23	4.81	24.8	27.5	34	34	3409	7045	transforming growth factor, beta-induced, 68kDa	Receptor binding	Extracellular	Ligand	Cell communication;Signal transduction	SP	Yes
MTDH	92140	protein LYRIC	NP_848927.2	1	18	18	45	0.99	0.95	5.29	6.95	26.6	33.9	25	25	17459	92140	None	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	TM	Yes
RPS11	6205	40S ribosomal protein S11	NP_001006.1	1	10	10	31	0.99	0.95	4.6	5.52	20	23.1	19	19	1599	6205	ribosomal protein S11	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
UQCRC2	7385	cytochrome b-c1 complex subunit 2, mitochondrial precursor	NP_003357.2	1	20	20	52	0.99	0.95	6.52	6.28	34.5	31.7	27	27	1876	7385	ubiquinol-cytochrome c reductase core proteinII	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	SP	Yes
PPP1R13L	10848	relA-associated inhibitor	NP_006654.2	1	20	20	44	0.99	0.94	3.34	5.35	17	26	26	26	9195	10848	protein phosphatase 1, regulatory(inhibitor) subunit 13 like	Translation regulator activity	Nucleus;Cytoplasm	Translation regulatory protein	Apoptosis	ANK;SH3;CC	Yes
SRGAP2	23380	SLIT-ROBO Rho GTPase-activating protein 2 isoform a	NP_056141.2	5	5	6	14	0.99	0.94	10.98	20.75	27.2	50.5	6	6	18520	23380	SLIT-ROBO Rho GTPase activating protein 2	GTPase activator activity	Nucleus;Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	FCH;CC;RHOGAP;SH3	Yes
REEP5	7905	receptor expression-enhancing protein 5	NP_005660.4	1	5	5	13	0.99	0.93	9.65	33.16	25.7	96.8	7	7	15918	7905	chromosome 5 open reading frame 18	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	Yes
DNPH1	10591	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 1	NP_006434.1	2	3	3	4	0.99	0.92	12.57	23.08	17.8	30.8	2	2									
DCBLD2	131566	discoidin, CUB and LCCL domain-containing protein 2 precursor	NP_563615.3	1	3	3	5	0.99	0.92	8.38	16.3	14.5	26.4	3	3	10567	131566	discoidin, CUB and LCCL domain containing 2	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;CUB;LCCL;F58C;TM	No
MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	NP_062552.2	1	5	5	8	0.99	0.92	3.72	9.33	9	21.2	6	6	7889	56257	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
VPS13D	55187	vacuolar protein sorting-associated protein 13D isoform 1	NP_056193.2	2	1	1	2	0.99	0.92					1	1	10593	55187	vacuolar protein sorting 13D (yeast)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC;UBA	Yes
ADCK4	79934	aarF domain-containing protein kinase 4 isoform a	NP_079152.3	2	1	1	2	0.99	0.91					1	1	10632	79934	aarF domain containing kinase 4	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
CCBL2	56267	kynurenine--oxoglutarate transaminase 3 isoform 1	NP_001008661.1	2	12	13	26	0.99	0.91	2.04	8.14	7.3	27.2	13	13	13752	56267	None	Transaminase activity	-	Enzyme: Aminotransferase	Metabolism;Energy pathways	-	Yes
PGAM5	192111	serine/threonine-protein phosphatase PGAM5, mitochondrial isoform 1	NP_001164014.1	2	1	8	14	0.99	0.91	3.41	18.97	4.8	24.7	2	2	14681	192111	None	Catalytic activity	Cytosol	Enzyme: Mutase	Metabolism;Energy pathways	SP	No
DCTN2	10540	dynactin subunit 2 isoform 1	NP_006391.1	3	19	19	56	0.99	0.9	3.86	6.85	21.1	34.7	30	30	9568	10540	dynactin 2 (p50)	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	CC	Yes
TMEM2	23670	transmembrane protein 2 isoform a	NP_037522.1	2	1	1	1	0.99	0.9					1	1	9317	23670	transmembrane protein 2	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
HIST1H1B	3009	histone H1.5	NP_005313.1	1	9	11	72	0.99	0.89	2.97	3.19	18.1	17.4	37	37	821	3009	histone 1, H1b	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H15	Yes
GRB7	2886	growth factor receptor-bound protein 7 isoform b	NP_001229371.1	2	1	1	2	0.99	0.89					1	1	3311	2886	growth factor receptor-bound protein 7	Binding	Plasma membrane	Adapter molecule	Cell migration	RA;PH;SH2	Yes
PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 1	NP_002703.1	7	9	9	29	0.99	0.88	5.99	10.33	23.3	36.3	15	15	4192	5510	protein phosphatase 1, regulatory subunit 7	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LRR	Yes
TBCC	6903	tubulin-specific chaperone C	NP_003183.1	1	2	2	4	0.99	0.87	23.87	24.2	34.3	30.3	2	2	4276	6903	tubulin-specific chaperone c	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CARP;CC	Yes
TCIRG1	10312	V-type proton ATPase 116 kDa subunit a isoform 3 isoform a	NP_006010.2	2	8	8	14	0.99	0.87	12.99	11.22	34.9	26.2	7	7	5207	10312	T-cell, immune regulator 1, ATPase, H+transporting, lysosomal V0 protein a isoform 3	Transporter activity	Integral to membrane	Unclassified	Transport	TM;SP;CC	Yes
COMMD3-BMI1	100532731	COMMD3-BMI1 read-through protein	NP_001190991.1	2	1	1	1	0.99	0.87					1	1									
VAC14	55697	protein VAC14 homolog	NP_060522.3	1	4	4	9	0.99	0.86	12.34	3.45	27.7	6.6	5	5	7660	55697	Vac14 homolog (S. cerevisiae)	Molecular function unknown	Microsome;Centrosome	Unclassified	Biological_process unknown	HEAT	No
NUP133	55746	nuclear pore complex protein Nup133	NP_060700.2	1	11	11	23	0.99	0.86	3.28	5.91	11.8	18.5	13	13	6354	55746	nucleoporin 133kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
HSPA6	3310	heat shock 70 kDa protein 6	NP_002146.2	1	1	11	117	0.99	0.86	2.87	11.79	4.9	17.7	3	3	775	3310	heat shock 70kDa protein 6 (HSP70B`)	Heat shock protein activity	Nucleus	Heat shock protein	Protein metabolism	CC	Yes
LRRC40	55631	leucine-rich repeat-containing protein 40	NP_060238.3	1	9	9	23	0.99	0.86	2	8.13	6.2	22.2	10	10	8622	55631	leucine rich repeat containing 40	Molecular function unknown	-	Unclassified	Biological_process unknown	LRR	No
CEP170	9859	centrosomal protein of 170 kDa isoform alpha	NP_055627.2	1	3	20	38	0.99	0.85	24.74	14.64	44.2	21.8	3	3	17172	9859	KIAA0470	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	FHA;CC	No
EMC10	284361	ER membrane protein complex subunit 10 isoform 2 precursor	NP_996261.1	2	1	1	6	0.99	0.85	7.49	9.14	12.9	13.4	3	3									

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
APLP2	334	amyloid-like protein 2 isoform 1 precursor	NP_001633.1	5	4	4	6	0.99	0.84	19.9	12.56	40.8	21.4	4	4	103	334	amyloid beta (A4) precursor-like protein 2	Protein binding	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	KUNITZ;TM;CC;NPXY;SP	Yes
SDR39U1	56948	epimerase family protein SDR39U1 isoform 1	NP_064580.2	1	1	1	2	0.99	0.84					1	1	16598	56948	chromosome 14 open reading frame 124	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PDSS2	57107	decaprenyl-diphosphate synthase subunit 2	NP_065114.3	1	1	1	1	0.99	0.83					1	1	12879	57107	chromosome 6 open reading frame 210	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	SP	No
YWHAG	7532	14-3-3 protein gamma	NP_036611.2	1	10	15	120	0.99	0.82	2.65	9.3	12.4	37.1	22	22	5639	7532	tyrosine 3-monooxygenase/tryptophan5-monooxygenase activation protein, gamma polypeptide	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
SMAP1	60682	stromal membrane-associated protein 1 isoform A	NP_001037770.1	3	1	1	2	0.99	0.82					1	1	18072	60682	stromal membrane-associated protein 1	Binding	Integral to membrane	Integral membrane protein	Cell growth and/or maintenance	TM;CXXC	No
DOCK9	23348	dedicator of cytokinesis protein 9 isoform a	NP_056111.1	4	3	3	4	0.99	0.81	7.76	26.62	13.3	38.8	3	3	9542	23348	dedicator of cytokinesis 9	Guanyl-nucleotide exchange factor activity	Plasma membrane	Guanine nucleotide exchange factor	Cell communication;Signal transduction	PH;CC	Yes
VPS11	55823	vacuolar protein sorting-associated protein 11 homolog isoform 1	NP_068375.3	2	2	2	2	0.99	0.81	2.56	38.93	3.6	47	2	2	12258	55823	vacuolar protein sorting 11 (yeast)	Transporter activity	Endosome	Transport/cargo protein	Transport	CC;RING	Yes
MICAL3	57553	protein-methionine sulfoxide oxidase MICAL3 isoform 1	NP_056056.2	3	3	4	9	0.99	0.78	9.42	9.6	16.2	13	3	3	19352	57553	microtubule associated monoxygenase, calponin and LIM domain containing 3	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell motility;Transport	CC	Yes
EPHX2	2053	bifunctional epoxide hydrolase 2 isoform a	NP_001970.2	3	1	1	2	0.99	0.74					1	1	582	2053	epoxide hydrolase 2, cytoplasmic	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	ABH	Yes
POGZ	23126	pogo transposable element with ZNF domain isoform 1	NP_055915.2	5	5	5	8	0.99	0.72	30.17	2.18	55.4	2.7	3	3	11445	23126	pogo transposable element with ZNF domain	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
SH3PXD2A	9644	SH3 and PX domain-containing protein 2A	NP_055446.2	3	2	2	2	0.99	0.69					1	1	10228	9644	SH3 multiple domains 1	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	PX;SH3;CC	No
INTS4	92105	integrator complex subunit 4	NP_291025.3	1	4	4	11	0.99	0.69	13.11	28.68	32.6	51.2	6	6	12386	92105	None	Transcription regulator activity	-	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ADAP	Yes
CBX1	10951	chromobox protein homolog 1	NP_001120700.1	1	3	4	18	0.99	0.68	7.85	29.47	15.7	41.7	4	4	5149	10951	chromobox homolog 1 (HP1 beta homolog Drosophila)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CHROMO	No
ABHD12	26090	monoacylglycerol lipase ABHD12 isoform b	NP_056415.1	2	3	3	6	0.99	0.6	10.43	8.04	18	8.4	3	3	7094	26090	chromosome 20 open reading frame 22	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM;ABH	Yes
HSBP1	3281	heat shock factor-binding protein 1	NP_001528.1	1	3	3	5	0.99	0.57	5.7	31.97	8	26.2	2	2	5185	3281	heat shock factor binding protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
TOMM22	56993	mitochondrial import receptor subunit TOM22 homolog	NP_064628.1	1	4	4	38	0.98	1.75	13.02	14.62	56.4	142.9	17	17	6130	56993	translocase of outer mitochondrial membrane 22homolog (yeast)	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	TM	Yes
MEA1	4201	male-enhanced antigen 1	NP_055438.1	1	1	1	3	0.98	1.74	18.26	6.27	25.8	15.6	2	2	885	4201	male-enhanced antigen 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
EXOSC5	56915	exosome complex component RRP46	NP_064543.3	1	2	2	7	0.98	1.61	15.58	1.37	31.4	4.4	4	4	16222	56915	exosome component 5	Ribonuclease activity	Nucleolus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
AUP1	550	ancient ubiquitous protein 1	NP_853553.1	1	3	3	7	0.98	1.56	8.7	13.06	19.2	47.9	5	5	3892	550	ancient ubiquitous protein 1	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	PISC;CUE;SP	Yes
SLC4A1AP	22950	kanadaptin	NP_060628.2	1	3	3	5	0.98	1.51	18.4	13.86	25.9	30.4	2	2	4038	22950	solute carrier family 4 (anion exchanger),member 1, adaptor protein	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	FHA;DSRM;CC;NLS	No
MAGOHB	55110	protein mago nashi homolog 2 isoform 1	NP_060518.1	3	7	7	13	0.98	1.45	7.47	2.85	23.6	13.1	10	10	8544	55110	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
AGFG1	3267	arf-GAP domain and FG repeat-containing protein 1 isoform 1	NP_001128659.1	4	3	3	5	0.98	1.37	4.81	4.38	8.2	10.4	3	3	2918	3267	HIV-1 Rev binding protein	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ARFGAP	Yes
FUBP1	8880	far upstream element-binding protein 1 isoform 2	NP_003893.2	2	15	17	31	0.98	1.35	6.18	6.33	24.6	35.3	16	16	10349	8880	far upstream element (FUSE) binding protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH;NLS	Yes

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
COPS5	10987	COP9 signalosome complex subunit 5	NP_006828.2	1	6	6	20	0.98	1.31	9.77	21.01	34.1	122	12	12	6888	10987	COP9 constitutive photomorphogenic homologsubunit 5 (Arabidopsis)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	JAB	Yes
KLC3	147700	kinesin light chain 3	NP_803136.2	1	5	5	7	0.98	1.29	1.63	1.78	3.6	5.2	5	5	3212	147700	None	Motor activity	-	Motor protein	Cell growth and/or maintenance	CC;TPR	No
DDB1	1642	DNA damage-binding protein 1	NP_001914.3	1	40	40	110	0.98	1.26	2.93	3.22	23.4	33.7	65	65	10952	1642	damage-specific DNA binding protein 1, 127kDa	DNA repair protein	Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
KPNA4	3840	importin subunit alpha-3	NP_002259.1	1	7	11	35	0.98	1.25	2.88	4.1	9.4	17.1	11	11	4275	3840	karyopherin alpha 4 (importin alpha 3)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ARM	No
LTN1	26046	E3 ubiquitin-protein ligase listerin	NP_056380.2	1	3	3	4	0.98	1.24	9.5	12.78	13.1	22.6	2	2									
CSDE1	7812	cold shock domain-containing protein E1 isoform 4	NP_001229820.1	4	15	15	29	0.98	1.23	9.38	4.94	39.5	25.5	17	17	15949	7812	None	RNA binding	Cytoplasm	RNA binding protein	Regulation of gene expression, epigenetic	CSP	Yes
EIF3L	51386	eukaryotic translation initiation factor 3 subunit L isoform 1	NP_057175.1	2	20	20	53	0.98	1.22	5.94	4.02	31.7	26.4	28	28	10932	51386	eukaryotic translation initiation factor 3,subunit 6 interacting protein	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	No
MSTO1	55154	protein misato homolog 1 isoform a	NP_060586.2	3	2	2	3	0.98	1.21	10.72	1.48	14.9	2.5	2	2	16904	55154	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
EIF4E2	9470	eukaryotic translation initiation factor 4E type 2 isoform A	NP_004837.1	4	3	3	11	0.98	1.18	1.63	3.33	3.6	8.8	5	5	5798	9470	eukaryotic translation initiation factor 4Emember 2	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 1	NP_006658.1	2	7	7	20	0.98	1.18	7.27	7.11	22.8	27	10	10	2338	10857	progesterone receptor membrane component 1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;CC	Yes
FJX1	24147	four-jointed box protein 1 precursor	NP_055159.2	1	1	1	2	0.98	1.16					1	1	16897	24147	four jointed box 1 (Drosophila)	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
EIF5B	9669	eukaryotic translation initiation factor 5B	NP_056988.3	1	26	26	63	0.98	1.16	3.51	4.34	20.2	30	34	34	7304	9669	eukaryotic translation initiation factor 5B	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC;GTP_EFTU;GTP_EFTU_D2	Yes
NNMT	4837	nicotinamide N-methyltransferase	NP_006160.1	1	5	5	15	0.98	1.16	15.13	11.86	44	40.5	8	8	2478	4837	nicotinamide N-methyltransferase	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	Yes
ADPRHL2	54936	poly(ADP-ribose) glycohydrolase ARH3	NP_060295.1	1	1	1	4	0.98	1.16	5.53	7.2	7.6	11.8	2	2	12432	54936	ADP-ribosylhydrolase like 2	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	No
COL6A1	1291	collagen alpha-1(VI) chain precursor	NP_001839.2	1	1	1	1	0.98	1.15					1	1	370	1291	collagen, type VI, alpha 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	VWA;COLL;SP	Yes
ECHDC1	55862	ethylmalonyl-CoA decarboxylase isoform 5	NP_001132982.1	5	6	6	15	0.98	1.14	9.27	5.26	26	17.1	8	8	13260	55862	enoyl Coenzyme A hydratase domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
CTSC	1075	dipeptidyl peptidase 1 isoform a preproprotein	NP_001805.3	1	4	4	13	0.98	1.14	9.81	9.81	25.9	30.3	7	7	3841	1075	cathepsin C	Cysteine-type peptidase activity	Lysosome	Cysteine protease	Protein metabolism	PPTC1;SP	Yes
PSMA4	5685	proteasome subunit alpha type-4 isoform 1	NP_002780.1	2	10	10	62	0.98	1.14	2.17	3.28	11.8	21	31	31	10168	5685	proteasome (prosome, macropain) subunit, alphatype, 4	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
CDK13	8621	cyclin-dependent kinase 13 isoform 1	NP_003709.3	47	3	4	21	0.98	1.13	2.04	7.43	3.4	14.6	3	3	4496	8621	cell division cycle 2-like 5(cholinesterase-related cell division controller)	Protein serine/threonine kinase activity	Nucleus;Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
ACACA	31	acetyl-CoA carboxylase 1 isoform 1	NP_942131.1	5	31	31	68	0.98	1.1	2.68	2.46	16.4	16.9	38	38	1938	31	acetyl-Coenzyme A carboxylase alpha	Ligase activity	Cytoplasm;Nucleus	Enzyme: Carboxylase	Metabolism;Energy pathways	-	Yes
CSTF3	1479	cleavage stimulation factor subunit 3 isoform 1	NP_001317.1	2	4	4	8	0.98	1.09	2.66	5.97	5.8	14.6	5	5	2651	1479	cleavage stimulation factor, 3` pre-RNA,subunit 3, 77kDa	RNA binding	Nucleus	RNA binding protein	RNA metabolism	NLS;HAT	Yes
GAK	2580	cyclin-G-associated kinase isoform 1	NP_005246.2	2	10	10	21	0.98	1.09	10.24	12.65	35.9	50.8	12	12	3631	2580	cyclin G associated kinase	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	SP;DNAJ;S_T_kinase	Yes
DNAJA3	9093	dnaJ homolog subfamily A member 3, mitochondrial isoform 1	NP_005138.3	3	4	4	9	0.98	1.08	7.4	14.36	16.3	35.9	5	5	9758	9093	DnaJ (Hsp40) homolog, subfamily A, member 3	Chaperone activity	Mitochondrion	Chaperone	Apoptosis	DNAJ;SP	Yes
OXNAD1	92106	oxidoreductase NAD-binding domain-containing protein 1 precursor	NP_612390.1	1	2	2	6	0.98	1.07	2.71	5.7	4.6	10.6	3	3	14446	92106	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PPME1	51400	protein phosphatase methylesterase 1 isoform b	NP_001258522.1	2	9	9	23	0.98	1.07	5.65	8.91	19.4	34.1	12	12	17864	51400	None	Methyltransferase activity	-	Enzyme: Methyltransferase	Metabolism;Energy pathways	ABH	Yes
B3GAT3	26229	galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 isoform 1	NP_036332.2	4	1	1	2	0.98	1.06					1	1	7564	26229	beta-1,3-glucuronyltransferase 3(glucuronosyltransferase I)	Transferase activity	Golgi apparatus	Integral membrane protein	Metabolism;Energy pathways	TM	Yes
VCPIP1	80124	deubiquitinating protein VCIP135	NP_079330.2	1	4	4	6	0.98	1.05	9.21	13.43	12.8	20.1	2	2	15645	80124	valosin containing protein (p97)/p47 complexinteracting protein 1	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes

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AP1M1	8907	AP-1 complex subunit mu-1 isoform 1	NP_001123996.1	2	7	9	29	0.98	1.05	4.55	7.02	14.8	24.7	11	11	4639	8907	adaptor-related protein complex 1, mu 1 subunit	Receptor signaling complex scaffold activity	Golgi apparatus	Adapter molecule	Cell communication;Signal transduction	-	Yes
GTPBP1	9567	GTP-binding protein 1	NP_004277.2	1	9	9	20	0.98	1.04	4.56	3.53	14.9	12.2	11	11	3765	9567	GTP binding protein 1	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	-	Yes
PTCD3	55037	pentatricopeptide repeat domain-containing protein 3, mitochondrial precursor	NP_060422.4	3	13	13	33	0.98	1.03	5.7	5.68	21.2	23	14	15	8631	55037	None	Protein binding	-	Unclassified	Biological_process unknown	-	Yes
NDUFAF4	29078	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NP_054884.1	1	3	3	5	0.98	1.03					1	1	10795	29078	chromosome 6 open reading frame 66	Molecular function unknown	-	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
GORASP1	64689	Golgi reassembly-stacking protein 1 isoform 1	NP_114105.1	2	1	1	1	0.98	1.02					1	1	6038	64689	golgi reassembly stacking protein 1, 65kDa	Structural molecule activity	Golgi apparatus	Structural protein	Cell growth and/or maintenance	-	Yes
KIAA1598	57698	shootin-1 isoform a	NP_001120683.1	5	6	6	11	0.98	1.01	11.55	3.23	28.4	8	6	6	11155	57698	KIAA1598	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
SRFBP1	153443	serum response factor-binding protein 1	NP_689759.2	1	2	2	5	0.98	1	0.27	1.29	0.5	2.2	3	3	8685	153443	serum response factor binding protein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Metabolism	CC	No
UPF1	5976	regulator of nonsense transcripts 1 isoform 1	NP_001284478.1	2	32	32	89	0.98	1	3.36	3.51	22.5	23.9	45	45	3254	5976	regulator of nonsense transcripts 1	Helicase activity	Cytoplasm;Nucleus	RNA binding protein	Regulation of translation;RNA metabolism	ZNFC2;ZnF_C4;DEAD	Yes
SORD	6652	sorbitol dehydrogenase	NP_003095.2	1	7	7	26	0.98	1	4.84	3.16	16.6	11	12	12	1679	6652	sorbitol dehydrogenase	Catalytic activity	Plasma membrane	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
LMAN1	3998	protein ERGIC-53 precursor	NP_005561.1	1	13	14	42	0.98	0.99	5.74	5.26	24.9	23	19	19	3338	3998	lectin, mannose-binding, 1	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	TM;SP;CC	Yes
RPS20	6224	40S ribosomal protein S20 isoform 1	NP_001139699.1	2	4	5	22	0.98	0.99	3.97	4.99	13	16.5	11	11	4728	6224	ribosomal protein S20	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
NMT2	9397	glycylpeptide N-tetradecanoyltransferase 2 isoform 1	NP_004799.1	2	1	4	7	0.98	0.99					1	1	11948	9397	N-myristoyltransferase 2	Transferase activity	Cytoplasm	Enzyme: Transferase	Metabolism;Energy pathways	-	Yes
ARHGAP1	392	rho GTPase-activating protein 1	NP_004299.1	1	17	17	58	0.98	0.99	6.6	3.72	34.6	19.3	27	27	4108	392	Rho GTPase activating protein 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	SEC14;RHOGAP	Yes
PYCR2	29920	pyrroline-5-carboxylate reductase 2 isoform 1	NP_037460.2	2	5	6	19	0.98	0.98	2.63	7.21	7.8	21.5	9	9	17939	29920	pyrroline-5-carboxylate reductase family,member 2	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	No
UNC45A	55898	protein unc-45 homolog A isoform 2	NP_061141.2	2	21	21	49	0.98	0.97	3.31	4.81	16.4	23.6	25	25	18070	55898	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	TPR;ARM	Yes
KLC1	3831	kinesin light chain 1 isoform 3	NP_001123579.1	4	6	11	20	0.98	0.97	6.06	4.91	14.6	11.7	6	6	2489	3831	kinesin 2 60/70kDa	Motor activity	Cytoplasm	Motor protein	Signal transduction	TPR;CC	Yes
NXN	64359	nucleoredoxin isoform 1	NP_071908.2	2	9	9	39	0.98	0.97	5.49	8.63	23.1	36.7	18	18	14858	64359	nucleoredoxin	Oxidoreductase activity	Nucleus	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
DDX42	11325	ATP-dependent RNA helicase DDX42	NP_031398.2	1	15	15	37	0.98	0.97	4.08	5.62	17	22.8	18	17	9909	11325	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;DEXDc;HELIC	Yes
GALNT7	51809	N-acetylgalactosaminyltransferase 7	NP_059119.2	1	7	7	17	0.98	0.97	7.88	7.28	20.5	18.9	7	7	10386	51809	UDP-N-acetyl-alpha-D-galactosamine:polypeptideN-acetylgalactosaminyltransferase 7 (GalNAc-T7)	Transferase activity	Integral to membrane	Enzyme: Transferase	Metabolism;Energy pathways	TM	Yes
VPS26A	9559	vacuolar protein sorting-associated protein 26A isoform 1	NP_004887.2	2	9	9	25	0.98	0.97	5.96	18.21	22.2	74.4	14	14	8385	9559	vacuolar protein sorting 26 (yeast)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
EIF3F	8665	eukaryotic translation initiation factor 3 subunit F	NP_003745.1	1	9	9	25	0.98	0.97	5.17	8	19.2	29.6	14	14	4887	8665	eukaryotic translation initiation factor 3,subunit 5 epsilon, 47kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	JAB	Yes
CDK9	1025	cyclin-dependent kinase 9	NP_001252.1	50	5	7	35	0.98	0.97	5.1	10.63	13.2	27.7	7	7	16016	1025	cyclin-dependent kinase 9 (CDC2-related kinase)	Protein serine/threonine kinase activity	Nucleus;Cytoplasm	Serine/threonine kinase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_kinase	Yes
GTPBP4	23560	nucleolar GTP-binding protein 1	NP_036473.2	1	14	14	25	0.98	0.96	2.86	9.08	10.9	34.9	15	15	9976	23560	GTP binding protein 4	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	CC	Yes
SBNO1	55206	protein strawberry notch homolog 1 isoform 1	NP_001161328.1	2	1	1	2	0.98	0.96					1	1	11533	55206	sno, strawberry notch homolog 1 (Drosophila)	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;CC;HELIC	No
OPA1	4976	dynamin-like 120 kDa protein, mitochondrial isoform 8	NP_570850.2	8	16	16	56	0.98	0.95	3.41	5.13	18.1	26.8	29	29	5596	4976	optic atrophy 1 (autosomal dominant)	GTPase activity	Mitochondrion	GTPase	Cell communication;Signal transduction	DYNC;CC	Yes
SMS	6611	spermine synthase isoform 1	NP_004586.2	2	8	8	25	0.98	0.95	6.87	9.67	26.5	36.6	15	15	2115	6611	spermine synthase	Transferase activity	-	Enzyme: Synthase	Metabolism;Energy pathways	-	No
AKAP13	11214	A-kinase anchor protein 13 isoform 1	NP_006729.4	3	9	9	14	0.98	0.94	2.36	6.41	6.5	17.2	8	8	5253	11214	A kinase (PRKA) anchor protein 13	Guanyl-nucleotide exchange factor activity	Plasma membrane	Guanine nucleotide exchange factor	Cell communication;Signal transduction	SP;CC;C1;RHOGEF;PH	Yes
CRTAP	10491	cartilage-associated protein precursor	NP_006362.1	1	3	3	4	0.98	0.94	5.92	37.52	10.1	67.4	3	3	16110	10491	cartilage associated protein	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	SP	Yes
RPS2	6187	40S ribosomal protein S2	NP_002943.2	1	15	16	85	0.98	0.94	3.39	3.66	21.2	21.9	40	40	4690	6187	ribosomal protein S2	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PFN2	5217	profilin-2 isoform b	NP_002619.1	2	3	3	5	0.98	0.92	8.89	6.57	15.2	10.5	3	3	1451	5217	profilin 2	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	PROF	Yes

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ILF3	3609	interleukin enhancer-binding factor 3 isoform d	NP_060090.2	7	32	32	131	0.98	0.92	4.71	5.14	39	39.8	66	66	4420	3609	interleukin enhancer binding factor 3, 90kDa	Transcription factor activity;Transcription regulator activity	Nucleus	Transcription factor;RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Regulation of gene expression, epigenetic	NLS;RBD;DZF;DSRM	Yes
NUP153	9972	nuclear pore complex protein Nup153 isoform 1	NP_001265138.1	3	13	13	21	0.98	0.92	6.9	5.43	26.6	19.5	15	15	4899	9972	nucleoporin 153kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	ZnF_RBZ	Yes
SIN3A	25942	paired amphipathic helix protein Sin3a	NP_001138829.1	1	3	3	3	0.98	0.91	7.41	5.39	12.7	8.5	3	3	9690	25942	SIN3 homolog A, transcription regulator (yeast)	Transcription regulator activity;DNA binding	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PAH	Yes
EEA1	8411	early endosome antigen 1	NP_003557.2	1	37	37	73	0.98	0.91	2.99	4.28	19.4	25.9	43	43	5460	8411	early endosome antigen 1, 162kD	Auxiliary transport protein activity	Endosome	Membrane transport protein	Transport	CC;ZNFC2;FYVE	Yes
AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	NP_001248755.1	2	16	16	44	0.98	0.91	5.54	5.1	24.7	21	20	20	6260	8943	adaptor-related protein complex 3, delta 1subunit	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ADAP	Yes
LGALS3BP	3959	galectin-3-binding protein precursor	NP_005558.1	1	12	12	61	0.98	0.91	3.01	3.98	16.8	20.8	32	32	2796	3959	lectin, galactoside-binding, soluble, 3binding protein	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Immune response	SP;SR	Yes
SERPINB6	5269	serpin B6 isoform d	NP_001258752.1	4	15	15	60	0.98	0.9	3.31	11.71	17.6	61.5	29	29	1413	5269	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 6	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism	SERPIN	Yes
PPP1R8	5511	nuclear inhibitor of protein phosphatase 1 isoform alpha	NP_054829.2	3	3	3	5	0.98	0.89	0.58	16.83	1	26.5	3	3	4028	5511	protein phosphatase 1, regulatory (inhibitor)subunit 8	RNA binding	Nucleus	Ribonuclease	RNA metabolism	FHA	Yes
H2AFY	9555	core histone macro-H2A.1 isoform 3	NP_613258.2	3	13	15	76	0.98	0.89	2.93	3.5	17.6	19.2	37	37	13624	9555	H2A histone family, member Y	DNA binding	Centrosome;Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H2A;A1pp	Yes
PRSS23	11098	serine protease 23 isoform a	NP_009104.2	3	2	2	4	0.98	0.89	19.56	2.75	27.6	3.5	2	2	7149	11098	protease, serine, 23	Serine-type peptidase activity	-	Serine protease	Protein metabolism	TRYPSIN;SP	Yes
MAP7D1	55700	MAP7 domain-containing protein 1 isoform 1	NP_060537.3	3	15	15	30	0.98	0.88	7.63	7.5	30.5	27	16	16	7666	55700	proline arginine rich coiled coil 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
MYOF	26509	myoferlin isoform a	NP_038479.1	16	85	85	242	0.98	0.87	1.98	3.07	23.3	32.2	140	140	6857	26509	fer-1-like 3, myoferlin (C. elegans)	Molecular function unknown	Plasma membrane;Nucleus	Integral membrane protein	Cell growth and/or maintenance	C2;SH3;NLS;TM	Yes
CLASP2	23122	CLIP-associating protein 2 isoform 1	NP_055912.2	1	1	6	20	0.98	0.87					1	1	12054	23122	cytoplasmic linker associated protein 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	-	No
ERGIC2	51290	endoplasmic reticulum-Golgi intermediate compartment protein 2	NP_057654.2	1	2	2	4	0.98	0.87	0.94	27.56	1.3	35	2	2	17932	51290	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	NLS	Yes
TOMM6	100188893	mitochondrial import receptor subunit TOM6 homolog	NP_001127965.1	1	1	1	6	0.98	0.86	1.45	0.9	2.5	1.3	3	3	19464	100188893	translocase of outer mitochondrial membrane 6 homolog (yeast)	Protein transporter activity	Mitochondrial membrane	Transport/cargo protein	Protein transport	-	No
APPL1	26060	DCC-interacting protein 13-alpha	NP_036228.1	1	8	8	13	0.98	0.85	3.58	4.23	9.3	9.5	7	7	5053	26060	None	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PH;PTB;CC	No
NOC4L	79050	nucleolar complex protein 4 homolog	NP_076983.1	1	7	7	13	0.98	0.85	3.04	18.09	7.3	42.3	6	7	14543	79050	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
BROX	148362	BRO1 domain-containing protein BROX isoform a	NP_653296.2	3	7	7	16	0.98	0.85	3.51	3.11	10.4	7.5	9	8									
RPL18	6141	60S ribosomal protein L18 isoform 1	NP_000970.1	2	7	7	53	0.98	0.82	3.94	4.52	21.3	20.6	30	30	16046	6141	ribosomal protein L18	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
TAP1	6890	antigen peptide transporter 1 isoform 1	NP_000584.2	2	6	6	23	0.98	0.79	9.28	12.59	32.4	35.5	12	12	1359	6890	transporter 1, ATP-binding cassette, sub-familyB (MDR/TAP)	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM;AAA	Yes
TMEM230	29058	transmembrane protein 230 isoform 1	NP_001009923.1	2	1	1	2	0.98	0.78					1	1									
DBT	1629	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial precursor	NP_001909.3	1	5	5	12	0.98	0.78	21.14	63.46	54.4	183.2	6	6	2010	1629	dihydrolipoamide branched chain transacylase E2	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	SP	Yes
TC2N	123036	tandem C2 domains nuclear protein isoform 1	NP_689545.1	2	2	2	2	0.98	0.77	13.95	33.94	19.5	38.5	2	2	11375	123036	membrane targeting (tandem) C2 domaincontaining 1	Transporter activity	Nucleus	Transport/cargo protein	Transport	C2	Yes
RABEP2	79874	rab GTPase-binding effector protein 2	NP_079092.2	1	2	2	4	0.98	0.76	7.85	21.99	10.9	23.9	2	2	17948	79874	rabaptin, RAB GTPase binding effector protein2	GTPase activator activity	Cytoplasm	GTPase activating protein	Transport	CC	No
TP53BP2	7159	apoptosis-stimulating of p53 protein 2 isoform 1	NP_001026855.2	2	3	3	4	0.98	0.75	16.95	4.2	23.8	4.5	2	2	11803	7159	tumor protein p53 binding protein, 2	Protein binding	Cytoplasm;Nucleus	Cell cycle control protein	Cell communication;Signal transduction	ANK;SH3;CC;RA	Yes
ACTC1	70	actin, alpha cardiac muscle 1 proprotein	NP_005150.1	4	2	27	749	0.98	0.75	4.72	27.92	19.2	105.2	17	17	15	70	actin, alpha, cardiac muscle	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	ACTIN	Yes
IFIT3	3437	interferon-induced protein with tetratricopeptide repeats 3 isoform a	NP_001540.2	3	8	9	22	0.98	0.74	6.47	10.21	19.2	22.8	9	9	5228	3437	interferon-induced protein withtetratricopeptide repeats 3	Molecular function unknown	Cytoplasm	Unclassified	Immune response	TPR	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
CA12	771	carbonic anhydrase 12 isoform 1 precursor	NP_001209.1	3	5	5	10	0.98	0.73	24.17	47.4	49.9	78.6	4	4	4464	771	carbonic anhydrase XII	Catalytic activity	Plasma membrane	Enzyme: Carbonic anhydrase	Metabolism;Energy pathways	SP;TM	Yes
MRPS36	92259	28S ribosomal protein S36, mitochondrial	NP_150597.1	1	2	2	4	0.98	0.73	16.39	23.7	23	24.9	2	2	17600	92259	mitochondrial ribosomal protein S36	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
MKI67	4288	antigen KI-67 isoform 1	NP_002408.3	2	6	6	7	0.98	0.71	3.93	15.72	8.6	25.3	5	5	8902	4288	antigen identified by monoclonal antibody Ki-67	Protein binding	Nucleolus	Cell cycle control protein	Cell communication;Signal transduction	FHA	Yes
PTPRK	5796	receptor-type tyrosine-protein phosphatase kappa isoform a precursor	NP_001129120.1	6	5	5	9	0.98	0.7	3.37	17.5	7.4	28	5	5	3968	5796	protein tyrosine phosphatase, receptor type, K	Receptor signaling protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine phosphatase	Cell communication;Signal transduction	SP;MAM;IG;FN3;TM;Tyr_Phos	Yes
TP53I3	9540	quinone oxidoreductase PIG3 isoform 1	NP_004872.2	2	4	4	6	0.98	0.67	9.15	7.62	15.6	8.9	3	3	5527	9540	tumor protein p53 inducible protein 3	Oxidoreductase activity	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
ARAP1	116985	arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform c	NP_001035207.1	3	1	1	5	0.98	0.64	47.69	10.86	74	9.8	2	2	9440	116985	centaurin, delta 2	GTPase activator activity	Golgi apparatus	GTPase activating protein	Cell communication;Signal transduction	PH;ARFGAP;ANK;RHOGAP;RA	Yes
SPTBN5	51332	spectrin beta chain, non-erythrocytic 5	NP_057726.4	1	1	1	1	0.98	0.63					1	1	10438	51332	spectrin, beta, non-erythrocytic 5	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;SPECTRIN;CC	Yes
BTAF1	9044	TATA-binding protein-associated factor 172	NP_003963.1	1	1	1	1	0.98	0.58					1	1	5546	9044	BTAF1 RNA polymerase II, B-TFIID transcriptionfactor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PHLDA1	22822	pleckstrin homology-like domain family A member 1	NP_031376.3	1	2	2	5	0.97	1.72	1.68	0.03	2.8	0.1	3	3	5625	22822	pleckstrin homology-like domain, family A,member 1	Transcription factor activity	Cytoplasm	Transcription factor	Protein metabolism;Apoptosis	PH	Yes
PTMA	5757	prothymosin alpha isoform 2	NP_002814.3	4	7	7	48	0.97	1.53	7.62	2.84	34.7	20.1	21	21	1778	5757	prothymosin, alpha (gene sequence 28)	Molecular function unknown	Nucleus	Unclassified	Cell proliferation	CC;NLS	Yes
DUT	1854	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 1 precursor	NP_001020419.1	3	3	3	5	0.97	1.46	5.34	4.98	9	12.7	3	3	3165	1854	dUTP pyrophosphatase	Hydrolase activity	Cytoplasm;Nucleus;Mitochondrion	Enzyme: Hydrolase	DNA replication	NLS	Yes
RUVBL1	8607	ruvB-like 1	NP_003698.1	1	19	19	90	0.97	1.44	3.95	3.3	26.8	33.4	47	47	9143	8607	RuvB-like 1 (E. coli)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA	Yes
DCTN4	51164	dynactin subunit 4 isoform b	NP_057305.1	3	10	10	32	0.97	1.37	4.63	10.84	15.7	54.9	12	12	13126	51164	dynactin 4 (p62)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
MYL12A	10627	myosin regulatory light chain 12A isoform 2	NP_001289978.1	3	5	10	181	0.97	1.37	5.04	4.8	34.1	47.3	46	47	14735	10627	None	Calcium ion binding	Cytoskeleton	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
SAP30BP	29115	SAP30-binding protein isoform 1	NP_001288784.1	3	3	3	4	0.97	1.37	4.56	15.88	7.7	38.9	3	3	17094	29115	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Biological_process unknown	NLS	No
UFD1L	7353	ubiquitin fusion degradation protein 1 homolog isoform A	NP_005650.2	2	6	6	15	0.97	1.34	8.69	14.13	25.6	61.9	9	9	6778	7353	ubiquitin fusion degradation 1-like	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
CEACAM1	634	carcinoembryonic antigen-related cell adhesion molecule 1 isoform 1 precursor	NP_001703.2	6	1	1	2	0.97	1.29					1	1	191	634	carcinoembryonic antigen-related celladhesion molecule 1 (biliary glycoprotein)	Molecular function unknown	Plasma membrane	Adhesion molecule	Signal transduction	SP;IGC2;TM;Ig_LIKE;IG	Yes
SLC7A5	8140	large neutral amino acids transporter small subunit 1	NP_003477.4	1	4	4	13	0.97	1.26	3.34	5.47	7.9	17	6	6	2552	8140	solute carrier family 7 (cationic amino acidtransporter, y+ system), member 5	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	Yes
USP47	55031	ubiquitin carboxyl-terminal hydrolase 47 isoform a	NP_001269588.1	2	7	7	15	0.97	1.22	5.8	7.86	16	27.6	8	8	11668	55031	ubiquitin specific protease 47	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UCH;CC	No
HSPA1B	3304	heat shock 70 kDa protein 1A/1B	NP_005337.2	1	26	35	266	0.97	1.2	2.84	3.18	28.5	40.5	103	104	6784	3304	heat shock 70kDa protein 1B	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CC	Yes
DHCR7	1717	7-dehydrocholesterol reductase	NP_001157289.1	1	4	4	11	0.97	1.2	15.39	0.41	34.2	1.1	5	5	4174	1717	7-dehydrocholesterol reductase	Catalytic activity	Peroxisome	Enzyme: Reductase	Metabolism;Energy pathways	TM	Yes
NFKB1	4790	nuclear factor NF-kappa-B p105 subunit isoform 1	NP_003989.2	2	10	11	20	0.97	1.18	12.6	7.46	40	28.5	10	10	1238	4790	nuclear factor of kappa light polypeptide geneenhancer in B-cells 1 (p105)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RHD;IPT;ANK;DEATH	Yes
MRPL43	84545	39S ribosomal protein L43, mitochondrial isoform d	NP_789764.1	5	3	3	8	0.97	1.18	7.77	2.57	16.9	6.8	5	5	14762	84545	mitochondrial ribosomal protein L43	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
HMOX2	3163	heme oxygenase 2 isoform a	NP_001273196.1	3	13	13	38	0.97	1.16	5.6	9.41	25.2	53.1	21	21	783	3163	heme oxygenase (decycling) 2	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase	Metabolism;Energy pathways	TM	Yes
RNMT	8731	mRNA cap guanine-N7 methyltransferase isoform 1	NP_001295192.1	2	4	4	15	0.97	1.15	3.43	11.69	9.4	39.6	8	8	4622	8731	RNA (guanine-7-) methyltransferase	RNA methyltransferase activity	Cytoplasm	RNA methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
GCAT	23464	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial isoform 1 precursor	NP_001165161.1	2	2	2	3	0.97	1.15	1.36	10.04	1.9	16.4	2	2	7602	23464	glycine C-acetyltransferase(2-amino-3-ketobutyrate coenzyme A ligase)	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
MRPL27	51264	39S ribosomal protein L27, mitochondrial	NP_057588.1	1	3	3	3	0.97	1.14	1.13	19.72	1.5	32.7	2	2	14750	51264	mitochondrial ribosomal protein L27	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	Yes
PSMB7	5695	proteasome subunit beta type-7 proprotein	NP_002790.1	1	6	6	26	0.97	1.13	11.62	9.27	38.9	37.5	11	12	4940	5695	proteasome (prosome, macropain) subunit, betatype, 7	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
NECAP2	55707	adaptin ear-binding coat-associated protein 2 isoform 2	NP_001138749.1	3	2	2	8	0.97	1.13	14.16	3.49	28.1	7.9	4	4	7674	55707	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
MBP	4155	Golli-MBP isoform 1	NP_001020272.1	2	1	1	1	0.97	1.12					1	1	1158	4155	myelin basic protein	Structural constituent of myelin sheath	Plasma membrane;Cytoplasm	Structural protein	Immune response;Neurogenesis	-	Yes
SUPV3L1	6832	ATP-dependent RNA helicase SUPV3L1, mitochondrial isoform 1	NP_003162.2	2	6	6	12	0.97	1.12	3.04	15.69	7.8	48.9	7	7	5493	6832	suppressor of var1, 3-like 1 (S. cerevisiae)	RNA binding	Mitochondrion	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;SP	No
MRPL34	64981	39S ribosomal protein L34, mitochondrial	NP_076426.1	1	1	1	2	0.97	1.09					1	1	14754	64981	mitochondrial ribosomal protein L34	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	Yes
ZC3HC1	51530	nuclear-interacting partner of ALK isoform 1	NP_057562.3	3	2	2	3	0.97	1.09	21.69	16.63	30.3	26.2	2	2	11390	51530	zinc finger, C3HC-type containing 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
GOT2	2806	aspartate aminotransferase, mitochondrial isoform 1 precursor	NP_002071.2	2	20	20	74	0.97	1.09	3.4	3.96	21.8	28.9	43	43	684	2806	glutamic-oxaloacetic transaminase 2,mitochondrial (aspartate aminotransferase 2)	Transaminase activity	Mitochondrion	Enzyme: Aminotransferase	Metabolism;Energy pathways	SP	Yes
CTAGE5	4253	cTAGE family member 5 isoform 6	NP_001234918.1	7	3	3	4	0.97	1.08	27.26	26.65	38.9	42.3	2	2	3680	4253	CTAGE family, member 5	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	CC;TM	Yes
HEATR5A	25938	HEAT repeat-containing protein 5A	NP_056288.2	1	1	1	2	0.97	1.08					1	1	10709	25938	chromosome 14 open reading frame 125	Molecular function unknown	-	Unclassified	Biological_process unknown	HEAT	No
LRRC8C	84230	volume-regulated anion channel subunit LRRC8C	NP_115646.2	1	3	4	14	0.97	1.07	19.75	4.22	39.7	9.1	4	4	13284	84230	None	Cytoskeletal anchoring activity	Endoplasmic reticulum	Anchor protein	Cell growth and/or maintenance	LRR;TM	No
RPS13	6207	40S ribosomal protein S13	NP_001008.1	1	14	14	50	0.97	1.06	3.37	8.9	15.7	47.8	23	23	1604	6207	ribosomal protein S13	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PAFAH1B1	5048	platelet-activating factor acetylhydrolase IB subunit alpha	NP_000421.1	1	12	12	34	0.97	1.06	5.75	4.32	24.8	20.1	19	19	3329	5048	platelet-activating factor acetylhydrolase,isoform Ib, alpha subunit 45kDa	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	LISH;WD40;CC	Yes
KRT8	3856	keratin, type II cytoskeletal 8 isoform 1	NP_001243211.1	4	30	36	215	0.97	1.06	4.79	4.05	42.7	39.3	78	78	1015	3856	keratin 8	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
MB21D1	115004	cyclic GMP-AMP synthase	NP_612450.2	1	5	5	8	0.97	1.05	3.54	7.35	6.9	15.5	4	4									
SNX12	29934	sorting nexin-12 isoform 1	NP_037478.2	2	4	5	6	0.97	1.05	15.03	0.79	25.7	1.4	3	3	6719	29934	sorting nexin 12	Molecular function unknown	Cytoplasm	Unclassified	Protein metabolism	PX	Yes
PDIA5	10954	protein disulfide-isomerase A5 precursor	NP_006801.1	1	6	6	11	0.97	1.04	8.03	4.4	20.9	12.2	7	7	8334	10954	protein disulfide isomerase-associated 5	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP	Yes
AIMP2	7965	aminoacyl tRNA synthase complex-interacting multifunctional protein 2	NP_006294.2	1	10	10	26	0.97	1.04	7.47	7.61	28.5	31.4	15	15	2915	7965	None	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	LZ	Yes
RNF40	9810	E3 ubiquitin-protein ligase BRE1B isoform 1	NP_055586.1	4	5	7	12	0.97	1.04	1.32	10.77	2.2	19.7	3	3	7411	9810	ring finger protein 40	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC;RING;LZ;NLS	Yes
PLCH2	9651	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2 isoform 1	NP_055453.2	3	11	11	16	0.97	1.04	9.95	17.68	29.5	59.6	9	9	18986	9651	phospholipase C, eta 2	Phospholipase activity	Plasma membrane	Enzyme: Phospholipase	Cell growth and/or maintenance	SP;PH;EF;PLCXc;PLCYc;C2	Yes
TBRG4	9238	protein TBRG4 isoform 3	NP_001248763.1	3	11	11	17	0.97	1.03	2.5	2.73	7.7	8.9	10	10	10263	9238	transforming growth factor beta regulator 4	Molecular function unknown	Mitochondrion;Nucleus	Cell cycle control protein	Cell communication;Signal transduction	-	No
APOA1BP	128240	NAD(P)H-hydrate epimerase precursor	NP_658985.2	1	9	9	30	0.97	1.03	3.33	3.19	13	13.2	16	16	16397	128240	apolipoprotein A-I binding protein	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	SP	Yes
PURB	5814	transcriptional activator protein Pur-beta	NP_150093.1	1	7	7	21	0.97	1.03	7.2	9.34	23.5	32.9	11	11	12325	5814	purine-rich element binding protein B	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
PTPMT1	114971	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 isoform 1	NP_783859.1	2	2	2	6	0.97	1.02	5.49	5.76	7.5	8.3	2	2	15151	114971	protein tyrosine phosphatase, mitochondrial 1	Protein tyrosine/serine/threonine phosphatase activity	-	Dual specificity phosphatase	Cell communication;Signal transduction	DSPC	No
AP3B1	8546	AP-3 complex subunit beta-1 isoform 1	NP_003655.3	5	21	21	59	0.97	1.02	3.43	3.33	17.7	18.1	28	28	4551	8546	adaptor-related protein complex 3, beta 1subunit	Receptor signaling complex scaffold activity	Plasma membrane;Nucleus;Cytoplasm	Adapter molecule	Protein metabolism	ADAP	Yes
LIPA	3988	lysosomal acid lipase/cholesteryl ester hydrolase isoform 1 precursor	NP_001121077.1	2	2	2	6	0.97	1.02	2.9	7.17	4.9	12.7	3	3	2044	3988	lipase A, lysosomal acid, cholesterol esterase(Wolman disease)	Lipase activity	Lysosome	Enzyme: Lipase	Metabolism;Energy pathways	ABH;SP	No
ATP6V1A	523	V-type proton ATPase catalytic subunit A	NP_001681.2	1	19	19	53	0.97	1.01	5.99	10.48	32.2	61.7	29	29	6120	523	ATPase, H+ transporting, lysosomal 70kDa, V1subunit A	Transporter activity	Endosome	Transport/cargo protein	Metabolism;Energy pathways	-	Yes
LARS	51520	leucine--tRNA ligase, cytoplasmic	NP_064502.9	1	44	44	117	0.97	1.01	3.21	2.89	24.7	23	61	61	1042	51520	leucyl-tRNA synthetase	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
CHP1	11261	calcineurin B homologous protein 1	NP_009167.1	1	7	7	22	0.97	1	11.38	5.06	38	16.9	11	11									

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Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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VPS25	84313	vacuolar protein-sorting-associated protein 25	NP_115729.1	1	4	4	10	0.97	1	10.47	3.38	25.1	8.3	6	6	14396	84313	None	Transporter activity	Endosome	Transport/cargo protein	Transport	-	No
SWAP70	23075	switch-associated protein 70 isoform 1	NP_055870.2	2	10	10	17	0.97	0.99	2.93	7.17	9.1	22.7	10	10	10378	23075	None	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	PH;CC;NLS;NES	Yes
NR3C1	2908	glucocorticoid receptor isoform gamma	NP_001019265.1	5	1	1	2	0.97	0.99					1	1	679	2908	nuclear receptor subfamily 3, group C, member 1(glucocorticoid receptor)	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor;Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C4;HOLI	Yes
IKBKAP	8518	elongator complex protein 1	NP_003631.2	1	18	18	45	0.97	0.99	3.68	3.65	17.2	17.5	23	23	4763	8518	inhibitor of kappa light polypeptide geneenhancer in B-cells, kinase complex-associated protein	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 1	NP_851997.1	4	3	3	5	0.97	0.98	3.51	27.46	5.9	49.2	3	3	9811	55729	activating transcription factor 7 interactingprotein	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;FN3	Yes
MIPEP	4285	mitochondrial intermediate peptidase	NP_005923.2	1	6	6	14	0.97	0.98	3.43	4.29	9.4	11.9	8	8	3761	4285	mitochondrial intermediate peptidase	Metallopeptidase activity	Mitochondrion	Metallo protease	Protein metabolism	-	Yes
PPIB	5479	peptidyl-prolyl cis-trans isomerase B precursor	NP_000933.1	1	16	16	91	0.97	0.98	5.39	7.52	37.3	54.7	48	48	458	5479	peptidylprolyl isomerase B (cyclophilin B)	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP	Yes
GIT1	28964	ARF GTPase-activating protein GIT1 isoform 1	NP_001078923.1	3	3	5	11	0.97	0.98	7.13	13.63	15.6	30.6	5	5	6577	28964	G protein-coupled receptor kinase interactor 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	ARFGAP;CC	Yes
SMC2	10592	structural maintenance of chromosomes protein 2	NP_001252531.1	1	20	20	35	0.97	0.98	2.34	4.67	10	20.2	19	19	9277	10592	SMC2 structural maintenance of chromosomes2-like 1 (yeast)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
HELZ2	85441	helicase with zinc finger domain 2 isoform 1	NP_001032412.2	2	23	23	52	0.97	0.97	2.63	7.15	13.6	37.8	28	28									
COPA	1314	coatomer subunit alpha isoform 1	NP_001091868.1	2	48	48	150	0.97	0.97	2.55	3.43	22.5	30.7	80	81	3564	1314	coatomer protein complex, subunit alpha	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	WD40	Yes
BST2	684	bone marrow stromal antigen 2 precursor	NP_004326.1	1	1	1	3	0.97	0.95	12.57	12.22	17.4	16.5	2	2	2759	684	bone marrow stromal cell antigen 2	Molecular function unknown	Plasma membrane	Integral membrane protein	Immune response	CC;TM	Yes
WDR46	9277	WD repeat-containing protein 46 isoform 1	NP_005443.3	2	6	6	12	0.97	0.95	6.78	5.79	16.2	13.6	6	6	12839	9277	WD repeat domain 46	Molecular function unknown	Nucleolus	Unclassified	Cell communication;Signal transduction	WD40	Yes
AGPS	8540	alkyldihydroxyacetonephosphate synthase, peroxisomal precursor	NP_003650.1	1	18	18	43	0.97	0.94	5.58	6.6	26.5	30.3	23	23	4337	8540	alkylglycerone phosphate synthase	Transferase activity	Peroxisome	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
EPRS	2058	bifunctional glutamate/proline--tRNA ligase	NP_004437.2	1	55	55	175	0.97	0.94	3.42	3.33	32.8	30.9	93	93	703	2058	glutamyl-prolyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
CAD	790	CAD protein isoform 1	NP_004332.2	2	46	46	125	0.97	0.93	2.5	3.54	20.2	27.6	68	68	6437	790	carbamoyl-phosphate synthetase 2, aspartatetranscarbamylase, and dihydroorotase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
NELFB	25920	negative elongation factor B	NP_056271.2	1	9	9	18	0.97	0.93	2.9	9.73	8.4	27.6	9	9									
TXNDC12	51060	thioredoxin domain-containing protein 12 precursor	NP_056997.1	1	3	3	6	0.97	0.92	20.99	47.96	36.4	89.4	3	3	11633	51060	thioredoxin domain containing 12 (endoplasmicreticulum)	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase	Protein metabolism	SP	Yes
SLC20A2	6575	sodium-dependent phosphate transporter 2	NP_001244109.1	1	1	1	2	0.97	0.92					1	1	8865	6575	solute carrier family 20 (phosphatetransporter), member 2	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
ZC3H7B	23264	zinc finger CCCH domain-containing protein 7B	NP_060060.3	1	4	4	5	0.97	0.91	9.52	12.63	18.6	23.3	4	4	6711	23264	zinc finger CCCH-type containing 7B	Translation regulator activity	Nucleus	Translation regulatory protein	Protein metabolism	TPR;CC;ZNFC2;ZnF_C3H1	Yes
NKRF	55922	NF-kappa-B-repressing factor isoform 1	NP_001166958.1	2	4	4	7	0.97	0.91	2.52	4.5	4.9	8.2	4	4	2341	55922	NF-kappaB repressing factor	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;DSRM;G_PATCH;R3H	Yes
ARIH1	25820	E3 ubiquitin-protein ligase ARIH1	NP_005735.2	1	5	5	11	0.97	0.91	5.68	1.42	12.4	2.9	5	5	5730	25820	ariadne homolog, ubiquitin-conjugating enzymeE2 binding protein, 1 (Drosophila)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	RING;IBR	Yes
INPP1	3628	inositol polyphosphate 1-phosphatase	NP_002185.1	1	3	3	8	0.97	0.9	12.5	2.96	27.6	6	5	5	923	3628	inositol polyphosphate-1-phosphatase	Catalytic activity	Cytoplasm	Enzyme: Phosphohydrolase	Cell communication;Signal transduction	I_Phosphatase	Yes
SNRPD1	6632	small nuclear ribonucleoprotein Sm D1 isoform 1	NP_008869.1	2	4	4	15	0.97	0.9	8.58	14.56	23.8	38.2	8	8	3040	6632	small nuclear ribonucleoprotein D1 polypeptide16kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
STX5	6811	syntaxin-5 isoform 1	NP_003155.2	2	5	5	8	0.97	0.9	11.21	19.45	22.1	36.1	4	4	4426	6811	syntaxin 5A	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	TM;CC;t_SNARE	Yes
EMC7	56851	ER membrane protein complex subunit 7 precursor	NP_064539.1	1	2	2	3	0.97	0.89	7.1	16.55	9.8	21	2	2									

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GTF2I	2969	general transcription factor II-I isoform 1	NP_127492.1	8	17	17	28	0.97	0.89	3.05	4.83	13	18.9	19	19	3399	2969	general transcription factor II, i	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ASCC3	10973	activating signal cointegrator 1 complex subunit 3 isoform a	NP_006819.2	2	16	16	28	0.97	0.89	4.59	7.36	18	26.7	16	16	9980	10973	activating signal cointegrator 1 complexsubunit 3	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;DEXDc;HELIC	Yes
EARS2	124454	probable glutamate--tRNA ligase, mitochondrial isoform 2	NP_001295140.1	2	2	2	6	0.97	0.89	0.31	36.73	0.5	61.4	3	3	11174	124454	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ZC3HAV1	56829	zinc finger CCCH-type antiviral protein 1 isoform 1	NP_064504.2	2	20	21	44	0.97	0.88	7.69	4.75	34.2	18.8	20	20	9534	56829	zinc finger CCCH-type, antiviral 1	Defense/immunity protein activity	Cytoplasm;Nucleus	-	Immune response	SP	Yes
RPL10A	4736	60S ribosomal protein L10a	NP_009035.3	1	10	10	58	0.97	0.88	4.85	5.04	27	25.7	32	32	10199	4736	ribosomal protein L10a	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
LARP7	51574	la-related protein 7 isoform 2	NP_001253968.1	2	9	9	13	0.97	0.88	3.06	7.98	8.4	20	8	8	17095	51574	None	Molecular function unknown	-	Unclassified	Biological_process unknown	LA;RRM;CC	No
PTK2B	2185	protein-tyrosine kinase 2-beta isoform a	NP_775266.1	2	6	7	13	0.97	0.88	6.41	11.49	15.4	25.2	6	6	3131	2185	PTK2B protein tyrosine kinase 2 beta	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase	Signal transduction	B41;Tyr_Kinase;CC	Yes
DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 1	NP_001354.1	3	16	16	41	0.97	0.88	4.99	6.46	24	28.3	24	24	2129	1736	dyskeratosis congenita 1, dyskerin	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
METTL1	4234	tRNA (guanine-N(7)-)-methyltransferase isoform a	NP_005362.3	1	4	4	8	0.97	0.88	4.87	18.07	9.5	32.8	4	4	6834	4234	methyltransferase like 1	RNA methyltransferase activity	-	RNA methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MTHFD1	4522	C-1-tetrahydrofolate synthase, cytoplasmic	NP_005947.3	1	42	42	135	0.97	0.88	2.39	3.78	19.9	28.6	72	72	1403	4522	methylenetetrahydrofolate dehydrogenase (NADP+dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolatesynthetase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
THOC3	84321	THO complex subunit 3	NP_115737.1	1	3	3	4	0.97	0.88	10.64	11.61	18	17.8	3	3	9497	84321	THO complex 3	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
NCSTN	23385	nicastrin isoform 1 precursor	NP_056146.1	3	4	4	10	0.97	0.87	6.11	18.72	13.3	37.7	5	5	5584	23385	nicastrin	Protein binding	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	SP;TM	Yes
TUBGCP3	10426	gamma-tubulin complex component 3 isoform 1	NP_006313.1	4	9	9	18	0.97	0.87	9.68	13.62	30.3	38.7	10	10	10289	10426	tubulin, gamma complex associated protein 3	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
AFG3L2	10939	AFG3-like protein 2	NP_006787.2	1	18	18	37	0.97	0.87	3.31	6.62	14.1	25.5	19	19	5205	10939	AFG3 ATPase family gene 3-like 2 (yeast)	ATPase activity	Mitochondrion	ATPase	Transport	AAA;TM	Yes
LRRFIP2	9209	leucine-rich repeat flightless-interacting protein 2 isoform 3	NP_001127841.1	4	4	4	6	0.97	0.87	13.52	5.86	22.9	8.9	3	3	10061	9209	leucine rich repeat (in FLII) interactingprotein 2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
CAPN7	23473	calpain-7	NP_055111.1	1	2	2	2	0.97	0.87					1	1	5908	23473	calpain 7	Cysteine-type peptidase activity	Nucleus	Cysteine protease	Protein metabolism	CYSPC;CALPAIN_III;CC	Yes
VPS37B	79720	vacuolar protein sorting-associated protein 37B	NP_078943.1	1	3	3	8	0.97	0.87	6.53	26.57	11	41.7	3	3	7794	79720	None	Protein transporter activity	Cytoplasm	Transport/cargo protein	Protein transport	-	Yes
MAN2A1	4124	alpha-mannosidase 2	NP_002363.2	1	8	8	16	0.97	0.87	5.05	7.23	15.6	20.1	10	10	1110	4124	mannosidase, alpha, class 2A, member 1	Catalytic activity	Golgi apparatus	Enzyme: Glycosidase	Metabolism;Energy pathways	TM;CC	Yes
LOC102723897	102723897	LOW QUALITY PROTEIN: WAS protein family homolog 2-like isoform X7	XP_011542112.1	2	2	2	9	0.97	0.86	1.62	5.99	3.1	10.3	4	4									
RPS6KA3	6197	ribosomal protein S6 kinase alpha-3	NP_004577.1	21	4	10	37	0.97	0.85	9.48	10.9	24.7	25	7	7	2092	6197	ribosomal protein S6 kinase, 90kDa,polypeptide 3	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
AR	367	androgen receptor isoform 2	NP_001011645.1	1	1	1	2	0.97	0.82	21.3	26.14	29.9	31.1	2	2	2437	367	androgen receptor (dihydrotestosterone receptor;testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	Ligand-dependent nuclear receptor activity	Nucleus;Cytoplasm	Nuclear receptor	Cell communication;Signal transduction	ZnF_C4;CC;HOLI	Yes
CASP4	837	caspase-4 isoform alpha precursor	NP_001216.1	3	3	3	5	0.97	0.82	2.81	38.36	3.9	47	2	2	4047	837	caspase 4, apoptosis-related cysteine protease	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Apoptosis	CARD;CASc	Yes
MFF	56947	mitochondrial fission factor isoform a	NP_064579.3	7	5	5	12	0.97	0.82	11	9.91	26.6	20.1	6	6	16653	56947	chromosome 2 open reading frame 33	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	CC;TM	Yes
CCDC120	90060	coiled-coil domain-containing protein 120 isoform 1	NP_001156793.2	4	1	1	2	0.97	0.82					1	1	6595	90060	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No

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YKT6	10652	synaptobrevin homolog YKT6	NP_006546.1	1	6	6	19	0.97	0.81	4.52	4.21	13.2	10.3	9	9	16205	10652	None	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Transport	-	No
STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	NP_849193.1	1	9	9	23	0.97	0.81	6.65	10.64	23.5	31.7	13	13	12268	201595	None	Catalytic activity;Phosphoprotein phosphatase activity	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
UQCRQ	27089	cytochrome b-c1 complex subunit 8	NP_055217.2	1	4	4	9	0.97	0.81	3.3	8.1	7.2	14.8	5	5	17941	27089	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
COG1	9382	conserved oligomeric Golgi complex subunit 1	NP_061184.1	1	6	6	12	0.97	0.79	23.26	15.69	59.6	31.2	6	6	7371	9382	component of oligomeric golgi complex 1	Structural molecule activity	Golgi apparatus	Structural protein	Transport	-	Yes
HAAO	23498	3-hydroxyanthranilate 3,4-dioxygenase	NP_036337.2	1	1	1	2	0.97	0.79					1	1	5158	23498	3-hydroxyanthranilate 3,4-dioxygenase	Catalytic activity	Cytoplasm	Enzyme: Oxygenase	Metabolism;Energy pathways	-	Yes
TRIP6	7205	thyroid receptor-interacting protein 6	NP_003293.2	1	6	6	9	0.97	0.78	8.93	7.17	17.4	11.2	4	4	4242	7205	thyroid hormone receptor interactor 6	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LIM	Yes
PTPN23	25930	tyrosine-protein phosphatase non-receptor type 23 isoform 1	NP_056281.1	2	10	10	26	0.97	0.78	9.28	15.63	33.2	46.4	13	13	5959	25930	protein tyrosine phosphatase, non-receptortype 23	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	CC;Tyr_Phos	Yes
OCLN	100506658	occludin isoform a	NP_002529.1	2	1	1	1	0.97	0.77					1	1	4191	4950	occludin	Cell adhesion molecule activity	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	TM;CC	No
TRIM56	81844	E3 ubiquitin-protein ligase TRIM56	NP_112223.1	1	6	6	15	0.97	0.75	4.57	12.18	11.8	24.6	7	7	10284	81844	tripartite motif-containing 56	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;BBOX;CC	Yes
WIPF2	147179	WAS/WASL-interacting protein family member 2	NP_573571.1	1	2	2	2	0.97	0.75					1	1	18304	147179	None	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	WH2	Yes
PPP1R14B	26472	protein phosphatase 1 regulatory subunit 14B	NP_619634.1	1	1	1	3	0.97	0.73	7.8	23.67	13.1	30.4	3	3	18513	26472	protein phosphatase 1, regulatory(inhibitor) subunit 14B	Phosphatase regulator activity	Cytoplasm	Enzyme regulator	Metabolism;Energy pathways	SP;CC	Yes
PTGS1	5742	prostaglandin G/H synthase 1 isoform 1 precursor	NP_000953.2	6	2	2	2	0.97	0.71	2.77	47.25	3.8	50.5	2	2	7518	5742	prostaglandin-endoperoxide synthase 1(prostaglandin G/H synthase and cyclooxygenase)	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase	Lipid metabolism	EGF;TM	Yes
CDC42EP4	23580	cdc42 effector protein 4	NP_036253.2	1	1	1	2	0.97	0.58					1	1	8383	23580	CDC42 effector protein (Rho GTPase binding)4	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	-	Yes
SH2D3A	10045	SH2 domain-containing protein 3A	NP_005481.2	1	1	1	2	0.97	0.56					1	1	5283	10045	SH2 domain containing 3A	Receptor signaling complex scaffold activity	-	Adapter molecule	Cell communication;Signal transduction	SH2	No
SPCS3	60559	signal peptidase complex subunit 3	NP_068747.1	1	4	4	14	0.96	1.78	10.59	6.05	29.3	31.2	8	8	8001	60559	signal peptidase complex subunit 3 homolog (S.cerevisiae)	Protease activator activity	-	Protease	Protein metabolism;Protein modification	SP	No
OXSM	54995	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial isoform 1 precursor	NP_060367.1	2	1	1	1	0.96	1.63					1	1	7931	54995	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
GPX4	2879	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform C precursor	NP_001034937.1	3	2	2	4	0.96	1.27	2.19	3.72	3	6.7	2	2	11819	2879	glutathione peroxidase 4 (phospholipidhydroperoxidase)	Peroxidase activity	Mitochondrion	Enzyme: Peroxidase	Metabolism;Energy pathways	SP	Yes
UBL4A	8266	ubiquitin-like protein 4A	NP_055050.1	1	3	3	10	0.96	1.24	1.98	7.47	4.6	23.1	6	6	2417	8266	ubiquitin-like 4	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBQ	Yes
LDHA	3939	L-lactate dehydrogenase A chain isoform 3	NP_001158886.1	7	22	25	220	0.96	1.23	4.26	3.03	44.7	40.7	110	110	1025	3939	lactate dehydrogenase A	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
PSMC3	5702	26S protease regulatory subunit 6A	NP_002795.2	1	15	15	62	0.96	1.21	3.87	6.34	21.7	46.1	33	33	1733	5702	proteasome (prosome, macropain) 26S subunit,ATPase, 3	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	AAA	Yes
SON	6651	protein SON isoform F	NP_620305.2	4	15	15	32	0.96	1.21	6.57	9.62	26.4	50.7	17	17	1678	6651	SON DNA binding protein	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	COLL;CC;DSRM;G_PATCH	Yes
HDAC1	3065	histone deacetylase 1	NP_004955.2	1	5	8	25	0.96	1.2	1.86	4.08	4.7	13	7	7	3143	3065	histone deacetylase 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
IGFBP2	3485	insulin-like growth factor-binding protein 2 precursor	NP_000588.2	1	1	1	1	0.96	1.19					1	1	898	3485	insulin-like growth factor binding protein 2,36kDa	Growth factor activity	Extracellular	Secreted polypeptide	Cell communication;Signal transduction	SP;IB;THYRO	Yes
CARD10	29775	caspase recruitment domain-containing protein 10	NP_055365.2	1	1	1	1	0.96	1.18					1	1	6233	29775	caspase recruitment domain family, member 10	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Apoptosis	CC;CARD;PDZ;SH3;GuKinase	Yes
HGS	9146	hepatocyte growth factor-regulated tyrosine kinase substrate	NP_004703.1	1	10	10	16	0.96	1.18	15.23	12.81	43.1	44.6	8	8	5085	9146	hepatocyte growth factor-regulated tyrosinekinase substrate	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	VHS;FYVE;UIM;CC	Yes

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AIMP1	9255	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 isoform b precursor	NP_001135888.1	2	10	10	23	0.96	1.17	3.66	5.35	13.2	23.7	14	14	4676	9255	small inducible cytokine subfamily E, member 1(endothelial monocyte-activating)	Cytokine activity	Extracellular	Cytokine	Immune response	CC;SP	Yes
GATB	5188	glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial precursor	NP_004555.1	1	4	4	4	0.96	1.15	12.2	7.98	20.5	16	3	3									
PYCRL	65263	pyrroline-5-carboxylate reductase 3	NP_075566.2	1	1	1	4	0.96	1.14	11.38	12.4	15.6	20.2	2	2	15196	65263	pyrroline-5-carboxylate reductase-like	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
XPO1	7514	exportin-1	NP_003391.1	1	29	29	104	0.96	1.13	3.21	6.11	22.2	52.3	51	51	3975	7514	exportin 1 (CRM1 homolog, yeast)	Transporter activity	Nucleus	Transport/cargo protein	Cell communication;Signal transduction	IBN_NT	Yes
DAXX	1616	death domain-associated protein 6 isoform b	NP_001135442.1	3	1	1	2	0.96	1.13					1	1	4424	1616	death-associated protein 6	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	NLS;CC	Yes
RAB11B	9230	ras-related protein Rab-11B	NP_004209.2	3	11	11	44	0.96	1.13	4.46	4.22	21.7	24.2	25	25	5009	9230	RAB11B, member RAS oncogene family	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	RAB	No
PREB	10113	prolactin regulatory element-binding protein	NP_037520.1	1	5	5	11	0.96	1.13	3.19	0.82	7.5	2.3	6	6	16216	10113	prolactin regulatory element binding	Transcription factor activity	Endoplasmic reticulum	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP;WD40;TM	Yes
TMED10	10972	transmembrane emp24 domain-containing protein 10 precursor	NP_006818.3	1	9	9	38	0.96	1.12	9.16	17.45	41	107.4	20	20	12013	10972	None	Transporter activity	Integral to membrane	Integral membrane protein	Transport	TM;SP	Yes
ITPR2	3709	inositol 1,4,5-trisphosphate receptor type 2	NP_002214.2	1	4	10	16	0.96	1.12	14.44	17.24	24.3	34.3	3	3	2536	3709	inositol 1,4,5-triphosphate receptor, type 2	Transporter activity	Plasma membrane	Transport/cargo protein	Cell communication;Signal transduction	MIR;RYDR;TM;CC	Yes
PDLIM4	8572	PDZ and LIM domain protein 4 isoform 1	NP_003678.2	2	3	3	5	0.96	1.12	16.38	20.2	27.8	40.9	3	3	4571	8572	PDZ and LIM domain 4	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	LIM;PDZ	Yes
PACSIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	NP_001171904.1	1	11	11	25	0.96	1.11	5.51	6.85	18.6	26.8	12	12	5937	29763	protein kinase C and casein kinase substratein neurons 3	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	FCH;CC;SH3	Yes
ETV6	2120	transcription factor ETV6	NP_001978.1	1	1	1	2	0.96	1.11					1	1	15976	2120	ets variant gene 6 (TEL oncogene)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAM_PNT;ETS	Yes
RPE	6120	ribulose-phosphate 3-epimerase isoform 1	NP_954699.1	3	1	1	2	0.96	1.11					1	1	1608	6120	ribulose-5-phosphate-3-epimerase	Racemase and epimerase activity	Cytoplasm	Enzyme: Epimerase	Metabolism;Energy pathways	-	Yes
ATP6V1C1	528	V-type proton ATPase subunit C 1	NP_001686.1	1	9	9	15	0.96	1.1	4.32	8.68	11.7	27.4	8	8	4371	528	ATPase, H+ transporting, lysosomal 42kDa, V1subunit C, isoform 1	ATPase activity	-	ATPase	Transport	CC	Yes
NUF2	83540	kinetochore protein Nuf2	NP_113611.2	1	1	1	1	0.96	1.1					1	1	10817	83540	cell division cycle associated 1	Cytoskeletal protein binding	Kinetochore	Cytoskeletal associated protein;Cell cycle control protein	Cell communication;Signal transduction;Spindle assembly;Chromosome segregation	CC	Yes
MSMO1	6307	methylsterol monooxygenase 1 isoform 1	NP_006736.1	2	1	1	3	0.96	1.1					1	1									
TEX264	51368	testis-expressed sequence 264 protein isoform 1 precursor	NP_001230654.1	2	2	2	4	0.96	1.1	19.42	11.44	26.8	18	2	2	15492	51368	testis expressed sequence 264	Molecular function unknown	Extracellular	Secreted polypeptide	Biological_process unknown	SP	Yes
ATP11C	286410	phospholipid-transporting ATPase IG isoform a	NP_775965.2	2	1	1	2	0.96	1.1					1	1	9814	286410	ATPase, Class VI, type 11C	ATPase activity	-	ATPase	Transport	TM	Yes
TERF2IP	54386	telomeric repeat-binding factor 2-interacting protein 1	NP_061848.2	1	1	1	2	0.96	1.1					1	1	5452	54386	telomeric repeat binding factor 2,interacting protein	DNA binding	Nucleus	DNA binding protein;Cell cycle control protein	Cell communication;Signal transduction;Chromosome organization and biogenesis (sensu Eukarya)	CC;NLS;BRCT	Yes
UBTF	7343	nucleolar transcription factor 1 isoform a	NP_055048.1	2	5	5	11	0.96	1.1	4.68	13.85	12.8	45	8	8	2814	7343	upstream binding transcription factor, RNApolymerase I	Transcription factor activity	Nucleolus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	Yes
ADPGK	83440	ADP-dependent glucokinase precursor	NP_112574.3	1	2	2	5	0.96	1.09	3.21	5.11	5.3	9.7	3	3	12429	83440	ADP-dependent glucokinase	Phosphorylase activity	-	Enzyme: Phosphorylase	Metabolism;Energy pathways	SP	No
PEBP1	5037	phosphatidylethanolamine-binding protein 1 preproprotein	NP_002558.1	1	6	6	31	0.96	1.09	8.3	4.66	33.6	21.3	17	17	6850	5037	prostatic binding protein	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Cell communication;Signal transduction	-	Yes
UBA52	7311	ubiquitin-60S ribosomal protein L40 precursor	NP_001029102.1	3	1	8	72	0.96	1.08					1	1	8931	7311	ubiquitin A-52 residue ribosomal protein fusionproduct 1	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	UBQ	No
TSN	7247	translin isoform 1	NP_004613.1	2	11	11	25	0.96	1.07	4.17	4.31	15.6	18	15	15	8993	7247	translin	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes

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XRCC5	7520	X-ray repair cross-complementing protein 5	NP_066964.1	1	37	37	170	0.96	1.07	4.37	4.09	40.5	42.5	86	86	8935	7520	X-ray repair complementing defective repair inChinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)	DNA repair protein	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	VWA;Ku78	Yes
LOC102724985	102724985	pyridoxal-dependent decarboxylase domain-containing protein 1 isoform X1	XP_006726658.1	8	8	8	15	0.96	1.07	5.5	8.38	12.9	22.3	6	6									
NUDT21	11051	cleavage and polyadenylation specificity factor subunit 5	NP_008937.1	1	7	7	14	0.96	1.07	4.84	6.81	13.3	20.8	8	8	5400	11051	cleavage and polyadenylation specific factor 5,25 kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
MIOS	54468	WD repeat-containing protein mio	NP_061878.3	1	2	2	4	0.96	1.07	10.25	21.29	14	33	2	2	7898	54468	None	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	WD40	Yes
RCOR1	23186	REST corepressor 1	NP_055971.2	5	2	2	3	0.96	1.05	23.85	6.37	33.3	9.5	2	2	9645	23186	REST corepressor 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT;CC	Yes
CASP8	841	caspase-8 isoform G precursor	NP_001073594.1	5	6	6	13	0.96	1.04	11.76	6.94	28.2	17.7	6	6	3459	841	caspase 8, apoptosis-related cysteine protease	Cysteine-type peptidase activity	Cytosol;Cytoplasm	Cysteine protease	Apoptosis	DED;CASc	Yes
EGFR	1956	epidermal growth factor receptor isoform a precursor	NP_005219.2	10	32	32	79	0.96	1.04	3.09	2.73	19	18.2	40	40	579	1956	epidermal growth factor receptor (erythroblasticleukemia viral (v-erb-b) oncogene homolog, avian)	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane;Nucleus;Cytoplasm	Receptor tyrosine kinase	Cell communication;Signal transduction	REC;FU;Tyr_Kinase;TM;SP	Yes
IMP4	92856	U3 small nucleolar ribonucleoprotein protein IMP4	NP_219484.1	1	2	2	4	0.96	1.04	1.2	26.39	1.6	40.5	2	2	10002	92856	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Ribonucleoprotein	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
METTL8	79828	methyltransferase-like protein 8	NP_079046.2	1	1	1	1	0.96	1.04					1	1	7845	79828	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PICALM	8301	phosphatidylinositol-binding clathrin assembly protein isoform 1	NP_009097.2	9	10	10	28	0.96	1.04	4.93	4.46	16.4	16.1	12	12	4320	8301	phosphatidylinositol binding clathrin assemblyprotein	Clathrin binding	Plasma membrane	Transport/cargo protein	Regulation of endocytosis	CC	Yes
DHX37	57647	probable ATP-dependent RNA helicase DHX37	NP_116045.2	1	1	1	2	0.96	1.03					1	1	10883	57647	DEAH (Asp-Glu-Ala-His) box polypeptide 37	Helicase activity	Nucleolus	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
GUF1	60558	translation factor GUF1, mitochondrial	NP_068746.2	1	3	3	7	0.96	1.03	5.65	15.45	10.8	32.6	4	4	7821	60558	None	Molecular function unknown	-	Unclassified	Biological_process unknown	GTP_EFTU;GTP_EFTU_D2	No
MTOR	2475	serine/threonine-protein kinase mTOR	NP_004949.1	2	12	13	22	0.96	1.03	7.13	2.86	20.7	8.8	9	9	3134	2475	FK506 binding protein 12-rapamycin associatedprotein 1	Kinase activity	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	PI3KC	Yes
PSMD3	5709	26S proteasome non-ATPase regulatory subunit 3	NP_002800.2	1	24	24	75	0.96	1.03	3.91	3	24.5	20	41	41	10170	5709	proteasome (prosome, macropain) 26S subunit,non-ATPase, 3	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CC;PINT	Yes
RPL7	6129	60S ribosomal protein L7	NP_000962.2	1	19	20	109	0.96	1.03	2.4	2.74	17.6	21.8	58	58	5004	6129	ribosomal protein L7	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PPP2CA	5515	serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	NP_002706.1	1	2	13	46	0.96	1.01	24.08	4.22	41.6	7.4	3	3	8912	5515	protein phosphatase 2 (formerly 2A), catalyticsubunit, alpha isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2A	Yes
ATG7	10533	ubiquitin-like modifier-activating enzyme ATG7 isoform a	NP_006386.1	3	10	10	21	0.96	1.01	5.44	3.63	17.4	12.2	11	11	12293	10533	APG7 autophagy 7-like (S. cerevisiae)	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	SP	No
DHX29	54505	ATP-dependent RNA helicase DHX29	NP_061903.2	1	16	17	43	0.96	1.01	4.03	5.67	18.3	27.4	22	22	10882	54505	DEAH (Asp-Glu-Ala-His) box polypeptide 29	Helicase activity	-	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;DEXDc;HELIC;SP	Yes
AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	NP_001611.1	3	310	310	1517	0.96	1.01	1.46	2.23	40.9	70.6	796	796	14684	79026	AHNAK nucleoprotein (desmoyokin)	Protein binding	Nucleus	Unclassified	Muscle contraction	PDZ;NLS	Yes
TMEM131	23505	transmembrane protein 131	NP_056163.1	1	1	1	2	0.96	1.01					1	1	19388	23505	transmembrane protein 131	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
DPYSL2	1808	dihydropyrimidinase-related protein 2 isoform 1	NP_001184222.1	7	18	21	93	0.96	1.01	3.55	5.96	21.3	38.6	38	38	3914	1808	dihydropyrimidinase-like 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell communication;Signal transduction	-	Yes
DPP9	91039	dipeptidyl peptidase 9	NP_631898.3	1	17	17	36	0.96	1	3.74	4.06	16.6	18.8	21	21	7001	91039	dipeptidylpeptidase 9	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Metabolism;Energy pathways	-	No
PRKRA	8575	interferon-inducible double-stranded RNA-dependent protein kinase activator A isoform 1	NP_003681.1	3	2	2	2	0.96	1	1.42	21.1	1.9	30.5	2	2	4573	8575	protein kinase, interferon-inducible doublestranded RNA dependent activator	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DSRM	No

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SACM1L	22908	phosphatidylinositide phosphatase SAC1	NP_054735.3	1	10	10	25	0.96	1	5.3	5.66	18.6	20.6	13	13	7587	22908	SAC1 suppressor of actin mutations 1-like(yeast)	Lipid phosphatase activity	Endoplasmic reticulum	Lipid phosphatase	Cell communication;Signal transduction	TM	No
NUDT19	390916	nucleoside diphosphate-linked moiety X motif 19, mitochondrial precursor	NP_001099040.1	3	4	4	9	0.96	1	8.9	28.27	14.9	52.3	3	3	19584	390916	nudix (nucleoside diphosphate linked moiety X)-type motif 19	Hydrolase activity	-	Unclassified	Biological_process unknown	-	No
EIF1B	10289	eukaryotic translation initiation factor 1b	NP_005866.1	2	2	2	3	0.96	1	35.43	10.95	51.2	15.5	2	2	17032	10289	None	Translation regulator activity	Nucleus	Translation regulatory protein	Protein metabolism	-	No
ALG5	29880	dolichyl-phosphate beta-glucosyltransferase isoform 1	NP_037470.1	2	4	4	7	0.96	0.98	23.59	20.75	53.8	47.7	5	5	5193	29880	asparagine-linked glycosylation 5 homolog(yeast, dolichyl-phosphate beta-glucosyltransferase)	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase	Protein metabolism	TM	Yes
DPP3	10072	dipeptidyl peptidase 3 isoform 1	NP_005691.2	2	17	17	50	0.96	0.97	3.65	4.08	17.7	20	25	25	6012	10072	dipeptidylpeptidase 3	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	-	Yes
AP1M2	10053	AP-1 complex subunit mu-2 isoform 1	NP_001287816.1	2	2	4	6	0.96	0.96					1	1	6296	10053	adaptor-related protein complex 1, mu 2 subunit	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
VPS45	11311	vacuolar protein sorting-associated protein 45 isoform 1	NP_009190.2	4	5	5	10	0.96	0.96	8.24	16.42	17.8	36.5	5	5	10301	11311	vacuolar protein sorting 45A (yeast)	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	Yes
BUD31	8896	protein BUD31 homolog	NP_003901.2	1	3	3	7	0.96	0.95	4.35	5.22	9.4	11.2	5	5	10351	8896	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
DCTN1	1639	dynactin subunit 1 isoform 3	NP_001128512.1	6	32	32	65	0.96	0.94	4.25	6.05	25.2	35.6	37	37	7206	1639	dynactin 1 (p150, glued homolog, Drosophila)	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein	Transport	CC	Yes
EML4	27436	echinoderm microtubule-associated protein-like 4 isoform a	NP_061936.2	2	9	9	15	0.96	0.94	8.61	9.7	25.2	28	9	9	6310	27436	echinoderm microtubule associated protein like 4	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC;WD40;TM	Yes
AP1G2	8906	AP-1 complex subunit gamma-like 2 isoform 1	NP_003908.1	3	5	5	7	0.96	0.94	2.39	9	5.1	19.1	5	5	4638	8906	adaptor-related protein complex 1, gamma 2subunit	Transporter activity	Cytosol	Transport/cargo protein	Transport	ADAP	Yes
RALBP1	10928	ralA-binding protein 1	NP_006779.1	1	2	2	6	0.96	0.93	0.91	8.75	1.5	14.1	3	3	9013	10928	ralA binding protein 1	GTPase activator activity	Plasma membrane	GTPase activating protein	Cell communication;Signal transduction	RHOGAP;CC	Yes
IARS	3376	isoleucine--tRNA ligase, cytoplasmic	NP_002152.2	1	34	34	107	0.96	0.93	3.45	4.25	24.9	29.9	55	55	2832	3376	isoleucine-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	-	Yes
FASN	2194	fatty acid synthase	NP_004095.4	1	109	110	543	0.96	0.92	1.36	1.69	22.3	26.7	283	283	2567	2194	fatty acid synthase	Catalytic activity	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
SLC25A10	1468	mitochondrial dicarboxylate carrier isoform 1	NP_001257817.1	3	3	3	4	0.96	0.92	17.23	2.63	23.7	3.4	2	2	8424	1468	solute carrier family 25 (mitochondrialcarrier; dicarboxylate transporter), member 10	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	-	No
SNX1	6642	sorting nexin-1 isoform a	NP_003090.2	3	9	12	44	0.96	0.92	4.45	5.54	17.8	21.2	17	17	3171	6642	sorting nexin 1	Transporter activity	Endosome;Plasma membrane	Transport/cargo protein	Cell communication;Signal transduction	PX;CC	Yes
NIPBL	25836	nipped-B-like protein isoform A	NP_597677.2	2	4	4	5	0.96	0.92	9	3.54	15	5.6	3	3	10560	25836	Nipped-B homolog (Drosophila)	DNA repair protein	Nucleus	-	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
POLR2B	5431	DNA-directed RNA polymerase II subunit RPB2 isoform 1	NP_000929.1	3	15	15	31	0.96	0.91	7.24	12.14	27.5	44.9	15	15	15943	5431	polymerase (RNA) II (DNA directed) polypeptideB, 140kDa	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PHC2	1912	polyhomeotic-like protein 2 isoform a	NP_932157.1	2	1	1	1	0.96	0.89					1	1	10340	1912	polyhomeotic-like 2 (Drosophila)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	SAM	No
SEC24B	10427	protein transport protein Sec24B isoform c	NP_001287742.1	3	9	10	29	0.96	0.89	4.1	11.21	13.2	34.1	11	11	6216	10427	SEC24 related gene family, member B (S.cerevisiae)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	GEL	Yes
HPS6	79803	Hermansky-Pudlak syndrome 6 protein	NP_079023.2	1	3	3	6	0.96	0.85	13.16	34	22.1	53.5	3	3	8471	79803	Hermansky-Pudlak syndrome 6	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes
RRBP1	6238	ribosome-binding protein 1	NP_004578.2	12	58	59	236	0.96	0.85	2	2.74	21.4	26	121	120	11796	6238	ribosome binding protein 1 homolog 180kDa (dog)	Transmembrane receptor activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Integral membrane protein	Transport	TM;CC	Yes
SEC22B	9554	vesicle-trafficking protein SEC22b precursor	NP_004883.3	1	7	7	32	0.96	0.84	5.53	4.98	22.8	17.9	18	18	4939	9554	SEC22 vesicle trafficking protein-like 1 (S.cerevisiae)	Transporter activity	Endoplasmic reticulum	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
STX4	6810	syntaxin-4 isoform 3	NP_004595.2	3	4	4	4	0.96	0.83	2.4	21.65	4	31.8	3	3	1722	6810	syntaxin 4A (placental)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Cell communication;Signal transduction	TM;CC;SynN	Yes
AARS	16	alanine--tRNA ligase, cytoplasmic	NP_001596.2	1	33	33	116	0.96	0.83	3.2	4.8	24.4	31.8	61	61	3042	16	alanyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism;Translation	CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
TEAD2	8463	transcriptional enhancer factor TEF-4 isoform 2	NP_001243589.1	7	1	1	1	0.96	0.82					1	1	3432	8463	TEA domain family member 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TEA	No
ECI1	1632	enoyl-CoA delta isomerase 1, mitochondrial isoform 1 precursor	NP_001910.2	2	6	6	18	0.96	0.79	15.33	6.18	49.1	15.6	10	10									
UPF3B	65109	regulator of nonsense transcripts 3B isoform 1	NP_542199.1	2	2	2	2	0.96	0.79					1	1	2247	65109	UPF3 regulator of nonsense transcripts homologB (yeast)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NES;NLS	No
SMC3	9126	structural maintenance of chromosomes protein 3	NP_005436.1	1	22	22	43	0.96	0.79	4.56	4.99	22.9	20.8	27	27	5829	9126	chondroitin sulfate proteoglycan 6 (bamacan)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
FAM210A	125228	protein FAM210A	NP_689565.2	1	2	2	3	0.96	0.78	7.01	38.63	9.6	44.3	2	2									
DDB2	1643	DNA damage-binding protein 2	NP_000098.1	2	5	5	10	0.96	0.76	3.14	2.55	7.4	4.7	6	6	2886	1643	damage-specific DNA binding protein 2, 48kDa	DNA binding	Nucleus;Cytoplasm	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
ATP5L	10632	ATP synthase subunit g, mitochondrial	NP_006467.4	1	7	7	23	0.96	0.75	5.76	5.54	20.9	15.6	14	14	9815	10632	ATP synthase, H+ transporting, mitochondrial F0complex, subunit g	ATPase activity	Mitochondrion	ATPase	Metabolism;Energy pathways	-	Yes
KIAA1217	56243	sickle tail protein homolog isoform 1	NP_062536.2	6	7	7	12	0.96	0.75	3.85	10.26	9.8	20.7	7	7	11132	56243	KIAA1217	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
SMAD2	4087	mothers against decapentaplegic homolog 2 isoform 1	NP_005892.1	2	3	5	13	0.96	0.74	12.96	5.05	25.2	7.5	4	4	3221	4087	SMAD, mothers against DPP homolog 2(Drosophila)	Transcription regulator activity	Cytoplasm;Nucleus	DNA binding protein	Signal transduction;Regulation of gene expression, epigenetic	MH1;MH2	Yes
POLR3A	11128	DNA-directed RNA polymerase III subunit RPC1	NP_008986.2	1	1	1	2	0.96	0.74					1	1	17879	11128	polymerase (RNA) III (DNA directed)polypeptide A, 155kDa	DNA-directed RNA polymerase activity	-	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
STAT1	6772	signal transducer and activator of transcription 1-alpha/beta isoform alpha	NP_009330.1	1	3	36	118	0.96	0.69	1.3	53.57	3.5	142.5	8	8	2777	6772	signal transducer and activator oftranscription 1, 91kDa	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SH2;CC	Yes
ARHGDIA	396	rho GDP-dissociation inhibitor 1 isoform e	NP_001288172.1	5	6	6	22	0.96	0.69	5.78	5.74	19.4	13.8	12	12	3565	396	Rho GDP dissociation inhibitor (GDI) alpha	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	-	Yes
CUTA	51596	protein CutA isoform 1	NP_001014433.1	3	1	1	5	0.96	0.69	7.69	33.3	12.8	41.3	3	3	12902	51596	chromosome 6 open reading frame 82	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	SP;TM	Yes
COQ9	57017	ubiquinone biosynthesis protein COQ9, mitochondrial precursor	NP_064708.1	1	2	2	2	0.96	0.57	7.85	80.65	10.7	73.1	2	2	13157	57017	chromosome 16 open reading frame 49	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
USE1	55850	vesicle transport protein USE1	NP_060937.1	1	1	1	2	0.96	0.54					1	1	11299	55850	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;TM	Yes
RAB22A	57403	ras-related protein Rab-22A	NP_065724.1	1	1	3	7	0.96	0.53					1	1	6696	57403	RAB22A, member RAS oncogene family	GTPase activity	Endosome	GTPase	Cell communication;Signal transduction	RAB	Yes
SLC35C1	55343	GDP-fucose transporter 1 isoform a	NP_060859.4	2	1	1	1	0.95	1.44					1	1	9324	55343	solute carrier family 35, member C1	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	TM	Yes
MTERF4	130916	transcription termination factor 4, mitochondrial	NP_872307.2	1	1	1	1	0.95	1.3					1	1									
NELFA	7469	negative elongation factor A	NP_005654.3	1	5	5	8	0.95	1.3	7.9	8.21	16.9	24.2	5	5									
PSMC5	5705	26S protease regulatory subunit 8 isoform 1	NP_002796.4	2	14	15	43	0.95	1.25	6.24	6.4	28.2	38.9	22	22	3400	5705	proteasome (prosome, macropain) 26S subunit,ATPase, 5	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	AAA;CC	Yes
RPL31	6160	60S ribosomal protein L31 isoform 1	NP_000984.1	3	10	10	38	0.95	1.23	8.16	5.13	36.7	29.5	21	21	17994	6160	ribosomal protein L31	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
PPP1CB	5500	serine/threonine-protein phosphatase PP1-beta catalytic subunit isoform 1	NP_002700.1	1	4	15	54	0.95	1.23	13.62	16.15	35.3	56.3	7	7	11792	5500	protein phosphatase 1, catalytic subunit, betaisoform	Protein serine/threonine phosphatase activity	Nucleolus	Serine/threonine phosphatase	Cell growth and/or maintenance	PP2A	Yes
CHCHD4	131474	mitochondrial intermembrane space import and assembly protein 40 isoform 2	NP_653237.1	2	1	1	2	0.95	1.22					1	1	13045	131474	coiled-coil-helix-coiled-coil-helix domaincontaining 4	Molecular function unknown	-	Unclassified	Biological_process unknown	CHCH	No
NPEPPS	9520	puromycin-sensitive aminopeptidase	NP_006301.3	2	34	34	108	0.95	1.22	4	2.79	29.9	26.6	59	59	7366	9520	aminopeptidase puromycin sensitive	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	-	Yes
NOMO2	283820	nodal modulator 2 isoform 1 precursor	NP_001004060.1	5	2	29	97	0.95	1.21	6.68	6.59	12.8	16	4	4	12375	283820	NODAL modulator 2	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;CC	Yes
CLUH	23277	clustered mitochondria protein homolog	NP_056044.3	3	19	19	35	0.95	1.17	5.5	3.82	24.9	21.1	22	22									
ARHGEF18	23370	rho guanine nucleotide exchange factor 18 isoform b	NP_001124427.1	2	8	9	16	0.95	1.15	1.96	13.75	5.2	47	8	8	12479	23370	rho/rac guanine nucleotide exchange factor(GEF) 18	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH;CC	No
TXLNG	55787	gamma-taxilin isoform 1	NP_060830.2	2	4	4	8	0.95	1.14	6.36	7.41	10.5	14.7	3	3									
GNA11	2767	guanine nucleotide-binding protein subunit alpha-11	NP_002058.2	2	8	11	22	0.95	1.14	7.01	2.54	18.9	8.2	8	8	759	2767	guanine nucleotide binding protein (G protein),alpha 11 (Gq class)	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	CC;GALP	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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TMED4	222068	transmembrane emp24 domain-containing protein 4 isoform 1 precursor	NP_872353.2	5	5	7	26	0.95	1.13	10.64	8.29	20.3	18.8	4	4	13666	222068	transmembrane emp24 protein transport domaincontaining 4	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	SP;CC;TM	No
GNPDA1	10007	glucosamine-6-phosphate isomerase 1	NP_005462.1	1	6	9	24	0.95	1.11	10.5	4.03	28.8	12.7	8	8	9048	10007	glucosamine-6-phosphate deaminase 1	Deaminase activity	-	Enzyme: Deaminase	Metabolism;Energy pathways	-	Yes
RPL12	6136	60S ribosomal protein L12	NP_000967.1	1	9	9	40	0.95	1.1	5.58	4.57	24.1	22.7	20	20	1603	6136	ribosomal protein L12	Structural constituent of ribosome	Nucleus	Ribosomal subunit	Protein metabolism	-	Yes
ARHGEF5	7984	rho guanine nucleotide exchange factor 5	NP_005426.2	2	4	5	10	0.95	1.1	7.74	26.68	16.6	73	5	5	2932	7984	Rho guanine nucleotide exchange factor (GEF)5	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH;SH3	Yes
UBE2D3	7323	ubiquitin-conjugating enzyme E2 D3 isoform 3	NP_871622.1	9	2	2	10	0.95	1.1	4.47	4.05	9.5	10	5	5	4269	7323	ubiquitin-conjugating enzyme E2D 3 (UBC4/5homolog, yeast)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBC	Yes
PDHB	5162	pyruvate dehydrogenase E1 component subunit beta, mitochondrial isoform 1 precursor	NP_000916.2	2	10	10	26	0.95	1.1	5.28	13.3	18.2	56.8	13	13	1530	5162	pyruvate dehydrogenase (lipoamide) beta	Carboxy-lyase activity	Mitochondrion	Enzyme: Decarboxylase	Metabolism;Energy pathways	-	Yes
PAK1IP1	55003	p21-activated protein kinase-interacting protein 1	NP_060376.2	1	3	3	10	0.95	1.1	2.56	3.65	5.5	9	5	5	7424	55003	PAK1 interacting protein 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell communication;Signal transduction	WD40	No
NUP37	79023	nucleoporin Nup37	NP_076962.2	1	3	3	8	0.95	1.1	13.26	7.89	25.7	17.4	4	4	14853	79023	nucleoporin 37kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	WD40	Yes
CS	1431	citrate synthase, mitochondrial precursor	NP_004068.2	1	14	14	69	0.95	1.08	5.17	3.57	28.4	22.1	32	32	349	1431	citrate synthase	Acyltransferase activity	Mitochondrial matrix	Enzyme: Acyltransferase	Metabolism;Energy pathways	SP	Yes
BZW2	28969	basic leucine zipper and W2 domain-containing protein 2	NP_001153239.1	1	4	7	14	0.95	1.08	8.92	13.21	17.1	29.2	4	4	16571	28969	basic leucine zipper and W2 domains 2	Translation regulator activity	Nucleolus	Translation regulatory protein	Protein metabolism	-	No
EIF3K	27335	eukaryotic translation initiation factor 3 subunit K isoform 1	NP_037366.1	2	7	7	18	0.95	1.07	2.36	2.44	7.4	8.7	11	11	11740	27335	eukaryotic translation initiation factor 3,subunit 12	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
EYA3	2140	eyes absent homolog 3 isoform a	NP_001981.2	4	1	1	2	0.95	1.07					1	1	9042	2140	eyes absent homolog 3 (Drosophila)	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	-	Yes
ZKSCAN1	7586	zinc finger protein with KRAB and SCAN domains 1 isoform a	NP_003430.1	3	1	1	2	0.95	1.06					1	1	3161	7586	zinc finger with KRAB and SCAN domains 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LER;KRAB;ZNFC2	Yes
USP5	8078	ubiquitin carboxyl-terminal hydrolase 5 isoform 1	NP_001092006.1	2	21	21	63	0.95	1.04	2.49	2.57	14.3	16.1	36	36	3265	8078	ubiquitin specific protease 5 (isopeptidase T)	Ubiquitin-specific protease activity	Extracellular	Ubiquitin proteasome system protein	Protein metabolism	ZnF_UBP;UBA;CC	Yes
LGR6	59352	leucine-rich repeat-containing G-protein coupled receptor 6 isoform 1 precursor	NP_001017403.1	3	1	1	3	0.95	1.04					1	1	5974	59352	leucine-rich repeat containing G protein-coupledreceptor 6	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Cell communication;Signal transduction	LRR;TM;SP	Yes
DYNC1LI1	51143	cytoplasmic dynein 1 light intermediate chain 1	NP_057225.2	1	9	9	19	0.95	1.04	6.46	3.44	20.6	11.9	11	11	10917	51143	dynein, cytoplasmic, light intermediatepolypeptide 1	Motor activity	Cytoskeleton	Motor protein	Cell growth and/or maintenance	-	Yes
DDX58	23586	probable ATP-dependent RNA helicase DDX58	NP_055129.2	1	15	15	33	0.95	1.03	6.15	13.43	23.7	59.6	16	16	13131	23586	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Molecular function unknown	Cytoplasm	RNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	No
SRI	6717	sorcin isoform A	NP_003121.1	4	7	7	26	0.95	1.03	12.4	6.69	44.3	25.3	13	13	1680	6717	sorcin	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
PRMT5	10419	protein arginine N-methyltransferase 5 isoform a	NP_006100.2	6	11	11	34	0.95	1.03	3.76	4.49	15.6	20.4	19	19	4955	10419	SKB1 homolog (S. pombe)	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase	Cell communication;Signal transduction	-	Yes
CEP170B	283638	centrosomal protein of 170 kDa protein B isoform 2	NP_055820.2	2	6	6	11	0.95	1.03	12.2	14.94	26.2	35.4	5	5									
PRPF8	10594	pre-mRNA-processing-splicing factor 8	NP_006436.3	1	46	46	112	0.95	1.03	3.49	3.39	25.7	27	58	58	6295	10594	PRP8 pre-mRNA processing factor 8 homolog(yeast)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	JAB	Yes
CTNNB1	1499	catenin beta-1	NP_001895.1	1	19	23	73	0.95	1.01	4.77	11.39	24.4	65.2	28	27	286	1499	catenin (cadherin-associated protein), beta 1,88kDa	Cell adhesion molecule activity	Plasma membrane;Nucleus;Cytoplasm	Adhesion molecule	Cell communication;Signal transduction	ARM	Yes
CCNL2	81669	cyclin-L2 isoform A	NP_112199.2	1	2	2	3	0.95	1					1	1	10815	81669	cyclin L2	Transcription regulator activity	Nucleus	Cell cycle control protein	Cell communication;Signal transduction;Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CYCLIN	No
TYMP	1890	thymidine phosphorylase isoform 1 proprotein	NP_001944.1	2	21	21	67	0.95	1	3.6	4.73	19.5	26.2	32	30	8833	1890	endothelial cell growth factor 1(platelet-derived)	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	-	Yes
NOC2L	26155	nucleolar complex protein 2 homolog	NP_056473.2	1	8	8	14	0.95	1	5.28	4.63	14.3	13.1	8	8	13166	26155	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
BRIX1	55299	ribosome biogenesis protein BRX1 homolog	NP_060791.3	1	8	8	14	0.95	1	11.24	13.48	28.7	36.7	7	7	16563	55299	brix domain containing 2	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	Yes
TRIT1	54802	tRNA dimethylallyltransferase, mitochondrial precursor	NP_060116.2	1	2	2	3	0.95	1	12.66	21.38	17	31	2	2	18226	54802	tRNA isopentenyltransferase 1	Transferase activity	Cytoplasm	Enzyme: Transferase	Metabolism;Energy pathways	SP;NLS	Yes
SNRPE	6635	small nuclear ribonucleoprotein E isoform 1	NP_003085.1	1	5	5	17	0.95	0.99	10.6	23.68	29	74.2	8	8	548	6635	small nuclear ribonucleoprotein polypeptide E	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM	Yes
MRPS26	64949	28S ribosomal protein S26, mitochondrial	NP_110438.1	1	1	1	2	0.95	0.99					1	1	17595	64949	mitochondrial ribosomal protein S26	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	CC	No
INPP4B	8821	type II inositol 3,4-bisphosphate 4-phosphatase	NP_003857.2	1	2	2	3	0.95	0.98					1	1	6322	8821	inositol polyphosphate-4-phosphatase, type II,105kDa	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Cell communication;Signal transduction	CC	No
FAM91A1	157769	protein FAM91A1	NP_659400.2	1	5	5	11	0.95	0.98	19.12	10.43	50.9	27.4	7	7	8676	157769	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
CUL5	8065	cullin-5	NP_003469.2	1	6	7	8	0.95	0.97	15.3	21.73	29.5	43.9	4	4	3444	8065	cullin 5	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	CULL	Yes
TTC37	9652	tetratricopeptide repeat protein 37	NP_055454.1	1	14	14	36	0.95	0.96	3.91	12.21	15.4	51.3	17	17	11079	9652	KIAA0372	Molecular function unknown	-	Unclassified	Biological_process unknown	TPR	No
MRPL16	54948	39S ribosomal protein L16, mitochondrial	NP_060310.1	1	3	3	11	0.95	0.96	1.59	12.97	4	33.9	7	7	14743	54948	mitochondrial ribosomal protein L16	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	No
COX11	1353	cytochrome c oxidase assembly protein COX11, mitochondrial isoform 1	NP_004366.1	1	1	1	1	0.95	0.95					1	1	4709	1353	COX11 homolog, cytochrome c oxidase assemblyprotein (yeast)	Chaperone activity	Mitochondrion	Chaperone	Metabolism;Energy pathways	TM	Yes
RPL35A	6165	60S ribosomal protein L35a	NP_000987.2	1	6	6	15	0.95	0.95	8.12	19.02	22.2	54.4	8	8	1596	6165	ribosomal protein L35a	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
ANK3	288	ankyrin-3 isoform 1	NP_066267.2	4	2	2	2	0.95	0.95					1	1	2715	288	ankyrin 3, node of Ranvier (ankyrin G)	Receptor signaling complex scaffold activity	Plasma membrane	Adapter molecule	Cell communication;Signal transduction	ANK;ZU5;DEATH	Yes
OAS3	4940	2'-5'-oligoadenylate synthase 3	NP_006178.2	1	19	19	52	0.95	0.95	6.4	7.77	31.8	38.9	26	26	4519	4940	2`-5`-oligoadenylate synthetase 3, 100kDa	Ligase activity	Cytoplasm	Enzyme: Ligase	Immune response	-	Yes
MRPL37	51253	39S ribosomal protein L37, mitochondrial	NP_057575.2	1	9	9	21	0.95	0.95	5.23	3.55	17.4	11.7	12	12	14757	51253	mitochondrial ribosomal protein L37	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
MRPL21	219927	39S ribosomal protein L21, mitochondrial isoform d	NP_852615.1	2	5	5	9	0.95	0.94	9.23	4.81	19.8	10.2	5	5	14747	219927	mitochondrial ribosomal protein L21	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	No
TLDC1	57707	TLD domain-containing protein 1	NP_065998.3	1	8	8	19	0.95	0.93	7.14	6.84	21.6	20.2	10	10									
XPO7	23039	exportin-7	NP_055839.3	1	11	11	19	0.95	0.93	9.26	6.32	29.8	19.8	11	11	5846	23039	exportin 7	Transporter activity	Nucleus	Transport/cargo protein	Transport	IBN_NT	Yes
TMEM205	374882	transmembrane protein 205	NP_940938.1	1	3	3	5	0.95	0.92	11.33	30.6	15.3	41.7	2	2	18605	374882	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	SP;TM	No
GALT	2592	galactose-1-phosphate uridylyltransferase isoform 1	NP_000146.2	2	4	4	7	0.95	0.92	10.84	12.18	20.7	22.7	4	4	6106	2592	galactose-1-phosphate uridylyltransferase	Nucleotidyltransferase activity	-	Enzyme: Nucleotidyltransferase	Energy pathways;Metabolism	-	No
MYH10	4628	myosin-10 isoform 2	NP_005955.3	12	51	77	375	0.95	0.91	2.83	3.59	25.9	31.3	89	88	1178	4628	myosin, heavy polypeptide 10, non-muscle	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC;IQ;MYOSIN	Yes
STRIP1	85369	striatin-interacting protein 1 isoform 1	NP_149079.2	2	5	5	11	0.95	0.91	12.44	16.99	29.5	39.2	6	6									
BCKDK	10295	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial isoform a precursor	NP_005872.2	3	2	2	5	0.95	0.89	0.89	5.88	1.5	9.1	3	3	12523	10295	branched chain ketoacid dehydrogenase kinase	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
RRAS	6237	ras-related protein R-Ras precursor	NP_006261.1	1	4	6	26	0.95	0.87	2.32	6.42	5.4	13.7	6	6	1299	6237	related RAS viral (r-ras) oncogene homolog	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	Yes
C2orf43	60526	UPF0554 protein C2orf43 isoform X1	XP_011531316.1	5	2	2	5	0.95	0.87	9.15	6.73	12.3	8.3	2	2	7113	60526	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
MRPS16	51021	28S ribosomal protein S16, mitochondrial	NP_057149.1	1	2	2	3	0.95	0.87					1	1	14778	51021	mitochondrial ribosomal protein S16	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
SCAMP1	9522	secretory carrier-associated membrane protein 1 isoform 1	NP_004857.4	2	8	8	20	0.95	0.86	10.2	8.52	29.7	22.2	9	9	6072	9522	secretory carrier membrane protein 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM;CC	Yes
ARPC1B	10095	actin-related protein 2/3 complex subunit 1B	NP_005711.1	1	10	10	28	0.95	0.86	7.77	3.39	23.7	9.3	10	10	10366	10095	actin related protein 2/3 complex, subunit 1B,41kDa	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	WD40	Yes
TARS2	80222	threonine--tRNA ligase, mitochondrial isoform a	NP_079426.2	3	6	6	14	0.95	0.85	7.16	4.73	19.5	11.4	8	8	18148	80222	threonyl-tRNA synthetase-like 1	Ligase activity	-	Enzyme: Ligase	Protein metabolism	-	Yes
TXNDC17	84817	thioredoxin domain-containing protein 17	NP_116120.1	1	4	4	12	0.95	0.83	3.38	12.34	7.9	25.6	6	6	11656	84817	thioredoxin-like 5	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
STK25	10494	serine/threonine-protein kinase 25 isoform 1	NP_006365.2	4	2	9	25	0.95	0.82	32.57	2.26	45.8	2.6	2	2	3770	10494	serine/threonine kinase 25 (STE20 homolog,yeast)	Protein serine/threonine kinase activity	Golgi apparatus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
MYD88	4615	myeloid differentiation primary response protein MyD88 isoform 1	NP_001166038.1	5	5	5	6	0.95	0.82	11.7	16.51	22.5	27.6	4	4	3703	4615	myeloid differentiation primary response gene(88)	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	DEATH;TIR	Yes
HPS3	84343	Hermansky-Pudlak syndrome 3 protein isoform 1	NP_115759.2	2	1	1	1	0.95	0.8					1	1	5835	84343	Hermansky-Pudlak syndrome 3	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes

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MLLT4	4301	afadin isoform 1	NP_001193937.1	1	1	17	31	0.95	0.79					1	1	1164	4301	myeloid/lymphoid or mixed-lineage leukemia(trithorax homolog, Drosophila); translocated to, 4	Cell adhesion molecule activity	Cytoplasm	Cell junction protein	Cell communication;Signal transduction	RA;CC;FHA;PDZ	Yes
BPHL	670	valacyclovir hydrolase isoform 1 precursor	NP_004323.2	2	1	1	1	0.95	0.77					1	1	4403	670	biphenyl hydrolase-like (serine hydrolase;breast epithelial mucin-associated antigen)	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
WDR47	22911	WD repeat-containing protein 47 isoform 1	NP_001136022.1	3	3	3	5	0.95	0.74	1.71	11.17	2.8	14.4	3	3	15670	22911	WD repeat domain 47	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	LISH;CTLH;WD40;CC	Yes
TRIM5	85363	tripartite motif-containing protein 5 isoform alpha	NP_149023.2	3	2	2	3	0.95	0.72	3.38	44.89	4.6	48.3	2	2	7004	85363	tripartite motif-containing 5	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	RING;BBOX;SPRY;CC	Yes
FKBP1A	2280	peptidyl-prolyl cis-trans isomerase FKBP1A isoform a	NP_000792.1	2	3	3	4	0.95	0.72	14.52	4.21	19.6	4.3	2	2	1741	2280	FK506 binding protein 1A, 12kDa	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Cell communication;Signal transduction	-	Yes
DDRGK1	65992	DDRGK domain-containing protein 1 precursor	NP_076424.1	1	6	6	19	0.95	0.71	11.7	9.55	34.1	20.5	9	9	12741	65992	chromosome 20 open reading frame 116	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;CC	Yes
NCKAP1	10787	nck-associated protein 1 isoform 2	NP_995314.1	2	15	15	35	0.95	0.68	4.7	12.34	19	37.6	18	19	5353	10787	NCK-associated protein 1	Protein binding	Cytoplasm	Integral membrane protein	Cell communication;Signal transduction;Anti-apoptosis	TM	Yes
RAB7B	338382	ras-related protein Rab-7b isoform a	NP_001157994.1	2	2	2	3	0.95	0.65	29.09	35.23	40.8	33.1	2	2	15202	338382	RAB7B, member RAS oncogene family	RNA binding	Lysosome	RNA binding protein	Biological_process unknown	RAB	No
RFX1	5989	MHC class II regulatory factor RFX1	NP_002909.4	1	1	1	7	0.95						1		2476	5989	regulatory factor X, 1 (influences HLA class IIexpression)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ADRB2	154	beta-2 adrenergic receptor	NP_000015.1	1	1	1	2	0.94	1.53					1	1	187	154	adrenergic, beta-2-, receptor, surface	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Cell communication;Signal transduction	TM	No
NPEPL1	79716	probable aminopeptidase NPEPL1 isoform 1	NP_078939.3	3	2	2	4	0.94	1.5	3.25	3.66	4.3	7.8	2	2	7496	79716	aminopeptidase-like 1	Aminopeptidase activity	-	Aminopeptidase	Protein metabolism	-	Yes
OCRL	4952	inositol polyphosphate 5-phosphatase OCRL-1 isoform a	NP_000267.2	2	3	3	3	0.94	1.49	23.96	27.01	40.6	79.3	3	3	2395	4952	oculocerebrorenal syndrome of Lowe	Catalytic activity;Acid phosphatase activity	Golgi membrane	Enzyme: Phosphatase;Enzyme: Phosphohydrolase	Metabolism;Energy pathways;Vesicle-mediated transport;Signal transduction;Cell-cell adhesion	I_Phosphatase;RHOGAP	Yes
RPP40	10799	ribonuclease P protein subunit p40 isoform a	NP_006629.2	3	2	2	3	0.94	1.42					1	1	9361	10799	ribonuclease P 40kDa subunit	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MVB12A	93343	multivesicular body subunit 12A isoform 1	NP_612410.1	2	3	3	8	0.94	1.37	15.21	8.66	32.7	27.1	5	5									
VDAC2	7417	voltage-dependent anion-selective channel protein 2 isoform 1	NP_001171712.1	2	14	14	63	0.94	1.37	5.37	4.04	29.6	32.5	33	33	1904	7417	voltage-dependent anion channel 2	Voltage-gated ion channel activity	Mitochondrion	Voltage gated channel	Transport	-	Yes
WDHD1	11169	WD repeat and HMG-box DNA-binding protein 1 isoform 1	NP_009017.1	2	3	3	4	0.94	1.35	0.69	17.44	1.1	42.4	3	3	10483	11169	WD repeat and HMG-box DNA binding protein 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40;CC;HMG	Yes
UBE2I	7329	SUMO-conjugating enzyme UBC9	NP_003336.1	1	2	2	5	0.94	1.35	3.95	7.76	7.4	21.2	4	4	9045	7329	ubiquitin-conjugating enzyme E2I (UBC9 homolog,yeast)	Ubiquitin-specific protease activity;Protein binding	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBC	Yes
TMED7-TICAM2	100302736	TRAM adaptor with GOLD domain isoform 1 precursor	NP_001157940.1	3	8	8	21	0.94	1.35	4.12	10.94	12.3	49.6	10	10									
EIF3G	8666	eukaryotic translation initiation factor 3 subunit G	NP_003746.2	1	12	12	22	0.94	1.33	3.77	4.54	12.8	22	13	13	4886	8666	eukaryotic translation initiation factor 3,subunit 4 delta, 44kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	RRM	Yes
RNF25	64320	E3 ubiquitin-protein ligase RNF25	NP_071898.2	1	1	1	2	0.94	1.31					1	1	9737	64320	ring finger protein 25	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	RWD;RING	Yes
TK2	7084	thymidine kinase 2, mitochondrial isoform 1 precursor	NP_004605.4	7	1	1	2	0.94	1.3					1	1	1770	7084	thymidine kinase 2, mitochondrial	Phosphorylase activity	Mitochondrion	Enzyme: Phosphorylase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
DPYD	1806	dihydropyrimidine dehydrogenase [NADP(+)] isoform 1	NP_000101.2	1	2	2	3	0.94	1.27	11.33	0.75	15.2	1.3	2	2	2036	1806	dihydropyrimidine dehydrogenase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
THUMPD3	25917	THUMP domain-containing protein 3	NP_056268.2	1	3	3	5	0.94	1.27	10.92	4.68	18	10.3	3	3	15507	25917	THUMP domain containing 3	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RPL36	25873	60S ribosomal protein L36	NP_378669.1	1	5	5	21	0.94	1.22	5.54	10.14	18.1	44.9	12	12	10201	25873	ribosomal protein L36	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
HNRNPH2	3188	heterogeneous nuclear ribonucleoprotein H2	NP_062543.1	1	4	9	35	0.94	1.22	13.62	10.92	32.3	33.4	6	6	3022	3188	heterogeneous nuclear ribonucleoprotein H2(H`)	RNA binding	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes

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PSMC4	5704	26S protease regulatory subunit 6B isoform 1	NP_006494.1	2	13	13	29	0.94	1.21	6.12	3.66	24.7	18.3	18	17	4085	5704	proteasome (prosome, macropain) 26S subunit,ATPase, 4	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	AAA;CC	Yes
CNOT6	57472	CCR4-NOT transcription complex subunit 6	NP_001290170.1	2	1	1	2	0.94	1.18					1	1	12341	57472	CCR4-NOT transcription complex, subunit 6	Endonuclease activity	Nucleus	DNA endonuclease	Protein metabolism	LRR	Yes
PSMD12	5718	26S proteasome non-ATPase regulatory subunit 12 isoform 1	NP_002807.1	2	19	20	55	0.94	1.18	9.9	11.19	51.2	77.6	27	27	5120	5718	proteasome (prosome, macropain) 26S subunit,non-ATPase, 12	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	PINT	Yes
PDP1	54704	pyruvate dehyrogenase phosphatase catalytic subunit 1 isoform 2	NP_001155252.1	2	6	6	8	0.94	1.17	19.53	12.41	42.7	33.3	5	5	16185	54704	protein phosphatase 2C, magnesium-dependent,catalytic subunit	Protein serine/threonine phosphatase activity	Mitochondrion	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2C	Yes
TRIM32	22954	E3 ubiquitin-protein ligase TRIM32	NP_036342.2	1	4	4	15	0.94	1.16	2.98	10.51	7.4	33.2	7	7	3797	22954	tripartite motif-containing 32	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;BBOX;CC	Yes
UROD	7389	uroporphyrinogen decarboxylase	NP_000365.3	1	5	5	27	0.94	1.15	6.52	5.5	21.4	21.3	12	11	1441	7389	uroporphyrinogen decarboxylase	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase	Metabolism;Energy pathways	-	Yes
HMGXB4	10042	HMG domain-containing protein 4	NP_001003681.1	1	1	1	2	0.94	1.14					1	1	5267	10042	high-mobility group protein 2-like 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG	Yes
PSMG3	84262	proteasome assembly chaperone 3	NP_115678.1	1	2	2	3	0.94	1.14	22.33	7.55	30.2	12.2	2	2	14404	84262	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
BIN1	274	myc box-dependent-interacting protein 1 isoform 1	NP_647593.1	10	1	1	4	0.94	1.14	29.7	23.47	41.2	39.2	2	2	3150	274	bridging integrator 1	Receptor signaling complex scaffold activity	Cytoplasm;Nucleus	Adapter molecule	Cell communication;Signal transduction	BAR;SH3;CC	Yes
ZADH2	284273	zinc-binding alcohol dehydrogenase domain-containing protein 2 isoform 1	NP_787103.1	2	2	2	4	0.94	1.14	8.7	32.89	11.6	57.1	2	2	15685	284273	zinc binding alcohol dehydrogenase, domaincontaining 2	Catalytic activity	-	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
CHCHD6	84303	MICOS complex subunit MIC25	NP_115719.1	1	1	1	1	0.94	1.14					1	1	13047	84303	coiled-coil-helix-coiled-coil-helix domaincontaining 6	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
NUBP2	10101	cytosolic Fe-S cluster assembly factor NUBP2 isoform 1	NP_036357.1	2	5	5	11	0.94	1.13	18.39	7.54	40.3	19.3	5	5	14846	10101	nucleotide binding protein 2 (MinD homolog, E.coli)	Molecular function unknown	Cytoplasm	Unclassified	Protein metabolism	-	No
UBR1	197131	E3 ubiquitin-protein ligase UBR1	NP_777576.1	1	3	3	5	0.94	1.13	40.5	1.2	57.7	1.9	2	2	9342	197131	ubiquitin protein ligase E3 component n-recognin1	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
KIF3B	9371	kinesin-like protein KIF3B	NP_004789.1	2	3	4	5	0.94	1.12	5.13	3.27	8.4	6.3	3	3	4781	9371	kinesin family member 3B	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	KISC;CC	Yes
PSMF1	9491	proteasome inhibitor PI31 subunit	NP_006805.2	1	2	2	3	0.94	1.12	4.11	7.15	5.5	11.3	2	2	17919	9491	proteasome (prosome, macropain) inhibitorsubunit 1 (PI31)	Protease inhibitor activity	Nuclear membrane	Protease inhibitor	Protein metabolism	-	Yes
TRAPPC4	51399	trafficking protein particle complex subunit 4	NP_057230.1	1	4	4	11	0.94	1.11	7.07	4.21	14.9	10.5	5	5	18220	51399	trafficking protein particle complex 4	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
ACTN4	81	alpha-actinin-4	NP_004915.2	1	46	67	490	0.94	1.1	2.6	2.42	32.6	35.7	168	168	5222	81	actinin, alpha 4	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CH;SPECTRIN;EF;CC	Yes
HTATIP2	10553	oxidoreductase HTATIP2 isoform a precursor	NP_001091990.1	3	5	5	11	0.94	1.09	9.17	7.81	23.1	22.8	7	7	9288	10553	HIV-1 Tat interactive protein 2, 30kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP;TM	No
EMC6	83460	ER membrane protein complex subunit 6	NP_001014764.1	1	1	1	2	0.94	1.08	7.8	4.56	10.4	6.9	2	2									
DAD1	1603	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	NP_001335.1	1	3	3	7	0.94	1.08	1.47	1.76	2.4	3.3	3	3	2589	1603	defender against cell death 1	Receptor signaling complex scaffold activity	Endoplasmic reticulum	Adapter molecule	Apoptosis	TM	No
NOTCH1	4851	neurogenic locus notch homolog protein 1 preproprotein	NP_060087.3	2	11	11	18	0.94	1.07	5.83	4.98	16.5	16	9	9	1827	4851	Notch homolog 1, translocation-associated(Drosophila)	Transcription regulator activity	Plasma membrane	Cell surface receptor	Anti-apoptosis	SP;EGF;EGFCA;NOTCH;ANK;TM;NLS	Yes
ANXA5	308	annexin A5	NP_001145.1	1	20	21	132	0.94	1.07	5.18	4.14	41	37.1	65	66	568	308	annexin A5	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	ANX;SP	Yes
PPT1	5538	palmitoyl-protein thioesterase 1 isoform 1 precursor	NP_000301.1	2	3	3	5	0.94	1.07	8.45	2.19	13.9	4.1	3	3	7203	5538	palmitoyl-protein thioesterase 1(ceroid-lipofuscinosis, neuronal 1, infantile)	Hydrolase activity	Lysosome	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
FAM21A	387680	WASH complex subunit FAM21A isoform 1	NP_001005751.1	2	2	17	34	0.94	1.07	13.04	4.47	17.4	6.8	2	2	17364	387680	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
MTCH2	23788	mitochondrial carrier homolog 2	NP_055157.1	1	7	7	18	0.94	1.06	12.73	17.12	39.1	62.5	10	10	14788	23788	mitochondrial carrier homolog 2 (C. elegans)	Molecular function unknown	Mitochondrion	Unclassified	Cell communication;Signal transduction	SP	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
ALDH9A1	223	4-trimethylaminobutyraldehyde dehydrogenase	NP_000687.3	1	20	20	62	0.94	1.05	5.39	7.8	29.1	48.9	32	32	4109	223	aldehyde dehydrogenase 9 family, member A1	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
SNRNP200	23020	U5 small nuclear ribonucleoprotein 200 kDa helicase	NP_054733.2	1	43	43	95	0.94	1.04	3.74	2.74	25	20.2	49	49	3391	23020	activating signal cointegrator 1 complexsubunit 3-like 1	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
TEX10	54881	testis-expressed sequence 10 protein isoform 1	NP_060216.2	2	7	7	18	0.94	1.04	9.62	6.15	29.1	20.3	10	10	15489	54881	testis expressed sequence 10	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
FAM45A	404636	protein FAM45A isoform 1	NP_996892.1	4	2	2	4	0.94	1.03	17.23	6.32	23.3	9.2	2	2	13310	404636	family with sequence similarity 45, member A	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
MKLN1	4289	muskelin isoform 2	NP_037387.2	2	2	2	2	0.94	1.03					1	1	16129	4289	muskelin 1, intracellular mediator containingkelch motifs	Cell adhesion molecule activity	Cytoplasm	Adhesion molecule	Cell growth and/or maintenance	LISH;KELCH;CTLH	Yes
PSMB4	5692	proteasome subunit beta type-4	NP_002787.2	1	9	9	48	0.94	1.03	3.98	7.76	18.1	39	23	22	3710	5692	proteasome (prosome, macropain) subunit, betatype, 4	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
OTUD7B	56957	OTU domain-containing protein 7B	NP_064590.2	1	1	1	2	0.94	1.02					1	1	10313	56957	zinc finger, A20 domain containing 1	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	ZnFA20	Yes
SIL1	64374	nucleotide exchange factor SIL1 precursor	NP_001032722.1	1	1	1	2	0.94	1.01					1	1	12150	64374	None	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	SP	Yes
CTNND1	1500	catenin delta-1 isoform 1ABC	NP_001078927.1	15	35	35	113	0.94	1.01	3.77	4.21	26.2	31.8	53	53	3026	1500	catenin (cadherin-associated protein), delta 1	Cell adhesion molecule activity	Cytoplasm;Nucleus	Adhesion molecule	Cell communication;Signal transduction	ARM;CC	Yes
CNPY3	10695	protein canopy homolog 3 precursor	NP_006577.2	1	4	4	7	0.94	1.01	18.12	11.41	43.5	28.9	6	6	6745	10695	trinucleotide repeat containing 5	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes
KCTD15	79047	BTB/POZ domain-containing protein KCTD15 isoform 2	NP_001123466.1	2	1	1	1	0.94	1					1	1	13765	79047	potassium channel tetramerisation domaincontaining 15	Ion channel activity	-	Ion channel	Transport	BTB	No
CNOT1	23019	CCR4-NOT transcription complex subunit 1 isoform a	NP_057368.3	3	27	27	54	0.94	1	3.96	3.88	19.1	20	26	26	11999	23019	CCR4-NOT transcription complex, subunit 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Transcription	TM	Yes
PMM2	5373	phosphomannomutase 2	NP_000294.1	1	7	7	9	0.94	1	5.18	11.86	10.9	27.1	5	5	3472	5373	phosphomannomutase 2	Catalytic activity	Cytoplasm	Enzyme: Mutase	Metabolism;Energy pathways	SP	Yes
AKT1	207	RAC-alpha serine/threonine-protein kinase	NP_005154.2	8	4	7	11	0.94	1	7.06	7.38	13.3	14.9	4	4	1261	207	v-akt murine thymoma viral oncogene homolog 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	PH;S_T_kinase	No
UBA6	55236	ubiquitin-like modifier-activating enzyme 6	NP_060697.4	1	28	28	60	0.94	1	5.02	4.78	28	28.5	34	34	13341	55236	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	-	No
SUCLA2	8803	succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial precursor	NP_003841.1	1	9	9	27	0.94	1	6.49	3.69	24.7	14.8	16	16	6798	8803	succinate-CoA ligase, ADP-forming, betasubunit	Ligase activity	Mitochondrion	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
RECQL	5965	ATP-dependent DNA helicase Q1	NP_002898.2	4	24	24	77	0.94	1	6.38	8.19	38.7	54.8	39	39	2762	5965	RecQ protein-like (DNA helicase Q1-like)	DNA repair protein	Nucleus	DNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC	Yes
APEX1	328	DNA-(apurinic or apyrimidinic site) lyase	NP_001632.2	1	11	11	34	0.94	0.99	4.4	3.89	17.6	16.4	18	18	136	328	APEX nuclease (multifunctional DNA repairenzyme) 1	DNA repair protein;Transcription regulator activity	Cytoplasm	DNA repair protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
NUP155	9631	nuclear pore complex protein Nup155 isoform 1	NP_705618.1	3	17	17	38	0.94	0.99	5.84	3.15	23.6	13.4	18	18	5984	9631	nucleoporin 155kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
EPHB2	2048	ephrin type-B receptor 2 isoform 2 precursor	NP_004433.2	10	3	4	12	0.94	0.99	14.86	14.11	28.4	28.5	4	4	2997	2048	EPH receptor B2	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	TM;FN3;Tyr_Kinase;SAM;SP	Yes
ZFYVE16	9765	zinc finger FYVE domain-containing protein 16 isoform a	NP_001271165.1	1	2	2	8	0.94	0.99	27.67	5.43	55.8	10.7	4	4	10319	9765	zinc finger, FYVE domain containing 16	Auxiliary transport protein activity	Endosome	Membrane transport protein	Transport	FYVE	Yes
USP14	9097	ubiquitin carboxyl-terminal hydrolase 14 isoform a	NP_005142.1	2	25	25	75	0.94	0.98	3.89	4.9	23.8	31.6	41	41	6279	9097	ubiquitin specific protease 14 (tRNA-guaninetransglycosylase)	Ubiquitin-specific protease activity	Cytosol	Ubiquitin proteasome system protein	Protein metabolism	UBQ	Yes
VPS53	55275	vacuolar protein sorting-associated protein 53 homolog isoform 1	NP_001121631.1	2	3	3	6	0.94	0.98	6.21	8.24	11.7	16.2	4	4	7720	55275	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
MRPS11	64963	28S ribosomal protein S11, mitochondrial isoform a	NP_073750.2	2	5	5	16	0.94	0.97	4.17	2.9	11.8	8.5	9	9	14776	64963	mitochondrial ribosomal protein S11	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
FDFT1	2222	squalene synthase isoform 1	NP_004453.3	5	14	14	63	0.94	0.97	4.88	8.51	26.5	49.5	32	32	1694	2222	farnesyl-diphosphate farnesyltransferase 1	Transferase activity	Endoplasmic reticulum	Enzyme: Synthase	Metabolism;Energy pathways	-	No
DOCK7	85440	dedicator of cytokinesis protein 7 isoform 1	NP_001258928.1	5	8	8	11	0.94	0.96	9.22	8.81	23.3	22.5	7	7	16833	85440	dedicator of cytokinesis 7	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	CC	Yes
NUP35	129401	nucleoporin NUP53 isoform a	NP_612142.2	3	5	5	8	0.94	0.96	11.7	6.06	22.3	11.7	4	4	10486	129401	nucleoporin 35kDa	Transporter activity	Nuclear membrane	Transport/cargo protein	Transport	-	No
COMMD4	54939	COMM domain-containing protein 4 isoform 1	NP_060298.2	4	3	3	5	0.94	0.95	20.94	30	28.5	42.2	2	2	13083	54939	COMM domain containing 4	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
UFL1	23376	E3 UFM1-protein ligase 1	NP_056138.1	1	12	12	24	0.94	0.95	8.13	5.32	28.1	18.3	13	13									

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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TJP1	7082	tight junction protein ZO-1 isoform d	NP_001287955.1	4	28	28	51	0.94	0.95	3.62	3.11	18.5	16	29	29	3002	7082	tight junction protein 1 (zona occludens 1)	Cell adhesion molecule activity	Cell surface;Nucleus;Cytoplasm	Cell junction protein	Cell growth and/or maintenance	PDZ;SH3;GuKinase;ZU5	Yes
TMEM201	199953	transmembrane protein 201 isoform 1	NP_001124396.2	2	1	1	2	0.94	0.95					1	1	17991	199953	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No
NIT2	56954	omega-amidase NIT2	NP_064587.1	1	11	11	31	0.94	0.95	4.95	5.35	19.3	21.3	17	17	17634	56954	nitrilase family, member 2	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
EML2	24139	echinoderm microtubule-associated protein-like 2 isoform 1	NP_001180197.1	3	12	12	38	0.94	0.94	4.18	3.69	18.1	16	21	21	16860	24139	echinoderm microtubule associated protein like 2	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	WD40	Yes
RPL10	6134	60S ribosomal protein L10 isoform a	NP_006004.3	5	11	11	80	0.94	0.94	8	12.95	49.4	88.1	39	39	2421	6134	ribosomal protein L10	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
SREK1IP1	285672	protein SREK1IP1	NP_776190.1	1	1	1	2	0.94	0.93					1	1									
HECTD3	79654	E3 ubiquitin-protein ligase HECTD3	NP_078878.3	1	4	4	15	0.94	0.91	4.92	5.4	9.3	9.9	4	4	13383	79654	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	HECT	No
GMDS	2762	GDP-mannose 4,6 dehydratase isoform 1	NP_001491.1	2	6	6	10	0.94	0.91	3.82	15.79	8	32.8	5	5	11925	2762	GDP-mannose 4,6-dehydratase	Hydro-lyase activity	Cytoplasm	Enzyme: Dehydratase	Metabolism;Energy pathways	-	Yes
SMARCE1	6605	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	NP_003070.3	1	4	4	8	0.94	0.9	6.52	6.85	12.3	12.3	4	4	4382	6605	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily e, member 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG;CC	Yes
ARHGEF1	9138	rho guanine nucleotide exchange factor 1 isoform 1	NP_945353.1	3	15	15	26	0.94	0.89	3.84	3.5	14.5	12.5	16	16	3511	9138	Rho guanine nucleotide exchange factor (GEF)1	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH;CC	Yes
DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 1	NP_006132.1	2	8	8	26	0.94	0.89	4.65	7.79	15.8	25.5	13	13	9923	1783	dynein, cytoplasmic, light intermediatepolypeptide 2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
HTT	3064	huntingtin	NP_002102.4	1	4	4	5	0.94	0.88	21.38	25.71	35.9	40.7	3	3	883	3064	huntingtin (Huntington disease)	DNA binding	-	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HEAT	Yes
PLOD3	8985	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor	NP_001075.1	1	19	19	64	0.94	0.88	3.64	3.24	19.5	16.3	32	32	4347	8985	procollagen-lysine, 2-oxoglutarate5-dioxygenase 3	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Protein metabolism	SP;P4HC	Yes
APOO	79135	apolipoprotein O precursor	NP_077027.1	1	2	2	3	0.94	0.88	4.19	10.95	5.6	13.7	2	2	6657	79135	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	SP;TM	No
RNF20	56254	E3 ubiquitin-protein ligase BRE1A	NP_062538.5	1	3	4	8	0.94	0.87	7.76	10.98	14.7	19.2	4	4	7410	56254	ring finger protein 20	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC;RING	Yes
GCSH	2653	glycine cleavage system H protein, mitochondrial precursor	NP_004474.2	1	1	1	5	0.94	0.87	27.82	23.59	48	36.7	3	3	1998	2653	glycine cleavage system protein H (aminomethylcarrier)	Transferase activity	Mitochondrion	Enzyme: Transferase	Metabolism;Energy pathways	SP	Yes
DIS3L2	129563	DIS3-like exonuclease 2 isoform 1	NP_689596.4	2	3	3	4	0.94	0.87	2.06	9.5	3.4	14.4	3	3	14619	129563	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NOMO1	23420	nodal modulator 1 precursor	NP_055102.3	2	1	28	91	0.94	0.86					1	1	11398	23420	NODAL modulator 1	Molecular function unknown	Endoplasmic reticulum	Growth inhibitory factor	Cell communication;Signal transduction	SP;CC	Yes
STXBP2	6813	syntaxin-binding protein 2 isoform a	NP_008880.2	3	12	12	22	0.94	0.86	7.01	9.16	24	28.8	13	13	3423	6813	syntaxin binding protein 2	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
PARVB	29780	beta-parvin isoform a	NP_001003828.1	4	1	2	5	0.94	0.85					1	1	16284	29780	parvin, beta	Cytoskeletal protein binding	-	Adhesion molecule	Cell adhesion	CH	Yes
DERA	51071	deoxyribose-phosphate aldolase isoform 1	NP_057038.2	2	4	4	7	0.94	0.84	9.1	7.34	14.9	10.7	3	3	13138	51071	2-deoxyribose-5-phosphate aldolase homolog (C.elegans)	Lyase activity	-	Enzyme: Lyase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PTAR1	375743	protein prenyltransferase alpha subunit repeat-containing protein 1	NP_001093136.1	1	1	1	1	0.94	0.83					1	1	19564	375743	protein prenyltransferase alpha subunit repeat containing 1	Transferase activity	-	Unclassified	Biological_process unknown	-	No
SPG7	6687	paraplegin isoform 1 precursor	NP_003110.1	2	2	2	4	0.94	0.83	8.4	2.69	11.2	3.2	2	2	4149	6687	spastic paraplegia 7, paraplegin (pure andcomplicated autosomal recessive)	Metallopeptidase activity	Mitochondrion	Metallo protease	Protein metabolism	SP;TM;CC;AAA	Yes
MAD2L1	4085	mitotic spindle assembly checkpoint protein MAD2A	NP_002349.1	1	2	2	3	0.94	0.81					1	1	3274	4085	MAD2 mitotic arrest deficient-like 1 (yeast)	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
TRADD	8717	tumor necrosis factor receptor type 1-associated DEATH domain protein	NP_003780.1	1	3	3	5	0.94	0.81	5.98	22.6	11.2	37.9	4	4	4610	8717	TNFRSF1A-associated via death domain	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction;Apoptosis	DEATH;CC	Yes
MFSD6	54842	major facilitator superfamily domain-containing protein 6	NP_060164.3	1	2	2	4	0.94	0.81	28.4	26.59	39.1	31.2	2	2	13369	54842	None	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	TM	No
CAPZA2	830	F-actin-capping protein subunit alpha-2	NP_006127.1	1	6	8	58	0.94	0.8	5.36	14.17	23.4	55.8	21	21	11871	830	capping protein (actin filament) muscleZ-line, alpha 2	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	-	Yes
RAB3GAP2	25782	rab3 GTPase-activating protein non-catalytic subunit	NP_036546.2	2	24	25	42	0.94	0.79	3.74	5.66	17	21.7	23	23	11471	25782	None	GTPase activator activity	Cytoplasmic vesicle	GTPase activating protein	Cell communication;Signal transduction	CC	No

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
CHTF18	63922	chromosome transmission fidelity protein 18 homolog	NP_071375.1	1	1	1	2	0.94	0.79					1	1	13059	63922	CTF18, chromosome transmission fidelity factor18 homolog (S. cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA;CC	Yes
ASS1	445	argininosuccinate synthase	NP_446464.1	1	3	3	5	0.94	0.78	10.14	1.48	16.6	2	3	3	4590	445	argininosuccinate synthetase	Ligase activity;Catalytic activity	Cytosol	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
ARHGEF10	9639	rho guanine nucleotide exchange factor 10 isoform 3	NP_001295082.1	3	2	2	2	0.94	0.78	10.46	4.25	14	4.7	2	2	9735	9639	Rho guanine nucleotide exchange factor (GEF)10	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;CC	Yes
ATP1B3	483	sodium/potassium-transporting ATPase subunit beta-3	NP_001670.1	1	6	6	10	0.94	0.78	13.48	8.53	37.2	19.1	8	8	3521	483	ATPase, Na+/K+ transporting, beta 3polypeptide	ATPase activity	Plasma membrane	ATPase	Transport	TM	No
APPL2	55198	DCC-interacting protein 13-beta isoform 2	NP_001238833.1	3	3	3	6	0.94	0.78	9.19	28.8	15	40.3	3	3	6945	55198	None	Molecular function unknown	Endosome	Unclassified	Cell communication;Signal transduction	PH	No
UBXN4	23190	UBX domain-containing protein 4	NP_055422.1	1	2	2	10	0.94	0.77	11.42	8.55	24.5	14.9	5	5	18254	23190	UBX domain containing 2	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;CC;UBX	Yes
KIAA0196	9897	WASH complex subunit strumpellin	NP_055661.3	1	6	6	8	0.94	0.75	3.25	8.64	6.1	13.1	4	4	13786	9897	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
SLC16A1	6566	monocarboxylate transporter 1	NP_001159968.1	1	2	2	2	0.94	0.75	3.88	3.07	5.1	3.3	2	2	2816	6566	solute carrier family 16 (monocarboxylic acidtransporters), member 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
GDAP2	54834	ganglioside-induced differentiation-associated protein 2 isoform a	NP_060156.1	2	1	1	2	0.94	0.73					1	1	6576	54834	ganglioside induced differentiation associatedprotein 2	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	SEC14;A1pp	No
USP28	57646	ubiquitin carboxyl-terminal hydrolase 28 isoform 1	NP_065937.1	1	1	1	1	0.94	0.73					1	1	15632	57646	ubiquitin specific protease 28	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UIM;UCH;CC	Yes
PCBP1	5093	poly(rC)-binding protein 1	NP_006187.2	3	9	12	88	0.94	0.7	4.74	8.03	25.7	32.4	32	32	3128	5093	poly(rC) binding protein 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
SMARCAL1	50485	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1	NP_054859.2	1	1	1	1	0.94	0.68					1	1	5969	50485	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily a-like 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;CC	Yes
RNASEL	6041	2-5A-dependent ribonuclease	NP_066956.1	1	2	2	6	0.94	0.66	27.13	6.26	46.4	7.2	3	3	1590	6041	ribonuclease L (2`,5`-oligoisoadenylatesynthetase-dependent)	Ribonuclease activity	Cytoplasm	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_Y_Kinase;PUG;ANK	Yes
SERF2	10169	small EDRK-rich factor 2 isoform a	NP_001186804.1	4	1	1	2	0.94	0.61					1	1	5447	10169	small EDRK-rich factor 2	Nucleic acid binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
SLC25A40	55972	solute carrier family 25 member 40	NP_061331.2	1	1	1	2	0.94	0.58					1	1	14372	55972	None	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	-	No
FAM96B	51647	mitotic spindle-associated MMXD complex subunit MIP18	NP_057146.1	1	3	3	6	0.94	0.57	8.69	19.24	11.6	15.5	2	2	13033	51647	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
TRAF2	7186	TNF receptor-associated factor 2	NP_066961.2	1	3	3	6	0.93	1.86	1.72	14.29	2.3	38.9	2	2	3538	7186	TNF receptor-associated factor 2	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	RING;MATH;CC;TRAF	Yes
PNO1	56902	RNA-binding protein PNO1	NP_064528.1	1	2	2	5	0.93	1.54	12.32	24.77	20.1	74.1	3	3	14250	56902	None	Molecular function unknown	-	Unclassified	Biological_process unknown	KH	Yes
UCK2	7371	uridine-cytidine kinase 2	NP_036606.2	1	4	4	9	0.93	1.33	4.19	7.2	8.7	21.6	5	5	1882	7371	uridine-cytidine kinase 2	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
DNAJA1	3301	dnaJ homolog subfamily A member 1	NP_001530.1	4	13	13	54	0.93	1.29	6.26	5.8	31.7	41.3	28	28	4159	3301	DnaJ (Hsp40) homolog, subfamily A, member 1	Heat shock protein activity	Acrosome	Heat shock protein	Protein metabolism	DNAJ	Yes
ETFA	2108	electron transfer flavoprotein subunit alpha, mitochondrial isoform a	NP_000117.1	2	10	10	44	0.93	1.28	5.83	2.07	25.9	12.5	22	22	1979	2108	electron-transfer-flavoprotein, alphapolypeptide (glutaric aciduria II)	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Metabolism;Energy pathways	-	Yes
GSTCD	79807	glutathione S-transferase C-terminal domain-containing protein isoform 1	NP_001026890.2	2	1	1	1	0.93	1.27					1	1	7823	79807	None	Molecular function unknown	-	Unclassified	Protein metabolism	-	No
SLC1A5	6510	neutral amino acid transporter B(0) isoform 1	NP_005619.1	3	10	10	52	0.93	1.26	6.38	5.63	28.9	34.9	23	23	173	6510	solute carrier family 1 (neutral amino acidtransporter), member 5	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
NHP2	55651	H/ACA ribonucleoprotein complex subunit 2 isoform a	NP_060308.1	2	7	7	22	0.93	1.25	5.13	12.9	15.9	57.5	11	11	7570	55651	nucleolar protein family A, member 2 (H/ACAsmall nucleolar RNPs)	RNA binding	Nucleolus	Ribonucleoprotein	Ribosome biogenesis and assembly	-	Yes

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IDH3A	3419	isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor	NP_005521.1	1	5	5	13	0.93	1.25	4.55	6.64	12	23.9	8	8	3094	3419	isocitrate dehydrogenase 3 (NAD+) alpha [Homosapiens]Other Aliases: HGNC:5384Other Designations: H-IDH alpha; NAD(H)-specificisocitrate dehydrogenase alpha subunit precursor; NAD+-specific ICDH; isocitratedehydrogenase (NAD+) alpha chain precursor; isocitrate dehydrogenase	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
GNB4	59345	guanine nucleotide-binding protein subunit beta-4	NP_067642.1	3	3	7	27	0.93	1.23	7.76	2.47	10.2	4.3	2	2	9973	59345	guanine nucleotide binding protein (G protein),beta polypeptide 4	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	CC;WD40	No
PARS2	25973	probable proline--tRNA ligase, mitochondrial precursor	NP_689481.2	1	3	3	6	0.93	1.21	10.34	0.37	16.8	0.8	3	3	13220	25973	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PNISR	25957	arginine/serine-rich protein PNISR	NP_116259.2	1	2	2	4	0.93	1.2	25.17	9.87	33.9	16.9	2	2									
MCTS1	28985	malignant T-cell-amplified sequence 1 isoform 2	NP_001131026.1	2	4	4	28	0.93	1.2	12.33	20.36	43.1	109	13	13	6634	28985	malignant T cell amplified sequence 1	DNA binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
RRS1	23212	ribosome biogenesis regulatory protein homolog	NP_055984.1	1	7	7	12	0.93	1.19	4.84	5.69	11.1	16.7	6	6	15277	23212	RRS1 ribosome biogenesis regulator homolog (S.cerevisiae)	Ribonucleoprotein;Molecular function unknown	Nucleus	Unclassified	Cell growth and/or maintenance;Biological_process unknown	-	Yes
OSBPL5	114879	oxysterol-binding protein-related protein 5 isoform a	NP_065947.1	2	4	5	7	0.93	1.19	19.22	35.18	31.8	83.4	3	3	9475	114879	oxysterol binding protein-like 5	Transporter activity;Lipid transporter activity	Cytoplasm	Transport/cargo protein	Transport;Lipid transport	PH;CC	Yes
EIF2D	1939	eukaryotic translation initiation factor 2D isoform 1	NP_008824.2	2	6	6	13	0.93	1.18	3.54	7.52	8.7	23.9	7	7									
PTK2	5747	focal adhesion kinase 1 isoform b	NP_005598.3	3	9	10	19	0.93	1.17	6.61	5.1	18.6	18	9	9	2859	5747	PTK2 protein tyrosine kinase 2	Protein-tyrosine kinase activity	Cytoplasm;Nucleus	Tyrosine kinase	Cell communication;Signal transduction	B41;Tyr_Kinase;CC	Yes
PPAN-P2RY11	692312	PPAN-P2RY11 protein isoform 1	NP_001035754.1	3	4	4	10	0.93	1.16	3.86	2.98	8	7.8	5	5	19032	692312	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;TM	Yes
ETF1	2107	eukaryotic peptide chain release factor subunit 1 isoform 1	NP_004721.1	3	14	14	50	0.93	1.16	7.32	6.24	35.6	38.1	26	26	2616	2107	eukaryotic translation termination factor 1	Translation regulator activity	Ribosome	Translation regulatory protein	Protein metabolism	-	Yes
STXBP1	6812	syntaxin-binding protein 1 isoform a	NP_003156.1	2	6	6	13	0.93	1.16	8.62	7.46	23	24.8	8	8	4235	6812	syntaxin binding protein 1	Transporter activity	Plasma membrane;Cytosol	Transport/cargo protein	Neurotransmitter transport	-	Yes
RAPGEF1	2889	rap guanine nucleotide exchange factor 1 isoform b	NP_941372.1	3	4	4	7	0.93	1.14	9.05	12.13	12	19.8	2	2	2627	2889	Rap guanine nucleotide exchange factor (GEF)1	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RasGEFN;RasGEF	Yes
NDC1	55706	nucleoporin NDC1 isoform 1	NP_060557.3	2	4	4	10	0.93	1.14	2.51	7.67	5.2	19.7	5	5									
MRPL54	116541	39S ribosomal protein L54, mitochondrial	NP_758455.1	1	1	1	2	0.93	1.14					1	1	14772	116541	mitochondrial ribosomal protein L54	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
POLE3	54107	DNA polymerase epsilon subunit 3	NP_001265184.1	1	1	1	2	0.93	1.13					1	1	6274	54107	polymerase (DNA directed), epsilon 3 (p17subunit)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
WDR11	55717	WD repeat-containing protein 11	NP_060587.8	1	5	5	12	0.93	1.13	7.5	12.49	17.2	35.6	6	6	16218	55717	bromodomain and WD repeat domain containing 2	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
PRCP	5547	lysosomal Pro-X carboxypeptidase isoform 2 preproprotein	NP_955450.2	2	3	3	4	0.93	1.12	6.76	3.18	12.6	7.2	4	4	8352	5547	prolylcarboxypeptidase (angiotensinase C)	Carboxypeptidase activity	Lysosome	Carboxypeptidase	Protein metabolism	SP	Yes
RAN	5901	GTP-binding nuclear protein Ran isoform 1	NP_006316.1	2	10	10	60	0.93	1.12	5.82	5.41	30.9	34.7	31	31	3109	5901	RAN, member RAS oncogene family	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	RAS	Yes
MET	4233	hepatocyte growth factor receptor isoform a precursor	NP_001120972.1	2	6	6	10	0.93	1.11	9.12	7.84	19.1	19.7	5	5	1280	4233	met proto-oncogene (hepatocyte growth factorreceptor)	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	SEMA;PSI;IPT;Tyr_Kinase;SP	Yes
GRIPAP1	56850	GRIP1-associated protein 1	NP_064522.3	1	6	6	17	0.93	1.11	9.52	8.22	23.7	24.4	7	7	2325	56850	GRIP1 associated protein 1	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	CC	No
KIF15	56992	kinesin-like protein KIF15	NP_064627.1	1	1	1	1	0.93	1.1					1	1	10037	56992	kinesin family member 15	Protein binding;Protein domain specific binding	Centrosome	Cell cycle control protein	Cell communication;Signal transduction	KISC;CC	Yes
EIF2B5	8893	translation initiation factor eIF-2B subunit epsilon	NP_003898.2	1	10	10	22	0.93	1.09	6.09	5.76	20.5	23	13	13	4898	8893	eukaryotic translation initiation factor 2B,subunit 5 epsilon, 82kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
ETFB	2109	electron transfer flavoprotein subunit beta isoform 1	NP_001976.1	2	16	16	45	0.93	1.08	5.58	5.06	27	28.3	26	26	557	2109	electron-transfer-flavoprotein, beta polypeptide	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes

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SLU7	10569	pre-mRNA-splicing factor SLU7	NP_006416.3	1	2	2	2	0.93	1.07	18.82	23.03	25.1	36	2	2	12074	10569	None	Ribonucleoprotein	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C2HC;CC;LRR	No
BECN1	8678	beclin-1	NP_003757.1	1	1	1	2	0.93	1.07					1	1	5087	8678	beclin 1 (coiled-coil, myosin-like BCL2interacting protein)	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	CC	Yes
IPO7	10527	importin-7	NP_006382.1	1	14	14	50	0.93	1.07	5.39	6.87	26.4	39.8	27	27	9280	10527	importin 7	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
NHLRC2	374354	NHL repeat-containing protein 2	NP_940916.2	1	9	9	26	0.93	1.06	9.8	7.76	32.4	29	12	12	14827	374354	NHL repeat containing 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RNASEH2B	79621	ribonuclease H2 subunit B isoform 1	NP_078846.2	2	2	2	4	0.93	1.05	11.59	0.59	15.4	0.9	2	2	7757	79621	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
SLC35B2	347734	adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform a precursor	NP_835361.1	6	2	2	6	0.93	1.05	14.46	13.98	23.5	25.9	3	3	11576	347734	solute carrier family 35, member B2	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	TM	No
DNAJC17	55192	dnaJ homolog subfamily C member 17	NP_060633.1	1	2	2	3	0.93	1.05					1	1	7111	55192	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	DNAJ;CC	No
RRM2B	50484	ribonucleoside-diphosphate reductase subunit M2 B isoform 2	NP_001165948.1	3	2	3	5	0.93	1.04	3.3	0.05	4.3	0.1	2	2	5276	50484	ribonucleotide reductase M2 B (TP53 inducible)	Catalytic activity	Nucleus	Enzyme: Reductase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TM	No
OVCA2	124641	ovarian cancer-associated gene 2 protein	NP_543012.1	1	4	4	7	0.93	1.03	6.99	3.16	11.3	5.6	3	3	7437	124641	None	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	-	No
ACLY	47	ATP-citrate synthase isoform 3	NP_001290203.1	4	43	43	179	0.93	1.02	3.51	2.56	31.8	25.3	91	91	155	47	ATP citrate lyase	ATPase activity	Cytoplasm	ATPase	Metabolism;Energy pathways	-	Yes
ZCCHC6	79670	terminal uridylyltransferase 7 isoform 1	NP_001171988.1	2	4	4	11	0.93	1.02	14.53	9.22	30.8	21.3	5	5	11697	79670	zinc finger, CCHC domain containing 6	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C2HC	Yes
SPARC	6678	SPARC precursor	NP_003109.1	1	2	2	3	0.93	1.01	71.55	6.34	119.3	9	2	2	1631	6678	secreted protein, acidic, cysteine-rich(osteonectin)	Extracellular matrix structural constituent	Extracellular	Secreted polypeptide	Cell growth and/or maintenance	SP;FOLN;KAZAL	Yes
TTLL12	23170	tubulin--tyrosine ligase-like protein 12	NP_055955.1	1	23	23	55	0.93	1.01	4.98	4.63	25.8	26	30	30	13782	23170	None	Ligase activity	Nucleus;Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
MTX1	4580	metaxin-1 isoform 1	NP_002446.3	2	4	4	11	0.93	1.01	8.93	12.14	22.4	33.2	7	7	11861	4580	metaxin 1	Auxiliary transport protein activity;Transporter activity	Mitochondrion	Membrane transport protein	Transport	TM	No
TPP2	7174	tripeptidyl-peptidase 2	NP_003282.2	1	21	21	52	0.93	1.01	4.8	4.8	23.5	25.5	27	27	1834	7174	tripeptidyl peptidase II	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	CC	Yes
EIF2B1	1967	translation initiation factor eIF-2B subunit alpha	NP_001405.1	1	8	8	18	0.93	0.98	9.86	9.08	29.6	28.6	10	10	9458	1967	eukaryotic translation initiation factor 2B,subunit 1 alpha, 26kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	-	Yes
TUBGCP4	27229	gamma-tubulin complex component 4 isoform a	NP_001273343.1	2	3	3	4	0.93	0.98	2.78	0.15	4.5	0.2	3	3	10616	27229	None	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein	Cell growth and/or maintenance	SP	Yes
FHOD1	29109	FH1/FH2 domain-containing protein 1	NP_037373.2	1	12	12	24	0.93	0.97	7.63	5.78	24.9	19.6	12	12	6049	29109	formin homology 2 domain containing 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	FH2;CC;NLS	Yes
USP9X	8239	probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 3	NP_001034679.2	5	20	20	47	0.93	0.97	4.15	3.52	17.9	15.7	21	21	2091	8239	ubiquitin specific protease 9, X-linked (fatfacets-like, Drosophila)	Ubiquitin-specific protease activity	Cytoplasm;Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UCH	Yes
YARS2	51067	tyrosine--tRNA ligase, mitochondrial precursor	NP_001035526.1	2	11	12	18	0.93	0.96	6.52	8.97	18.3	26.3	9	9	13025	51067	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes
NCLN	56926	nicalin precursor	NP_064555.2	1	9	9	25	0.93	0.96	4.25	8.39	13.2	27.2	11	11	7126	56926	nicalin homolog (zebrafish)	Peptidase activity	Plasma membrane	Protease	Protein metabolism	SP;TM	No
MAPK1	5594	mitogen-activated protein kinase 1	NP_002736.3	1	9	12	25	0.93	0.95	8.67	6.22	20	14.5	6	6	1496	5594	mitogen-activated protein kinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
TRAPPC3	27095	trafficking protein particle complex subunit 3 isoform 2	NP_001257823.1	3	2	2	6	0.93	0.95	5.74	10.43	9.3	17.2	3	3	11644	27095	trafficking protein particle complex 3	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	No
MOGS	7841	mannosyl-oligosaccharide glucosidase isoform 1	NP_006293.2	2	17	17	51	0.93	0.95	2.99	3.65	14.5	18.1	27	27	3214	7841	None	Glucosidase activity	Endoplasmic reticulum	Enzyme: Glucosidase	Metabolism;Energy pathways	TM	Yes
LAS1L	81887	ribosomal biogenesis protein LAS1L isoform 1	NP_112483.1	3	5	5	7	0.93	0.94	2.1	1.95	3.4	3.2	3	3	6519	81887	LAS1-like (S. cerevisiae)	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	CC	No
RPS18	6222	40S ribosomal protein S18	NP_072045.1	1	10	10	40	0.93	0.92	6.18	6.17	28.1	27.8	23	23	1601	6222	ribosomal protein S18	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
MX2	4600	interferon-induced GTP-binding protein Mx2	NP_002454.1	1	14	18	67	0.93	0.91	5.24	9.46	22	40.1	20	20	1001	4600	myxovirus (influenza virus) resistance 2 (mouse)	GTPase activity	Nucleus	GTPase	Immune response	GED;DYNC;NLS	Yes
MOB1B	92597	MOB kinase activator 1B isoform 1	NP_001231695.1	4	4	4	13	0.93	0.9	1.92	3.33	4.7	7.9	7	7									
GRHPR	9380	glyoxylate reductase/hydroxypyruvate reductase	NP_036335.1	1	9	9	36	0.93	0.9	5.98	6.67	25.2	27.5	20	20	5052	9380	glyoxylate reductase/hydroxy pyruvate reductase	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	2HD	Yes
RCC2	55920	protein RCC2	NP_061185.1	1	22	22	60	0.93	0.9	3.04	7.97	16.4	42.8	33	33	18171	55920	regulator of chromosome condensation 2	Protein binding	Nucleus	Cell cycle control protein	Cell growth and/or maintenance	-	Yes
SUGT1	10910	suppressor of G2 allele of SKP1 homolog isoform SGT1B	NP_001124384.1	2	4	4	7	0.93	0.9	10.82	10.37	20.3	18.9	4	4	9160	10910	SGT1, suppressor of G2 allele of SKP1 (S.cerevisiae)	Ubiquitin-specific protease activity	Nucleus	Cell cycle control protein;Ubiquitin proteasome system protein	Cell communication;Signal transduction;Protein metabolism	TPR	Yes

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FH	2271	fumarate hydratase, mitochondrial	NP_000134.2	6	17	17	71	0.93	0.9	4.05	5.29	22.7	28.7	35	35	652	2271	fumarate hydratase	Catalytic activity	Mitochondrion	Enzyme: Hydratase	Metabolism;Energy pathways	SP	Yes
ATP6V1H	51606	V-type proton ATPase subunit H isoform 1	NP_057025.2	2	5	5	17	0.93	0.89	3.59	2.3	9.4	5.8	8	8	10591	51606	ATPase, H+ transporting, lysosomal 50/57kDa,V1 subunit H	ATPase activity	-	ATPase	Transport	ARM	No
GDF15	9518	growth/differentiation factor 15 precursor	NP_004855.2	1	3	3	4	0.93	0.89	19.22	9.94	31.8	15.4	3	3	5608	9518	growth differentiation factor 15	Growth factor activity	Extracellular	Growth factor	Cell communication;Signal transduction	SP;TGFB	Yes
ACSS2	55902	acetyl-coenzyme A synthetase, cytoplasmic isoform 2	NP_001070020.2	3	7	7	17	0.93	0.89	9.51	5.49	26.9	14.7	9	9	12053	55902	acetyl-Coenzyme A synthetase 2 (ADP forming)	Catalytic activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
SHC1	6464	SHC-transforming protein 1 isoform 3	NP_001123512.1	6	6	6	18	0.93	0.89	6.33	10.46	17.7	28.6	9	9	2780	6464	SHC (Src homology 2 domain containing)transforming protein 1	Protein binding	Cytoplasm	Adapter molecule	Signal transduction;Cell communication	PTB;SH2	Yes
SRP19	6728	signal recognition particle 19 kDa protein isoform 1	NP_003126.1	4	6	6	10	0.93	0.89	17.28	1.47	37.2	2.9	5	5	1644	6728	signal recognition particle 19kDa	RNA binding	Cytoplasm	RNA binding protein	Protein metabolism	-	No
SNTB2	6645	beta-2-syntrophin	NP_006741.1	1	5	5	9	0.93	0.87	11.08	13.21	23.2	26.1	5	5	2491	6645	syntrophin, beta 2 (dystrophin-associatedprotein A1, 59kDa, basic component 2)	Receptor signaling complex scaffold activity	Cytoplasm;Nucleus	Adapter molecule	Signal transduction	PDZ;PH	Yes
ESRP2	80004	epithelial splicing regulatory protein 2	NP_079215.2	1	5	5	9	0.93	0.86	15.43	11.27	29.4	17	4	3	7971	80004	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	No
STAT3	6774	signal transducer and activator of transcription 3 isoform 1	NP_644805.1	3	18	18	38	0.93	0.85	3.36	5.52	14.7	22.2	22	22	26	6774	signal transducer and activator oftranscription 3 (acute-phase response factor)	Transcription factor activity	Nucleus;Extracellular matrix	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SH2;CC	Yes
DNM2	1785	dynamin-2 isoform 1	NP_001005360.1	5	16	21	57	0.93	0.83	4.33	11.14	19.9	47.9	24	24	3852	1785	dynamin 2 [Homo sapiens]Other Aliases:HGNC:2974, DYN2, DYNIIOther Designations: DYN2_HUMAN [AA 474- 870]; cytoskeletalprotein; dynamin II; dynamin II {AA 474- 866]	GTPase activity	Cytoskeleton	GTPase	Cell communication;Signal transduction	DYNC;PH;GED	Yes
TMTC3	160418	transmembrane and TPR repeat-containing protein 3	NP_861448.2	1	10	10	17	0.93	0.82	3.67	12.34	10.8	32.9	10	10	10243	160418	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM;TPR	No
NEFL	4747	neurofilament light polypeptide	NP_006149.2	4	8	9	24	0.93	0.81	6.29	14.48	15.6	31.7	7	7	1206	4747	neurofilament, light polypeptide 68kDa	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
MYO10	4651	unconventional myosin-X	NP_036466.2	1	3	3	3	0.93	0.8	2.58	34.56	3.4	40.5	2	2	3283	4651	myosin X	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	MYOSIN;IQ;PH;B41;CC	Yes
APOOL	139322	MICOS complex subunit MIC27 precursor	NP_940852.3	1	3	3	5	0.93	0.8	10.95	10.18	14.5	11.5	2	2	16775	139322	chromosome X open reading frame 33	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
NRAS	4893	GTPase NRas	NP_002515.1	1	3	9	27	0.93	0.77	8.05	5.56	18.4	10.6	6	6	1273	4893	neuroblastoma RAS viral (v-ras) oncogene homolog	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	Yes
SCP2	6342	non-specific lipid-transfer protein isoform 1 proprotein	NP_002970.2	6	1	1	1	0.93	0.77					1	1	1700	6342	sterol carrier protein 2	Auxiliary transport protein activity;Sterol transporter activity	Cytoplasm	Membrane transport protein	Transport;Lipid metabolism	-	Yes
MFSD10	10227	major facilitator superfamily domain-containing protein 10	NP_001111.3	1	4	4	9	0.93	0.73	11.28	4.4	21.2	6.4	4	4	10265	10227	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ATL2	64225	atlastin-2 isoform 2	NP_001129145.1	3	2	2	7	0.93	0.71	49.97	38.63	73.3	40.2	2	2	10662	64225	ADP-ribosylation factor-like 6 interactingprotein 2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	TM;CC	No
MAN2C1	4123	alpha-mannosidase 2C1 isoform 2	NP_001243423.1	4	1	1	2	0.93	0.69					1	1	1109	4123	mannosidase, alpha, class 2C, member 1	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
RPAP1	26015	RNA polymerase II-associated protein 1	NP_056355.2	1	1	1	2	0.93	0.69					1	1	11522	26015	RNA polymerase II associated protein 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
VAPA	9218	vesicle-associated membrane protein-associated protein A isoform 2	NP_919415.2	2	10	11	40	0.93	0.68	3.9	13.74	15.8	42.6	19	19	9299	9218	VAMP (vesicle-associated membraneprotein)-associated protein A, 33kDa	Auxiliary transport protein activity	Endoplasmic reticulum membrane;Golgi membrane	Membrane transport protein	Vesicle docking;Transport	CC;TM	Yes
STMN1	3925	stathmin isoform a	NP_005554.1	4	7	7	43	0.93	0.67	3.6	9.32	14.2	26.8	18	18	1047	3925	stathmin 1/oncoprotein 18	Structural molecule activity;Signal transducer activity	Cytoplasm	Structural protein	Cell growth and/or maintenance;Signal transduction	CC	Yes
CCNJL	79616	cyclin-J-like protein isoform a	NP_078841.3	1	1	1	1	0.93	0.62					1	1	7853	79616	None	Molecular function unknown	-	Cell cycle control protein	Cell communication;Signal transduction	CYCLIN	No

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SIN3B	23309	paired amphipathic helix protein Sin3b isoform 1	NP_056075.1	2	1	1	2	0.92	1.98					1	1	9691	23309	SIN3 homolog B, transcription regulator (yeast)	Translation regulator activity	Nucleus	Translation regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PAH;CC	Yes
PRR12	57479	proline-rich protein 12	NP_065770.1	1	1	1	2	0.92	1.94					1	1	19620	57479	proline rich 12	DNA binding	-	DNA binding protein	Biological_process unknown	AT_hook	No
PNPLA4	8228	patatin-like phospholipase domain-containing protein 4 isoform 1 precursor	NP_004641.1	2	2	2	6	0.92	1.58	58.54	13.52	117.1	38.4	3	3	2112	8228	patatin-like phospholipase domain containing 4	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
UBE4A	9354	ubiquitin conjugation factor E4 A isoform 1	NP_004779.2	2	4	4	8	0.92	1.5	5.82	11.3	9.3	29.9	3	3	6793	9354	ubiquitination factor E4A (UFD2 homolog, yeast)	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBOX	Yes
MRPS25	64432	28S ribosomal protein S25, mitochondrial	NP_071942.1	1	3	3	6	0.92	1.49	7.77	6.26	12.4	16.2	3	3	17594	64432	mitochondrial ribosomal protein S25	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	CC	Yes
SDHB	6390	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor	NP_002991.2	1	11	11	34	0.92	1.4	2.37	2.09	8.7	11.8	16	16	1707	6390	succinate dehydrogenase complex, subunit B, ironsulfur (Ip)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
OARD1	221443	O-acetyl-ADP-ribose deacetylase 1	NP_659500.1	1	1	1	2	0.92	1.34					1	1									
PPM1B	5495	protein phosphatase 1B isoform 1	NP_002697.1	4	1	3	4	0.92	1.29					1	1	4796	5495	protein phosphatase 1B (formerly 2C),magnesium-dependent, beta isoform	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Signal transduction	PP2C	Yes
PWP1	11137	periodic tryptophan protein 1 homolog	NP_008993.1	1	5	5	9	0.92	1.27	12.69	2.7	29.1	8.4	6	6	11464	11137	PWP1 homolog (S. cerevisiae)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Cell growth and/or maintenance	CC;WD40	No
CCT4	10575	T-complex protein 1 subunit delta isoform a	NP_006421.2	2	32	33	193	0.92	1.24	3.21	4.47	28	55.2	86	86	5506	10575	chaperonin containing TCP1, subunit 4 (delta)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
PSMB8	5696	proteasome subunit beta type-8 isoform E2 proprotein	NP_683720.2	2	5	5	7	0.92	1.19	22.71	15.44	49.1	43.1	5	5	1515	5696	proteasome (prosome, macropain) subunit, betatype, 8 (large multifunctional protease 7)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
INTS10	55174	integrator complex subunit 10	NP_060612.2	1	2	2	4	0.92	1.17					1	1	7686	55174	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
NARS	4677	asparagine--tRNA ligase, cytoplasmic	NP_004530.1	1	14	14	46	0.92	1.16	4.55	9.06	20.8	55	24	24	154	4677	asparaginyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	TRNAA;CC	Yes
TOR1AIP2	163590	torsin-1A-interacting protein 2 isoform b	NP_659471.1	1	7	8	23	0.92	1.14	19.13	10.58	57	32.9	9	7	10048	163590	torsin A interacting protein 2	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	TM	No
SRSF9	8683	serine/arginine-rich splicing factor 9	NP_003760.1	1	3	3	5	0.92	1.13	31.85	3.59	54.4	7	3	3									
LDLR	3949	low-density lipoprotein receptor isoform 1 precursor	NP_000518.1	9	15	15	39	0.92	1.11	5.8	6.64	24.2	33.9	20	20	6091	3949	low density lipoprotein receptor (familialhypercholesterolemia)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	LDLA;EGF;EGFCA;LDLRB;EGFL;TM;SP	Yes
BLMH	642	bleomycin hydrolase	NP_000377.1	1	6	6	12	0.92	1.1	5.88	2.87	14.4	8.3	7	7	3870	642	bleomycin hydrolase	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
AHCTF1	25909	protein ELYS	NP_056261.4	1	13	13	28	0.92	1.08	10.74	2.18	36.7	8.5	13	13	9935	25909	None	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AT_hook	No
PLRG1	5356	pleiotropic regulator 1 isoform 1	NP_002660.1	2	5	5	16	0.92	1.08	5.53	8.09	12.5	21.6	6	6	16181	5356	pleiotropic regulator 1 (PRL1 homolog,Arabidopsis)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Cell communication;Signal transduction	WD40	Yes
SRPK2	6733	SRSF protein kinase 2 isoform a	NP_872634.1	5	3	5	9	0.92	1.07	0.83	18.57	1.3	35.4	3	3	4280	6733	SFRS protein kinase 2	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Regulation of gene expression, epigenetic	CC;S_T_Y_Kinase	No
RPL9	6133	60S ribosomal protein L9	NP_001020092.1	1	7	7	47	0.92	1.07	1.86	5.9	8.2	31	23	23	4732	6133	ribosomal protein L9	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
CPOX	1371	oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial precursor	NP_000088.3	1	8	8	14	0.92	1.06	3.64	5.14	10.1	16.4	9	9	417	1371	coproporphyrinogen oxidase	Catalytic activity	Mitochondrion	Enzyme: Oxidase	Metabolism;Energy pathways	-	Yes
SNRPA	6626	U1 small nuclear ribonucleoprotein A	NP_004587.1	1	6	7	20	0.92	1.05	13.33	11.93	46.6	47.6	13	13	1658	6626	small nuclear ribonucleoprotein polypeptide A	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
IMPAD1	54928	inositol monophosphatase 3	NP_060283.3	1	4	4	6	0.92	1.05	9.11	2.64	16.9	5.6	4	4	6531	54928	None	Catalytic activity	-	Enzyme: Phosphatase	Metabolism;Energy pathways	I_Phosphatase;TM	No
UBE4B	10277	ubiquitin conjugation factor E4 B isoform 1	NP_001099032.1	2	4	4	7	0.92	1.05	9.47	9.75	19.7	23.2	5	5	11659	10277	ubiquitination factor E4B (UFD2 homolog, yeast)	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBOX	Yes
YARS	8565	tyrosine--tRNA ligase, cytoplasmic	NP_003671.1	1	26	26	61	0.92	1.04	5.6	5.65	30.3	34.9	33	33	9153	8565	tyrosyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes

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SH3GL1	6455	endophilin-A2 isoform 1	NP_003016.1	4	10	10	35	0.92	1.03	3.93	4.71	14.5	19.6	16	16	3462	6455	SH3-domain GRB2-like 1 [Homo sapiens]OtherAliases: HGNC:10830, CNSA1, EEN, SH3D2B, SH3P8Other Designations: SH3-containingGrb-2-like 1 protein; SH3-containing protein EEN	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	BAR;SH3;CC	Yes
GTF3C3	9330	general transcription factor 3C polypeptide 3 isoform 1	NP_036218.1	2	5	5	10	0.92	1.03	11.83	2.02	24.7	4.6	5	5	11997	9330	general transcription factor IIIC, polypeptide3, 102kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;TPR	Yes
LMNB1	4001	lamin-B1 isoform 1	NP_005564.1	2	36	39	138	0.92	1.02	3.18	3.74	24.7	32.6	69	69	1036	4001	lamin B1	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	CC;NLS	Yes
UTP6	55813	U3 small nucleolar RNA-associated protein 6 homolog	NP_060898.2	1	4	4	6	0.92	1.02	24.06	4.53	46.4	9.3	4	4	11020	55813	chromosome 17 open reading frame 40	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	HAT	Yes
GXYLT1	283464	glucoside xylosyltransferase 1 isoform 1	NP_775872.1	2	1	1	2	0.92	1.02					1	1	19529	283464	glycosyltransferase 8 domain containing 3	Transferase activity	-	Unclassified	Biological_process unknown	TM	No
PITPNB	23760	phosphatidylinositol transfer protein beta isoform isoform 3	NP_001271207.1	3	10	10	20	0.92	1.01	13.12	8.99	43.5	32.3	12	12	6044	23760	phosphatidylinositol transfer protein, beta	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
ACSL4	2182	long-chain-fatty-acid--CoA ligase 4 isoform 2	NP_075266.1	2	12	15	50	0.92	1	4.83	12.76	16.8	50.5	14	14	2152	2182	acyl-CoA synthetase long-chain family member 4	Ligase activity	Microsome	Enzyme: Ligase	Metabolism;Energy pathways	SP	Yes
VPS35	55737	vacuolar protein sorting-associated protein 35	NP_060676.2	1	20	20	60	0.92	0.99	3.93	4.32	19.7	23.8	29	30	6085	55737	vacuolar protein sorting 35 (yeast)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
DCD	117159	dermcidin isoform 2 preproprotein	NP_001287783.1	2	2	2	2	0.92	0.98					1	1	7363	117159	dermcidin	Molecular function unknown	Extracellular	Secreted polypeptide	Immune response	SP	Yes
SF3B1	23451	splicing factor 3B subunit 1 isoform 1	NP_036565.2	3	34	34	74	0.92	0.98	4.99	7.01	29.7	45.5	40	40	9281	23451	splicing factor 3b, subunit 1, 155kDa	Ribonucleoprotein	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
ACTR1A	10121	alpha-centractin	NP_005727.1	1	5	10	47	0.92	0.98	4.6	5.04	13.4	15.7	10	10	5507	10121	ARP1 actin-related protein 1 homolog A,centractin alpha (yeast)	Structural constituent of cytoskeleton	Centrosome	Cytoskeletal protein	Cell growth and/or maintenance	ACTIN	Yes
DUSP11	8446	RNA/RNP complex-1-interacting phosphatase	NP_003575.2	1	1	1	1	0.92	0.98					1	1	4368	8446	dual specificity phosphatase 11 (RNA/RNPcomplex 1-interacting)	Protein tyrosine/serine/threonine phosphatase activity	Nucleus	Dual specificity phosphatase	Cell communication;Signal transduction	DSPC	No
DICER1	23405	endoribonuclease Dicer isoform 1	NP_803187.1	4	2	2	8	0.92	0.98	8.17	3.74	10.7	5.2	2	2	5875	23405	Dicer1, Dcr-1 homolog (Drosophila)	Ribonuclease activity	Cytoplasm	Ribonuclease	Gene silencing	DEXDc;HELIC;DSRM;CC	Yes
DNAJC11	55735	dnaJ homolog subfamily C member 11	NP_060668.2	1	8	8	13	0.92	0.98	4.81	8.4	13.3	25.1	9	9	7112	55735	DnaJ (Hsp40) homolog, subfamily C, member 11	Molecular function unknown	-	Unclassified	Biological_process unknown	DNAJ;NLS;CC	No
MDH1	4190	malate dehydrogenase, cytoplasmic isoform 1	NP_001186040.1	3	17	17	62	0.92	0.97	3.51	4.9	19.4	28.6	35	35	1100	4190	malate dehydrogenase 1, NAD (soluble)	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
HBS1L	10767	HBS1-like protein isoform 1	NP_006611.1	3	7	7	12	0.92	0.97	7.88	7.9	20.6	21.9	8	8	6582	10767	HBS1-like (S. cerevisiae)	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	GTP_EFTU;GTP_EFTU_D2;GTP_EFTU_D3	Yes
ASAH1	427	acid ceramidase isoform b	NP_004306.3	3	5	5	14	0.92	0.97	7.32	14.05	19.1	40.1	8	8	1969	427	N-acylsphingosine amidohydrolase (acidceramidase) 1	Hydrolase activity	Lysosome	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
GBA	2629	glucosylceramidase isoform 1 precursor	NP_001005742.1	3	8	8	27	0.92	0.95	8.17	7	28.5	25.3	14	14	6973	2629	glucosidase, beta; acid (includesglucosylceramidase)	Glucosidase activity	Lysosome	Enzyme: Glucosidase	Lipid metabolism	SP	Yes
TARBP1	6894	probable methyltransferase TARBP1	NP_005637.3	1	3	3	3	0.92	0.95	7.37	7.69	9.6	10.3	2	2	5445	6894	TAR (HIV) RNA binding protein 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MAT2A	4144	S-adenosylmethionine synthase isoform type-2	NP_005902.1	2	13	13	35	0.92	0.95	4.75	4.44	18.1	17.6	17	17	3275	4144	methionine adenosyltransferase II, alpha	Catalytic activity	Cytoplasm	Enzyme: Adenosyltransferase	Metabolism;Energy pathways	-	Yes
PRKDC	5591	DNA-dependent protein kinase catalytic subunit isoform 1	NP_008835.5	2	109	109	336	0.92	0.92	2.46	2.84	29.8	34.6	166	166	2941	5591	protein kinase, DNA-activated, catalyticpolypeptide	Protein serine/threonine kinase activity;DNA repair protein	Nucleus	Serine/threonine kinase;DNA repair protein	Cell communication;Signal transduction	PI3KC;LZ;HEAT	Yes
PRPSAP2	5636	phosphoribosyl pyrophosphate synthase-associated protein 2 isoform 1	NP_002758.1	4	8	11	31	0.92	0.92	6.2	9.79	21.6	34.7	14	14	4789	5636	phosphoribosyl pyrophosphatesynthetase-associated protein 2	Molecular function unknown	Nucleus;Cytoplasm	Regulatory/other subunit	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
RPL14	9045	60S ribosomal protein L14	NP_003964.3	1	4	4	39	0.92	0.91	4.98	6.63	21.2	28.3	21	21	10617	9045	ribosomal protein L14	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	KOW	Yes

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ABCD3	5825	ATP-binding cassette sub-family D member 3 isoform a	NP_002849.1	6	9	10	27	0.92	0.91	5.51	9.64	16.2	29.8	10	11	1368	5825	ATP-binding cassette, sub-family D (ALD),member 3	ATP binding	Peroxisome	Integral membrane protein	Transport	TM;AAA;SP	Yes
DYNC1H1	1778	cytoplasmic dynein 1 heavy chain 1	NP_001367.2	5	159	159	478	0.92	0.91	1.71	2.32	25.3	34.3	250	250	2524	1778	dynein, cytoplasmic, heavy polypeptide 1	ATPase activity	Cytoplasm	ATPase	Metabolism;Energy pathways	CC;AAA	Yes
ATP5A1	498	ATP synthase subunit alpha, mitochondrial isoform a precursor	NP_004037.1	3	30	30	237	0.92	0.91	2.99	3.09	29.5	30.1	110	110	1258	498	ATP synthase, H+ transporting, mitochondrialF1 complex, alpha subunit, isoform 1, cardiac muscle	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	SP	Yes
VPS16	64601	vacuolar protein sorting-associated protein 16 homolog isoform 1	NP_072097.2	2	4	4	12	0.92	0.9	7.24	8.36	16.4	18.7	6	6	12259	64601	vacuolar protein sorting 16 (yeast)	Transporter activity	Late endosome	Transport/cargo protein	Transport	CC	Yes
PEX11B	8799	peroxisomal membrane protein 11B isoform 1	NP_003837.1	2	3	3	4	0.92	0.9	12.69	12.64	16.7	16.3	2	2	4844	8799	peroxisomal biogenesis factor 11B	Molecular function unknown	Peroxisome	Integral membrane protein	Cell communication;Signal transduction	TPR;TM	No
SMC6	79677	structural maintenance of chromosomes protein 6	NP_078900.1	1	2	2	3	0.92	0.89					1	1	10242	79677	SMC6 structural maintenance of chromosomes6-like 1 (yeast)	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;CXC	No
LSS	4047	lanosterol synthase isoform 1	NP_001001438.1	3	14	14	34	0.92	0.89	8.78	5.44	35.5	20.7	18	18	2945	4047	lanosterol synthase (2,3-oxidosqualene-lanosterolcyclase)	Catalytic activity	Endoplasmic reticulum	Enzyme: Mutase	Metabolism;Energy pathways	-	Yes
GNAI2	2771	guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 1	NP_002061.1	13	6	10	83	0.92	0.88	5.65	7.55	22.8	29.7	19	19	764	2771	guanine nucleotide binding protein (G protein),alpha inhibiting activity polypeptide 2	GTPase activity;G-protein-coupled receptor binding	Plasma membrane	GTPase;G protein	Cell communication;Signal transduction	-	Yes
COL1A2	1278	collagen alpha-2(I) chain precursor	NP_000080.2	1	2	2	3	0.92	0.88	45.17	49.12	64.6	67.4	2	2	363	1278	collagen, type I, alpha 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	COLFI;SP;COLL	Yes
CDK16	5127	cyclin-dependent kinase 16 isoform 3	NP_001163931.1	48	1	2	18	0.92	0.88					1	1	2409	5127	PCTAIRE protein kinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
TSG101	7251	tumor susceptibility gene 101 protein	NP_006283.1	1	6	6	21	0.92	0.88	5.23	9.47	17.4	30.7	13	13	3229	7251	tumor susceptibility gene 101	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBC;CC	Yes
SPATA5L1	79029	spermatogenesis-associated protein 5-like protein 1	NP_076968.2	1	3	3	5	0.92	0.87	9.91	41.97	12.9	55.6	2	2	11596	79029	spermatogenesis associated 5-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	AAA	No
IMMT	10989	MICOS complex subunit MIC60 isoform 1	NP_006830.2	3	44	44	121	0.92	0.87	3.13	3.85	23.5	27.6	65	65	2658	10989	inner membrane protein, mitochondrial(mitofilin)	Motor activity	Mitochondrion	Motor protein	Cell growth and/or maintenance	SP;CC;TM	Yes
PRPF38B	55119	pre-mRNA-splicing factor 38B	NP_060531.2	1	2	2	4	0.92	0.86	1.09	8.65	1.4	10.6	2	2	7664	55119	PRP38 pre-mRNA processing factor 38 (yeast)domain containing B	RNA binding	-	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
PYCR1	5831	pyrroline-5-carboxylate reductase 1, mitochondrial isoform 5	NP_001269210.1	4	4	5	10	0.92	0.86	13.23	9.97	27.9	19.3	5	5	1528	5831	pyrroline-5-carboxylate reductase 1	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
HIBADH	11112	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	NP_689953.1	1	10	10	24	0.92	0.86	4.56	10.47	14.6	32.1	12	12	12238	11112	3-hydroxyisobutyrate dehydrogenase	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
EXOC8	149371	exocyst complex component 8	NP_787072.2	1	9	9	17	0.92	0.86	10.37	5.03	30.9	13.7	10	10	9943	149371	exocyst complex component 8	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	PH	No
MTPAP	55149	poly(A) RNA polymerase, mitochondrial precursor	NP_060579.3	1	5	5	9	0.92	0.85	11.57	17.95	24.2	35.2	5	5	15097	55149	PAP associated domain containing 1	DNA-directed RNA polymerase activity	Mitochondrion	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 1	NP_004184.1	3	14	15	34	0.92	0.84	3.14	11.54	11.2	38.9	15	15	4740	8729	golgi-specific brefeldin A resistance factor 1	Guanyl-nucleotide exchange factor activity	Golgi apparatus	Guanine nucleotide exchange factor	Cell communication;Signal transduction	Sec7	Yes
RAB14	51552	ras-related protein Rab-14	NP_057406.2	10	14	15	100	0.92	0.83	4.88	6.43	26.2	31.3	33	33	6693	51552	RAB14, member RAS oncogene family	GTPase activity	Integral to membrane	GTPase	Cell communication;Signal transduction	RAB	Yes
PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	NP_055847.1	1	8	9	21	0.92	0.83	7.07	4.64	19.7	11.7	9	9	5624	23047	androgen-induced proliferation inhibitor	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AT_hook	No
FDPS	2224	farnesyl pyrophosphate synthase isoform a	NP_001995.1	3	9	9	35	0.92	0.83	4.88	14.09	19.9	54.6	19	19	606	2224	farnesyl diphosphate synthase (farnesylpyrophosphate synthetase, dimethylallyltranstransferase,geranyltranstransferase)	Transferase activity	Peroxisome	Enzyme: Prenyltransferase	Metabolism;Energy pathways	35EXO;SP;TM	Yes
VAMP3	9341	vesicle-associated membrane protein 3	NP_004772.1	2	4	4	16	0.92	0.82	4.9	22.34	11	47.3	6	6	4711	9341	vesicle-associated membrane protein 3(cellubrevin)	Protein binding;Transporter activity	Plasma membrane	Integral membrane protein	Transport	TM;CC	No

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FAF2	23197	FAS-associated factor 2	NP_055428.1	1	13	13	37	0.92	0.82	9.86	9.24	43.2	35.7	21	21	16870	23197	None	Molecular function unknown	Cytoplasm	Unclassified	Apoptosis	CC;UBX;UBA	No
FLYWCH2	114984	FLYWCH family member 2	NP_612448.1	1	2	2	3	0.92	0.82	2.12	14.11	2.8	16.5	2	2	14007	114984	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
LYRM7	90624	complex III assembly factor LYRM7 isoform 1	NP_859056.2	1	1	1	2	0.92	0.81	2.73	11.14	3.5	12.9	2	2	14276	90624	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
MCMBP	79892	mini-chromosome maintenance complex-binding protein isoform 1	NP_079110.1	3	6	6	11	0.92	0.81	3.5	5.2	7.9	10.4	6	6									
ELF1	1997	ETS-related transcription factor Elf-1 isoform a	NP_758961.1	2	3	3	5	0.92	0.8	18.22	24.83	24.1	28.7	2	2	1808	1997	E74-like factor 1 (ets domain transcriptionfactor)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ETS	Yes
TTF2	8458	transcription termination factor 2	NP_003585.3	1	2	2	5	0.92	0.8	20.63	42.39	27.3	51	2	2	5280	8458	transcription termination factor, RNA polymeraseII	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
IGBP1	3476	immunoglobulin-binding protein 1	NP_001542.1	1	3	3	5	0.92	0.79	15.88	2.45	25.8	3.4	3	3	2140	3476	immunoglobulin (CD79A) binding protein 1	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	CC	Yes
SLC30A5	64924	zinc transporter 5 isoform 1	NP_075053.2	1	1	1	2	0.92	0.78					1	1	6381	64924	solute carrier family 30 (zinc transporter),member 5	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	Yes
NENF	29937	neudesin precursor	NP_037481.1	1	3	3	7	0.92	0.77	6.56	6.06	12.1	9.4	4	4	11603	29937	None	Kinase regulator activity	Extracellular	Secreted polypeptide	Biological_process unknown	SP	Yes
ADAR	103	double-stranded RNA-specific adenosine deaminase isoform a	NP_001102.2	4	35	35	83	0.92	0.76	3.14	5.83	18.5	28.4	40	40	7528	103	adenosine deaminase, RNA-specific	Deaminase activity	Nucleus	Enzyme: Deaminase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DSRM;NLS	Yes
VAMP8	8673	vesicle-associated membrane protein 8	NP_003752.2	1	2	2	9	0.92	0.74	3.93	8.09	9.6	16	7	7	4415	8673	vesicle-associated membrane protein 8(endobrevin)	Auxiliary transport protein activity	Endosome	Membrane transport protein	Transport	TM	No
DARS2	55157	aspartate--tRNA ligase, mitochondrial	NP_060592.2	1	16	16	36	0.92	0.74	5.21	9.72	21.7	33	20	20	7677	55157	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	TRNAA	Yes
CDC42	998	cell division control protein 42 homolog isoform 1 precursor	NP_001782.1	4	6	7	48	0.92	0.74	3.31	6.18	15.3	23.1	25	25	309	998	cell division cycle 42 (GTP binding protein,25kDa)	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	RHO	Yes
TPM1	7168	tropomyosin alpha-1 chain isoform Tpm1.8cy	NP_001288218.1	2	2	14	32	0.92	0.66	4.23	51.79	5.5	51.6	2	2	1839	7168	tropomyosin 1 (alpha)	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
MPC2	25874	mitochondrial pyruvate carrier 2	NP_056230.1	1	2	2	3	0.92	0.64	0.32	15.35	0.4	14.1	2	2									
CISD1	55847	CDGSH iron-sulfur domain-containing protein 1	NP_060934.1	1	3	3	7	0.92	0.63	12.03	12.73	22.4	16.1	4	4	12587	55847	chromosome 10 open reading frame 70	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
ARL8A	127829	ADP-ribosylation factor-like protein 8A isoform 1	NP_620150.1	2	1	4	9	0.92	0.57					1	1	9807	127829	ADP-ribosylation factor-like 10B	GTPase activity	-	GTPase	Cell communication;Signal transduction	ARF	Yes
FTH1	2495	ferritin heavy chain	NP_002023.2	1	6	6	12	0.92	0.54	6.32	20.72	14.4	28.2	6	6	615	2495	ferritin, heavy polypeptide 1	Storage protein	Cytoplasm	Storage protein	Transport	-	Yes
COL1A1	1277	collagen alpha-1(I) chain preproprotein	NP_000079.2	1	1	1	11	0.92	0.52	9.01	23.11	20.6	30.3	6	6	362	1277	collagen, type I, alpha 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	VWC;COLL;COLFI;RGD;SP	Yes
MKRN2	23609	probable E3 ubiquitin-protein ligase makorin-2 isoform 1	NP_054879.3	2	1	1	1	0.91	1.75					1	1	9761	23609	makorin, ring finger protein, 2	Ribonucleoprotein	-	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1;RING	No
SPTLC2	9517	serine palmitoyltransferase 2	NP_004854.1	1	3	3	9	0.91	1.73	12.83	3.08	23.6	10.7	4	4	5755	9517	serine palmitoyltransferase, long chain basesubunit 2	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
LIG1	3978	DNA ligase 1 isoform 1	NP_000225.1	3	1	1	2	0.91	1.62					1	1	534	3978	ligase I, DNA, ATP-dependent	DNA ligase activity	Nucleus	DNA ligase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
SRSF4	6429	serine/arginine-rich splicing factor 4	NP_005617.2	1	6	10	23	0.91	1.42	13.97	23.13	29.1	84.7	5	5									
PPM1A	5494	protein phosphatase 1A isoform 3	NP_808821.2	5	2	3	5	0.91	1.36	6.23	8.66	8	16.7	2	2	16199	5494	protein phosphatase 1A (formerly 2C),magnesium-dependent, alpha isoform	Protein serine/threonine phosphatase activity	Cytoplasm;Nucleus	Serine/threonine phosphatase	Signal transduction	PP2C	Yes
TUBG1	7283	tubulin gamma-1 chain	NP_001061.2	2	9	9	23	0.91	1.29	10.33	4.77	31.8	20.7	11	11	1853	7283	tubulin, gamma 1	Structural constituent of cytoskeleton	Nucleus	Cytoskeletal protein	Cell growth and/or maintenance	TUBULIN	Yes
RFC5	5985	replication factor C subunit 5 isoform 1	NP_031396.1	4	3	3	5	0.91	1.29	20.36	7.71	26.6	14.1	2	2	2677	5985	replication factor C (activator 1) 5, 36.5kDa	DNA binding	Nucleus	DNA binding protein	DNA replication	AAA	Yes
NCBP1	4686	nuclear cap-binding protein subunit 1	NP_002477.1	1	10	10	22	0.91	1.28	3.12	7.32	9.4	31.9	11	11	2717	4686	nuclear cap binding protein subunit 1, 80kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MIF4G;CC;NLS	Yes

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TOP2B	7155	DNA topoisomerase 2-beta	NP_001059.2	1	7	15	36	0.91	1.27	4.51	3.99	12.4	15.3	9	9	537	7155	topoisomerase (DNA) II beta 180kDa	DNA topoisomerase activity	Nucleus	Enzyme: Topoisomerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NES	Yes
KIAA0020	9933	pumilio domain-containing protein KIAA0020	NP_055693.4	1	4	4	7	0.91	1.27	13.61	9.5	25	24.5	4	4	8822	9933	KIAA0020	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	Pumilio	Yes
EIF3M	10480	eukaryotic translation initiation factor 3 subunit M isoform 1	NP_006351.2	2	7	7	25	0.91	1.24	7.28	4.86	24.1	21.9	13	13	9969	10480	None	Molecular function unknown	-	Unclassified	Biological_process unknown	PINT	Yes
MRS2	57380	magnesium transporter MRS2 homolog, mitochondrial isoform a	NP_001273193.1	4	2	2	4	0.91	1.19	16.14	2.99	20.9	5	2	2	17603	57380	MRS2-like, magnesium homeostasis factor (S.cerevisiae)	Transporter activity	Mitochondrion	Integral membrane protein	Transport	TM	Yes
MYBBP1A	10514	myb-binding protein 1A isoform 1	NP_001099008.1	2	26	26	70	0.91	1.19	5.83	9.13	32.8	72.4	36	36	5349	10514	MYB binding protein (P160) 1a	Transcription regulator activity	Nucleolus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
DENR	8562	density-regulated protein	NP_003668.2	1	6	6	12	0.91	1.18	5.01	12.32	12.9	42.9	8	8	5182	8562	density-regulated protein	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	-	Yes
BDH1	622	D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	NP_976060.1	1	4	4	6	0.91	1.17	12.73	9.89	20.4	20.3	3	3	4344	622	3-hydroxybutyrate dehydrogenase (heart,mitochondrial)	Catalytic activity	Mitochondrial membrane	Enzyme: Dehydrogenase	Fatty acid metabolism	SP	Yes
ERO1L	30001	ERO1-like protein alpha precursor	NP_055399.1	1	20	21	77	0.91	1.17	4.51	2.7	26.1	20	39	39	13278	30001	ERO1-like (S. cerevisiae)	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
DAGLB	221955	sn1-specific diacylglycerol lipase beta isoform 1	NP_631918.3	2	3	3	4	0.91	1.16	13.17	44.55	21	84.3	3	2	17324	221955	None	Lipase activity	-	Enzyme: Lipase	Metabolism;Energy pathways	TM	No
NUP54	53371	nucleoporin p54 isoform 1	NP_059122.2	2	5	5	12	0.91	1.15	9.11	5.95	20.6	16.9	6	6	6352	53371	nucleoporin 54kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
ZMPSTE24	10269	CAAX prenyl protease 1 homolog	NP_005848.2	1	10	10	22	0.91	1.14	9.68	25.13	32.5	138	13	13	7349	10269	zinc metallopeptidase (STE24 homolog, yeast)	Metallopeptidase activity	Endoplasmic reticulum	Metallo protease	Protein metabolism	TM	No
OSTC	58505	oligosaccharyltransferase complex subunit OSTC isoform 3	NP_001254747.1	3	1	1	2	0.91	1.12					1	1	13120	58505	None	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
WDR5	11091	WD repeat-containing protein 5	NP_060058.1	1	4	4	12	0.91	1.1	4.27	0.68	9.5	1.9	6	6	10614	11091	WD repeat domain 5	Histone binding	Cytoplasm	Cell cycle control protein	Cell growth and/or maintenance	WD40	Yes
CAMSAP3	57662	calmodulin-regulated spectrin-associated protein 3 isoform 1	NP_001073898.1	2	2	2	3	0.91	1.1					1	1									
PSPH	5723	phosphoserine phosphatase	NP_004568.2	1	2	2	3	0.91	1.1	6.59	21.2	8.5	33.9	2	2	1406	5723	phosphoserine phosphatase	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Metabolism;Energy pathways	-	Yes
DNAJB11	51726	dnaJ homolog subfamily B member 11 precursor	NP_057390.1	1	5	5	14	0.91	1.07	6.67	4.17	14.9	11	6	6	7485	51726	DnaJ (Hsp40) homolog, subfamily B, member 11	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein metabolism	DNAJ;SP	Yes
PPCS	79717	phosphopantothenate--cysteine ligase isoform a	NP_078940.2	4	6	6	10	0.91	1.07	11.22	10.09	23.1	24.6	5	5	7760	79717	None	Ligase activity	-	Enzyme: Synthase	Metabolism	-	Yes
OXSR1	9943	serine/threonine-protein kinase OSR1	NP_005100.1	1	11	12	39	0.91	1.07	7.17	6.71	29.1	32.2	19	19	6809	9943	oxidative-stress responsive 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	No
GALNT2	2590	polypeptide N-acetylgalactosaminyltransferase 2 precursor	NP_004472.1	6	17	17	35	0.91	1.07	8.44	5.23	32.6	23.4	17	17	3782	2590	UDP-N-acetyl-alpha-D-galactosamine:polypeptideN-acetylgalactosaminyltransferase 2 (GalNAc-T2)	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase	Metabolism;Energy pathways	TM	Yes
MRPS14	63931	28S ribosomal protein S14, mitochondrial	NP_071383.1	1	1	1	10	0.91	1.07	14.43	10.86	30	26.5	5	5	14777	63931	mitochondrial ribosomal protein S14	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
ACAD9	28976	acyl-CoA dehydrogenase family member 9, mitochondrial	NP_054768.2	1	10	10	27	0.91	1.07	6.2	8.51	21.4	35.1	14	14	12412	28976	acyl-Coenzyme A dehydrogenase family, member 9	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
Sep-11	55752	septin-11 isoform 1	NP_001293076.1	3	6	8	51	0.91	1.06	11.16	16.18	25.3	44.2	6	6									
NUP188	23511	nucleoporin NUP188 homolog	NP_056169.1	3	6	6	20	0.91	1.06	3.47	7.85	7.8	20.6	6	6	18582	23511	nucleoporin 188kDa	Molecular function unknown	Nuclear membrane	Unclassified	Biological_process unknown	-	Yes
ILVBL	10994	acetolactate synthase-like protein	NP_006835.2	1	10	10	28	0.91	1.05	10.67	10.22	34.8	38.3	12	12	16152	10994	ilvB (bacterial acetolactate synthase)-like	Coenzyme binding	-	Enzyme: Synthase	Metabolism;Energy pathways	TM	No
CDK5RAP3	80279	CDK5 regulatory subunit-associated protein 3 isoform c	NP_001265126.1	11	4	5	25	0.91	1.05	1.23	5.6	2.8	14.5	6	6	12190	80279	CDK5 regulatory subunit associated protein 3	Molecular function unknown	-	Cell cycle control protein	Cell communication;Signal transduction;Regulation of cell cycle	CC	Yes
TMED9	54732	transmembrane emp24 domain-containing protein 9 precursor	NP_059980.2	1	5	7	38	0.91	1.04	6.6	15.69	17.2	48.6	8	8	9975	54732	transmembrane emp24 protein transport domaincontaining 9	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	SP;CC;TM	No
RPLP0	6175	60S acidic ribosomal protein P0	NP_444505.1	1	12	12	87	0.91	1.03	3.23	4.03	19.5	27.9	43	43	1610	6175	ribosomal protein, large, P0	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
FAM175B	23172	BRISC complex subunit Abro1	NP_115558.3	1	5	5	9	0.91	1.03	4.68	3.21	9.5	7.4	5	5	13783	23172	KIAA0157	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC	No

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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CARM1	10498	histone-arginine methyltransferase CARM1	NP_954592.1	1	8	8	12	0.91	1.02	10.48	7.53	23.6	18.9	6	6	9158	10498	coactivator-associated argininemethyltransferase 1	Methyltransferase activity	Nucleus	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	Yes
GLG1	2734	Golgi apparatus protein 1 isoform 1 precursor	NP_036333.2	3	18	18	33	0.91	1.01	6.43	4.49	26.5	20.5	20	20	2855	2734	golgi apparatus protein 1	Receptor binding	Golgi apparatus	Integral membrane protein	Biological_process unknown	TM;SP	No
CAPN1	823	calpain-1 catalytic subunit	NP_005177.2	1	27	27	77	0.91	1.01	2.94	5.53	17.9	38.3	44	44	253	823	calpain 1, (mu/I) large subunit	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Protein metabolism	CYSPC;CALPAIN_III;EF	Yes
FOSL2	2355	fos-related antigen 2	NP_005244.1	1	3	3	6	0.91	0.99	3.76	5.36	5.9	9.2	3	3	3343	2355	FOS-like antigen 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
PRKAA1	5562	5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform 2	NP_996790.3	3	6	6	12	0.91	0.99	11.77	11.04	28.9	29.5	7	7	4115	5562	protein kinase, AMP-activated, alpha 1catalytic subunit	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Signal transduction	S_T_kinase	Yes
CLTC	1213	clathrin heavy chain 1 isoform 2	NP_001275582.1	4	76	76	434	0.91	0.99	1.78	1.99	23.1	28.3	198	198	350	1213	clathrin, heavy polypeptide (Hc)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CLH	Yes
PAK1	5058	serine/threonine-protein kinase PAK 1 isoform 2	NP_002567.3	2	1	5	11	0.91	0.97					1	1	3995	5058	p21/Cdc42/Rac1-activated kinase 1 (STE20homolog, yeast)	Protein serine/threonine kinase activity	Plasma membrane;Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	PBD;S_T_kinase	Yes
FAM134C	162427	protein FAM134C	NP_835227.1	1	3	3	11	0.91	0.97	41.64	4.88	102.4	10.6	5	5	14108	162427	None	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
PDLIM1	9124	PDZ and LIM domain protein 1	NP_066272.1	1	17	17	50	0.91	0.97	6.53	6.01	32	31.5	28	28	9326	9124	PDZ and LIM domain 1 (elfin)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	PDZ;LIM	Yes
STXBP3	6814	syntaxin-binding protein 3	NP_009200.2	1	8	8	19	0.91	0.97	5.45	11.28	15.9	35.6	10	10	10517	6814	syntaxin binding protein 3	Transporter activity	Cytoplasmic vesicle	Transport/cargo protein	Transport	-	Yes
OTULIN	90268	ubiquitin thioesterase otulin	NP_612357.4	1	4	4	9	0.91	0.96	5.99	8.95	12.2	19.4	5	5									
CDC27	996	cell division cycle protein 27 homolog isoform 1	NP_001107563.1	4	4	4	8	0.91	0.96	17.01	12.22	31.9	23.9	4	4	304	996	cell division cycle 27	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	TPR	Yes
SMTN	6525	smoothelin isoform d	NP_001193946.1	5	4	4	6	0.91	0.96	7.23	8.46	11.5	14.1	3	3	3675	6525	smoothelin	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;CC	Yes
GTF3C5	9328	general transcription factor 3C polypeptide 5 isoform 1	NP_001116295.1	3	4	4	7	0.91	0.95	25.43	36.17	41.6	64.9	3	3	16077	9328	general transcription factor IIIC, polypeptide5, 63kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
C18orf8	29919	uncharacterized protein C18orf8 isoform 1	NP_037458.3	1	1	1	2	0.91	0.95					1	1	12693	29919	chromosome 18 open reading frame 8	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
YWHAE	7531	14-3-3 protein epsilon	NP_006752.1	1	19	21	181	0.91	0.95	4.56	5.6	35.8	46.8	70	70	5457	7531	tyrosine 3-monooxygenase/tryptophan5-monooxygenase activation protein, epsilon polypeptide	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
CDC23	8697	cell division cycle protein 23 homolog	NP_004652.2	1	4	4	8	0.91	0.94	22.84	13.25	43.4	25.3	4	4	7221	8697	CDC23 (cell division cycle 23, yeast, homolog)	Binding	Nucleus	Ubiquitin proteasome system protein;Cell cycle control protein	Cell communication;Signal transduction;Regulation of cell cycle	TPR	Yes
XPNPEP1	7511	xaa-Pro aminopeptidase 1 isoform 1	NP_065116.3	2	14	14	53	0.91	0.94	4.99	5.05	24.8	25.9	29	29	3899	7511	X-prolyl aminopeptidase (aminopeptidase P) 1,soluble	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	-	Yes
CCNYL1	151195	cyclin-Y-like protein 1 isoform 1	NP_001135772.1	2	1	1	3	0.91	0.94					1	1	8809	151195	None	Molecular function unknown	-	Cell cycle control protein	Cell communication;Signal transduction	CYCLIN	No
PHB2	11331	prohibitin-2 isoform 1	NP_001138303.1	2	19	19	72	0.91	0.93	3.6	4.07	21.7	25.6	43	44	17843	11331	prohibitin 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;CC;PHB	Yes
ADSSL1	122622	adenylosuccinate synthetase isozyme 1 isoform 2	NP_689541.1	2	1	3	4	0.91	0.93					1	1	12433	122622	adenylosuccinate synthase like 1	Molecular function unknown	Cytoplasm	Enzyme: Synthase	Metabolism;Energy pathways	SP	Yes
DRG1	4733	developmentally-regulated GTP-binding protein 1	NP_004138.1	1	11	11	30	0.91	0.92	4.86	6.2	16.6	21.6	14	14	16034	4733	developmentally regulated GTP binding protein 1	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	-	Yes
RPS9	6203	40S ribosomal protein S9	NP_001004.2	1	19	19	77	0.91	0.91	3.83	3.13	23.6	19.3	45	45	4696	6203	ribosomal protein S9	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
RPUSD3	285367	RNA pseudouridylate synthase domain-containing protein 3 isoform 1	NP_775930.2	2	1	1	1	0.91	0.9					1	1	14532	285367	RNA pseudouridylate synthase domain containing3	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
SCARB2	950	lysosome membrane protein 2 isoform 1 precursor	NP_005497.1	2	5	5	12	0.91	0.89	13.75	9.24	36.5	23.6	8	8	3772	950	scavenger receptor class B, member 2	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;SP	Yes
ANKFY1	51479	rabankyrin-5 isoform 3	NP_001244928.1	2	14	14	31	0.91	0.88	10.26	4.59	37.5	15.8	15	15	9717	51479	ankyrin repeat and FYVE domain containing 1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	BTB;CC;ANK;FYVE	Yes
ACOT9	23597	acyl-coenzyme A thioesterase 9, mitochondrial isoform a precursor	NP_001032248.1	2	20	20	51	0.91	0.88	3.66	7.66	17.9	37	28	28	6438	23597	None	Hydrolase activity	Mitochondrion	Enzyme: Esterase	Metabolism	-	Yes
CORO2A	7464	coronin-2A	NP_438171.1	1	7	8	20	0.91	0.87	18.18	16.13	53.1	44	9	9	3695	7464	coronin, actin binding protein, 2A	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	WD40;CC	Yes

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GEMIN5	25929	gem-associated protein 5 isoform 1	NP_056280.2	2	17	17	38	0.91	0.87	3.18	6.05	12.7	23.4	19	19	6109	25929	gem (nuclear organelle) associated protein 5	Ribonucleoprotein	Cytoplasm	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40;CC	Yes
MMAA	166785	methylmalonic aciduria type A protein, mitochondrial precursor	NP_758454.1	1	1	1	3	0.91	0.86					1	1	7394	166785	methylmalonic aciduria (cobalamin deficiency)type A	ATPase activity	Mitochondrion	ATPase	Metabolism;Energy pathways	AAA	Yes
MVD	4597	diphosphomevalonate decarboxylase	NP_002452.1	1	8	8	13	0.91	0.85	6.27	15.69	17.3	41.4	9	9	4454	4597	mevalonate (diphospho) decarboxylase	Carboxy-lyase activity	Cytoplasm	Enzyme: Decarboxylase	Metabolism;Energy pathways	-	Yes
BOLA2	552900	BolA-like protein 2	NP_001026997.1	1	1	1	2	0.91	0.85					1	1	18842	552900	BolA-like 2 (E. coli)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
VIPAS39	63894	spermatogenesis-defective protein 39 homolog isoform 1	NP_001180243.1	2	4	4	11	0.91	0.83	11.18	5.65	25.4	11.6	6	6									
C2CD2	25966	C2 domain-containing protein 2 isoform 1 precursor	NP_056315.1	2	2	2	4	0.91	0.81	26.96	18.66	35.9	21.5	2	2	10745	25966	chromosome 21 open reading frame 25	Molecular function unknown	-	Unclassified	Biological_process unknown	C2;SP	No
NOC3L	64318	nucleolar complex protein 3 homolog	NP_071896.8	1	3	3	6	0.91	0.81	24.14	9.26	39.4	13.1	3	3	12562	64318	chromosome 10 open reading frame 117	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
IARS2	55699	isoleucine--tRNA ligase, mitochondrial precursor	NP_060530.3	1	23	23	54	0.91	0.81	5.27	6.79	25.9	29.8	28	28	13334	55699	isoleucine-tRNA synthetase 2, mitochondrial	TRNA ligase activity	Mitochondrion	-	Metabolism;Energy pathways;Translation	-	No
ATP5B	506	ATP synthase subunit beta, mitochondrial precursor	NP_001677.2	1	23	23	267	0.91	0.81	2.41	6.38	25.8	65.9	134	134	44	506	ATP synthase, H+ transporting, mitochondrial F1complex, beta polypeptide	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	AAA	Yes
ROCK2	9475	rho-associated protein kinase 2	NP_004841.2	2	13	13	25	0.91	0.8	4.2	8.14	14.4	24.9	14	14	4922	9475	Rho-associated, coiled-coil containing proteinkinase 2	Protein serine/threonine kinase activity	Nucleus;Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;HR1;CC;PH	Yes
NOP10	55505	H/ACA ribonucleoprotein complex subunit 3	NP_061118.1	1	2	2	3	0.91	0.79					1	1	7571	55505	nucleolar protein family A, member 3 (H/ACAsmall nucleolar RNPs)	Ribonucleoprotein	Nucleolus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
RAP1GDS1	5910	rap1 GTPase-GDP dissociation stimulator 1 isoform 1	NP_001093896.1	6	11	12	36	0.91	0.78	8.42	17.6	32.5	61.5	17	17	11763	5910	RAP1, GTP-GDP dissociation stimulator 1	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	SP;ARM	Yes
ARF5	381	ADP-ribosylation factor 5	NP_001653.1	1	4	8	54	0.91	0.78	1.96	18.15	3.6	29	4	4	55	381	ADP-ribosylation factor 5	GTPase activity	Cytoplasm	G protein	Cell communication;Signal transduction	ARF	Yes
SLC25A13	10165	calcium-binding mitochondrial carrier protein Aralar2 isoform 1	NP_001153682.1	2	11	15	47	0.91	0.77	5.36	7.13	22	25	20	20	4837	10165	solute carrier family 25, member 13 (citrin)	Transporter activity;Carrier activity	Mitochondrion	Calcium binding protein;Transport/cargo protein	Transport	EF	Yes
PPAP2A	8611	lipid phosphate phosphohydrolase 1 isoform 2	NP_795714.1	2	1	1	2	0.91	0.75					1	1	6178	8611	phosphatidic acid phosphatase type 2A	Lipid phosphatase activity	Plasma membrane	Lipid phosphatase	Metabolism	TM;AcidPPc	No
CCDC93	54520	coiled-coil domain-containing protein 93	NP_061917.3	1	8	8	12	0.91	0.74	13.94	4.42	29	7.4	5	5	8557	54520	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
TMEM63B	55362	CSC1-like protein 2	NP_060896.1	1	1	1	1	0.91	0.67					1	1	16656	55362	chromosome 6 open reading frame 110	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	SP;TM	No
EIF2B4	8890	translation initiation factor eIF-2B subunit delta isoform 1	NP_751945.2	2	1	8	15	0.91	0.64					1	1	9459	8890	eukaryotic translation initiation factor 2B,subunit 4 delta, 67kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC	Yes
WWTR1	25937	WW domain-containing transcription regulator protein 1	NP_056287.1	1	1	1	2	0.91	0.64					1	1	9580	25937	WW domain containing transcription regulator 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WW	No
ADAMTS14	140766	A disintegrin and metalloproteinase with thrombospondin motifs 14 isoform 1 preproprotein	NP_631894.2	5	1	1	1	0.91	0.53					1	1	6329	140766	a disintegrin-like and metalloprotease(reprolysin type) with thrombospondin type 1 motif, 14	Metallopeptidase activity	Extracellular	Metallo protease	Protein metabolism	SP;REP;TSP1	Yes
TMPPE	643853	transmembrane protein with metallophosphoesterase domain isoform 1	NP_001034859.2	2	1	1	4	0.91						1		18951	643853	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM	No
MRPS18A	55168	28S ribosomal protein S18a, mitochondrial isoform 1 precursor	NP_060605.1	2	2	2	3	0.9	1.83	11.69	25.91	15	75.4	2	2	14780	55168	mitochondrial ribosomal protein S18A	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	Yes
RRP9	9136	U3 small nucleolar RNA-interacting protein 2	NP_004695.1	1	4	4	8	0.9	1.5	24.06	11.01	45.2	33.9	4	4	8827	9136	RNA, U3 small nucleolar interacting protein 2	Ribonucleoprotein	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40;NLS;CC	Yes
TUFM	7284	elongation factor Tu, mitochondrial precursor	NP_003312.3	1	20	20	59	0.9	1.49	3.82	3.45	20.2	30.6	34	34	3861	7284	Tu translation elongation factor, mitochondrial	Translation regulator activity	Mitochondrion	Translation regulatory protein	Protein metabolism	GTP_EFTU;GTP_EFTU_D2;GTP_EFTU_D3	Yes
EIF2B4	8890	translation initiation factor eIF-2B subunit delta isoform 2	NP_001029288.1	1	1	8	15	0.9	1.46					1	1	9459	8890	eukaryotic translation initiation factor 2B,subunit 4 delta, 67kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC	Yes
USP11	8237	ubiquitin carboxyl-terminal hydrolase 11	NP_004642.2	1	3	4	4	0.9	1.4					1	1	2081	8237	ubiquitin specific protease 11	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	DUSP;UCH	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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BCR	613	breakpoint cluster region protein isoform 1	NP_004318.3	2	4	5	9	0.9	1.39	25.09	2.32	47.5	6.5	4	4	1044	613	breakpoint cluster region	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	RHOGEF;RHOGAP;PH;C2;CC	Yes
LUC7L3	51747	luc7-like protein 3	NP_057508.2	1	6	6	23	0.9	1.34	10.04	2.56	29	10.9	10	10	16759	51747	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
DEGS1	8560	sphingolipid delta(4)-desaturase DES1	NP_003667.1	1	2	2	3	0.9	1.31					1	1	13133	8560	degenerative spermatocyte homolog 1, lipiddesaturase (Drosophila)	Oxidoreductase activity	Endoplasmic reticulum membrane	Enzyme: Oxidoreductase	Energy pathways;Lipid metabolism	TM	Yes
DAPK3	1613	death-associated protein kinase 3	NP_001339.1	2	2	2	5	0.9	1.25	0.35	1.52	0.4	2.7	2	2	4478	1613	death-associated protein kinase 3	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC;LZ	Yes
RBM22	55696	pre-mRNA-splicing factor RBM22	NP_060517.1	1	7	7	11	0.9	1.22	6.97	3.43	14.1	9.4	5	5	10186	55696	RNA binding motif protein 22	Molecular function unknown	-	Unclassified	Biological_process unknown	RRM;ZnF_C3H1	No
DNAJA2	10294	dnaJ homolog subfamily A member 2	NP_005871.1	1	10	10	21	0.9	1.22	7.34	4.94	23.2	21	12	12	7105	10294	DnaJ (Hsp40) homolog, subfamily A, member 2	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	DNAJ	Yes
RPP30	10556	ribonuclease P protein subunit p30 isoform a	NP_001098016.1	2	4	4	11	0.9	1.21	5.16	6.48	11.4	19.3	6	6	9359	10556	ribonuclease P/MRP 30kDa subunit	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MED27	9442	mediator of RNA polymerase II transcription subunit 27 isoform 1	NP_004260.2	2	2	2	2	0.9	1.21					1	1	5438	9442	cofactor required for Sp1 transcriptionalactivation, subunit 8, 34kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
PDCL3	79031	phosducin-like protein 3	NP_076970.1	1	6	6	12	0.9	1.2	2.17	17.98	5.2	62.1	7	7	17827	79031	phosducin-like 3	Molecular function unknown	Cytoplasm	Unclassified	Apoptosis	CC	Yes
LYPLA1	10434	acyl-protein thioesterase 1 isoform 1	NP_006321.1	6	6	6	13	0.9	1.2	0.49	10.61	1.2	34.7	7	7	7063	10434	lysophospholipase I	Phospholipase activity	Endoplasmic reticulum	Enzyme: Phospholipase	Metabolism;Energy pathways	-	Yes
BRAT1	221927	BRCA1-associated ATM activator 1	NP_689956.2	1	3	3	5	0.9	1.16	5.68	6.05	8.9	12.2	3	3									
RBM42	79171	RNA-binding protein 42	NP_077297.2	1	3	3	6	0.9	1.16	10.98	11.63	17.3	23.6	3	3	11303	79171	None	Molecular function unknown	-	Unclassified	Biological_process unknown	RRM	No
SGPL1	8879	sphingosine-1-phosphate lyase 1	NP_003892.2	1	8	8	15	0.9	1.14	12.46	5.39	34.8	18.6	9	9	7224	8879	sphingosine-1-phosphate lyase 1	Lyase activity	Endoplasmic reticulum	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
TRIO	7204	triple functional domain protein	NP_009049.2	1	7	7	12	0.9	1.13	13.14	7.49	32.3	22.8	7	7	3537	7204	triple functional domain (PTPRF interacting)	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	SEC14;SPECTRIN;RHOGEF;PH;SH3;IGC2;S_T_kinase	Yes
CD151	977	CD151 antigen	NP_004348.2	1	4	4	7	0.9	1.12	7.19	8.71	13	19.7	4	4	3763	977	CD151 antigen	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Cell motility	TM	No
ATP5O	539	ATP synthase subunit O, mitochondrial precursor	NP_001688.1	1	12	12	56	0.9	1.1	4.63	4.99	23.9	31.4	32	31	2899	539	ATP synthase, H+ transporting, mitochondrial F1complex, O subunit (oligomycin sensitivity conferring protein)	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	-	Yes
BIRC6	57448	baculoviral IAP repeat-containing protein 6	NP_057336.3	1	6	6	9	0.9	1.09	4.11	3.21	6.4	6.1	3	3	5731	57448	baculoviral IAP repeat-containing 6 (apollon)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Apoptosis	BIR;UBC;CC	Yes
RRP15	51018	RRP15-like protein	NP_057136.2	1	3	3	5	0.9	1.09	3.38	23.65	4.3	37.9	2	2	10822	51018	None	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	No
SPTAN1	6709	spectrin alpha chain, non-erythrocytic 1 isoform 2	NP_003118.2	4	99	99	274	0.9	1.08	2.49	2.11	28	28.2	148	147	1684	6709	spectrin, alpha, non-erythrocytic 1(alpha-fodrin)	Structural constituent of cytoskeleton	Cytoplasm;Nucleus	Cytoskeletal protein;Structural protein	Cell growth and/or maintenance	SPECTRIN;CC	Yes
PGAM1	5223	phosphoglycerate mutase 1	NP_002620.1	2	11	18	110	0.9	1.07	6.45	7.3	32.6	44.8	30	30	1392	5223	phosphoglycerate mutase 1 (brain)	Catalytic activity	Cytoplasm	Enzyme: Mutase	Metabolism;Energy pathways	-	Yes
PGM2	55276	phosphoglucomutase-2	NP_060760.2	1	12	12	28	0.9	1.06	3.17	5.15	12.6	24.2	19	19	11761	55276	phosphoglucomutase 2	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
SEC63	11231	translocation protein SEC63 homolog	NP_009145.1	1	16	16	38	0.9	1.06	4.47	6.29	19.4	32.9	23	23	9783	11231	SEC63-like (S. cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	TM;DNAJ;CC	Yes
NUP107	57122	nuclear pore complex protein Nup107	NP_065134.1	1	16	16	30	0.9	1.05	11.73	7.76	35.9	27.6	11	11	6356	57122	nucleoporin 107kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
PPP4C	5531	serine/threonine-protein phosphatase 4 catalytic subunit isoform 1	NP_002711.1	3	4	6	13	0.9	1.05	8.49	13.71	15.4	29.3	4	4	3615	5531	protein phosphatase 4 (formerly X), catalyticsubunit	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2A	No
MRPL53	116540	39S ribosomal protein L53, mitochondrial	NP_444278.1	1	1	1	1	0.9	1.04					1	1	14771	116540	mitochondrial ribosomal protein L53	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
ABCF3	55324	ATP-binding cassette sub-family F member 3	NP_060828.2	1	9	9	16	0.9	1.04	7.36	6.85	20	21.7	9	9	12404	55324	ATP-binding cassette, sub-family F (GCN20),member 3	Transporter activity	-	Transport/cargo protein	Transport	AAA	No
CSTF2	1478	cleavage stimulation factor subunit 2 isoform 1	NP_001293135.1	3	2	5	10	0.9	1.03	18.48	5.6	23.7	8.2	2	2	2652	1478	cleavage stimulation factor, 3` pre-RNA,subunit 2, 64kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes

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PDE5A	8654	cGMP-specific 3',5'-cyclic phosphodiesterase isoform 1	NP_001074.2	3	1	1	2	0.9	1.02					1	1	4497	8654	phosphodiesterase 5A, cGMP-specific	Phosphoric diester hydrolase activity	Nucleus	Enzyme: Phosphodiesterase	Cell communication;Signal transduction	GAF;HDc	Yes
EEF2	1938	elongation factor 2	NP_001952.1	1	46	47	305	0.9	1.02	3.39	2.75	39.5	35.9	156	155	561	1938	eukaryotic translation elongation factor 2	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism;Translation	-	Yes
PARN	5073	poly(A)-specific ribonuclease PARN isoform 1	NP_002573.1	3	3	3	4	0.9	1.02	17.29	13.27	22.2	19.3	2	2	7250	5073	poly(A)-specific ribonuclease (deadenylationnuclease)	Ribonuclease activity	Cytoplasm	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;R3H	Yes
GLYR1	84656	putative oxidoreductase GLYR1	NP_115958.2	1	4	4	6	0.9	1.01	8.36	8.35	15.2	16.9	4	4	17625	84656	None	Catalytic activity	Nucleus	Enzyme: Dehydrogenase	Metabolism;Energy pathways	PWWP;AT_hook	Yes
DNAJB4	11080	dnaJ homolog subfamily B member 4	NP_008965.2	1	4	5	10	0.9	1.01	31.72	23.42	52.7	42.8	3	3	7486	11080	DnaJ (Hsp40) homolog, subfamily B, member 4	Heat shock protein activity	-	Heat shock protein	Protein metabolism	DNAJ	Yes
YTHDF2	51441	YTH domain-containing family protein 2 isoform 1	NP_001166599.1	2	4	7	10	0.9	1.01	10.11	2.71	18.4	5.5	4	4	6587	51441	YTH domain family, member 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
DUS2	54920	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like isoform 1	NP_060273.1	2	1	1	2	0.9	1.01					1	1									
ZBTB33	10009	transcriptional regulator Kaiso	NP_006768.1	1	1	1	3	0.9	1					1	1	2269	10009	zinc finger and BTB domain containing 33	Transcription factor activity;Transcription regulator activity	Nucleus	Transcription regulatory protein;Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BTB;ZNFC2;NLS	Yes
TTC27	55622	tetratricopeptide repeat protein 27 isoform 1	NP_060205.3	2	3	3	7	0.9	0.99	9.04	6.21	16.3	12.4	4	4	8618	55622	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TPR	No
ASAP2	8853	arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2 isoform a	NP_003878.1	2	6	6	14	0.9	0.99	3.11	1.35	6.9	3.3	6	6	4820	8853	development and differentiation enhancingfactor 2	GTPase activator activity	Golgi apparatus;Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	PH;ARFGAP;ANK;SH3;BAR	Yes
GFM2	84340	ribosome-releasing factor 2, mitochondrial isoform 4	NP_001268231.1	4	4	4	15	0.9	0.99	3.26	11.49	7.8	30.6	7	7	9413	84340	G elongation factor, mitochondrial 2	Translation regulator activity	Mitochondrion	Translation regulatory protein	Regulation of translation	GTP_EFTU;GTP_EFTU_D2	Yes
GORASP2	26003	Golgi reassembly-stacking protein 2 isoform 1	NP_056345.3	2	4	4	12	0.9	0.99	8.39	11.99	18.7	29.6	6	6	8303	26003	golgi reassembly stacking protein 2, 55kDa	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	PDZ	Yes
NCAPG	64151	condensin complex subunit 3	NP_071741.2	1	10	10	20	0.9	0.99	8.11	4.96	24.7	16.4	11	11	12097	64151	None	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;HEAT	Yes
H3F3A	3020	histone H3.3	NP_002098.1	2	2	7	32	0.9	0.97	10.65	2.11	13.6	2.9	2	2	3082	3020	H3 histone, family 3A	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
RAB3GAP1	22930	rab3 GTPase-activating protein catalytic subunit isoform 2	NP_036365.1	2	15	15	29	0.9	0.97	6.94	7.36	27.6	31.8	19	19	16002	22930	None	GTPase activator activity	Nucleus	GTPase activating protein	Cell communication;Signal transduction	-	Yes
HIF1AN	55662	hypoxia-inducible factor 1-alpha inhibitor	NP_060372.2	1	1	1	1	0.9	0.97					1	1	9426	55662	hypoxia-inducible factor 1, alpha subunitinhibitor	Catalytic activity	Cytoplasm	Enzyme: Hydroxylase	Metabolism;Energy pathways	JMJC	Yes
EIF2AK2	5610	interferon-induced, double-stranded RNA-activated protein kinase isoform a	NP_001129123.1	2	15	15	54	0.9	0.97	3.28	3.24	14.8	15.8	25	25	1468	5610	eukaryotic translation initiation factor2-alpha kinase 2	Protein serine/threonine kinase activity	Ribosome	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;DSRM;S_T_Y_Kinase	Yes
TM9SF3	56889	transmembrane 9 superfamily member 3 precursor	NP_064508.3	1	4	4	9	0.9	0.96	11.92	7.74	26.7	18.3	6	6	18073	56889	None	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	SP;TM	Yes
ANXA1	301	annexin A1	NP_000691.1	1	28	28	273	0.9	0.96	2.72	2.62	29.2	30	136	136	1060	301	annexin A1	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	ANX	Yes
DARS	1615	aspartate--tRNA ligase, cytoplasmic isoform 1	NP_001340.2	2	28	28	90	0.9	0.96	4.16	4.41	26.6	30.2	49	49	4361	1615	aspartyl-tRNA synthetase	ATPase activity	Cytoplasm	ATPase	Metabolism;Energy pathways	TRNAA	Yes
ELP6	54859	elongator complex protein 6	NP_001026873.2	1	2	2	2	0.9	0.96	19.17	0.62	24.8	0.8	2	2									
EIF3C	8663	eukaryotic translation initiation factor 3 subunit C isoform a	NP_001032897.1	3	21	21	65	0.9	0.96	4.63	4.9	25.6	29.2	37	37	4889	8663	eukaryotic translation initiation factor 3,subunit 8, 110kDa	Translation regulator activity	Cytoplasm	Translation regulatory protein	Protein metabolism	CC;PINT	Yes
C21orf33	8209	ES1 protein homolog, mitochondrial isoform Ia precursor	NP_004640.3	2	6	6	13	0.9	0.95	1.56	10.96	3.7	28.1	7	7	9044	8209	chromosome 21 open reading frame 33	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	SP	Yes
IKBKB	3551	inhibitor of nuclear factor kappa-B kinase subunit beta isoform 1	NP_001547.1	3	2	3	4	0.9	0.95					1	1	4462	3551	inhibitor of kappa light polypeptide geneenhancer in B-cells, kinase beta	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
MTA1	9112	metastasis-associated protein MTA1 isoform MTA1	NP_004680.2	4	2	5	13	0.9	0.95	18.59	11.53	24	15.5	2	2	4633	9112	metastasis associated 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SANT;ZNF_GATA;BAH	Yes
SPR	6697	sepiapterin reductase	NP_003115.1	1	5	5	11	0.9	0.94	10.37	8.35	23.3	19.5	6	6	1632	6697	sepiapterin reductase (7,8-dihydrobiopterin: NADP+oxidoreductase)	Catalytic activity	-	Enzyme: Reductase	Metabolism;Energy pathways	SP	Yes
MYO1B	4430	unconventional myosin-Ib isoform 2	NP_036355.2	5	44	44	190	0.9	0.94	2.05	2.32	18.1	21.1	94	92	8407	4430	myosin IB	Motor activity	Plasma membrane	Motor protein	Cell growth and/or maintenance	MYOSIN;IQ	Yes

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Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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COG4	25839	conserved oligomeric Golgi complex subunit 4 isoform 1	NP_056201.2	2	5	5	9	0.9	0.93	7.85	12.91	14.3	24.5	4	4	8444	25839	component of oligomeric golgi complex 4	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	CC	Yes
CDK2	1017	cyclin-dependent kinase 2 isoform 1	NP_001789.2	49	3	5	25	0.9	0.93	6.32	2.45	9.9	3.9	3	3	310	1017	cyclin-dependent kinase 2	Kinase activity	Nucleus	Cell cycle control protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_kinase	Yes
SEH1L	81929	nucleoporin SEH1 isoform 1	NP_001013455.1	2	6	6	13	0.9	0.93	8.49	3.49	20.4	8.6	7	7	15319	81929	SEH1-like (S. cerevisiae)	Molecular function unknown	Kinetochore	Unclassified	Biological_process unknown	WD40	Yes
SDC1	6382	syndecan-1 precursor	NP_002988.3	1	3	3	11	0.9	0.92	5.77	4.54	12.8	10.3	6	6	1718	6382	syndecan 1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction;Cell surface receptor linked signal transduction;Cell adhesion	SP;TM;Band 4.1	Yes
EHHADH	1962	peroxisomal bifunctional enzyme isoform 1	NP_001957.2	2	3	3	5	0.9	0.92	17.15	6.46	27.3	10.3	3	3	6125	1962	enoyl-Coenzyme A, hydratase/3-hydroxyacylCoenzyme A dehydrogenase	Catalytic activity	Peroxisome	Enzyme: Hydratase	Metabolism;Energy pathways	-	Yes
SH3GLB1	51100	endophilin-B1 isoform 1	NP_057093.1	4	5	6	6	0.9	0.91	12.89	13.18	26.5	27.2	5	5	15333	51100	SH3-domain GRB2-like endophilin B1	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase	Metabolism;Energy pathways	SH3;CC	Yes
TBCD	6904	tubulin-specific chaperone D	NP_005984.3	1	16	16	31	0.9	0.91	8.92	4.94	30.8	16.9	14	14	5227	6904	tubulin-specific chaperone d	Chaperone activity	Microtubule	Chaperone	Protein metabolism;Protein folding	HEAT	No
UBR3	130507	E3 ubiquitin-protein ligase UBR3	NP_742067.3	1	2	2	2	0.9	0.9					1	1	15887	130507	zinc finger protein 650	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;ZFC3	Yes
PC	5091	pyruvate carboxylase, mitochondrial precursor	NP_071504.2	1	30	30	82	0.9	0.89	2.84	5.31	16.8	31.7	43	43	2032	5091	pyruvate carboxylase	Ligase activity	Mitochondrion	Enzyme: Carboxylase	Metabolism;Energy pathways	SP	Yes
FDXR	2232	NADPH:adrenodoxin oxidoreductase, mitochondrial isoform 3 precursor	NP_001244941.2	7	9	9	19	0.9	0.88	3.51	6.58	10.5	19.4	11	11	60	2232	ferredoxin reductase	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP	Yes
MYO1E	4643	unconventional myosin-Ie	NP_004989.2	1	22	22	50	0.9	0.87	4.74	7.01	21.1	30.6	24	24	3281	4643	myosin IE	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	MYOSIN;SH3;IQ	Yes
MRPL28	10573	39S ribosomal protein L28, mitochondrial	NP_006419.2	1	3	3	6	0.9	0.87	20.14	10.68	42.4	21.1	5	5	6889	10573	mitochondrial ribosomal protein L28	Structural molecule activity;Ribonucleoprotein	Mitochondrion	Structural protein	Protein metabolism;RNA metabolism	-	Yes
STAG2	10735	cohesin subunit SA-2 isoform a	NP_001036214.1	2	2	3	5	0.9	0.87	9.32	2.21	11.9	2.7	2	2	5077	10735	stromal antigen 2	Molecular function unknown	Nucleus	Cell cycle control protein	Cell growth and/or maintenance	CC	Yes
SSFA2	6744	sperm-specific antigen 2 isoform 1	NP_001123917.1	5	5	5	9	0.9	0.86	6.86	10.53	13.8	20.4	5	5	353	6744	sperm specific antigen 2	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	CC	Yes
TMEM43	79188	transmembrane protein 43	NP_077310.1	1	14	14	34	0.9	0.86	5.7	6.16	22.6	23.3	19	19	15541	79188	transmembrane protein 43	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
ATXN10	25814	ataxin-10 isoform 1	NP_037368.1	3	10	11	30	0.9	0.86	5.22	10.38	17.7	34.4	14	14	4624	25814	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
OGDH	4967	2-oxoglutarate dehydrogenase, mitochondrial isoform 1 precursor	NP_002532.2	6	21	21	59	0.9	0.86	5.67	7.21	29	35.5	31	31	8938	4967	oxoglutarate (alpha-ketoglutarate) dehydrogenase(lipoamide)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
MTPN	136319	myotrophin	NP_665807.1	1	2	2	8	0.9	0.85	2.31	8.72	4.2	14.8	4	4	7574	136319	myotrophin	Protein binding	Cytoplasm	Cell cycle control protein	Protein metabolism	ANK;NLS;NES	Yes
DLG1	1739	disks large homolog 1 isoform 2	NP_004078.2	11	10	10	19	0.9	0.84	8.58	8.18	27.1	24.2	12	12	3007	1739	discs, large homolog 1 (Drosophila)	Cell adhesion molecule activity	Plasma membrane;Nucleus;Cytoplasm;Membrane fraction;Cell junction	Cell junction protein	Cell communication;Signal transduction	PDZ;SH3;GuKinase;CC;L27	Yes
TP63	8626	tumor protein 63 isoform 1	NP_003713.3	19	8	8	16	0.9	0.84	9.19	14.97	25.2	39.1	9	9	4469	8626	tumor protein p73-like	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAM	Yes
SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	NP_003119.2	4	8	81	245	0.9	0.84	5.01	4.93	17.6	16.2	15	15	1683	6711	spectrin, beta, non-erythrocytic 1	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	SPECTRIN;CC;PH;CH	Yes
GLRX5	51218	glutaredoxin-related protein 5, mitochondrial precursor	NP_057501.2	1	1	1	1	0.9	0.83					1	1	12659	51218	chromosome 14 open reading frame 87	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
RPS4X	6191	40S ribosomal protein S4, X isoform X isoform	NP_000998.1	3	18	18	91	0.9	0.83	5.22	8.08	33.5	49.4	48	48	2427	6191	ribosomal protein S4, X-linked	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	KOW	Yes
DOCK5	80005	dedicator of cytokinesis protein 5	NP_079216.4	1	11	12	19	0.9	0.82	8.95	4.18	27.1	11.4	11	11	9925	80005	dedicator of cytokinesis 5	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	SH3	Yes
H2AFY2	55506	core histone macro-H2A.2	NP_061119.1	1	9	11	40	0.9	0.82	7.62	4.41	29	15	17	17	13625	55506	H2A histone family, member Y2	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H2A;A1pp	Yes
MAGT1	84061	magnesium transporter protein 1	NP_115497.4	1	3	3	4	0.9	0.81	7.16	6.87	11.2	9.6	3	3	6487	84061	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM	No
SUMO3	6612	small ubiquitin-related modifier 3 isoform 2	NP_001273345.1	2	1	2	7	0.9	0.81					1	1	3754	6612	SMT3 suppressor of mif two 3 homolog 3 (yeast)	Ubiquitin-specific protease activity	Cytosol;Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBQ	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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RAB24	53917	ras-related protein Rab-24	NP_001026847.1	1	2	2	4	0.9	0.81	8.61	12.08	10.9	13.9	2	2	6697	53917	RAB24, member RAS oncogene family	GTPase activity	Endoplasmic reticulum	GTPase	Cell communication;Signal transduction	RAB	Yes
PLBD2	196463	putative phospholipase B-like 2 isoform 1 precursor	NP_775813.2	2	6	6	8	0.9	0.81	10.1	9.7	20.6	17.7	5	5	14116	196463	None	Molecular function unknown	Lysosome	Unclassified	Biological_process unknown	SP	Yes
CLASP1	23332	CLIP-associating protein 1 isoform 1	NP_056097.1	4	11	14	34	0.9	0.8	16.22	13.34	48.7	34.9	10	10	9322	23332	cytoplasmic linker associated protein 1	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	No
NT5DC2	64943	5'-nucleotidase domain-containing protein 2 isoform 1	NP_001127703.1	2	3	3	4	0.9	0.75	16.93	0.16	21.7	0.2	2	2	7770	64943	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
SAMM50	25813	sorting and assembly machinery component 50 homolog	NP_056195.3	1	8	8	11	0.9	0.75	4.4	5.41	9.7	9.9	6	6	10826	25813	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	Yes
CCNB1	891	G2/mitotic-specific cyclin-B1	NP_114172.1	1	2	2	3	0.9	0.74	35.1	52.63	47.2	59.9	2	2	454	891	cyclin B1	Kinase binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	CYCLIN_N;CYCLIN_C;NES	Yes
PPM1F	9647	protein phosphatase 1F	NP_055449.1	1	3	3	4	0.9	0.73	32.99	30.69	54.9	40.6	3	3	10163	9647	protein phosphatase 1F (PP2C domain containing)	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2C	Yes
SNX27	81609	sorting nexin-27	NP_112180.4	1	3	3	7	0.9	0.72	5.46	30.75	9.9	46.3	4	4	11591	81609	sorting nexin family member 27	Transporter activity	Cytosol	Transport/cargo protein	Vesicle-mediated transport	PDZ;PX;RA	Yes
TMX4	56255	thioredoxin-related transmembrane protein 4 precursor	NP_066979.2	1	1	1	2	0.9	0.7					1	1	11128	56255	None	Molecular function unknown	-	Unclassified	Cell motility;Cellular morphogenesis	SP;TM;CC	No
GGCT	79017	gamma-glutamylcyclotransferase isoform 1	NP_076956.1	4	6	6	11	0.9	0.7	6.55	10.4	14.6	18	6	6	12912	79017	chromosome 7 open reading frame 24	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
FMN1	342184	formin-1 isoform b	NP_001096654.1	1	1	1	1	0.9	0.61					1	1	7031	342184	formin 1	Cell adhesion molecule activity	Cytoplasm	Cell junction protein	Cell growth and/or maintenance	FH2	No
MTSS1L	92154	MTSS1-like protein	NP_612392.1	1	1	1	2	0.9	0.51					1	1	14289	92154	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
KCMF1	56888	E3 ubiquitin-protein ligase KCMF1	NP_064507.3	1	2	2	4	0.89	1.95	20.5	30.95	26.1	103.5	2	2	13761	56888	potassium channel modulatory factor 1	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	ZNFC2;CC;RING;NLS	No
TMEM33	55161	transmembrane protein 33	NP_060596.2	1	3	3	11	0.89	1.6	1.5	10.6	3.3	43.5	6	6	7680	55161	transmembrane protein 33	Molecular function unknown	Membrane fraction	Unclassified	Biological_process unknown	TM	Yes
NBEAL1	65065	neurobeachin-like protein 1	NP_001107604.1	1	2	2	4	0.89	1.47	13.51	7.15	17.2	15	2	2	14811	65065	neurobeachin-like 1	Molecular function unknown	Lysosome	Unclassified	Cell-cell signaling	WD40	Yes
PTPRC	5788	receptor-type tyrosine-protein phosphatase C isoform 1 precursor	NP_002829.3	2	1	1	2	0.89	1.43					1	1	1050	5788	protein tyrosine phosphatase, receptor type, C	Receptor signaling protein tyrosine phosphatase activity	Plasma membrane	Receptor tyrosine phosphatase	Cell communication;Signal transduction	TM;FN3;Tyr_Phos;SP	Yes
CWC27	10283	peptidyl-prolyl cis-trans isomerase CWC27 homolog isoform 1	NP_005860.2	3	3	3	5	0.89	1.36	2.13	6.13	3.3	14.5	3	3	11541	10283	serologically defined colon cancer antigen10	Isomerase activity	-	Enzyme: Isomerase	Metabolism;Energy pathways	CC	Yes
VPS4A	27183	vacuolar protein sorting-associated protein 4A	NP_037377.1	3	7	9	23	0.89	1.35	15.14	13.06	27.4	36.3	4	4	11676	27183	vacuolar protein sorting 4A (yeast)	ATPase activity	Cytoplasm	ATPase	Cell communication;Signal transduction	AAA	No
RELA	5970	transcription factor p65 isoform 1	NP_068810.3	4	6	6	9	0.89	1.34	1.24	7.66	2.5	23.3	5	5	1241	5970	v-rel reticuloendotheliosis viral oncogenehomolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3,p65 (avian)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RHD;IPT	No
HNRNPK	3190	heterogeneous nuclear ribonucleoprotein K isoform a	NP_112553.1	2	29	29	185	0.89	1.33	3.89	2.31	31.9	27.9	80	80	2834	3190	heterogeneous nuclear ribonucleoprotein K	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH;NLS;NES	Yes
SMU1	55234	WD40 repeat-containing protein SMU1	NP_060695.2	1	11	11	30	0.89	1.3	7.2	5.93	25.2	30.5	15	15	11588	55234	smu-1 suppressor of mec-8 and unc-52 homolog (C.elegans)	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LISH;CTLH;WD40	Yes
PDHA1	5160	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform 2 precursor	NP_001166925.1	5	10	10	37	0.89	1.26	5.5	4.6	21.6	25.7	19	19	2420	5160	pyruvate dehydrogenase (lipoamide) alpha 1	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
STAM	8027	signal transducing adapter molecule 1	NP_003464.1	1	3	3	4	0.89	1.26	53.55	31.38	98.1	77.4	3	3	3542	8027	signal transducing adaptor molecule (SH3 domainand ITAM motif) 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	VHS;UIM;SH3;ITAM;CC	No
FKBP4	2288	peptidyl-prolyl cis-trans isomerase FKBP4	NP_002005.1	1	18	18	59	0.89	1.25	5.25	5.69	27.2	42.6	33	33	11794	2288	FK506 binding protein 4, 59kDa	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Metabolism;Energy pathways	TPR;CC	Yes
PSME1	5720	proteasome activator complex subunit 1 isoform 1	NP_006254.1	4	12	12	60	0.89	1.23	3.95	7.05	19	49.3	29	29	2803	5720	proteasome (prosome, macropain) activatorsubunit 1 (PA28 alpha)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC	Yes
CCDC124	115098	coiled-coil domain-containing protein 124	NP_612451.1	1	3	3	5	0.89	1.22	19.04	11.62	30.1	25	3	3	14008	115098	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
PPP6R1	22870	serine/threonine-protein phosphatase 6 regulatory subunit 1	NP_055746.3	1	4	4	6	0.89	1.22	8.68	53.07	13.4	158.5	3	3									

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EXOSC1	51013	exosome complex component CSL4	NP_057130.1	1	4	4	7	0.89	1.21	2.35	1.55	3.6	3.3	3	3	16223	51013	exosome component 1	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S1	Yes
SSR3	6747	translocon-associated protein subunit gamma isoform 1	NP_001295126.1	2	1	1	2	0.89	1.21					1	1	16206	6747	signal sequence receptor, gamma(translocon-associated protein gamma)	Auxiliary transport protein activity	Microsome	Membrane transport protein	Transport	TM	Yes
ARHGEF7	8874	rho guanine nucleotide exchange factor 7 isoform c	NP_001106983.1	4	2	2	4	0.89	1.21	8.16	4.5	10.3	7.7	2	2	5688	8874	Rho guanine nucleotide exchange factor (GEF)7	Guanyl-nucleotide exchange factor activity;Molecular function unknown	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction;Regulation of signal transduction	CH;SH3;RHOGEF;PH;CC;NLS	Yes
NOP9	161424	nucleolar protein 9 isoform 1	NP_777573.1	2	2	2	5	0.89	1.17	11.92	4.53	15	7.5	2	2									
ACY1	95	aminoacylase-1 isoform a	NP_000657.1	4	7	7	17	0.89	1.16	8.69	7.49	25	28	10	10	92	95	aminoacylase 1	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
CTTNBP2NL	55917	CTTNBP2 N-terminal-like protein	NP_061174.1	1	1	1	2	0.89	1.16					1	1	10906	55917	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
GLRX3	10539	glutaredoxin-3	NP_001186797.1	1	11	11	27	0.89	1.16	8.76	7.11	29.7	31.6	14	14	10153	10539	thioredoxin-like 2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
MKNK1	8569	MAP kinase-interacting serine/threonine-protein kinase 1 isoform 1	NP_003675.2	3	1	1	2	0.89	1.12					1	1	9468	8569	MAP kinase interacting serine/threonine kinase1	ATP binding;Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Apoptosis;Regulation of translation;Cell communication;Signal transduction	S_T_kinase;NLS;NES	Yes
C1orf27	54953	protein odr-4 homolog isoform 1	NP_060317.3	3	8	8	15	0.89	1.11	5.35	7.54	13.6	24.1	8	8	12723	54953	chromosome 1 open reading frame 27	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No
AGTRAP	57085	type-1 angiotensin II receptor-associated protein isoform a	NP_065083.3	2	2	2	13	0.89	1.11	6.07	6.85	15.3	21.8	8	8	16379	57085	angiotensin II receptor-associated protein	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	SP;TM	No
NCKIPSD	51517	NCK-interacting protein with SH3 domain isoform 1	NP_057537.1	2	1	1	2	0.89	1.1					1	1	9450	51517	NCK interacting protein with SH3 domain	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	SH3;NLS	Yes
MX1	4599	interferon-induced GTP-binding protein Mx1 isoform a	NP_001138397.1	2	31	35	141	0.89	1.06	4.13	3.57	29.2	30.7	61	62	919	4599	myxovirus (influenza virus) resistance 1,interferon-inducible protein p78 (mouse)	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	CC;GED;DYNC	Yes
SRC	6714	proto-oncogene tyrosine-protein kinase Src	NP_005408.1	1	6	9	17	0.89	1.04	3.98	7.09	8.7	18.2	6	6	1819	6714	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogenehomolog (avian)	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase	Signal transduction	SH3;SH2;Tyr_Kinase	Yes
PDPK1	5170	3-phosphoinositide-dependent protein kinase 1 isoform 1	NP_002604.1	2	1	1	2	0.89	1.03					1	1	5556	5170	3-phosphoinositide dependent protein kinase-1	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Signal transduction	S_T_kinase;S_T_Y_Kinase	Yes
CDC16	8881	cell division cycle protein 16 homolog	NP_003894.3	1	5	5	8	0.89	1.03	15.56	7.64	31.7	17.7	5	5	4587	8881	CDC16 cell division cycle 16 homolog (S.cerevisiae)	Protein binding	Centrosome	Cell cycle control protein	Cell communication;Signal transduction	TPR	Yes
ASL	435	argininosuccinate lyase isoform 1	NP_001020114.1	3	5	5	12	0.89	1.03	14.94	18.58	33.5	49.5	6	6	1948	435	argininosuccinate lyase	Lyase activity	-	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
CTPS2	56474	CTP synthase 2	NP_001137474.1	1	5	7	12	0.89	1.01	12.87	5.3	28.6	13.2	6	6	2305	56474	CTP synthase II	Ligase activity	-	Enzyme: Synthase;Enzyme: Ligase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
MTMR6	9107	myotubularin-related protein 6	NP_004676.3	1	2	2	3	0.89	1	9.8	3.29	12.4	4.6	2	2	11946	9107	myotubularin related protein 6	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase	Cell communication;Signal transduction	CC	Yes
RARS	5917	arginine--tRNA ligase, cytoplasmic	NP_002878.2	1	33	33	128	0.89	0.99	4.15	3.15	30.8	25.8	66	66	142	5917	arginyl-tRNA synthetase	Ligase activity	Cytoplasm	Enzyme: Ligase	Protein metabolism	CC	Yes
LCN2	3934	neutrophil gelatinase-associated lipocalin precursor	NP_005555.2	1	2	2	3	0.89	0.98	16.05	34.58	20.5	50.9	2	2	2551	3934	lipocalin 2 (oncogene 24p3)	Transporter activity	Extracellular	Transport/cargo protein	Transport	SP	Yes
VPS39	23339	vam6/Vps39-like protein isoform a	NP_001288067.1	2	1	1	1	0.89	0.98					1	1	10300	23339	vacuolar protein sorting 39 (yeast)	Transporter activity	Lysosome	Transport/cargo protein	Transport	CNH	Yes
SYNJ1	8867	synaptojanin-1 isoform a	NP_003886.3	4	1	1	1	0.89	0.98					1	1	9182	8867	synaptojanin 1	Hydrolase activity	Synaptic vesicle	Enzyme: Phosphatase	Metabolism	I_Phosphatase;RRM	Yes
ACTR10	55860	actin-related protein 10	NP_060947.1	2	6	6	16	0.89	0.96	11.51	10.75	29.5	29.8	8	8	12420	55860	actin-related protein 10 homolog (S.cerevisiae)	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	ACTIN	Yes
MRPL4	51073	39S ribosomal protein L4, mitochondrial isoform a	NP_666499.1	2	8	8	19	0.89	0.95	3.68	5.01	9.9	14.4	9	9	14759	51073	mitochondrial ribosomal protein L4	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
UBE2Z	65264	ubiquitin-conjugating enzyme E2 Z	NP_075567.2	1	2	2	2	0.89	0.95	21.57	57.44	27.5	89.9	2	2	8589	65264	None	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBC	No
ENOPH1	58478	enolase-phosphatase E1 isoform 1	NP_067027.1	2	5	5	7	0.89	0.95	8.59	16.82	17.1	37	5	5	17467	58478	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RABGAP1	23637	rab GTPase-activating protein 1	NP_036329.3	1	9	10	17	0.89	0.94	6.33	10.89	16	29.6	8	8	6575	23637	RAB GTPase activating protein 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	PTB;CC	No
HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	NP_113584.3	1	38	38	73	0.89	0.94	3.83	4.26	20.3	24	35	35	6608	10075	HECT, UBA and WWE domain containing 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UBA;CC;HECT;WWE;UIM	Yes

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Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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TRIM47	91107	tripartite motif-containing protein 47	NP_258411.2	1	5	5	8	0.89	0.93	7.49	11.68	15	24.6	5	5	15564	91107	tripartite motif-containing 47	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;BBOX;PRY;SPRY	Yes
ETFDH	2110	electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial isoform 1 precursor	NP_004444.2	3	2	2	5	0.89	0.92	12.04	12.2	15.2	16	2	2	1978	2110	electron-transferring-flavoproteindehydrogenase	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
CDKN2AIP	55602	CDKN2A-interacting protein	NP_060102.1	1	7	7	13	0.89	0.91	2.47	6.99	5.8	16.9	7	7	16683	55602	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DSRM	No
XRN1	54464	5'-3' exoribonuclease 1 isoform a	NP_061874.3	2	3	3	6	0.89	0.9	5.71	7.95	10.1	14.4	4	4	10470	54464	5`-3` exoribonuclease 1	Ribonuclease activity	Cytoplasm	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
CNP	1267	2',3'-cyclic-nucleotide 3'-phosphodiesterase	NP_149124.3	1	5	6	14	0.89	0.9	5.01	16.15	10	33.2	5	5	448	1267	2`,3`-cyclic nucleotide 3` phosphodiesterase	Phosphoric diester hydrolase activity	Cytoplasm	Enzyme: Phosphodiesterase	Metabolism;Energy pathways	-	Yes
WNK1	65125	serine/threonine-protein kinase WNK1 isoform 4	NP_001171914.1	4	4	4	6	0.89	0.9	6.1	6.65	10.9	12.1	4	4	5570	65125	WNK lysine deficient protein kinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
DNMT1	1786	DNA (cytosine-5)-methyltransferase 1 isoform a	NP_001124295.1	2	3	3	5	0.89	0.89	0.69	23.7	1.1	37.9	3	3	532	1786	DNA (cytosine-5-)-methyltransferase 1	DNA-methyltransferase activity	Nucleus	DNA methyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BAH	Yes
GDA	9615	guanine deaminase isoform b	NP_004284.1	2	1	18	48	0.89	0.88					1	1	8849	9615	guanine deaminase	Deaminase activity	Cytoplasm	Enzyme: Deaminase	Metabolism;Energy pathways	-	Yes
ATP2A2	488	sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform b	NP_733765.1	11	38	38	165	0.89	0.88	3.52	4.76	29.1	39.6	83	83	161	488	ATPase, Ca++ transporting, cardiac muscle,slow twitch 2	Auxiliary transport protein activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Membrane transport protein	Transport	TM	Yes
NMT1	4836	glycylpeptide N-tetradecanoyltransferase 1	NP_066565.1	1	7	10	32	0.89	0.88	3.94	4.31	12.6	13.8	13	13	1187	4836	N-myristoyltransferase 1	Molecular function unknown;Acyltransferase activity	Ribosome	Enzyme: Acyltransferase;Unclassified	Metabolism;Energy pathways;Protein metabolism	-	Yes
DNAJC13	23317	dnaJ homolog subfamily C member 13	NP_056083.3	1	18	18	33	0.89	0.87	4.17	4.29	16.2	16.3	19	19	10915	23317	DnaJ (Hsp40) homolog, subfamily C, member 13	Chaperone activity;Molecular function unknown	Endosome	Unclassified;Chaperone	Protein metabolism;Biological_process unknown	DNAJ	Yes
AP1S1	1174	AP-1 complex subunit sigma-1A	NP_001274.1	1	3	3	7	0.89	0.87	16.16	2.07	25.3	3.1	3	3	4635	1174	adaptor-related protein complex 1, sigma 1subunit	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	-	Yes
BCS1L	617	mitochondrial chaperone BCS1	NP_001244271.1	1	10	10	26	0.89	0.87	11.34	5.27	37.8	16.7	13	13	4708	617	BCS1-like (yeast)	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	AAA;SP	Yes
AKR1A1	10327	alcohol dehydrogenase [NADP(+)]	NP_697021.1	1	10	11	45	0.89	0.86	5.88	9.69	23.1	37.6	19	19	69	10327	aldo-keto reductase family 1, member A1(aldehyde reductase)	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism	ALDKR	Yes
SLC25A12	8604	calcium-binding mitochondrial carrier protein Aralar1	NP_003696.2	1	8	12	27	0.89	0.86	7.38	3.01	19.9	7.8	9	9	4719	8604	solute carrier family 25 (mitochondrialcarrier, Aralar), member 12	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	EF	Yes
EVPL	2125	envoplakin	NP_001979.2	1	3	3	9	0.89	0.86	9.03	18.77	18.1	37.3	5	5	3352	2125	envoplakin	Structural molecule activity	Plasma membrane	Structural protein	Cell growth and/or maintenance	SPECTRIN;PLEC;CC	Yes
GBE1	2632	1,4-alpha-glucan-branching enzyme	NP_000149.3	1	13	13	32	0.89	0.86	5.69	5.36	22.3	20.3	19	19	1985	2632	glucan (1,4-alpha-), branching enzyme 1(glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	Transferase activity	-	Enzyme: Glycosyltransferase	Metabolism;Energy pathways	AMY	Yes
DSG2	1829	desmoglein-2 preproprotein	NP_001934.2	1	24	24	92	0.89	0.86	4.19	5.08	23.9	27.8	40	39	516	1829	desmoglein 2	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	SP;Cadherin;TM	Yes
M6PR	4074	cation-dependent mannose-6-phosphate receptor isoform 1 precursor	NP_002346.1	2	4	4	14	0.89	0.86	11.77	7.55	28.3	17.2	7	7	1106	4074	mannose-6-phosphate receptor (cation dependent)	Receptor activity	Plasma membrane	Integral membrane protein	Protein metabolism	SP;TM	Yes
SVIL	6840	supervillin isoform 2	NP_068506.2	2	6	6	13	0.89	0.85	13.09	11.6	31.5	26.6	7	7	4992	6840	supervillin	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	GEL;VHP	Yes
INF2	64423	inverted formin-2 isoform 1	NP_071934.3	3	14	14	42	0.89	0.85	6.43	5.26	25.9	20.2	20	20	8648	64423	chromosome 14 open reading frame 173	Molecular function unknown;Cytoskeletal protein binding	Nucleus;Cytoplasm	Cytoskeletal associated protein;Unclassified	Biological_process unknown;Cytoskeleton organization and biogenesis	CC;FH2	Yes
DIP2B	57609	disco-interacting protein 2 homolog B	NP_775873.2	7	9	9	16	0.89	0.84	6.83	9.45	17.3	22.8	8	8	11148	57609	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes
FGD4	121512	FYVE, RhoGEF and PH domain-containing protein 4 isoform 1	NP_001291409.1	5	3	3	6	0.89	0.84	8.93	70.94	13.8	138.2	3	3	16891	121512	FYVE, RhoGEF and PH domain containing 4	Guanyl-nucleotide exchange factor activity	Cytoskeleton	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;FYVE	Yes
SDSL	113675	serine dehydratase-like	NP_612441.1	1	3	3	8	0.89	0.84	9.9	3	17.7	5	4	4	11542	113675	serine dehydratase-like	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No

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COPG2	26958	coatomer subunit gamma-2 isoform 1	NP_036265.3	3	15	17	47	0.89	0.83	3.17	7.77	12.1	27.7	18	18	5074	26958	coatomer protein complex, subunit gamma 2	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	ADAP	Yes
FN3KRP	79672	ketosamine-3-kinase	NP_078895.2	1	4	4	7	0.89	0.82	11.74	2.15	21.1	3.5	4	4	13546	79672	None	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
ARFGAP3	26286	ADP-ribosylation factor GTPase-activating protein 3 isoform 1	NP_055385.3	2	6	6	11	0.89	0.82	5.67	16.8	12.4	34.7	6	6	6444	26286	ADP-ribosylation factor GTPase activatingprotein 3	GTPase activator activity	Cytoplasm	GTPase activating protein	Protein metabolism	ARFGAP	Yes
NT5E	4907	5'-nucleotidase isoform 1 preproprotein	NP_002517.1	2	15	15	42	0.89	0.79	4.18	6.89	18	26	23	22	552	4907	5`-nucleotidase, ecto (CD73)	Hydrolase activity	Plasma membrane	Enzyme: Hydrolase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP;GPI	Yes
RAB5B	5869	ras-related protein Rab-5B isoform 1	NP_002859.1	2	6	9	47	0.89	0.79	10.07	31.43	35.6	122.4	15	15	1544	5869	RAB5B, member RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAB	Yes
ARVCF	421	armadillo repeat protein deleted in velo-cardio-facial syndrome	NP_001661.1	1	3	3	4	0.89	0.77					1	1	3778	421	armadillo repeat gene deletes invelocardiofacial syndrome	Molecular function unknown	Plasma membrane	Unclassified	Cell growth and/or maintenance	ARM;CC	Yes
PDXK	8566	pyridoxal kinase	NP_003672.1	1	9	9	33	0.89	0.77	9.67	19.55	34.3	64.1	15	15	1526	8566	pyridoxal (pyridoxine, vitamin B6) kinase	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
KIF4B	285643	chromosome-associated kinesin KIF4B	NP_001092763.1	5	3	4	6	0.89	0.76					1	1	19382	285643	kinesin family member 4B	Motor activity	-	Motor protein	Cell growth and/or maintenance	KISC;CC;PreSET	Yes
NCAM1	4684	neural cell adhesion molecule 1 isoform 5 precursor	NP_001229536.1	5	1	1	1	0.89	0.76					1	1	301	4684	neural cell adhesion molecule 1	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;IGC2;FN3;TM	Yes
TPMT	7172	thiopurine S-methyltransferase	NP_000358.1	1	2	2	2	0.89	0.76	5.66	9.68	7.1	10.5	2	2	1760	7172	thiopurine S-methyltransferase	Methyltransferase activity	Cytoplasm	Enzyme: Methyltransferase	Metabolism;Energy pathways	-	No
RAB8A	4218	ras-related protein Rab-8A	NP_005361.2	12	3	7	76	0.89	0.75	4.42	9.3	9.7	17.2	6	6	1296	4218	RAB8A, member RAS oncogene family	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	RAB	Yes
Sep-10	151011	septin-10 isoform 1	NP_653311.1	2	9	9	21	0.89	0.74	2.14	9.73	5.7	22	9	9									
SCAMP3	10067	secretory carrier-associated membrane protein 3 isoform 1	NP_005689.2	2	4	4	6	0.89	0.74	6.99	2.07	12.5	3.1	4	4	6074	10067	secretory carrier membrane protein 3	Auxiliary transport protein activity	Plasma membrane;Nucleus	Membrane transport protein	Transport	TM;CC	Yes
ARHGAP29	9411	rho GTPase-activating protein 29	NP_004806.3	1	6	6	10	0.89	0.74	15.05	6.23	30.8	10.3	5	5	6674	9411	Rho GTPase activating protein 29	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	C1;CC;RHOGAP	Yes
PPP1R21	129285	protein phosphatase 1 regulatory subunit 21 isoform 1	NP_001129101.1	3	3	3	8	0.89	0.73	8.17	54.57	14.6	94.7	4	4									
PPP3CA	5530	serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 1	NP_000935.1	4	10	17	54	0.89	0.73	7.7	13.68	29.8	41.4	18	16	234	5530	protein phosphatase 3 (formerly 2B), catalyticsubunit, alpha isoform (calcineurin A alpha)	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2A	Yes
OPTN	10133	optineurin	NP_001008212.1	1	10	10	15	0.89	0.73	7.89	10.47	21.4	23.1	9	9	3891	10133	optineurin	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;CC	No
NUDT1	4521	7,8-dihydro-8-oxoguanine triphosphatase isoform p22	NP_945187.1	2	4	4	7	0.89	0.7	1.62	26.78	2.9	38.8	4	4	2634	4521	nudix (nucleoside diphosphate linked moietyX)-type motif 1	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
MARK2	2011	serine/threonine-protein kinase MARK2 isoform d	NP_001034558.2	12	7	10	17	0.89	0.67	11.68	13.65	25.9	22.8	6	6	2753	2011	MAP/microtubule affinity-regulating kinase 2	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;UBA	No
RNF126	55658	E3 ubiquitin-protein ligase RNF126	NP_919442.1	1	2	2	4	0.89	0.66					1	1	11501	55658	ring finger protein 126	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	RING	No
C4orf27	54969	UPF0609 protein C4orf27	NP_060337.2	1	1	1	2	0.88	1.75					1	1	7924	54969	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
UBE2H	7328	ubiquitin-conjugating enzyme E2 H isoform 1	NP_003335.1	2	3	3	8	0.88	1.4	1.29	6.03	2.5	19	5	5	3052	7328	ubiquitin-conjugating enzyme E2H (UBC8 homolog,yeast)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBC	No
TPM3	7170	tropomyosin alpha-3 chain isoform Tpm3.1cy	NP_705935.1	4	4	27	95	0.88	1.37	48.47	54.81	85.6	209.8	3	3	1840	7170	tropomyosin 3	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein;Structural protein	Cell growth and/or maintenance	CC	Yes
POLR1C	9533	DNA-directed RNA polymerases I and III subunit RPAC1	NP_976035.1	1	5	5	13	0.88	1.29	14.39	21.76	34.5	85.9	7	7	9661	9533	polymerase (RNA) I polypeptide C, 30kDa	DNA-directed RNA polymerase activity	Nucleolus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RPOLD	Yes
ABHD10	55347	mycophenolic acid acyl-glucuronide esterase, mitochondrial isoform 1 precursor	NP_060864.1	1	1	1	2	0.88	1.28					1	1	7751	55347	abhydrolase domain containing 10	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism	SP	No
HRAS	3265	GTPase HRas isoform 1	NP_001123914.1	2	2	8	30	0.88	1.24	3.1	2.35	6.7	7.1	6	6	1813	3265	v-Ha-ras Harvey rat sarcoma viral oncogenehomolog	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	Yes
ARHGAP35	2909	rho GTPase-activating protein 35	NP_004482.4	1	2	2	3	0.88	1.23	30.78	8.69	39.8	15.2	2	2									

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HMGN1	3150	non-histone chromosomal protein HMG-14	NP_004956.5	1	5	5	11	0.88	1.21	11.04	13.14	26.2	44.1	7	7	1231	3150	high-mobility group nucleosome binding domain 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
TXLNA	200081	alpha-taxilin	NP_787048.1	1	11	11	34	0.88	1.2	6.26	8.31	22.2	41.6	16	16	9408	200081	None	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	CC	Yes
PSMG2	56984	proteasome assembly chaperone 2 isoform 1	NP_064617.2	2	6	6	11	0.88	1.16	8.32	3.81	16.5	9.9	5	5	11638	56984	tumor necrosis factor superfamily, member5-induced protein 1	Molecular function unknown	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	-	No
GNB2L1	10399	guanine nucleotide-binding protein subunit beta-2-like 1	NP_006089.1	1	19	19	92	0.88	1.12	3.37	3.5	21.4	28.5	51	51	1503	10399	guanine nucleotide binding protein (Gprotein), beta polypeptide 2-like 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	WD40	Yes
PPP3CB	5532	serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform a	NP_001135825.1	5	1	7	20	0.88	1.11	6.09	7.32	7.6	11.5	2	2	235	5532	protein phosphatase 3 (formerly 2B), catalyticsubunit, beta isoform (calcineurin A beta)	Protein serine/threonine phosphatase activity	Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2A	Yes
CBR1	873	carbonyl reductase [NADPH] 1 isoform 1	NP_001748.1	2	17	17	61	0.88	1.11	5.16	4.55	25.3	28.2	30	30	267	873	carbonyl reductase 1	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
PNP	4860	purine nucleoside phosphorylase	NP_000261.2	1	16	16	65	0.88	1.08	4.95	4.94	25.5	31.2	33	33	1247	4860	nucleoside phosphorylase	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase	Metabolism;Energy pathways	-	Yes
QTRT1	81890	queuine tRNA-ribosyltransferase	NP_112486.1	1	2	2	5	0.88	1.07					1	1	17943	81890	queuine tRNA-ribosyltransferase 1 (tRNA-guaninetransglycosylase)	Catalytic activity	-	Enzyme: Ribosyltransferase	Metabolism;Energy pathways	-	Yes
YIPF5	81555	protein YIPF5 isoform a	NP_001020118.1	2	2	2	6	0.88	1.06	9.83	3.97	15.1	7.3	3	3	18071	81555	None	Molecular function unknown	Golgi apparatus	Unclassified	Biological_process unknown	TM	No
CMTR2	55783	cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 2	NP_060818.4	1	1	1	2	0.88	1.05					1	1									
BDH2	56898	3-hydroxybutyrate dehydrogenase type 2	NP_064524.3	1	2	2	3	0.88	1.04					1	1	7103	56898	dehydrogenase/reductase (SDR family) member 6	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
DNPEP	23549	aspartyl aminopeptidase	NP_036232.2	1	9	9	20	0.88	1.04	6.2	8.15	18.3	28.6	11	11	9924	23549	aspartyl aminopeptidase	Aminopeptidase activity	Cytoplasm	Aminopeptidase	Protein metabolism	-	Yes
AP1B1	162	AP-1 complex subunit beta-1 isoform b	NP_663782.2	3	14	27	103	0.88	1.04	4.49	5.94	17.3	27.4	19	19	2541	162	adaptor-related protein complex 1, beta 1subunit	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	ADAP	Yes
QDPR	5860	dihydropteridine reductase isoform 1	NP_000311.2	2	4	4	7	0.88	1.04	10.97	19.42	19.5	42	4	4	2025	5860	quinoid dihydropteridine reductase	Catalytic activity	Extracellular	Enzyme: Reductase	Metabolism;Energy pathways	-	Yes
CLPP	8192	ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor	NP_006003.1	1	4	4	7	0.88	1.04	1.91	9.63	3.8	22.6	5	5	3074	8192	ClpP caseinolytic protease, ATP-dependent,proteolytic subunit homolog (E. coli)	Peptidase activity	Mitochondrion	Protease	Protein metabolism	-	Yes
RPL36A	6173	60S ribosomal protein L36a isoform a	NP_066357.2	5	6	6	11	0.88	1.02	8.62	4.5	21.7	13	8	8	6709	6173	ribosomal protein L36a	Structural constituent of ribosome	Cytoplasm	Ribosomal subunit	Protein metabolism	-	No
MAVS	57506	mitochondrial antiviral-signaling protein isoform 1	NP_065797.2	2	7	7	20	0.88	1	8.92	11.65	21.1	31.5	7	7	13847	57506	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
DRG2	1819	developmentally-regulated GTP-binding protein 2	NP_001379.1	1	8	8	18	0.88	1	7.49	8.01	21.2	25.8	10	10	4286	1819	developmentally regulated GTP binding protein 2	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	-	Yes
HCCS	3052	cytochrome c-type heme lyase	NP_001165462.1	1	2	2	3	0.88	0.99	42.77	36.24	57.5	54.3	2	2	2085	3052	holocytochrome c synthase (cytochrome cheme-lyase)	Lyase activity	Mitochondrion	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
DTYMK	1841	thymidylate kinase isoform 1	NP_036277.2	2	4	4	6	0.88	0.99	6.37	8.14	11.3	16.2	4	4	1773	1841	deoxythymidylate kinase (thymidylate kinase)	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	No
LMNB2	84823	lamin-B2	NP_116126.3	1	34	38	105	0.88	0.99	4.21	4.09	25.8	28.4	47	47	1037	84823	lamin B2	Structural molecule activity	Nucleus	Structural protein	Cell growth and/or maintenance	NLS;CC	Yes
MYH9	4627	myosin-9	NP_002464.1	9	127	159	1287	0.88	0.98	1.64	2.95	33.4	72.9	511	512	1177	4627	myosin, heavy polypeptide 9, non-muscle	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	MYOSIN;IQ;CC	Yes
DHRS1	115817	dehydrogenase/reductase SDR family member 1	NP_001129522.1	1	5	5	10	0.88	0.98	5.39	9.36	11.6	22.8	6	6	9914	115817	dehydrogenase/reductase (SDR family) member 1	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
RPA3	6119	replication protein A 14 kDa subunit	NP_002938.1	1	3	3	6	0.88	0.97	13.45	3.21	20.8	5.4	3	3	1567	6119	replication protein A3, 14kDa	DNA binding	Nucleolus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TRNAA	Yes
NONO	4841	non-POU domain-containing octamer-binding protein isoform 1	NP_031389.3	2	17	18	75	0.88	0.97	4.73	7.73	26.2	49	38	38	2098	4841	non-POU domain containing, octamer-binding	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM;CC	Yes
USP24	23358	ubiquitin carboxyl-terminal hydrolase 24	NP_056121.2	2	8	9	19	0.88	0.97	4.12	7.14	10.3	19.7	8	8	11664	23358	ubiquitin specific protease 24	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UCH	Yes
TBL2	26608	transducin beta-like protein 2 precursor	NP_036585.1	1	5	5	13	0.88	0.96	3.54	2.55	8.2	6.5	7	7	9319	26608	transducin (beta)-like 2	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	WD40;CC;TM	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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PIK3IP1	113791	phosphoinositide-3-kinase-interacting protein 1 isoform 1 precursor	NP_443112.2	1	1	1	4	0.88	0.96	41.11	15.43	54.5	21.2	2	2	17518	113791	None	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	SP;KRINGLE;TM	Yes
IPO9	55705	importin-9	NP_060555.2	1	18	18	41	0.88	0.96	5.46	5.36	23.8	25.6	24	24	17154	55705	importin 9	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	SP	Yes
FASTKD1	79675	FAST kinase domain-containing protein 1 isoform 1	NP_078898.3	2	2	2	3	0.88	0.95					1	1	7969	79675	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
PIK3R4	30849	phosphoinositide 3-kinase regulatory subunit 4	NP_055417.1	1	9	9	22	0.88	0.95	2.71	4.62	7.9	14.6	11	11	4010	30849	phosphoinositide-3-kinase, regulatory subunit4, p150	Receptor signaling complex scaffold activity	-	Adapter molecule	Protein metabolism	S_T_Y_Kinase;CC;WD40;HEAT	No
SNX17	9784	sorting nexin-17 isoform 1	NP_055563.1	4	5	5	8	0.88	0.94	7.53	20.88	15	46.3	5	5	5812	9784	sorting nexin 17	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PX;B41	Yes
SPTLC1	10558	serine palmitoyltransferase 1 isoform a	NP_006406.1	3	9	9	23	0.88	0.94	4.82	5.19	14.8	17	12	12	5754	10558	serine palmitoyltransferase, long chain basesubunit 1	Palmitoyltransferase activity	Endoplasmic reticulum	Enzyme: Palmitoyltransferase	Metabolism;Energy pathways	TM	Yes
SCRIB	23513	protein scribble homolog isoform a	NP_874365.3	2	15	16	27	0.88	0.93	5.82	5.43	19.4	19.8	14	15	6984	23513	scribbled homolog (Drosophila)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	LRR;CC;PDZ	Yes
CTNNA1	1495	catenin alpha-1 isoform 1	NP_001894.2	8	35	35	205	0.88	0.93	3.84	5	34	47.4	95	94	285	1495	catenin (cadherin-associated protein), alpha1, 102kDa	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
UBR5	51366	E3 ubiquitin-protein ligase UBR5 isoform 1	NP_056986.2	2	6	6	10	0.88	0.92	3.54	14.26	7	30	5	5	6436	51366	None	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBA;HECT;NLS	Yes
ESYT1	23344	extended synaptotagmin-1 isoform 1	NP_001171725.1	2	24	24	95	0.88	0.91	5.97	5.09	36.6	32.7	46	47	14367	23344	family with sequence similarity 62 (C2 domaincontaining), member A	Calcium ion binding	Plasma membrane	Calcium binding protein	Cell communication;Signal transduction	TM;C2	No
TSTA3	7264	GDP-L-fucose synthase	NP_003304.1	1	6	6	17	0.88	0.9	3.13	7.11	8.3	19.3	9	9	654	7264	tissue specific transplantation antigen P35B	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
UGGT1	56886	UDP-glucose:glycoprotein glucosyltransferase 1 precursor	NP_064505.1	2	33	33	93	0.88	0.9	3.84	4.21	24.4	27.5	51	51	12064	56886	UDP-glucose ceramide glucosyltransferase-like1	Transferase activity	Endoplasmic reticulum	Enzyme: Glycosyltransferase	Metabolism;Energy pathways	SP;CC	Yes
ARHGAP10	79658	rho GTPase-activating protein 10	NP_078881.3	1	1	1	2	0.88	0.89					1	1	7949	79658	Rho GTPase activating protein 10	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	RHOGAP;SH3;CC;PH	Yes
GUK1	2987	guanylate kinase isoform c	NP_001229769.1	3	2	2	2	0.88	0.89	6.07	4.63	7.6	5.8	2	2	755	2987	guanylate kinase 1	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Cell communication;Signal transduction	GuKinase	Yes
RPS10	6204	40S ribosomal protein S10	NP_001190174.1	2	14	14	51	0.88	0.87	3.72	11.8	16.2	54	24	24	4697	6204	ribosomal protein S10	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
ATP5H	10476	ATP synthase subunit d, mitochondrial isoform a	NP_006347.1	2	7	7	14	0.88	0.86	5.41	8.36	14.4	21.7	9	9	16519	10476	ATP synthase, H+ transporting, mitochondrial F0complex, subunit d	Transporter activity	Mitochondrial membrane	Transport/cargo protein	Metabolism;Energy pathways;Ion transport	CC	No
AP1G1	164	AP-1 complex subunit gamma-1 isoform a	NP_001025178.1	2	13	13	32	0.88	0.85	4.73	4.83	17.3	17	17	17	4637	164	adaptor-related protein complex 1, gamma 1subunit	Transporter activity	Golgi apparatus	Transport/cargo protein	Vesicle-mediated transport	ADAP	Yes
PTBP3	9991	polypyrimidine tract-binding protein 3 isoform 6	NP_001231827.1	6	9	12	43	0.88	0.85	4.35	10.75	13.3	32.4	12	12									
NDUFA10	4705	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor	NP_004535.1	1	6	6	15	0.88	0.85	15.09	17.48	38.9	44.1	8	8	11950	4705	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 10, 42kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP	Yes
NUBPL	80224	iron-sulfur protein NUBPL isoform 1 precursor	NP_079428.2	3	3	3	5	0.88	0.85	2.34	3.4	2.9	4.1	2	2	16600	80224	nucleotide binding protein-like	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
CAPZA1	829	F-actin-capping protein subunit alpha-1	NP_006126.1	1	11	13	88	0.88	0.85	4.42	5.99	22	28.9	31	31	3347	829	capping protein (actin filament) muscleZ-line, alpha 1	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	-	Yes
RAB7A	7879	ras-related protein Rab-7a	NP_004628.4	1	16	16	65	0.88	0.84	4.68	4.53	23.9	22.1	33	33	3805	7879	RAB7, member RAS oncogene family	GTPase activity	Endosome	GTPase	Cell communication;Signal transduction	RAB	Yes
ARRDC2	27106	arrestin domain-containing protein 2 isoform 2	NP_001020775.1	1	1	1	1	0.88	0.83					1	1	12492	27106	arrestin domain containing 2	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
PFKL	5211	ATP-dependent 6-phosphofructokinase, liver type isoform b	NP_002617.3	2	17	20	71	0.88	0.83	5.52	6.18	23	24.5	22	22	1385	5211	phosphofructokinase, liver	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
IDH2	3418	isocitrate dehydrogenase [NADP], mitochondrial isoform 1 precursor	NP_002159.2	3	11	12	41	0.88	0.83	4.97	6.24	20.6	24.5	22	22	973	3418	isocitrate dehydrogenase 2 (NADP+),mitochondrial	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
EXOC4	60412	exocyst complex component 4 isoform a	NP_068579.3	2	8	8	16	0.88	0.82	5.5	12.76	14.6	32	9	9	12185	60412	SEC8-like 1 (S. cerevisiae)	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	CC	Yes
STX6	10228	syntaxin-6 isoform 1	NP_005810.1	2	3	3	4	0.88	0.81	0.45	4.62	0.7	6.5	3	3	7231	10228	syntaxin 6	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Cell communication;Signal transduction	CC;TM	Yes
EXOC1	55763	exocyst complex component 1 isoform 1	NP_060731.2	2	10	10	17	0.88	0.79	3.27	11.05	9.1	28.2	10	10	7615	55763	SEC3-like 1 (S. cerevisiae)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC	Yes
HINT1	3094	histidine triad nucleotide-binding protein 1	NP_005331.1	1	3	3	4	0.88	0.78	8.09	13.11	12.4	17.9	3	3	3204	3094	histidine triad nucleotide binding protein 1	ATPase activity	Cytoplasm	ATPase	Cell communication;Signal transduction	-	Yes
ABRACL	58527	costars family protein ABRACL	NP_067066.1	1	2	2	3	0.88	0.77					1	1									
FASTKD2	22868	FAST kinase domain-containing protein 2	NP_055744.2	1	3	3	5	0.88	0.75	9.79	4.52	15	5.9	3	3	13825	22868	KIAA0971	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No

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PKP3	11187	plakophilin-3 isoform PKP3b	NP_001289958.1	2	28	28	75	0.88	0.75	4.25	5.46	23.4	25.7	38	38	5711	11187	plakophilin 3	Cell adhesion molecule activity	Plasma membrane	Cell junction protein	Cell communication;Signal transduction	ARM	Yes
MORC3	23515	MORC family CW-type zinc finger protein 3	NP_056173.1	1	6	6	9	0.88	0.75	20.34	4.81	41.9	8.1	5	5	10316	23515	zinc finger, CW type with coiled-coil domain 3	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;NLS	Yes
KLHL36	79786	kelch-like protein 36 isoform 1	NP_079007.2	2	1	1	1	0.88	0.75					1	1	12675	79786	chromosome 16 open reading frame 44	Molecular function unknown	-	Unclassified	Biological_process unknown	BTB;KELCH	No
UBFD1	56061	ubiquitin domain-containing protein UBFD1	NP_061989.2	1	1	1	2	0.88	0.73					1	1	15606	56061	None	Molecular function unknown	-	Unclassified	Protein metabolism	UBQ	No
RHOT2	89941	mitochondrial Rho GTPase 2	NP_620124.1	9	12	12	38	0.88	0.72	4.03	7.85	14.6	23.6	17	17	15248	89941	ras homolog gene family, member T2	GTPase activity	Mitochondrion	GTPase	Cell communication;Signal transduction	EF;TM	Yes
RPA2	6118	replication protein A 32 kDa subunit isoform 3	NP_001284487.1	3	4	4	20	0.88	0.71	3.61	35.24	7.1	60.8	5	5	1566	6118	replication protein A2, 32kDa	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TRNAA	Yes
SMG1	23049	serine/threonine-protein kinase SMG1	NP_055907.3	1	2	2	3	0.88	0.69	34.93	47.39	45.6	48.6	2	2	6123	23049	None	Molecular function unknown	Nucleus	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PI3KC;CC	Yes
TMED3	23423	transmembrane emp24 domain-containing protein 3 isoform a precursor	NP_031390.1	1	2	2	4	0.88	0.68	1.13	16.99	1.4	16.5	2	2	18200	23423	transmembrane emp24 domain containing 3	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	SP;TM	Yes
FTL	2512	ferritin light chain	NP_000137.2	1	3	3	7	0.88	0.64	7.75	13.14	13.7	16.9	4	4	616	2512	ferritin, light polypeptide	Storage protein	Cytoplasm	Storage protein	Transport	-	Yes
RNF185	91445	E3 ubiquitin-protein ligase RNF185 isoform 1	NP_689480.2	1	2	2	3	0.88	0.58					1	1	8790	91445	ring finger protein 185	Molecular function unknown	-	Unclassified	Biological_process unknown	RING;TM	No
HINT2	84681	histidine triad nucleotide-binding protein 2, mitochondrial precursor	NP_115982.1	1	5	5	9	0.88	0.51	3.87	53.87	6.8	60	4	4	17106	84681	histidine triad nucleotide binding protein 2	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
ANKZF1	55139	ankyrin repeat and zinc finger domain-containing protein 1 isoform 1	NP_001035869.1	2	4	4	9	0.87	1.89	34.98	10.6	56.7	35.7	3	3	7673	55139	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	ANK;CC	No
FADD	8772	FAS-associated death domain protein	NP_003815.1	1	1	1	1	0.87	1.54					1	1	3909	8772	Fas (TNFRSF6)-associated via death domain	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	DED;DEATH	Yes
STK39	27347	STE20/SPS1-related proline-alanine-rich protein kinase	NP_037365.2	1	4	5	12	0.87	1.53	5.66	6.08	11	21.1	5	5	9627	27347	serine threonine kinase 39 (STE20/SPS1 homolog,yeast)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NLS	Yes
OSTM1	28962	osteopetrosis-associated transmembrane protein 1	NP_054747.2	1	2	2	5	0.87	1.42	1.53	44.87	1.9	112.4	2	2	9628	28962	osteopetrosis associated transmembrane protein1	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM	No
CSNK2B	1460	casein kinase II subunit beta isoform 1	NP_001311.3	2	4	4	9	0.87	1.4	24.25	22.44	49.8	79.5	5	5	278	1460	casein kinase 2, beta polypeptide	Protein serine/threonine kinase activity	-	Serine/threonine kinase	Cell communication;Signal transduction	-	Yes
GPKOW	27238	G patch domain and KOW motifs-containing protein	NP_056513.2	1	4	4	10	0.87	1.36	10.57	6.82	22.9	23.1	6	6	6737	27238	G patch domain and KOW motifs	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	G_PATCH	Yes
NUPL2	11097	nucleoporin-like protein 2	NP_031368.1	1	1	1	2	0.87	1.3					1	1	14855	11097	nucleoporin like 2	Transporter activity	Nuclear membrane	Transport/cargo protein	Transport	CC	No
CRKL	1399	crk-like protein	NP_005198.1	1	2	2	4	0.87	1.26					1	1	3596	1399	v-crk sarcoma virus CT10 oncogene homolog(avian)-like	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	SH2;SH3	Yes
METTL15	196074	probable methyltransferase-like protein 15 isoform 1	NP_001107000.1	1	4	4	9	0.87	1.22	8.98	16.1	17.6	46	5	5									
SNRPB2	6629	U2 small nuclear ribonucleoprotein B"	NP_937863.1	1	3	4	6	0.87	1.22	1.56	12.81	2.7	32	4	4	4628	6629	small nuclear ribonucleoprotein polypeptideB``	RNA binding	Nucleus	Ribonucleoprotein	RNA metabolism	RRM	Yes
RPL30	6156	60S ribosomal protein L30	NP_000980.1	1	7	7	61	0.87	1.2	7.5	6.78	37.4	47.5	31	31	1595	6156	ribosomal protein L30	Structural constituent of ribosome	-	Ribosomal subunit	Protein metabolism	-	Yes
VPS4B	9525	vacuolar protein sorting-associated protein 4B	NP_004860.2	3	11	13	39	0.87	1.19	4.98	8.11	15.1	34.3	12	12	15653	9525	vacuolar protein sorting 4B (yeast)	Transporter activity	Perinuclear region	Transport/cargo protein	Transport	CC;AAA	Yes
SLC25A46	91137	solute carrier family 25 member 46 isoform 1	NP_620128.1	3	1	1	2	0.87	1.18					1	1	14283	91137	None	Transporter activity	Mitochondrial membrane	Transport/cargo protein	Transport	-	Yes
RRP12	23223	RRP12-like protein isoform 1	NP_055994.2	3	14	14	25	0.87	1.18	13.83	6.81	39.2	25.9	10	10	11103	23223	KIAA0690	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	CC	No
MARCKS	4082	myristoylated alanine-rich C-kinase substrate	NP_002347.5	1	8	9	27	0.87	1.17	12.44	14.6	40.6	67.8	13	13	7519	4082	myristoylated alanine-rich protein kinase Csubstrate	Structural constituent of cytoskeleton	Plasma membrane	Cytoskeletal protein	Cell growth and/or maintenance	-	Yes
AK1	203	adenylate kinase isoenzyme 1	NP_000467.1	1	6	6	14	0.87	1.16	15.77	9.64	37.4	30.2	7	7	46	203	adenylate kinase 1	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
GTF2B	2959	transcription initiation factor IIB	NP_001505.1	1	4	4	4	0.87	1.15	8.93	4.88	13.5	9.7	3	3	8928	2959	general transcription factor IIB	Transcription factor activity	Nucleus	Transcription factor	-	CYCLIN	Yes
FAM160B1	57700	protein FAM160B1 isoform a	NP_065991.3	3	3	3	7	0.87	1.15	11.61	10.38	20.5	24.2	4	4	17219	57700	KIAA1600	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
TIMM17B	10245	mitochondrial import inner membrane translocase subunit Tim17-B isoform 2	NP_005825.1	2	3	3	5	0.87	1.14	7.14	39.44	8.8	70.4	2	2	2218	10245	translocase of inner mitochondrial membrane17 homolog B (yeast)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
COG7	91949	conserved oligomeric Golgi complex subunit 7	NP_705831.1	1	3	3	7	0.87	1.12	4.03	6.76	7	15.2	4	4	7373	91949	component of oligomeric golgi complex 7	Structural molecule activity	Golgi apparatus	Structural protein	Transport	CC	Yes
PAIP1	10605	polyadenylate-binding protein-interacting protein 1 isoform 1	NP_006442.2	3	8	8	20	0.87	1.12	6.75	6.02	18.7	21.6	10	10	5539	10605	poly(A) binding protein interacting protein 1	Translation regulator activity;Protein binding	Cytoplasm	Translation regulatory protein	Protein metabolism;Regulation of translation	MIF4G	Yes
COTL1	23406	coactosin-like protein	NP_066972.1	1	7	7	22	0.87	1.12	12.25	5.4	36.3	20.3	11	11	9482	23406	coactosin-like 1 (Dictyostelium)	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	ADF	Yes
POR	5447	NADPH--cytochrome P450 reductase	NP_000932.3	1	10	10	33	0.87	1.12	7.13	9.41	25	42.5	16	15	485	5447	P450 (cytochrome) oxidoreductase	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase	Metabolism;Energy pathways	TM	Yes
AK3	50808	GTP:AMP phosphotransferase AK3, mitochondrial isoform a	NP_057366.2	3	6	6	8	0.87	1.11	0.68	10.15	1.3	25.7	5	5	12439	50808	adenylate kinase 3	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
ALG1	56052	chitobiosyldiphosphodolichol beta-mannosyltransferase	NP_061982.3	3	5	5	8	0.87	1.11	18.42	16.37	37.1	42.4	5	5	10437	56052	asparagine-linked glycosylation 1 homolog(yeast, beta-1,4-mannosyltransferase)	Mannosyltransferase activity	Endoplasmic reticulum	Enzyme: Mannosyltransferase	Metabolism;Energy pathways	TM	No
GALNT1	2589	polypeptide N-acetylgalactosaminyltransferase 1	NP_065207.2	1	2	2	5	0.87	1.1	13.32	0.64	20.2	1.2	3	3	3781	2589	UDP-N-acetyl-alpha-D-galactosamine:polypeptideN-acetylgalactosaminyltransferase 1 (GalNAc-T1)	Galactosyltransferase activity	Endoplasmic reticulum	Enzyme: Galactosyltransferase	Metabolism;Energy pathways	TM	Yes
SNX9	51429	sorting nexin-9	NP_057308.1	1	6	6	12	0.87	1.1	7.41	18.41	17.2	57.9	7	7	12072	51429	sorting nexin 9	Receptor signaling complex scaffold activity	-	Adapter molecule	Cell communication;Signal transduction	SH3;PX	Yes
AKR1C3	8644	aldo-keto reductase family 1 member C3 isoform 1	NP_003730.4	6	6	15	53	0.87	1.1	10.75	10.34	34.6	42.9	13	13	4911	8644	aldo-keto reductase family 1, member C3(3-alpha hydroxysteroid dehydrogenase, type II)	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	ALDKR	Yes
NTPCR	84284	cancer-related nucleoside-triphosphatase	NP_115700.1	1	6	6	14	0.87	1.09	5.93	6.15	14.6	19.1	8	8									
CD59	966	CD59 glycoprotein preproprotein	NP_001120695.1	1	6	6	21	0.87	1.08	12.83	5.36	38.3	19.5	11	11	117	966	CD59 antigen p18-20 (antigen identified bymonoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	Receptor activity	Plasma membrane	Cell surface receptor	Immune response	GPI;SP	Yes
CEBPZ	10153	CCAAT/enhancer-binding protein zeta	NP_005751.2	1	5	5	9	0.87	1.07	5.73	6.73	11.2	16.3	5	5	9875	10153	CCAAT/enhancer binding protein zeta	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
CCDC6	8030	coiled-coil domain-containing protein 6	NP_005427.2	1	6	6	13	0.87	1.07	6.46	5.75	16	17.5	8	8	9064	8030	coiled-coil domain containing 6	Structural constituent of cytoskeleton	Cytoplasm	Unclassified;Cell cycle control protein	Apoptosis	CC	Yes
SKIV2L	6499	helicase SKI2W	NP_008860.4	1	12	12	39	0.87	1.06	4.12	4.6	14.9	19.8	17	16	2724	6499	superkiller viralicidic activity 2-like (S.cerevisiae)	RNA binding	Nucleolus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
SLC12A2	6558	solute carrier family 12 member 2 isoform 1	NP_001037.1	2	3	3	6	0.87	1.05	3.16	6.11	4.8	11.1	3	3	6775	6558	solute carrier family 12(sodium/potassium/chloride transporters), member 2	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
MED15	51586	mediator of RNA polymerase II transcription subunit 15 isoform a	NP_001003891.1	5	2	2	2	0.87	1.04					1	1	12117	51586	PC2 (positive cofactor 2, multiprotein complex)glutamine/Q-rich-associated protein	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Biological_process unknown	CC;NLS	Yes
GTF3C2	2976	general transcription factor 3C polypeptide 2	NP_001512.1	1	2	2	2	0.87	1.04	1.3	16.38	1.6	24.5	2	2	5347	2976	general transcription factor IIIC, polypeptide2, beta 110kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
PRPS1	5631	ribose-phosphate pyrophosphokinase 1 isoform 1	NP_002755.1	3	4	11	26	0.87	1.03	7.57	12.52	13.3	26.3	4	4	2413	5631	phosphoribosyl pyrophosphate synthetase 1	Ligase activity	-	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
DCXR	51181	L-xylulose reductase isoform 1	NP_057370.1	2	4	4	6	0.87	1.03	6.18	9	9.3	16.2	3	3	16320	51181	dicarbonyl/L-xylulose reductase	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
FSCN1	6624	fascin	NP_003079.1	1	33	33	179	0.87	1.02	2.23	2.04	18.5	20	89	89	4068	6624	fascin homolog 1, actin-bundling protein(Strongylocentrotus purpuratus)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	-	Yes
LRRC57	255252	leucine-rich repeat-containing protein 57	NP_694992.2	1	3	3	13	0.87	1.02	8.06	13.47	18.7	37.7	7	7	8212	255252	None	Molecular function unknown	-	Unclassified	Biological_process unknown	LRR	No
TIMM22	29928	mitochondrial import inner membrane translocase subunit Tim22	NP_037469.2	1	1	1	2	0.87	1.01					1	1	6262	29928	translocase of inner mitochondrial membrane 22homolog (yeast)	Transporter activity	Mitochondrial membrane	Transport/cargo protein	Transport	TM	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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CASK	8573	peripheral plasma membrane protein CASK isoform 1	NP_003679.2	3	6	6	7	0.87	1.01	7.82	1.15	13.6	2.3	4	4	2164	8573	calcium/calmodulin-dependent serine proteinkinase (MAGUK family)	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;PDZ;SH3;GuKinase;L27	Yes
HERC4	26091	probable E3 ubiquitin-protein ligase HERC4 isoform a	NP_071362.1	4	5	5	7	0.87	1	7.98	7.4	13.9	14.9	4	4	13646	26091	hect domain and RLD 4	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	HECT	Yes
FITM2	128486	fat storage-inducing transmembrane protein 2	NP_001073941.1	1	1	1	1	0.87	1					1	1	19101	128486	chromosome 20 open reading frame 142	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
GGPS1	9453	geranylgeranyl pyrophosphate synthase	NP_001032354.1	1	3	3	7	0.87	0.96	5.91	2.43	10.3	4.7	4	4	6099	9453	geranylgeranyl diphosphate synthase 1	Transferase activity	Cytoplasm	Enzyme: Prenyltransferase	Metabolism;Energy pathways	35EXO	Yes
ESD	2098	S-formylglutathione hydrolase	NP_001975.1	1	12	12	39	0.87	0.96	3.4	4.44	14.3	20.6	23	23	588	2098	esterase D/formylglutathione hydrolase	Hydrolase activity	Cytoplasm	Enzyme: Esterase	Metabolism;Energy pathways	-	Yes
TMEM214	54867	transmembrane protein 214 isoform 1	NP_060197.4	2	3	3	5	0.87	0.96	5.35	13.75	6.6	18.7	2	2	7887	54867	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
THOC5	8563	THO complex subunit 5 homolog	NP_003669.4	1	2	2	3	0.87	0.95	6.04	8	7.5	10.8	2	2	16650	8563	chromosome 22 open reading frame 19	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	NLS;LZ;WW	Yes
PFDN5	5204	prefoldin subunit 5 isoform alpha	NP_002615.2	2	2	2	5	0.87	0.95	0.02	13.04	0	21.7	3	3	5359	5204	prefoldin 5	Chaperone activity	Nucleus	Chaperone	Protein metabolism	CC	No
PCK2	5106	phosphoenolpyruvate carboxykinase [GTP], mitochondrial isoform 1 precursor	NP_004554.3	4	19	19	58	0.87	0.95	6.21	3.52	29.3	18.1	28	29	2026	5106	phosphoenolpyruvate carboxykinase 2(mitochondrial)	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
L2HGDH	79944	L-2-hydroxyglutarate dehydrogenase, mitochondrial precursor	NP_079160.1	1	3	3	6	0.87	0.94	13.6	10.52	20.6	17.3	3	3	12640	79944	L-2-hydroxyglutarate dehydrogenase	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	No
SQRDL	58472	sulfide:quinone oxidoreductase, mitochondrial	NP_067022.1	1	26	26	130	0.87	0.91	4.3	3.14	32.3	24.3	71	71	18102	58472	sulfide quinone reductase-like (yeast)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP	Yes
UBA7	7318	ubiquitin-like modifier-activating enzyme 7	NP_003326.2	1	5	5	10	0.87	0.9	27.05	11.67	56.1	23.8	5	5	1873	7318	ubiquitin-activating enzyme E1-like	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
IMPA1	3612	inositol monophosphatase 1 isoform 2	NP_001138350.1	3	5	5	8	0.87	0.9	11.88	15.13	23.4	31.2	5	5	3641	3612	inositol(myo)-1(or 4)-monophosphatase 1	Phosphoprotein phosphatase activity	Cytoplasm	Enzyme: Phosphatase	Metabolism;Energy pathways	I_Phosphatase	Yes
BCKDHA	593	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial isoform 1 precursor	NP_000700.1	2	1	1	2	0.87	0.89					1	1	2009	593	branched chain keto acid dehydrogenase E1,alpha polypeptide (maple syrup urine disease)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
VAV2	7410	guanine nucleotide exchange factor VAV2 isoform 1	NP_001127870.1	3	8	8	17	0.87	0.87	11.16	8.24	26	19.1	7	7	2694	7410	vav 2 oncogene	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	CH;RHOGEF;PH;C1;SH3;SH2;CC	Yes
ABCB7	22	ATP-binding cassette sub-family B member 7, mitochondrial isoform 1	NP_004290.2	5	4	4	10	0.87	0.85	10.16	8.18	19.9	15.6	5	5	2137	22	ATP-binding cassette, sub-family B (MDR/TAP),member 7	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	SP;TM	Yes
GDI2	2665	rab GDP dissociation inhibitor beta isoform 1	NP_001485.2	3	19	26	130	0.87	0.85	5.45	6.42	32	36.9	43	43	2863	2665	GDP dissociation inhibitor 2	Auxiliary transport protein activity	Cytoplasm	Membrane transport protein	Transport	SP	Yes
BNIP1	662	vesicle transport protein SEC20 isoform BNIP1-b	NP_053582.2	4	2	2	2	0.87	0.84	6.14	12.29	7.6	14.6	2	2	4480	662	BCL2/adenovirus E1B 19kDa interacting protein 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Apoptosis	TM;CC;ANK;BH3	Yes
TROVE2	6738	60 kDa SS-A/Ro ribonucleoprotein isoform 2	NP_004591.2	4	12	12	34	0.87	0.83	7.51	4.57	26.6	15.3	16	16	15964	6738	Sjogren syndrome antigen A2 (60kDa,ribonucleoprotein autoantigen SS-A/Ro)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
NDUFB9	4715	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 isoform 1	NP_004996.1	3	3	3	4	0.87	0.83	9.16	26.99	11.3	32.3	2	2	3264	4715	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 9, 22kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	CC	No
GSK3B	2932	glycogen synthase kinase-3 beta isoform 1	NP_002084.2	2	7	9	26	0.87	0.82	10.31	16.46	24	39.7	7	8	5418	2932	glycogen synthase kinase 3 beta	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Metabolism;Energy pathways	S_T_kinase	Yes
VCL	7414	vinculin isoform meta-VCL	NP_054706.1	2	60	60	252	0.87	0.81	3.8	4.28	39.5	41.6	133	132	1900	7414	vinculin	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
CPNE3	8895	copine-3	NP_003900.1	10	12	13	29	0.87	0.8	6.78	9.01	23.1	28.4	15	15	5016	8895	copine III	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	C2;VWA	Yes
KIAA1522	57648	uncharacterized protein KIAA1522 isoform 1	NP_065939.2	3	8	8	15	0.87	0.79	8.6	14.9	22.7	36.2	9	9	18852	57648	KIAA1522	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
UGP2	7360	UTP--glucose-1-phosphate uridylyltransferase isoform a	NP_006750.3	2	23	23	71	0.87	0.78	5.43	4.19	30.3	20.7	39	39	8934	7360	UDP-glucose pyrophosphorylase 2	Nucleotidyltransferase activity	-	Enzyme: Nucleotidyltransferase	Metabolism;Energy pathways	-	Yes
AMZ2	51321	archaemetzincin-2 isoform 1	NP_001275983.1	1	1	1	1	0.87	0.77					1	1	14237	51321	None	Metallopeptidase activity	-	Metallo protease	Protein metabolism	-	No
GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 1	NP_001511.2	2	4	4	6	0.87	0.77	9.21	14	16.2	21.9	4	4	7540	2975	general transcription factor IIIC, polypeptide1, alpha 220kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MICU2	221154	calcium uptake protein 2, mitochondrial	NP_689939.1	1	1	1	2	0.87	0.77					1	1									
TBCE	6905	tubulin-specific chaperone E isoform b	NP_001274730.1	3	6	6	9	0.87	0.75	5.98	4.23	10.4	6.3	4	4	5381	6905	tubulin-specific chaperone e	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	No
CNN3	1266	calponin-3 isoform 1	NP_001830.1	3	5	6	10	0.87	0.75	5.91	14.87	10.3	22.5	4	4	3848	1266	calponin 3, acidic	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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UIMC1	51720	BRCA1-A complex subunit RAP80	NP_057374.3	1	1	1	2	0.87	0.73					1	1	11482	51720	None	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	UIM;CC;NLS	Yes
RAB38	23682	ras-related protein Rab-38	NP_071732.1	1	3	5	15	0.87	0.7	0.16	13.35	0.2	16.4	3	3	5889	23682	RAB38, member RAS oncogene family	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	RAB	Yes
TBC1D2B	23102	TBC1 domain family member 2B isoform a	NP_653173.1	2	1	1	2	0.87	0.67					1	1	8310	23102	None	Transcription regulator activity	-	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;KRAB;PH;TBC	No
EFHD2	79180	EF-hand domain-containing protein D2	NP_077305.2	4	9	9	13	0.87	0.67	8.9	16.86	23.5	34.7	9	9	13266	79180	EF hand domain family, member D2	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	EF;CC	Yes
ZC3H7A	29066	zinc finger CCCH domain-containing protein 7A	NP_054872.2	1	1	1	2	0.87	0.64					1	1	11694	29066	zinc finger CCCH-type containing 7A	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;ZnF_C3H1;CC	No
PSIP1	11168	PC4 and SFRS1-interacting protein isoform 2	NP_150091.2	2	3	4	6	0.87	0.62	20.17	1.24	31.2	1.3	3	3	4688	11168	PC4 and SFRS1 interacting protein 1	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PWWP;CC;NLS	Yes
DIABLO	56616	diablo homolog, mitochondrial isoform 1 precursor	NP_063940.1	6	7	7	15	0.87	0.59	7.21	19.18	17.9	32.6	8	8	5560	56616	diablo homolog (Drosophila)	Caspase activator activity	Mitochondrion	Cell cycle control protein	Cell communication;Signal transduction;Apoptosis	CC;TM	Yes
C5orf22	55322	UPF0489 protein C5orf22	NP_060826.2	1	3	3	6	0.86	1.98	12.47	22.56	18.8	90.4	3	3	7740	55322	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	NP_078772.1	1	2	2	4	0.86	1.61	39.74	20.79	51.1	50.1	2	2									
ORMDL3	94103	ORM1-like protein 3	NP_644809.1	3	1	1	3	0.86	1.52	7.08	15.8	8.7	35	2	2	17803	94103	ORM1-like 3 (S. cerevisiae)	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Protein metabolism	TM	Yes
FAHD2A	51011	fumarylacetoacetate hydrolase domain-containing protein 2A	NP_057128.2	2	1	1	3	0.86	1.52	11.16	11.01	13.6	24	2	2	13287	51011	fumarylacetoacetate hydrolase domaincontaining 2A	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
URI1	8725	unconventional prefoldin RPB5 interactor 1 isoform a	NP_003787.2	1	2	2	3	0.86	1.51	19.74	21.33	24.5	47.9	2	2									
TPI1	7167	triosephosphate isomerase isoform 2	NP_001152759.1	3	19	19	123	0.86	1.49	3.49	2.93	24.6	36.3	65	65	1833	7167	triosephosphate isomerase 1	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
NDUFA4	4697	cytochrome c oxidase subunit NDUFA4	NP_002480.1	1	2	2	4	0.86	1.47	23.43	26.49	29.2	59.5	2	2	4831	4697	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 4, 9kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
ARPC5L	81873	actin-related protein 2/3 complex subunit 5-like protein	NP_112240.1	1	1	1	2	0.86	1.4					1	1	12490	81873	actin related protein 2/3 complex, subunit5-like	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
MAPKAP1	79109	target of rapamycin complex 2 subunit MAPKAP1 isoform 1	NP_001006618.1	5	2	2	3	0.86	1.38	2.12	19.33	2.6	39.1	2	2	17464	79109	mitogen-activated protein kinase associatedprotein 1	Molecular function unknown;Kinase binding	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
RHEB	6009	GTP-binding protein Rheb	NP_005605.1	1	3	3	7	0.86	1.24	18.12	6.24	36.1	17.4	5	5	3188	6009	Ras homolog enriched in brain	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	Yes
UBE2L3	7332	ubiquitin-conjugating enzyme E2 L3 isoform 4	NP_001243284.1	3	5	5	13	0.86	1.23	6.95	7.46	15.9	24.7	7	7	4762	7332	ubiquitin-conjugating enzyme E2L 3	Ubiquitin-specific protease activity;Ubiquitin binding	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	UBC	Yes
MRPS23	51649	28S ribosomal protein S23, mitochondrial	NP_057154.2	1	4	4	10	0.86	1.19	1.58	5.54	3	14.8	5	5	17592	51649	mitochondrial ribosomal protein S23	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
LRRC1	55227	leucine-rich repeat-containing protein 1	NP_060684.4	1	4	5	11	0.86	1.13	20.93	16.5	31.9	33	3	3	6430	55227	leucine rich repeat containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	LRR	No
NUP205	23165	nuclear pore complex protein Nup205	NP_055950.1	1	19	19	36	0.86	1.11	4.14	4.42	14.8	20.5	17	17	17653	23165	nucleoporin 205kDa	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
ARAF	369	serine/threonine-protein kinase A-Raf isoform 2	NP_001243125.1	4	2	3	5	0.86	1.11	30.22	8.43	38.1	13.3	2	2	2405	369	v-raf murine sarcoma 3611 viral oncogene homolog	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	RBD;C1;S_T_kinase	Yes
ELOVL7	79993	elongation of very long chain fatty acids protein 7 isoform 1	NP_079206.2	1	1	1	2	0.86	1.11	18.91	2.64	23.4	4.1	2	2	18700	79993	ELOVL family member 7, elongation of long chain fatty acids (yeast)	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
MED23	9439	mediator of RNA polymerase II transcription subunit 23 isoform a	NP_004821.2	4	2	2	3	0.86	1.1	2.7	9.18	3.3	14.3	2	2	5436	9439	cofactor required for Sp1 transcriptionalactivation, subunit 3, 130kDa	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ATG3	64422	ubiquitin-like-conjugating enzyme ATG3 isoform 1	NP_071933.2	2	5	5	15	0.86	1.07	4.18	5.17	10.2	15.7	8	8	10654	64422	APG3 autophagy 3-like (S. cerevisiae)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
GOLGA1	2800	Golgin subfamily A member 1	NP_002068.1	1	2	2	2	0.86	1.05					1	1	3934	2800	golgi autoantigen, golgin subfamily a, 1	Structural molecule activity	Golgi apparatus	Structural protein	Cell growth and/or maintenance	CC;SPECTRIN	Yes

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NSUN5	55695	probable 28S rRNA (cytosine-C(5))-methyltransferase isoform 3	NP_001161819.1	4	3	3	3	0.86	1.05	7.48	3.23	11.2	5.9	3	3	11678	55695	NOL1/NOP2/Sun domain family, member 5	Molecular function unknown	-	Cell cycle control protein	Cell growth and/or maintenance	SP	No
SUCLG1	8802	succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial precursor	NP_003840.2	1	5	5	8	0.86	1.04	8.94	17.16	15.4	37	4	4	18128	8802	succinate-CoA ligase, GDP-forming, alphasubunit	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
NRD1	4898	nardilysin isoform a	NP_002516.2	3	10	10	21	0.86	1.04	8.28	9.46	26.1	36.7	13	13	4036	4898	nardilysin (N-arginine dibasic convertase)	Metallopeptidase activity	Plasma membrane	Metallo protease	Protein metabolism	CC	Yes
CRNKL1	51340	crooked neck-like protein 1 isoform a	NP_057736.4	4	4	4	8	0.86	1.02	8.11	3.93	14.1	8.1	4	4	9898	51340	Crn, crooked neck-like 1 (Drosophila)	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;HAT	Yes
MRPL11	65003	39S ribosomal protein L11, mitochondrial isoform a	NP_057134.1	3	8	8	18	0.86	1.01	3.81	10.13	10.4	33.4	10	10	14739	65003	mitochondrial ribosomal protein L11	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
FABP5	2171	fatty acid-binding protein, epidermal	NP_001435.1	1	4	4	8	0.86	1.01	9.59	1.02	16.6	2	4	4	5524	2171	fatty acid binding protein 5(psoriasis-associated)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
ACTR3	10096	actin-related protein 3 isoform 1	NP_005712.1	5	21	21	113	0.86	1	3.92	3.15	26.2	24.4	58	58	5024	10096	ARP3 actin-related protein 3 homolog (yeast)	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	ACTIN	Yes
TMEM167A	153339	protein kish-A precursor	NP_777569.1	1	2	2	3	0.86	0.99					1	1	14490	153339	None	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	SP;TM	No
CARD6	84674	caspase recruitment domain-containing protein 6	NP_115976.2	1	2	2	6	0.86	0.99	8.99	3.6	13.4	6.2	3	3	9871	84674	caspase recruitment domain family, member 6	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	CARD	Yes
SC5D	6309	lathosterol oxidase	NP_008849.2	1	1	1	1	0.86	0.99					1	1									
TOMM20	9804	mitochondrial import receptor subunit TOM20 homolog	NP_055580.1	1	1	1	4	0.86	0.99	14.61	12.27	17.9	17.3	2	2	3507	9804	translocase of outer mitochondrial membrane 20homolog (yeast)	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	TM	No
SENP3	26168	sentrin-specific protease 3	NP_056485.2	1	2	2	2	0.86	0.99					1	1	8339	26168	SUMO1/sentrin/SMT3 specific protease 3	Peptidase activity	Nucleolus	Protease	Protein metabolism	CC	Yes
XYLT2	64132	xylosyltransferase 2	NP_071450.2	1	1	1	3	0.86	0.98	0.19	5.4	0.2	7.5	2	2	16286	64132	xylosyltransferase II	Transferase activity	Extracellular	Enzyme: Transferase	Metabolism;Energy pathways	SP	Yes
FAM129A	116496	protein Niban	NP_443198.1	1	14	14	42	0.86	0.98	7.99	4.53	33.1	21	22	22	10725	116496	chromosome 1 open reading frame 24	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
RPL26L1	51121	60S ribosomal protein L26-like 1	NP_057177.1	2	10	10	23	0.86	0.98	17.52	20.87	58.6	85	13	13	17993	51121	ribosomal protein L26-like 1	Molecular function unknown	Ribosome	Unclassified	Biological_process unknown	KOW	Yes
STRN	6801	striatin	NP_003153.2	1	8	8	16	0.86	0.97	4.54	7.32	11.1	20.2	8	8	18124	6801	striatin, calmodulin binding protein	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	CC;WD40	Yes
SUMO2	6613	small ubiquitin-related modifier 2 isoform a precursor	NP_008868.3	3	1	2	11	0.86	0.97	1.28	3.16	1.6	4.3	2	2	4332	6613	SMT3 suppressor of mif two 3 homolog 2 (yeast)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	UBQ	No
NEDD1	121441	protein NEDD1 isoform a	NP_001128647.1	3	1	1	2	0.86	0.96					1	1	2655	121441	neural precursor cell expressed,developmentally down-regulated 1	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	WD40	No
EHBP1	23301	EH domain-binding protein 1 isoform 1	NP_056067.2	3	8	8	18	0.86	0.96	8.84	2.33	21.7	6.4	8	8	10109	23301	EH domain binding protein 1	Molecular function unknown	-	Unclassified	Biological_process unknown	CH;CC	Yes
NPM3	10360	nucleoplasmin-3	NP_008924.1	1	4	4	13	0.86	0.96	10.43	6.7	22.2	15.8	6	6	7346	10360	nucleophosmin/nucleoplasmin, 3	Chaperone activity	Nucleus	Chaperone	Protein metabolism	-	Yes
CUX1	1523	protein CASP isoform b	NP_001904.2	7	4	4	7	0.86	0.95	4.46	3.62	7.7	6.9	4	4	295	1523	cut-like 1, CCAAT displacement protein(Drosophila)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;HOX;TM	Yes
JUNB	3726	transcription factor jun-B	NP_002220.1	1	6	6	19	0.86	0.95	2.2	8.56	6	26.2	10	10	1303	3726	jun B proto-oncogene	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRLZ;CC	Yes
FNTA	2339	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	NP_002018.1	1	5	5	11	0.86	0.95	7.29	5.86	15.5	13.8	6	6	607	2339	farnesyltransferase, CAAX box, alpha	Transferase activity	Cytoplasm	Enzyme: Transferase	Protein modification	CC	Yes
RP2	6102	protein XRP2	NP_008846.2	1	2	2	5	0.86	0.94	20.55	3.73	31.4	6	3	3	2424	6102	retinitis pigmentosa 2 (X-linked recessive)	Structural molecule activity	Plasma membrane	Structural protein	Cell growth and/or maintenance	CARP	Yes
HK1	3098	hexokinase-1 isoform HKI-ta/tb	NP_277033.1	6	34	37	128	0.86	0.94	3.35	3.37	23.1	25.5	63	63	809	3098	hexokinase 1	Catalytic activity	Cytoplasm	Enzyme: Sugar phosphotransferase	Metabolism;Energy pathways	-	Yes
ADK	132	adenosine kinase isoform b	NP_006712.2	4	13	13	28	0.86	0.93	5.25	10.5	17.6	39.3	15	15	39	132	adenosine kinase	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
RPS5	6193	40S ribosomal protein S5	NP_001000.2	1	10	10	64	0.86	0.9	3.44	4.69	17	24.7	33	33	4695	6193	ribosomal protein S5	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
MRPS2	51116	28S ribosomal protein S2, mitochondrial	NP_057118.1	1	4	4	6	0.86	0.9	13.54	28.68	23.6	55.4	4	4	14783	51116	mitochondrial ribosomal protein S2	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
GCN1L1	10985	translational activator GCN1	NP_006827.1	1	67	67	175	0.86	0.88	2.77	3.29	22.6	27.7	87	87	16127	10985	GCN1 general control of amino-acid synthesis1-like 1 (yeast)	Translation regulator activity	Nucleolus	Translation regulatory protein	Protein metabolism	HR1;CC	Yes

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NDUFAF1	51103	complex I intermediate-associated protein 30, mitochondrial precursor	NP_057097.2	1	1	1	2	0.86	0.88					1	1	9500	51103	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, assembly factor 1	Chaperone activity	Mitochondrion	Chaperone	Biological_process unknown	-	No
GPD2	2820	glycerol-3-phosphate dehydrogenase, mitochondrial precursor	NP_001076581.2	1	22	22	65	0.86	0.87	4.44	3.71	22.9	19.3	35	35	715	2820	glycerol-3-phosphate dehydrogenase 2(mitochondrial)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	EF;TM	Yes
NDUFS1	4719	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 5	NP_001186913.1	5	23	23	81	0.86	0.86	4.06	5.46	23.9	32.4	45	45	1145	4719	NADH dehydrogenase (ubiquinone) Fe-S protein1, 75kDa (NADH-coenzyme Q reductase)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
TCP11L1	55346	T-complex protein 11-like protein 1	NP_001139013.1	1	1	1	1	0.86	0.85					1	1	7750	55346	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
LAMA5	3911	laminin subunit alpha-5 precursor	NP_005551.3	1	8	8	27	0.86	0.85	4.16	5.84	13.5	18.7	14	14	3020	3911	laminin, alpha 5	Cell adhesion molecule activity	Extracellular	Adhesion molecule	Cell growth and/or maintenance	LAMNT;EGFLAM;LAMB;LAMG;SP;CC	Yes
CASP7	840	caspase-7 isoform delta	NP_203124.1	5	2	2	3	0.86	0.83	0.91	23.55	1.1	28.1	2	2	3457	840	caspase 7, apoptosis-related cysteine protease	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Apoptosis	CASc	Yes
UPF2	26019	regulator of nonsense transcripts 2	NP_542166.1	1	6	6	12	0.86	0.83	5.64	14.77	12	30.6	6	6	10405	26019	UPF2 regulator of nonsense transcripts homolog(yeast)	RNA binding;MRNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;RNA metabolism	CC;MIF4G	Yes
STAMBP	10617	STAM-binding protein	NP_006454.1	1	5	5	7	0.86	0.82	17.38	17.04	34.6	31.9	5	5	5877	10617	STAM binding protein	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	JAB;CC	No
PRKCD	5580	protein kinase C delta type	NP_006245.2	1	5	5	9	0.86	0.81	12.74	5.94	25	10.8	5	5	1501	5580	protein kinase C, delta	Protein serine/threonine kinase activity	Cytosol	Serine/threonine kinase	Cell communication;Signal transduction	C2;C1;S_T_kinase	Yes
DTD1	92675	D-tyrosyl-tRNA(Tyr) deacylase 1	NP_543010.3	1	2	2	5	0.86	0.8	13.26	27.8	20	39.9	3	3	13631	92675	histidyl-tRNA synthetase 2	ATPase activity	Nucleus	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
RPL15	6138	60S ribosomal protein L15 isoform 1	NP_002939.2	2	8	8	34	0.86	0.8	6.62	6.84	25.2	24.1	19	19	16043	6138	ribosomal protein L15	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
SFXN1	94081	sideroflexin-1	NP_073591.2	1	13	15	48	0.86	0.79	5.08	9.01	22.7	37.7	26	26	18044	94081	sideroflexin 1	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	TM	Yes
CCDC8	83987	coiled-coil domain-containing protein 8	NP_114429.2	1	3	3	10	0.86	0.79	17.82	13.23	35.4	23.7	5	5	13009	83987	coiled-coil domain containing 8	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ESYT2	57488	extended synaptotagmin-2	NP_065779.1	1	15	15	46	0.86	0.79	5.07	6.8	22.1	27.5	25	25	13053	57488	family with sequence similarity 62 (C2 domaincontaining) member B	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	TM;C2	Yes
TMEM115	11070	transmembrane protein 115	NP_008955.1	1	2	2	5	0.86	0.77	21.46	7.93	32.8	10.6	3	3	6144	11070	None	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM;SP;NLS	Yes
DHRS7B	25979	dehydrogenase/reductase SDR family member 7B	NP_056325.2	1	5	5	12	0.86	0.77	7.51	2.11	15.9	4	6	6	13215	25979	None	Oxidoreductase activity	Cytosol	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP	No
GAA	2548	lysosomal alpha-glucosidase preproprotein	NP_000143.2	1	8	8	17	0.86	0.76	14.08	13.74	37.4	32	9	9	6006	2548	glucosidase, alpha; acid (Pompe disease, glycogenstorage disease type II)	Glucosidase activity	Lysosome	Enzyme: Glucosidase	Metabolism;Energy pathways	Trefoil;SP	Yes
SERPINB1	1992	leukocyte elastase inhibitor	NP_109591.1	3	18	19	64	0.86	0.76	5.45	6.09	27	27.2	32	33	555	1992	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 1	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism	SERPIN	Yes
CASP3	836	caspase-3 preproprotein	NP_004337.2	1	2	2	3	0.86	0.75					1	1	2799	836	caspase 3, apoptosis-related cysteine protease	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Apoptosis	CASc	Yes
SLC9A3R1	9368	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	NP_004243.1	1	4	4	8	0.86	0.74	1.68	2.64	2.9	3.9	4	4	5406	9368	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Receptor binding	Cytoplasm;Membrane fraction	Membrane bound ligand	Cell communication;Signal transduction	PDZ	Yes
PRKCDBP	112464	protein kinase C delta-binding protein	NP_659477.2	1	7	7	19	0.86	0.73	4.99	13.16	13	29.3	9	9	17908	112464	protein kinase C, delta binding protein	Molecular function unknown	Nucleus	Unclassified	Cell communication;Signal transduction	-	No
RPS6KA1	6195	ribosomal protein S6 kinase alpha-1 isoform b	NP_001006666.1	22	14	20	48	0.86	0.72	6.19	12.12	21.6	35.8	16	16	3402	6195	ribosomal protein S6 kinase, 90kDa,polypeptide 1	Protein serine/threonine kinase activity	Cytosol	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
CCBL1	883	kynurenine--oxoglutarate transaminase 1 isoform c	NP_001274319.1	3	1	2	4	0.86	0.72					1	1	2769	883	cysteine conjugate-beta lyase; cytoplasmic(glutamine transaminase K, kyneurenine aminotransferase)	Lyase activity	Cytoplasm	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
ARPC5	10092	actin-related protein 2/3 complex subunit 5 isoform 1	NP_005708.1	2	5	5	19	0.86	0.72	8.65	20.78	25.1	52.9	11	11	11969	10092	actin related protein 2/3 complex, subunit 5,16kDa	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes

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TCOF1	6949	treacle protein isoform d	NP_001128715.1	6	28	28	59	0.86	0.72	3.75	5.23	18.6	22	33	33	6026	6949	Treacher Collins-Franceschetti syndrome 1	Transcription regulator activity	Nucleolus	Transcription regulatory protein	Transcription;Cell migration;Ribosome biogenesis and assembly	LISH;NLS;NES	Yes
FAM83F	113828	protein FAM83F	NP_612444.2	1	2	2	4	0.86	0.7	7.36	35.92	9	36.6	2	2	11228	113828	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
MCM7	4176	DNA replication licensing factor MCM7 isoform 1	NP_005907.3	2	16	16	35	0.86	0.69	7.28	7.24	26.9	21.6	18	18	1154	4176	MCM7 minichromosome maintenance deficient 7 (S.cerevisiae)	Helicase activity	Nucleus	Unclassified;DNA helicase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;DNA replication	MCM	Yes
ITPR1	3708	inositol 1,4,5-trisphosphate receptor type 1 isoform 3	NP_001161744.1	3	1	7	13	0.86	0.68					1	1	925	3708	inositol 1,4,5-triphosphate receptor, type 1	Intracellular ligand-gated ion channel activity	Endoplasmic reticulum	Intracellular ligand gated channel	Cell communication;Signal transduction	MIR;RYDR;CC;TM	Yes
OSTF1	26578	osteoclast-stimulating factor 1	NP_036515.4	1	3	3	10	0.86	0.62	14.47	14.19	28.2	19.8	5	5	17808	26578	osteoclast stimulating factor 1	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	SH3;ANK	Yes
LIMS1	3987	LIM and senescent cell antigen-like-containing domain protein 1 isoform e	NP_001180413.1	5	4	4	8	0.86	0.6	2.24	34.33	4.3	48.5	5	5	3978	3987	LIM and senescent cell antigen-like domains 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	LIM	Yes
PPAP2C	8612	lipid phosphate phosphohydrolase 2 isoform 3	NP_808211.1	3	1	1	2	0.86	0.58					1	1	6180	8612	phosphatidic acid phosphatase type 2C	Hydrolase activity;Lipid phosphatase activity	Integral to membrane	Lipid phosphatase;Enzyme: Hydrolase	Cell communication;Signal transduction;Lipid metabolism	TM;AcidPPc;SP	No
COL5A2	1290	collagen alpha-2(V) chain preproprotein	NP_000384.2	1	1	1	5	0.86	0.53	5.35	12.84	6.5	9.7	2	2	366	1290	collagen, type V, alpha 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	VWC;COLL;COLFI;SP	Yes
PPIF	10105	peptidyl-prolyl cis-trans isomerase F, mitochondrial precursor	NP_005720.1	8	3	4	8	0.86	0.51					1	1	6839	10105	peptidylprolyl isomerase F (cyclophilin F)	Isomerase activity	Mitochondrion	Enzyme: Isomerase	Protein metabolism	-	Yes
ASPSCR1	79058	tether containing UBX domain for GLUT4 isoform 2	NP_001238817.1	2	1	1	2	0.86						1		6947	79058	alveolar soft part sarcoma chromosome region,candidate 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	CC;UBX	Yes
RNF217	154214	probable E3 ubiquitin-protein ligase RNF217 isoform a	NP_001273327.1	1	1	1	1	0.85	1.93					1	1	17125	154214	IBR domain containing 1	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	IBR;TM	Yes
IMPDH1	3614	inosine-5'-monophosphate dehydrogenase 1 isoform a	NP_000874.2	8	4	5	12	0.85	1.63	5.54	11.74	9.5	39.6	4	4	8853	3614	IMP (inosine monophosphate) dehydrogenase 1	Catalytic activity	Cytosol	Enzyme: Dehydrogenase	Metabolism;Energy pathways	CBS	Yes
SDE2	163859	protein SDE2 homolog	NP_689821.3	1	2	2	2	0.85	1.58					1	1									
C19orf66	55337	UPF0515 protein C19orf66 isoform 1	NP_060851.2	2	2	2	3	0.85	1.51					1	1	7747	55337	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
SLC30A7	148867	zinc transporter 7	NP_598003.2	1	1	1	1	0.85	1.42					1	1	15369	148867	solute carrier family 30 (zinc transporter),member 7	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Transport	TM	Yes
SSR1	6745	translocon-associated protein subunit alpha isoform 1 precursor	NP_003135.2	2	4	4	33	0.85	1.33	19.43	12.18	58.9	57.8	11	11	2924	6745	signal sequence receptor, alpha(translocon-associated protein alpha)	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	SP;TM	Yes
GNB1	2782	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 isoform 1	NP_002065.1	4	6	11	53	0.85	1.32	8.31	6.28	25	29.4	12	12	766	2782	guanine nucleotide binding protein (G protein),beta polypeptide 1	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	CC;WD40	Yes
VBP1	7411	prefoldin subunit 3 isoform 2	NP_001290472.1	4	5	5	15	0.85	1.31	11.33	6.1	24.1	19.8	6	6	2135	7411	von Hippel-Lindau binding protein 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	CC	Yes
MRPL55	128308	39S ribosomal protein L55, mitochondrial isoform b	NP_852127.2	2	2	2	3	0.85	1.3	9.81	23.05	11.8	44.3	2	2	14773	128308	mitochondrial ribosomal protein L55	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	CC	No
SCYL3	57147	protein-associating with the carboxyl-terminal domain of ezrin isoform 2	NP_851607.2	2	2	2	3	0.85	1.23					1	1	7459	57147	SCY1-like 3 (S. cerevisiae)	Molecular function unknown	Golgi apparatus	Unclassified	Biological_process unknown	S_T_Y_Kinase;HEAT	No
FAM188A	80013	protein FAM188A	NP_079224.1	1	2	2	3	0.85	1.2					1	1	10702	80013	chromosome 10 open reading frame 97	Molecular function unknown	Nucleus	Cell cycle control protein	Apoptosis	CARD;EF	No
COPS6	10980	COP9 signalosome complex subunit 6	NP_006824.2	1	6	6	16	0.85	1.17	10.48	9.37	27.2	33.9	9	9	16735	10980	COP9 constitutive photomorphogenic homologsubunit 6 (Arabidopsis)	Protein binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	JAB	No
METTL13	51603	methyltransferase-like protein 13 isoform 1	NP_057019.3	3	3	3	4	0.85	1.13	0.34	10.42	0.5	20.5	3	3	13821	51603	KIAA0859	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ASNA1	439	ATPase ASNA1	NP_004308.2	1	8	8	23	0.85	1.13	11.06	8.97	33.6	36.2	12	12	3555	439	arsA arsenite transporter, ATP-binding, homolog1 (bacterial)	ATPase activity	Cytoplasm	ATPase	Metabolism;Energy pathways	-	Yes
MRPL3	11222	39S ribosomal protein L3, mitochondrial	NP_009139.1	1	2	2	4	0.85	1.11	5.18	7.08	6.3	11.1	2	2	6175	11222	mitochondrial ribosomal protein L3	Structural constituent of ribosome	Nucleolus	Ribosomal subunit	Protein metabolism	-	Yes
MAT2B	27430	methionine adenosyltransferase 2 subunit beta isoform 1	NP_037415.1	2	9	9	20	0.85	1.11	7.17	8.22	21.2	32.4	12	12	5701	27430	methionine adenosyltransferase II, beta	Catalytic activity	Cytoplasm	Enzyme: Adenosyltransferase	Metabolism	-	No
NUMB	8650	protein numb homolog isoform 1	NP_001005743.1	4	2	4	6	0.85	1.08	0.28	5.41	0.3	8.2	2	2	4767	8650	numb homolog (Drosophila)	Molecular function unknown	Plasma membrane;Nucleus;Cytoplasm	Unclassified	Development	PTB	Yes
WDR60	55112	WD repeat-containing protein 60	NP_060521.4	1	1	1	1	0.85	1.07					1	1	8545	55112	WD repeat domain 60	Molecular function unknown	-	Unclassified	Biological_process unknown	CC;WD40	No

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DENND4C	55667	DENN domain-containing protein 4C	NP_060395.5	1	2	2	3	0.85	1.06	37.56	8	47.7	12	2	2	12927	55667	chromosome 9 open reading frame 55	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
SCLY	51540	selenocysteine lyase	NP_057594.4	1	1	1	2	0.85	1.05					1	1	15303	51540	selenocysteine lyase	Lyase activity	Cytoplasm	Enzyme: Lyase	Metabolism;Energy pathways	-	No
CDK6	1021	cyclin-dependent kinase 6	NP_001250.1	46	7	8	26	0.85	1.02	3.83	17.37	8	45.6	6	6	4533	1021	cyclin-dependent kinase 6	Protein binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	S_T_kinase	Yes
NCDN	23154	neurochondrin isoform 1	NP_055099.1	2	7	7	10	0.85	1.02	5.85	7.01	12.2	17.7	6	6	10530	23154	neurochondrin	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	RGD	Yes
PKMYT1	9088	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase isoform 1	NP_004194.3	3	1	1	2	0.85	1.01					1	1	3920	9088	protein kinase, membrane associatedtyrosine/threonine 1	Protein threonine/tyrosine kinase activity	Endoplasmic reticulum	Dual specificity kinase	Negative regulation of enzyme activity	S_T_Y_Kinase	Yes
HSD17B10	3028	3-hydroxyacyl-CoA dehydrogenase type-2 isoform 1	NP_004484.1	2	9	9	34	0.85	1.01	2.88	7.93	10.2	33.8	17	17	2223	3028	hydroxyacyl-Coenzyme A dehydrogenase, type II	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	KRINGLE	Yes
NDUFA12	55967	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 isoform a	NP_061326.1	1	2	2	5	0.85	1	2.3	0.7	3.4	1.2	3	3	16781	55967	None	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
AP3S1	1176	AP-3 complex subunit sigma-1	NP_001275.1	1	3	3	9	0.85	0.99	10.62	3.79	20.4	8.4	5	5	3298	1176	adaptor-related protein complex 3, sigma 1subunit	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
MALSU1	115416	mitochondrial assembly of ribosomal large subunit protein 1	NP_612455.1	1	2	2	2	0.85	0.99	21.13	13.42	25.8	18.9	2	2									
MRPS22	56945	28S ribosomal protein S22, mitochondrial	NP_064576.1	1	7	7	12	0.85	0.98	14.67	2.43	34	6.3	7	7	10430	56945	mitochondrial ribosomal protein S22	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	SP	No
TOLLIP	54472	toll-interacting protein	NP_061882.2	1	3	3	5	0.85	0.98	22.32	14.6	27.5	20.4	2	2	5887	54472	toll interacting protein	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	C2;CUE	Yes
SLC25A19	60386	mitochondrial thiamine pyrophosphate carrier	NP_068380.3	1	2	2	4	0.85	0.97	17.83	10.84	21.6	14.9	2	2	8405	60386	solute carrier family 25 (mitochondrialdeoxynucleotide carrier), member 19	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	TM	Yes
PRDX6	9588	peroxiredoxin-6	NP_004896.1	1	20	20	116	0.85	0.96	6.13	7.88	42.3	63.2	60	59	3817	9588	peroxiredoxin 6	Peroxidase activity	Lysosome	Enzyme: Peroxidase	Metabolism;Energy pathways	-	Yes
BSG	682	basigin isoform 1 precursor	NP_001719.2	4	7	7	30	0.85	0.95	7.91	4.37	28.3	17.2	17	17	176	682	basigin (OK blood group)	Receptor activity	Plasma membrane;Nucleus;Cytoplasm	Cell surface receptor	Cell communication;Signal transduction	IG;TM;SP	Yes
PRDX2	7001	peroxiredoxin-2	NP_005800.3	1	8	9	35	0.85	0.93	6.22	9.68	21.5	37	16	16	2763	7001	peroxiredoxin 2	Peroxidase activity	Cytoplasm	Enzyme: Peroxidase	Metabolism;Energy pathways	-	Yes
UFM1	51569	ubiquitin-fold modifier 1 isoform 1 precursor	NP_057701.1	2	1	1	8	0.85	0.92	2.31	3.18	3.9	5.8	4	4	15644	51569	ubiquitin-fold modifier 1	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
TVP23C	201158	Golgi apparatus membrane protein TVP23 homolog C isoform 1	NP_660344.2	4	1	1	2	0.85	0.91					1	1									
NDUFS2	4720	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial isoform 1 precursor	NP_004541.1	2	10	10	28	0.85	0.9	12.55	6.75	41.5	23	14	14	4285	4720	NADH dehydrogenase (ubiquinone) Fe-S protein2, 49kDa (NADH-coenzyme Q reductase)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP	Yes
CISD3	284106	CDGSH iron-sulfur domain-containing protein 3, mitochondrial precursor	NP_001129970.1	1	1	1	1	0.85	0.89					1	1	19534	284106	CDGSH iron sulfur domain 3	Metal ion binding	-	Unclassified	Biological_process unknown	-	No
TUBGCP2	10844	gamma-tubulin complex component 2 isoform 1	NP_001243546.1	3	7	7	13	0.85	0.89	7.2	13.19	16.3	31.9	7	7	18245	10844	tubulin, gamma complex associated protein 2	Cytoskeletal protein binding	Centrosome	Cytoskeletal associated protein	Cell growth and/or maintenance	SP	Yes
NDUFV2	4729	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor	NP_066552.2	1	4	4	14	0.85	0.89	20.9	13.98	49.6	33.8	7	7	2757	4729	NADH dehydrogenase (ubiquinone) flavoprotein2, 24kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
REEP3	221035	receptor expression-enhancing protein 3	NP_001001330.1	1	2	2	3	0.85	0.88	19.2	5.57	23.5	6.9	2	2	16582	221035	chromosome 10 open reading frame 74	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PLXNB2	23654	plexin-B2 precursor	NP_036533.2	1	18	18	33	0.85	0.87	3.28	4.86	11.6	17.5	17	17	5050	23654	plexin B2	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	-	Yes
NPTN	27020	neuroplastin isoform b precursor	NP_036560.1	4	7	7	14	0.85	0.86	5.9	10.42	14.3	25.7	8	8	18033	27020	stromal cell derived factor receptor 1	Antigen binding	Plasma membrane	Immunoglobulin	Immune response	SP;IGC2;Ig_LIKE;TM	No
EXOC2	55770	exocyst complex component 2	NP_060773.3	1	7	7	13	0.85	0.86	11.09	3.97	27.1	9.7	8	8	11544	55770	SEC5-like 1 (S. cerevisiae)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	IPT	Yes
MINK1	50488	misshapen-like kinase 1 isoform 3	NP_722549.2	8	7	11	21	0.85	0.86	5.33	4.84	12.9	11.8	8	8	11366	50488	misshapen-like kinase 1 (zebrafish)	Protein serine/threonine kinase activity	Golgi apparatus;Nucleus;Cytoplasm	Serine/threonine kinase	Signal transduction	S_T_kinase;CNH;CC	Yes
AARS2	57505	alanine--tRNA ligase, mitochondrial	NP_065796.1	1	10	10	23	0.85	0.85	7.4	7.47	20.2	21.4	10	11	12397	57505	alanyl-tRNA synthetase like	Molecular function unknown	Mitochondrion	Unclassified;Enzyme: Synthase	Metabolism;Energy pathways;Biological_process unknown	-	Yes
UTRN	7402	utrophin	NP_009055.2	1	6	6	11	0.85	0.85	4.71	17.57	9	34.6	5	5	547	7402	utrophin (homologous to dystrophin)	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein	Cell growth and/or maintenance	CH;CC;WW;ZnF_ZZ;SPECTRIN	Yes
CPS1	1373	carbamoyl-phosphate synthase [ammonia], mitochondrial isoform a precursor	NP_001116105.1	3	7	7	18	0.85	0.85	2.88	13.64	5.5	26.4	5	5	1995	1373	carbamoyl-phosphate synthetase 1, mitochondrial	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
EFTUD1	79631	elongation factor Tu GTP-binding domain-containing protein 1 isoform 1	NP_078856.4	2	9	9	40	0.85	0.85	7.6	8.57	26.2	27.9	16	14	7812	79631	elongation factor Tu GTP binding domaincontaining 1	Translation regulator activity	-	Translation regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	GTP_EFTU;GTP_EFTU_D2	No
CCND2	894	G1/S-specific cyclin-D2	NP_001750.1	1	3	3	6	0.85	0.85	9.23	13.63	15.9	23.6	4	4	451	894	cyclin D2	Kinase binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	CYCLIN_N;CYCLIN_C	No
MACF1	23499	microtubule-actin cross-linking factor 1	NP_036222.3	1	52	54	94	0.85	0.85	3.55	4.01	21.7	24.4	50	50	9750	23499	microtubule-actin crosslinking factor 1	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein	Cell communication;Signal transduction	PLEC;CC;SPECTRIN;EF;CH	Yes
MGAT1	4245	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	NP_002397.2	1	4	4	7	0.85	0.84	20.88	16.58	31.7	24.5	3	3	1189	4245	mannosyl (alpha-1,3-)-glycoproteinbeta-1,2-N-acetylglucosaminyltransferase	Transferase activity	Golgi apparatus	Enzyme: Glucosaminyltransferase	Metabolism;Energy pathways	SP;TM	Yes
ZW10	9183	centromere/kinetochore protein zw10 homolog	NP_004715.1	1	9	9	23	0.85	0.83	6.14	3.77	17.5	10.5	11	11	4902	9183	ZW10 homolog, centromere/kinetochore protein(Drosophila)	DNA binding	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	CC	Yes
RPS6KA4	8986	ribosomal protein S6 kinase alpha-4 isoform a	NP_003933.1	3	4	4	8	0.85	0.81	9.11	17.14	15.7	28.4	4	4	4677	8986	ribosomal protein S6 kinase, 90kDa,polypeptide 4	Protein serine/threonine kinase activity;Transcription regulator activity	Nucleus	Translation regulatory protein;Serine/threonine kinase	Cell communication;Signal transduction;Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_kinase	Yes
SPECC1	92521	cytospin-B isoform 1	NP_001028725.1	5	2	2	3	0.85	0.81					1	1									
NDUFS3	4722	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	NP_004542.1	1	11	11	31	0.85	0.8	3.74	5.27	13.2	17.6	17	17	10355	4722	NADH dehydrogenase (ubiquinone) Fe-S protein3, 30kDa (NADH-coenzyme Q reductase)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
FRYL	285527	protein furry homolog-like	NP_055845.1	1	9	9	20	0.85	0.79	4.14	4.43	11.2	11	10	10	18995	285527	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ZFP36L2	678	zinc finger protein 36, C3H1 type-like 2	NP_008818.3	1	3	3	5	0.85	0.78	26.47	7.49	40.4	10.2	3	3	18319	678	zinc finger protein 36, C3H type-like 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1	Yes
HLA-E	3133	HLA class I histocompatibility antigen, alpha chain E precursor	NP_005507.3	1	1	2	13	0.85	0.78	10.29	21.85	12.4	24.6	2	2	877	3133	major histocompatibility complex, class I, E	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein	Immune response	SP;IGC;TM	Yes
IRF9	10379	interferon regulatory factor 9	NP_006075.3	1	2	2	2	0.85	0.77					1	1	960	10379	interferon-stimulated transcription factor 3,gamma 48kDa	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	IRF	Yes
HADHB	3032	trifunctional enzyme subunit beta, mitochondrial isoform 1 precursor	NP_000174.1	3	18	18	79	0.85	0.77	9.37	5.32	55.1	27	42	42	887	3032	hydroxyacyl-Coenzyme Adehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase(trifunctional protein), beta subunit	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
PON2	5445	serum paraoxonase/arylesterase 2 isoform 1	NP_000296.2	2	3	3	9	0.85	0.77	5.86	7.25	10	11.2	4	4	3903	5445	paraoxonase 2	Hydrolase activity;Antioxidant activity	Plasma membrane	Enzyme: Esterase	Metabolism;Energy pathways;Lipid metabolism	SP	Yes
STIM1	6786	stromal interaction molecule 1 isoform 2 precursor	NP_003147.2	3	7	7	13	0.85	0.77	6.11	15.2	13.8	31.8	7	7	5803	6786	stromal interaction molecule 1	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SAM;TM;SP;CC	Yes
SLK	9748	STE20-like serine/threonine-protein kinase isoform 1	NP_055535.2	2	20	21	45	0.85	0.76	3.15	4.99	13.2	18.8	24	24	11585	9748	STE20-like kinase (yeast)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
MKL2	57496	MKL/myocardin-like protein 2 isoform 1	NP_001295071.1	2	2	3	4	0.85	0.76					1	1	17577	57496	MKL/myocardin-like 2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAP;CC	Yes
TNS1	7145	tensin-1 isoform 1	NP_072174.3	3	1	1	3	0.85	0.75	32.87	19.77	41.2	21.2	2	2	2512	7145	tensin 1	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	DSPC;SH2;PTB	Yes
KDSR	2531	3-ketodihydrosphingosine reductase precursor	NP_002026.1	1	5	5	8	0.85	0.75	7.63	18.32	16	34.9	6	6	640	2531	follicular lymphoma variant translocation 1	Oxidoreductase activity	Extracellular	Secreted polypeptide	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP	Yes
WDR35	57539	WD repeat-containing protein 35 isoform 1	NP_001006658.1	2	1	1	2	0.85	0.75					1	1	15667	57539	WD repeat domain 35	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
GGCX	2677	vitamin K-dependent gamma-carboxylase isoform 1	NP_000812.2	2	3	3	4	0.85	0.74					1	1	665	2677	gamma-glutamyl carboxylase	Ligase activity	Endoplasmic reticulum	Enzyme: Carboxylase	Metabolism;Energy pathways	TM	Yes

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MYO9B	4650	unconventional myosin-IXb isoform 1	NP_004136.2	2	5	5	10	0.85	0.74	4.26	8.49	8.1	14.1	5	5	3677	4650	myosin IXB	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	RA;IQ;C1;RHOGAP;CC	Yes
LRRC16A	55604	leucine-rich repeat-containing protein 16A isoform 1	NP_060110.4	2	3	3	5	0.85	0.73	18.54	9.06	22.6	9.4	2	2	11285	55604	leucine rich repeat containing 16	Molecular function unknown	-	Unclassified	Biological_process unknown	LRR	No
ALDH3A2	224	fatty aldehyde dehydrogenase isoform 1	NP_001026976.1	6	14	15	42	0.85	0.73	9.22	6.03	35.1	19.3	19	19	7188	224	aldehyde dehydrogenase 3 family, member A2	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism	TM	Yes
FOXK2	3607	forkhead box protein K2	NP_004505.2	1	1	1	2	0.85	0.72					1	1	982	3607	forkhead box K2	Transcription factor activity;DNA binding	Nucleus	Transcription factor;DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	FHA;FH;NLS	Yes
AFAP1	60312	actin filament-associated protein 1 isoform A	NP_001128119.1	2	1	1	2	0.85	0.71					1	1	9747	60312	None	Receptor signaling complex scaffold activity;Cytoskeletal anchoring activity	Cytoplasm	Adapter molecule	Cell growth and/or maintenance	PH;CC	No
ERLEC1	27248	endoplasmic reticulum lectin 1 isoform 1 precursor	NP_056516.2	3	2	2	4	0.85	0.67	43.1	38.82	55.5	38.3	2	2	10310	27248	chromosome 2 open reading frame 30	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
PLEKHF1	79156	pleckstrin homology domain-containing family F member 1	NP_077286.3	1	1	2	5	0.85	0.66					1	1	15146	79156	pleckstrin homology domain containing, familyF (with FYVE domain) member 1	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;PH;FYVE	No
ERGIC1	57222	endoplasmic reticulum-Golgi intermediate compartment protein 1	NP_001026881.1	1	6	6	18	0.85	0.66	10.15	17.51	23	31.5	7	7	13836	57222	None	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	TM	No
CD63	967	CD63 antigen isoform A	NP_001771.1	3	1	1	2	0.85	0.58					1	1	1121	967	CD63 antigen (melanoma 1 antigen)	Molecular function unknown	Lysosome	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
NME1-NME2	654364	NME1-NME2 protein	NP_001018146.1	5	14	14	63	0.84	1.49	7.65	6.06	41.3	61.3	38	39									
SMYD2	56950	N-lysine methyltransferase SMYD2	NP_064582.2	1	1	1	2	0.84	1.34					1	1	15406	56950	SET and MYND domain containing 2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	SET	Yes
ARF1	375	ADP-ribosylation factor 1	NP_001649.1	2	6	10	81	0.84	1.3	10.55	19.32	40	151.2	19	19	54	375	ADP-ribosylation factor 1	GTPase activity	Golgi apparatus	GTPase	Signal transduction;Endosome transport	ARF	No
Sep-06	23157	septin-6 isoform B	NP_055944.2	4	1	3	40	0.84	1.26					1	1									
CSTB	1476	cystatin-B	NP_000091.1	1	2	2	3	0.84	1.26	16.9	39.74	20.4	80.9	2	2	3091	1476	cystatin B (stefin B)	Protease inhibitor activity	Nucleus	Protease inhibitor	Protein metabolism	CYSTATIN	Yes
HNRNPH3	3189	heterogeneous nuclear ribonucleoprotein H3 isoform a	NP_036339.1	2	9	9	28	0.84	1.25	5.88	3.66	18.6	17.3	14	14	3818	3189	heterogeneous nuclear ribonucleoprotein H3(2H9)	Ribonucleoprotein	Nucleus	Ribonucleoprotein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
ENY2	56943	transcription and mRNA export factor ENY2 isoform 1	NP_064574.1	2	1	1	2	0.84	1.25					1	1	13121	56943	enhancer of yellow 2 homolog (Drosophila)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
FAS	355	tumor necrosis factor receptor superfamily member 6 isoform 1 precursor	NP_000034.1	2	4	4	6	0.84	1.23	10.26	10.62	17.4	26.6	4	4	609	355	Fas (TNF receptor superfamily, member 6)	Receptor activity;Binding	Plasma membrane	Cell surface receptor;Unclassified	Cell communication;Signal transduction;Anti-apoptosis	TM;TNFR;DEATH;SP	No
ADSL	158	adenylosuccinate lyase isoform a	NP_000017.1	2	7	7	16	0.84	1.15	16.05	4.91	39.5	16.1	8	8	49	158	adenylosuccinate lyase	Lyase activity	Cytoplasm	Enzyme: Lyase	Metabolism;Energy pathways	CC	Yes
SLC30A6	55676	zinc transporter 6 isoform 1	NP_001180442.1	4	1	1	2	0.84	1.14					1	1	15368	55676	solute carrier family 30 (zinc transporter),member 6	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	TM	No
MRPL45	84311	39S ribosomal protein L45, mitochondrial isoform 1	NP_115727.5	1	1	1	3	0.84	1.12	3.67	11.66	5.3	22.9	3	3	14764	84311	mitochondrial ribosomal protein L45	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
DGKZ	8525	diacylglycerol kinase zeta isoform 4	NP_001099010.1	7	3	3	4	0.84	1.12	24.38	3.5	29.6	5.5	2	2	3260	8525	diacylglycerol kinase, zeta 104kDa	Catalytic activity	Nucleus	Enzyme: Phosphotransferase	Cell communication;Signal transduction;Vesicle-mediated transport	C1;DAGKC;ANK;DAGKa;ANX	Yes
MOB2	81532	MOB kinase activator 2 isoform 1	NP_001165694.1	2	1	1	2	0.84	1.11					1	1									
TBC1D15	64786	TBC1 domain family member 15 isoform 2	NP_001139686.1	3	4	4	6	0.84	1.11	18.38	10.18	22	16	2	2	15470	64786	TBC1 domain family, member 15	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	TBC	No
CAB39	51719	calcium-binding protein 39	NP_057373.1	2	12	12	32	0.84	1.11	13.91	14.08	47.4	66.5	15	15	10091	51719	calcium binding protein 39	Calcium ion binding	-	Calcium binding protein	Biological_process unknown	-	Yes
SCPEP1	59342	retinoid-inducible serine carboxypeptidase precursor	NP_067639.1	1	4	4	12	0.84	1.1	4.46	13.35	9.1	37.2	6	6	10194	59342	serine carboxypeptidase 1	Carboxypeptidase activity	Cytoplasm	Carboxypeptidase	Protein metabolism	SP	No
PRPSAP1	5635	phosphoribosyl pyrophosphate synthase-associated protein 1	NP_002757.2	1	7	10	31	0.84	1.07	12.03	9.83	34.5	36.1	11	11	3151	5635	phosphoribosyl pyrophosphatesynthetase-associated protein 1	Enzyme regulator activity	Cytoplasm	Regulatory/other subunit	Metabolism;Energy pathways	-	Yes
APOBEC3F	200316	DNA dC->dU-editing enzyme APOBEC-3F isoform a	NP_660341.2	3	1	3	6	0.84	1.07					1	1	16415	200316	apolipoprotein B mRNA editing enzyme,catalytic polypeptide-like 3F	RNA binding	-	RNA binding protein	RNA metabolism	-	Yes
ZYX	7791	zyxin	NP_003452.1	1	14	14	42	0.84	1.04	6.45	6.41	26.3	32.9	23	23	3592	7791	zyxin	Cell adhesion molecule activity	Plasma membrane;Cytoplasm	Adhesion molecule	Signal transduction	LIM	Yes

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ATP5C1	509	ATP synthase subunit gamma, mitochondrial isoform L (liver) precursor	NP_001001973.1	2	10	10	37	0.84	1.04	4.22	7.33	16.3	36.1	21	21	156	509	ATP synthase, H+ transporting, mitochondrialF1 complex, gamma polypeptide 1	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	-	Yes
AMIGO2	347902	amphoterin-induced protein 2 precursor	NP_862830.1	1	1	1	5	0.84	1.03	37.7	10.42	46.9	15.3	2	2	16483	347902	None	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	SP;LRR;IG;TM	No
GALK2	2585	N-acetylgalactosamine kinase isoform 1	NP_002035.1	3	4	4	9	0.84	1.03	3.86	6.82	8	17.3	6	6	657	2585	galactokinase 2	Galactosyltransferase activity	Cytoplasm	Enzyme: Sugar phosphotransferase	Metabolism;Energy pathways	-	Yes
SHMT1	6470	serine hydroxymethyltransferase, cytosolic isoform 1	NP_004160.3	3	1	2	21	0.84	1.03					1	1	1643	6470	serine hydroxymethyltransferase 1 (soluble)	Methyltransferase activity;RNA binding	Cytoplasm	Enzyme: Methyltransferase; RNA binding protein	Metabolism;Energy pathways	-	Yes
VWA8	23078	von Willebrand factor A domain-containing protein 8 isoform a precursor	NP_055873.1	2	14	14	28	0.84	1	6.06	4.86	19.9	18.9	15	15									
NCS1	23413	neuronal calcium sensor 1 isoform 1	NP_055101.2	2	1	1	2	0.84	1					1	1	4500	23413	frequenin homolog (Drosophila)	Calcium ion binding	Golgi apparatus	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
PPP2R5D	5528	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform isoform 1	NP_006236.1	4	7	10	19	0.84	1	19.67	13.43	52.5	42.2	9	9	9039	5528	protein phosphatase 2, regulatory subunit B(B56), delta isoform	Protein serine/threonine phosphatase activity	Nucleus;Cytoplasm	Serine/threonine phosphatase	Cell communication;Signal transduction	-	Yes
GNS	2799	N-acetylglucosamine-6-sulfatase precursor	NP_002067.1	1	3	3	8	0.84	0.99	12.67	3.73	24.2	8.3	5	5	9637	2799	glucosamine (N-acetyl)-6-sulfatase (Sanfilippodisease IIID)	Catalytic activity	Lysosome	Enzyme: Sulphatase	Metabolism;Energy pathways	TM;SULF	No
RANBP6	26953	ran-binding protein 6 isoform 1	NP_036548.1	2	3	5	24	0.84	0.97					1	1	17953	26953	RAN binding protein 6	Transporter activity	-	Transport/cargo protein	Transport	CC;HEAT	Yes
ACAT2	39	acetyl-CoA acetyltransferase, cytosolic isoform 1	NP_005882.2	2	15	15	75	0.84	0.97	4.12	6.13	21.8	39.1	39	40	6	39	acetyl-Coenzyme A acetyltransferase 2(acetoacetyl Coenzyme A thiolase)	Acyltransferase activity	Cytoplasm	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
CAPN2	824	calpain-2 catalytic subunit isoform 1	NP_001739.2	2	30	30	145	0.84	0.96	3.22	2.43	23.1	19.7	71	71	254	824	calpain 2, (m/II) large subunit [Homosapiens]Other Aliases: HGNC:1479, CANPL2, CANPml, mCANPOther Designations:Calpain 2, large	Cysteine-type peptidase activity	Cytoplasm	Cysteine protease	Protein metabolism	CYSPC;CALPAIN_III;EF	Yes
FARS2	10667	phenylalanine--tRNA ligase, mitochondrial precursor	NP_006558.1	1	2	2	3	0.84	0.96	0.95	0.83	1.1	1.1	2	2	9946	10667	phenylalanine-tRNA synthetase 2 (mitochondrial)	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
GNPDA2	132789	glucosamine-6-phosphate isomerase 2 isoform 1	NP_612208.1	3	4	7	16	0.84	0.94	8.89	37.1	13	66.6	3	3	13594	132789	glucosamine-6-phosphate deaminase 2	Deaminase activity	-	Enzyme: Deaminase	Metabolism;Energy pathways	CC	No
OXR1	55074	oxidation resistance protein 1 isoform 3	NP_001185461.1	6	2	2	2	0.84	0.93					1	1	16126	55074	oxidation resistance 1	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	Yes
CAP1	10487	adenylyl cyclase-associated protein 1	NP_001099000.1	2	27	27	209	0.84	0.91	4.17	4	37.5	38.3	106	104	9869	10487	CAP, adenylate cyclase-associated protein 1(yeast)	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	CARP	Yes
PRKAG1	5571	5'-AMP-activated protein kinase subunit gamma-1 isoform 3	NP_001193638.1	7	6	6	15	0.84	0.91	17.62	6.96	46.7	19.2	9	9	4118	5571	protein kinase, AMP-activated, gamma 1non-catalytic subunit	Molecular function unknown	-	Regulatory/other subunit	Signal transduction	CBS	Yes
LPP	4026	lipoma-preferred partner isoform a	NP_005569.1	2	4	4	11	0.84	0.91	21.45	8.18	37.5	14.9	4	4	2828	4026	LIM domain containing preferred translocationpartner in lipoma	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	CC;LIM;NLS	Yes
PHGDH	26227	D-3-phosphoglycerate dehydrogenase	NP_006614.2	1	17	17	62	0.84	0.9	4.83	3.61	22.5	17.9	30	30	6047	26227	phosphoglycerate dehydrogenase	Catalytic activity	Extracellular	Enzyme: Dehydrogenase	Metabolism;Energy pathways	2HD	Yes
PHLDB1	23187	pleckstrin homology-like domain family B member 1 isoform a	NP_001138230.1	2	12	12	20	0.84	0.89	4.96	9.64	14.5	30.3	12	12	15128	23187	pleckstrin homology-like domain, family B,member 1	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	FHA;CC;PH	No
NIF3L1	60491	NIF3-like protein 1 isoform 1	NP_001129511.1	3	7	7	13	0.84	0.89	14.7	15.55	33.4	37.7	7	7	10424	60491	NIF3 NGG1 interacting factor 3-like 1 (S.pombe)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PGLS	25796	6-phosphogluconolactonase	NP_036220.1	1	7	7	25	0.84	0.89	9.77	9.97	26.3	31.3	10	12	12001	25796	6-phosphogluconolactonase	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
NRM	11270	nurim isoform 2	NP_001257636.1	4	2	2	3	0.84	0.86	23.35	3.5	28.1	4.3	2	2	10120	11270	nurim (nuclear envelope membrane protein)	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	TM	No
STX12	23673	syntaxin-12	NP_803173.1	1	8	8	22	0.84	0.85	13.83	9.57	40.1	27.4	11	11	6059	23673	syntaxin 12	Auxiliary transport protein activity	Endosome	Membrane transport protein	Transport	SynN;TM;CC;t_SNARE	Yes
EZR	7430	ezrin	NP_003370.2	1	28	39	164	0.84	0.85	4.53	7.29	25.9	43.3	45	45	475	7430	villin 2 (ezrin)	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein	Cell growth and/or maintenance	B41;ERM;CC	Yes
TOM1L2	146691	TOM1-like protein 2 isoform 3	NP_001076437.1	4	1	1	2	0.84	0.84					1	1	18213	146691	target of myb1-like 2 (chicken)	Transporter activity	-	Transport/cargo protein	Transport	VHS;CC	No
NDEL1	81565	nuclear distribution protein nudE-like 1 isoform B	NP_110435.1	3	2	2	4	0.84	0.84	5.18	0.12	6.1	0.1	2	2	6340	81565	nudE nuclear distribution gene E homolog like 1(A. nidulans)	Molecular function unknown	Centrosome	Cell cycle control protein	Cell growth and/or maintenance	CC	Yes
WDR41	55255	WD repeat-containing protein 41	NP_060738.2	1	1	1	8	0.84	0.83					1	1	7714	55255	WD repeat domain 41	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes

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CAMK2G	818	calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 1	NP_751911.1	16	2	4	7	0.84	0.81	0.21	13.68	0.3	15.7	2	2	3672	818	calcium/calmodulin-dependent protein kinase(CaM kinase) II gamma	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
FAM114A2	10827	protein FAM114A2	NP_061161.2	1	8	8	25	0.84	0.8	5.55	23.62	14	62	9	9	12831	10827	chromosome 5 open reading frame 3	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
ATPIF1	93974	ATPase inhibitor, mitochondrial isoform 1 precursor	NP_057395.1	3	1	1	1	0.84	0.79					1	1	16529	93974	ATPase inhibitory factor 1	Enzyme inhibitor activity	Mitochondrion	Enzyme regulator	Energy pathways	-	No
SMAD4	4089	mothers against decapentaplegic homolog 4	NP_005350.1	1	2	2	2	0.84	0.79					1	1	2995	4089	SMAD, mothers against DPP homolog 4(Drosophila)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SAD;CC	No
CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 1	NP_001284636.1	3	8	8	14	0.84	0.76	9.54	22.49	21.4	47.8	7	7									
CYFIP1	23191	cytoplasmic FMR1-interacting protein 1 isoform a	NP_055423.1	2	19	19	48	0.84	0.76	5.48	7.07	23.7	27.8	26	26	5890	23191	cytoplasmic FMR1 interacting protein 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
RIPK1	8737	receptor-interacting serine/threonine-protein kinase 1	NP_003795.2	1	3	3	5	0.84	0.75	1.19	44.76	1.7	63.7	3	3	4583	8737	receptor (TNFRSF)-interacting serine-threoninekinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication	S_T_kinase;DEATH;CC	Yes
CDH1	999	cadherin-1 preproprotein	NP_004351.1	1	9	12	29	0.84	0.73	6.52	7.05	22.8	21.4	17	17	1885	999	cadherin 1, type 1, E-cadherin (epithelial)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	TM;Cadherin;SP	Yes
RPL22L1	200916	60S ribosomal protein L22-like 1	NP_001093115.1	1	1	1	2	0.84	0.72					1	1	19507	200916	ribosomal protein L22-like 1	Structural constituent of ribosome	-	Unclassified	Translation	-	Yes
ARL8B	55207	ADP-ribosylation factor-like protein 8B	NP_060654.1	2	2	5	19	0.84	0.69	16.9	33.07	28.9	47.7	4	4	12483	55207	ADP-ribosylation factor-like 10C	GTPase activity	Cytoskeleton	GTPase	Cell communication;Signal transduction	-	No
TPT1	7178	translationally-controlled tumor protein isoform 1	NP_001273201.1	4	9	9	68	0.84	0.69	12.76	29.51	63	144.4	29	27	15979	7178	tumor protein, translationally-controlled 1	Calcium ion binding	Nucleus	Calcium binding protein	Cell growth and/or maintenance	-	Yes
RAB31	11031	ras-related protein Rab-31	NP_006859.2	1	2	4	9	0.84	0.67	17.72	2.64	21.2	2.5	2	2	5751	11031	RAB31, member RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAB	Yes
RRAGB	10325	ras-related GTP-binding protein B long isoform	NP_057740.2	3	3	3	3	0.84	0.62	15.93	42.92	19.1	38.8	2	2	6710	10325	Ras-related GTP binding B	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	-	No
ANO10	55129	anoctamin-10 isoform 1	NP_060545.3	5	4	4	6	0.84	0.55	4.78	23	6.9	22	3	3	7667	55129	None	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
POTEI	653269	POTE ankyrin domain family member I	NP_001264335.1	1	2	12	272	0.84	0.52	4.44	11.7	21	34.8	31	31									
WDR13	64743	WD repeat-containing protein 13 isoform 1	NP_060353.2	2	1	1	1	0.83	1.49					1	1	6753	64743	WD repeat domain 13	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
RXRB	6257	retinoic acid receptor RXR-beta isoform 1	NP_001257330.1	8	3	3	3	0.83	1.46	47.27	43.57	59.7	111.9	2	2	1578	6257	retinoid X receptor, beta	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor	Cell communication;Signal transduction	ZnF_C4;HOLI	Yes
SSU72	29101	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	NP_054907.1	1	3	3	4	0.83	1.43	0.62	11.63	0.9	29.3	3	3	13712	29101	Ssu72 RNA polymerase II CTD phosphatase homolog(yeast)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RPS15A	6210	40S ribosomal protein S15a	NP_001010.2	1	10	10	43	0.83	1.41	9.61	13.86	37.9	110.7	21	21	4723	6210	ribosomal protein S15a	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
CRYZ	1429	quinone oxidoreductase isoform a	NP_001880.2	3	12	12	43	0.83	1.31	5.1	7.6	21.5	52.9	25	25	437	1429	crystallin, zeta (quinone reductase)	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
TMCO1	54499	transmembrane and coiled-coil domain-containing protein 1 isoform a	NP_061899.2	3	3	3	15	0.83	1.3	11.2	6.04	25.1	20.9	7	7	14243	54499	transmembrane and coiled-coil domains 4	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Biological_process unknown	CC;TM	Yes
GAPDH	2597	glyceraldehyde-3-phosphate dehydrogenase isoform 1	NP_002037.2	3	26	26	525	0.83	1.28	2.8	3.07	38.7	70.2	259	258	713	2597	glyceraldehyde-3-phosphate dehydrogenase	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
ENO1	2023	alpha-enolase isoform 1	NP_001419.1	2	28	31	407	0.83	1.28	3.04	2.6	34.6	46.3	177	177	1400	2023	enolase 1, (alpha)	Catalytic activity	Cytoplasm	Enzyme: Hydratase	Metabolism;Energy pathways	-	Yes
ASCL1	429	achaete-scute homolog 1	NP_004307.2	1	1	1	1	0.83	1.27					1	1	11	429	achaete-scute complex-like 1 (Drosophila)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HLH	No
MTRR	4552	methionine synthase reductase isoform 2	NP_076915.2	2	2	2	4	0.83	1.2	25.02	28.96	30.1	52.3	2	2	3979	4552	5-methyltetrahydrofolate-homocysteinemethyltransferase reductase [Homo sapiens]Other Aliases: HGNC:7473, MSROtherDesignations:	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
ATG12	9140	ubiquitin-like protein ATG12 isoform 1	NP_004698.3	1	1	1	1	0.83	1.18					1	1	8496	9140	APG12 autophagy 12-like (S. cerevisiae)	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes

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NCEH1	57552	neutral cholesterol ester hydrolase 1 isoform a	NP_001139748.1	3	6	6	34	0.83	1.14	5.45	5.2	17	22.5	14	14	7489	57552	arylacetamide deacetylase-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
FSCN2	25794	fascin-2 isoform 2	NP_001070650.1	2	1	1	2	0.83	1.14	13.01	5.86	15.3	9.5	2	2	6366	25794	fascin homolog 2, actin-bundling protein,retinal (Strongylocentrotus purpuratus)	Structural molecule activity	Cytoplasm;Plasma membrane	Structural protein	Cell growth and/or maintenance	-	Yes
VPS26B	112936	vacuolar protein sorting-associated protein 26B	NP_443107.1	1	4	4	7	0.83	1.1	9	26.25	15	63	4	4	14395	112936	None	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	-	No
PPIG	9360	peptidyl-prolyl cis-trans isomerase G	NP_004783.2	1	4	4	6	0.83	1.07	14.93	23.4	17.7	36.6	2	2	12083	9360	peptidyl-prolyl isomerase G (cyclophilin G)	Isomerase activity	Nucleus	Enzyme: Isomerase	Metabolism;Energy pathways	-	Yes
THNSL1	79896	threonine synthase-like 1	NP_079114.3	1	1	1	1	0.83	1.06					1	1	7974	79896	threonine synthase-like 1 (bacterial)	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
NUP160	23279	nuclear pore complex protein Nup160	NP_056046.1	1	11	11	24	0.83	1.05	9.11	5.62	29	22.3	14	14	16254	23279	nucleoporin 160kDa	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
ORC5	5001	origin recognition complex subunit 5 isoform 1	NP_002544.1	2	3	3	5	0.83	1.04	9.61	1.5	13.8	2.7	3	3									
OAS2	4939	2'-5'-oligoadenylate synthase 2 isoform 2	NP_002526.2	4	16	16	33	0.83	1.03	3.35	5.36	11.8	23.6	18	18	4518	4939	2`-5`-oligoadenylate synthetase 2, 69/71kDa	Ligase activity	Cytoplasm	Enzyme: Ligase	Immune response	-	Yes
UFC1	51506	ubiquitin-fold modifier-conjugating enzyme 1	NP_057490.2	1	2	2	3	0.83	1.01	3.16	7.24	3.7	10.4	2	2	15643	51506	ubiquitin-fold modifier conjugating enzyme 1	Molecular function unknown	-	Unclassified	Protein metabolism	-	Yes
MRPS24	64951	28S ribosomal protein S24, mitochondrial precursor	NP_114403.1	1	1	1	1	0.83	1					1	1	17593	64951	mitochondrial ribosomal protein S24	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
UNG	7374	uracil-DNA glycosylase isoform UNG2	NP_550433.1	2	1	1	1	0.83	0.98					1	1	1881	7374	uracil-DNA glycosylase	DNA binding;DNA repair protein	Nucleus;Cytoplasm	DNA binding protein;DNA repair protein	DNA repair	-	Yes
LSM1	27257	U6 snRNA-associated Sm-like protein LSm1	NP_055277.1	1	2	2	4	0.83	0.98					1	1	6281	27257	LSM1 homolog, U6 small nuclear RNA associated(S. cerevisiae)	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SM;CC	Yes
COG6	57511	conserved oligomeric Golgi complex subunit 6 isoform 1	NP_065802.1	2	5	5	8	0.83	0.96	2.39	6.59	4.4	14.3	5	5	8445	57511	component of oligomeric golgi complex 6	Structural molecule activity	Golgi apparatus	Structural protein	Transport	CC	Yes
RPL18A	6142	60S ribosomal protein L18a	NP_000971.1	1	12	12	46	0.83	0.95	9.74	7	38.5	31.2	21	21	16045	6142	ribosomal protein L18a	RNA binding	Cytoplasm	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
UCKL1	54963	uridine-cytidine kinase-like 1 isoform 1	NP_060329.2	1	1	1	2	0.83	0.95					1	1	15607	54963	uridine-cytidine kinase 1-like 1	Transferase activity	Cytoplasm	Enzyme: Transferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
AGL	178	glycogen debranching enzyme isoform 1	NP_000019.2	3	7	7	10	0.83	0.93	3.19	8.09	6.5	18.6	6	6	1984	178	amylo-1, 6-glucosidase,4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storagedisease type III)	Glucosidase activity	Cytoplasm	Enzyme: Glucosidase	Carbohydrate metabolism;Energy pathways	-	Yes
VTA1	51534	vacuolar protein sorting-associated protein VTA1 homolog isoform a	NP_057569.2	3	4	4	13	0.83	0.93	17.15	12.37	35.9	28.8	6	6	9855	51534	chromosome 6 open reading frame 55	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
PCDHB16	57717	protocadherin beta-16 precursor	NP_066008.2	1	1	1	2	0.83	0.92					1	1	6961	57717	protocadherin beta 16	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;Cadherin;TM	Yes
LRCH1	23143	leucine-rich repeat and calponin homology domain-containing protein 1 isoform 1	NP_001157683.1	5	2	2	7	0.83	0.92	9.19	1.97	15.3	3.6	4	4	14307	23143	leucine-rich repeats and calponin homology (CH)domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	LRR;CH	Yes
ARFGEF1	10565	brefeldin A-inhibited guanine nucleotide-exchange protein 1	NP_006412.2	1	4	7	10	0.83	0.92	7.41	3.73	12.3	6.9	4	4	9163	10565	ADP-ribosylation factor guaninenucleotide-exchange factor 1(brefeldin A-inhibited)	Guanyl-nucleotide exchange factor activity	Golgi apparatus	Guanine nucleotide exchange factor	Cell communication;Signal transduction	Sec7	Yes
RB1	5925	retinoblastoma-associated protein	NP_000312.2	1	1	1	2	0.83	0.91					1	1	1574	5925	retinoblastoma 1 (including osteosarcoma)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CYCLIN_N	Yes
EXOC3	11336	exocyst complex component 3	NP_009208.2	1	4	4	7	0.83	0.9	1.31	5.25	2.2	9.4	4	4	9738	11336	SEC6-like 1 (S. cerevisiae)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	-	Yes
FKBP8	23770	peptidyl-prolyl cis-trans isomerase FKBP8 isoform 1	NP_036313.3	2	7	7	20	0.83	0.89	10.01	7.58	26.9	21.5	10	10	5327	23770	FK506 binding protein 8, 38kDa	Receptor signaling complex scaffold activity;Protease inhibitor activity	Mitochondrion	Adapter molecule	Apoptosis	TPR;LZ;TM	Yes
GCC2	9648	GRIP and coiled-coil domain-containing protein 2	NP_852118.1	5	2	3	6	0.83	0.88	24.86	30.95	29.8	40	2	2	11001	9648	GRIP and coiled-coil domain containing 2	Structural molecule activity	Golgi apparatus	Structural protein	Cell growth and/or maintenance	CC;GRIP	Yes

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MDN1	23195	midasin	NP_055426.1	1	2	2	3	0.83	0.88					1	1	10069	23195	MDN1, midasin homolog (yeast)	Chaperone activity	Nucleus	Chaperone	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA;VWA;CC	Yes
STAT6	6778	signal transducer and activator of transcription 6 isoform 1	NP_003144.3	2	7	7	7	0.83	0.88	13.41	13.01	25.4	25.9	5	5	3302	6778	signal transducer and activator oftranscription 6, interleukin-4 induced	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SH2	Yes
GLUD1	2746	glutamate dehydrogenase 1, mitochondrial precursor	NP_005262.1	2	26	26	94	0.83	0.87	4.23	4.24	26.1	27.8	54	54	11748	2746	glutamate dehydrogenase 1	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
CAND1	55832	cullin-associated NEDD8-dissociated protein 1	NP_060918.2	1	41	43	140	0.83	0.86	3.01	3.41	20.5	24.1	65	65	6983	55832	cullin-associated and neddylation-dissociated 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ARHGAP5	394	rho GTPase-activating protein 5 isoform a	NP_001025226.1	2	7	7	11	0.83	0.86	2.6	18.09	5.3	39.7	6	6	4060	394	Rho GTPase activating protein 5	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	RHOGAP;FF;Small_GTPase	Yes
ERLIN2	11160	erlin-2 isoform 1	NP_009106.1	2	9	12	44	0.83	0.86	9.59	18.14	32.6	66.6	16	15	15437	11160	SPFH domain family, member 2	Molecular function unknown	-	Unclassified	Biological_process unknown	PHB;TM	Yes
TPM2	7169	tropomyosin beta chain isoform Tpm2.1sm/cy	NP_998839.1	4	13	23	51	0.83	0.86	8.01	5.65	25.4	18.4	14	14	11768	7169	tropomyosin 2 (beta)	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	-	Yes
ALCAM	214	CD166 antigen isoform 1 precursor	NP_001618.2	4	16	16	56	0.83	0.85	5.88	3.94	24.2	16.6	24	24	3389	214	activated leukocyte cell adhesion molecule	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Immune response	SP;Ig_LIKE;IG;TM	Yes
SLC29A1	2030	equilibrative nucleoside transporter 1 isoform 5	NP_001291391.1	5	1	1	2	0.83	0.85					1	1	3724	2030	solute carrier family 29 (nucleosidetransporters), member 1	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
PLXNA1	5361	plexin-A1 precursor	NP_115618.3	1	2	2	4	0.83	0.84	4.81	30.33	5.6	37.2	2	2	11868	5361	plexin A1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SEMA;PSI;IPT	No
RABGGTA	5875	geranylgeranyl transferase type-2 subunit alpha	NP_878256.1	1	11	11	32	0.83	0.84	5.82	5.53	19.5	18.7	16	16	3547	5875	Rab geranylgeranyltransferase, alpha subunit	Transferase activity	Cytoplasm	Enzyme: Prenyltransferase	Protein modification	LRR	Yes
NDUFB11	54539	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial isoform 1	NP_061929.2	2	2	2	6	0.83	0.83	3.95	21.02	5.7	31	3	3	2323	54539	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 11, 17.3kDa	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM;PEST	Yes
LAGE3	8270	EKC/KEOPS complex subunit LAGE3	NP_006005.2	1	2	2	3	0.83	0.82					1	1	2087	8270	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
MYO6	4646	unconventional myosin-VI isoform 2	NP_001287828.1	2	23	23	52	0.83	0.81	4.68	5.47	22.1	25.3	32	32	2985	4646	myosin VI	Motor activity	Golgi apparatus	Motor protein	Cell growth and/or maintenance	MYOSIN;IQ;CC	Yes
DGKH	160851	diacylglycerol kinase eta isoform 2	NP_821077.1	5	2	2	3	0.83	0.81	4.56	10.42	5.3	11.9	2	2	7237	160851	diacylglycerol kinase, eta	Lipid kinase activity	Cytoplasm	Lipid Kinase	Signal transduction	PH;C1;DAGKC;SAM;DAGKa	Yes
WDR66	144406	WD repeat-containing protein 66 isoform 1	NP_653269.3	2	2	2	4	0.83	0.79	40.47	13.68	50.3	15.4	2	2	14570	144406	WD repeat domain 66	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	No
STK3	6788	serine/threonine-protein kinase 3 isoform 2	NP_001243241.1	3	5	7	15	0.83	0.76	10.29	8.8	21.2	16.6	6	6	5433	6788	serine/threonine kinase 3 (STE20 homolog, yeast)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	Yes
AASS	10157	alpha-aminoadipic semialdehyde synthase, mitochondrial	NP_005754.2	1	7	7	13	0.83	0.75	4.91	13.87	10	25.8	6	6	5489	10157	aminoadipate-semialdehyde synthase	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase;Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
SEC14L2	23541	SEC14-like protein 2 isoform 1	NP_036561.1	7	13	13	39	0.83	0.74	8.44	11.16	31.1	37.3	19	19	6344	23541	SEC14-like 2 (S. cerevisiae)	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SEC14	Yes
MAPKAPK2	9261	MAP kinase-activated protein kinase 2 isoform 2	NP_116584.2	4	1	2	3	0.83	0.73					1	1	11882	9261	mitogen-activated protein kinase-activatedprotein kinase 2	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NLS;CC;NES	Yes
NAA25	80018	N-alpha-acetyltransferase 25, NatB auxiliary subunit	NP_079229.2	1	3	3	5	0.83	0.71	15.97	2.25	23.3	2.8	3	3	8578	80018	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
H1FX	8971	histone H1x	NP_006017.1	1	6	6	22	0.83	0.68	11.87	9.1	30.2	18.8	9	9	4151	8971	H1 histone family, member X	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H15	Yes
VAMP4	8674	vesicle-associated membrane protein 4 isoform 1	NP_003753.2	2	1	1	1	0.83	0.65					1	1	6070	8674	vesicle-associated membrane protein 4	Auxiliary transport protein activity	Golgi apparatus	Membrane transport protein	Protein transport	CC;TM	Yes
CCNA2	890	cyclin-A2	NP_001228.1	1	1	1	1	0.83	0.56					1	1	453	890	cyclin A2	Kinase binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CYCLIN_N;CYCLIN_C	Yes
GGA2	23062	ADP-ribosylation factor-binding protein GGA2	NP_055859.1	4	1	2	3	0.83	0.55					1	1	9347	23062	golgi associated, gamma adaptin ear containing,ARF binding protein 2	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	SP;VHS;CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
RSRC2	65117	arginine/serine-rich coiled-coil protein 2	NP_075388.2	1	2	2	3	0.82	1.97	42.5	24.85	52.6	78.6	2	2	13342	65117	None	Molecular function unknown;Transcription factor activity	Nucleus	Unclassified	Biological_process unknown;Cell proliferation	CC	No
MARS2	92935	methionine--tRNA ligase, mitochondrial precursor	NP_612404.1	1	1	1	2	0.82	1.86					1	1	14363	92935	methionine-tRNA synthetase 2 (mitochondrial)	Ligase activity	-	Enzyme: Synthase	Metabolism;Energy pathways	SP	No
SORBS3	10174	vinexin isoform 1	NP_005766.3	2	1	1	1	0.82	1.6					1	1	11535	10174	None	Cell adhesion molecule activity	Cytoplasm	Adhesion molecule	Cell growth and/or maintenance;Cytoskeleton organization and biogenesis	SH3;SORB	Yes
BCAS2	10286	pre-mRNA-splicing factor SPF27	NP_005863.1	1	1	1	1	0.82	1.54					1	1	5777	10286	breast carcinoma amplified sequence 2	Pre-mRNA splicing factor activity	Nucleus	Cell cycle control protein	Cell communication;Signal transduction;Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
HERC2	8924	E3 ubiquitin-protein ligase HERC2	NP_004658.3	2	1	2	3	0.82	1.38					1	1	6905	8924	hect domain and RLD 2	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	CC;ZnF_ZZ;HECT	No
ASUN	55726	protein asunder homolog	NP_060634.2	1	1	1	1	0.82	1.37					1	1									
MBLAC2	153364	metallo-beta-lactamase domain-containing protein 2	NP_981951.1	1	2	2	7	0.82	1.11	5.33	18.9	7.6	37.6	3	3	14099	153364	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
TDRKH	11022	tudor and KH domain-containing protein isoform a	NP_006853.2	2	2	2	5	0.82	1.03	0.63	0.62	0.7	0.9	2	2	15485	11022	tudor and KH domain containing	RNA binding	-	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	TM;KH;TUDOR	Yes
EXOSC6	118460	exosome complex component MTR3	NP_478126.1	1	4	4	9	0.82	1.02	6.07	8.14	10	16.8	4	4	12107	118460	exosome component 6	Ribonuclease activity	Nucleus	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
CTSB	1508	cathepsin B preproprotein	NP_001899.1	1	7	7	24	0.82	1	7.26	11.66	21.8	43.8	13	13	287	1508	cathepsin B	Cysteine-type peptidase activity	Lysosome	Cysteine protease	Protein metabolism;Apoptosis	PPTC1;SP	Yes
TRIM22	10346	E3 ubiquitin-protein ligase TRIM22 isoform 1	NP_006065.2	2	4	4	8	0.82	1	23.2	3.43	39.7	6.9	4	4	5951	10346	tripartite motif-containing 22	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;BBOX;PRY;CC;SPRY	Yes
COG2	22796	conserved oligomeric Golgi complex subunit 2 isoform 1	NP_031383.1	2	5	5	13	0.82	0.99	8.16	13.47	15.1	33.7	5	6	7372	22796	component of oligomeric golgi complex 2	Structural molecule activity	Golgi apparatus	Structural protein	Transport	CC	Yes
RAB18	22931	ras-related protein Rab-18 isoform 1	NP_067075.1	5	7	7	24	0.82	0.98	4.61	6.59	13.2	22.6	12	12	3731	22931	RAB18, member RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAB	Yes
C19orf70	125988	protein QIL1 isoform 1	NP_001295169.1	2	2	2	6	0.82	0.98	38.65	10.72	58.9	18.3	3	3	15198	125988	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NSDHL	50814	sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NP_001123237.1	1	10	10	22	0.82	0.98	8.97	4.03	25.9	13.8	12	12	2229	50814	NAD(P) dependent steroid dehydrogenase-like	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM	Yes
RAB4A	5867	ras-related protein Rab-4A isoform 1	NP_004569.2	11	3	5	41	0.82	0.97	10.93	2.13	15.7	3.6	3	3	1541	5867	RAB4A, member RAS oncogene family	GTPase activity	Endosome	GTPase	Cell communication;Signal transduction	RAB	Yes
BAG3	9531	BAG family molecular chaperone regulator 3	NP_004272.2	1	3	3	5	0.82	0.96	2.78	10.53	3.2	14.4	2	2	4860	9531	BCL2-associated athanogene 3	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Apoptosis	WW;BAG;CC	Yes
AKR1C1	1645	aldo-keto reductase family 1 member C1	NP_001344.2	4	1	15	58	0.82	0.94					1	1	7194	1645	aldo-keto reductase family 1, member C1(dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	ALDKR	Yes
CYB5R3	1727	NADH-cytochrome b5 reductase 3 isoform 3	NP_001165131.1	3	10	10	51	0.82	0.92	8.39	8.3	36.9	41.4	27	27	8942	1727	diaphorase (NADH) (cytochrome b-5 reductase)	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	-	Yes
NEK9	91754	serine/threonine-protein kinase Nek9	NP_149107.4	1	8	8	20	0.82	0.92	5.94	6.7	16.2	20.7	11	11	11386	91754	NIMA (never in mitosis gene a)-related kinase 9	Kinase activity	Cytoplasm	Serine/threonine kinase;Cell cycle control protein	Cell growth and/or maintenance	NLS;CC	Yes
LPCAT4	254531	lysophospholipid acyltransferase LPCAT4	NP_705841.2	1	4	4	13	0.82	0.92	10.88	15.24	20.1	32.1	5	5	8315	254531	None	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM;PISC	No
TMEM109	79073	transmembrane protein 109 precursor	NP_076997.1	1	3	3	7	0.82	0.92	16.14	3.52	27	6.5	4	4	14687	79073	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP;TM;CC	No
CLEC14A	161198	C-type lectin domain family 14 member A precursor	NP_778230.1	1	1	1	1	0.82	0.89					1	1	10711	161198	C-type lectin domain family 14, member A	Molecular function unknown	-	Unclassified	Biological_process unknown	LECTIN_C;SP;TM	Yes
OSBPL3	26031	oxysterol-binding protein-related protein 3 isoform a	NP_056365.1	4	13	14	25	0.82	0.89	10.81	10.2	34.3	34.9	14	14	9474	26031	oxysterol binding protein-like 3	Steroid binding	Endoplasmic reticulum membrane	Unclassified	Steroid metabolism	PH;CC	Yes
PGRMC2	10424	membrane-associated progesterone receptor component 2	NP_006311.2	1	3	3	9	0.82	0.89	26.06	13.33	38.2	20.7	3	3	9665	10424	progesterone receptor membrane component 2	Steroid hormone receptor activity	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	TM	No

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CSPG4	1464	chondroitin sulfate proteoglycan 4 precursor	NP_001888.2	1	3	3	4	0.82	0.88	1.39	24.99	1.6	31.8	2	2	3105	1464	chondroitin sulfate proteoglycan 4(melanoma-associated)	Protein binding	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	SP;TM;LAMG	No
ACO2	50	aconitate hydratase, mitochondrial precursor	NP_001089.1	1	26	26	129	0.82	0.88	4.15	5.15	27.4	37.2	62	63	12	50	aconitase 2, mitochondrial	Catalytic activity	Mitochondrion	Enzyme: Hydratase	Metabolism;Energy pathways	-	Yes
LRBA	987	lipopolysaccharide-responsive and beige-like anchor protein isoform 1	NP_001186211.2	4	17	21	45	0.82	0.86	3.5	4.55	12.9	17.5	20	20	7344	987	LPS-responsive vesicle trafficking, beach andanchor containing	Cytoskeletal anchoring activity	Golgi apparatus	Anchor protein	Cell communication;Signal transduction	WD40	Yes
ARPC4	10093	actin-related protein 2/3 complex subunit 4 isoform c	NP_001185709.1	4	7	7	24	0.82	0.85	5.81	7.23	18.6	24.2	15	15	10368	10093	actin related protein 2/3 complex, subunit 4,20kDa	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
CAPZB	832	F-actin-capping protein subunit beta isoform 4	NP_001269091.1	4	12	12	47	0.82	0.84	3.52	2.93	14.1	12.1	24	24	11872	832	capping protein (actin filament) muscle Z-line,beta	Structural constituent of cytoskeleton	Cytoskeleton	Cytoskeletal protein	Cell growth and/or maintenance	-	Yes
RAB35	11021	ras-related protein Rab-35 isoform 1	NP_006852.1	13	5	7	88	0.82	0.84	3.97	7.43	8.7	16.5	7	7	5010	11021	RAB35, member RAS oncogene family	GTPase activity	-	GTPase	Cell communication;Signal transduction	RAB	Yes
NME3	4832	nucleoside diphosphate kinase 3 precursor	NP_002504.2	1	1	1	2	0.82	0.83					1	1	3488	4832	non-metastatic cells 3, protein expressed in	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	SP;NDK	Yes
ATP1A1	476	sodium/potassium-transporting ATPase subunit alpha-1 isoform a	NP_000692.2	11	43	43	209	0.82	0.83	3.65	4.79	32.3	43.2	111	108	1662	476	ATPase, Na+/K+ transporting, alpha 1polypeptide	ATPase activity	Plasma membrane	ATPase	Transport	TM	Yes
SLC16A3	9123	monocarboxylate transporter 4	NP_004198.1	1	5	5	16	0.82	0.82	5.05	2.78	12.5	6.8	9	9	4854	9123	solute carrier family 16 (monocarboxylic acidtransporters), member 3	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	Yes
APOBEC3C	27350	DNA dC->dU-editing enzyme APOBEC-3C	NP_055323.2	2	2	3	6	0.82	0.82	1.71	20.23	2	23.9	2	2	9671	27350	apolipoprotein B mRNA editing enzyme,catalytic polypeptide-like 3C	Deaminase activity	-	Enzyme: Deaminase	Metabolism;Energy pathways	-	No
MSN	4478	moesin	NP_002435.1	1	37	48	319	0.82	0.81	4.72	10.4	44	110.1	118	113	2399	4478	moesin	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	B41;ERM;CC	Yes
DHRS4	10901	dehydrogenase/reductase SDR family member 4 isoform 1	NP_066284.2	3	2	2	4	0.82	0.81	4.98	32.02	5.8	38.1	2	2	7484	10901	dehydrogenase/reductase (SDR family) member 4	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
H6PD	9563	GDH/6PGL endoplasmic bifunctional protein isoform 1 precursor	NP_001269516.1	2	6	6	8	0.82	0.8	17	12.6	35.1	25.1	6	6	681	9563	hexose-6-phosphate dehydrogenase (glucose1-dehydrogenase)	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
ACAD11	84129	acyl-CoA dehydrogenase family member 11	NP_115545.3	1	2	2	2	0.82	0.79	3.19	6.17	3.7	6.9	2	2	13352	84129	None	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
MTIF2	4528	translation initiation factor IF-2, mitochondrial precursor	NP_002444.2	1	5	5	10	0.82	0.79	8.95	17.77	18	35.5	6	6	4792	4528	mitochondrial translational initiation factor 2	Translation regulator activity	Mitochondrion	Translation regulatory protein	Protein metabolism	GTP_EFTU;GTP_EFTU_D2;CC	Yes
PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	NP_060895.1	2	14	15	21	0.82	0.79	6.28	3.11	19.5	9.2	14	14	11431	55361	None	Lipid kinase activity	Golgi apparatus	Lipid Kinase	Cell communication;Signal transduction	PI3KC	Yes
ATP5I	521	ATP synthase subunit e, mitochondrial	NP_009031.1	1	2	2	7	0.82	0.77	3.66	37.46	6	63.2	4	4	3308	521	ATP synthase, H+ transporting, mitochondrial F0complex, subunit e	Transporter activity	Mitochondrion	Transport/cargo protein	Metabolism;Energy pathways	CC	Yes
SYPL1	6856	synaptophysin-like protein 1 isoform a	NP_006745.1	2	3	3	8	0.82	0.73	7.58	7.21	15.3	12.9	6	6	15459	6856	synaptophysin-like 1	Transporter activity	Cytoplasmic vesicle	Integral membrane protein	Transport	TM	No
TSC1	7248	hamartin isoform 1	NP_000359.1	3	1	1	2	0.82	0.73					1	1	5594	7248	tuberous sclerosis 1	Protein binding	Cytoplasm	Cytoskeletal associated protein	Regulation of cell growth	CC	Yes
HP1BP3	50809	heterochromatin protein 1-binding protein 3	NP_057371.2	1	15	15	35	0.82	0.73	4.95	8.22	19.2	28.8	22	22	11026	50809	heterochromatin protein 1, binding protein 3	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H15	Yes
MCM3	4172	DNA replication licensing factor MCM3 isoform 1	NP_002379.3	2	22	22	56	0.82	0.73	5.01	5.31	22.5	21.1	29	29	4072	4172	MCM3 minichromosome maintenance deficient 3 (S.cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA;CC	Yes
C6orf120	387263	UPF0669 protein C6orf120 precursor	NP_001025034.1	1	1	1	4	0.82	0.7	25.21	1.81	29.9	1.8	2	2	18800	387263	Chromosome 6 open reading frame 120	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
MPZL1	9019	myelin protein zero-like protein 1 isoform a precursor	NP_003944.1	3	4	4	6	0.82	0.7	11.29	10.77	18.7	15.2	4	4	5086	9019	myelin protein zero-like 1	Binding	Integral to membrane	Unclassified	Cell-cell signaling	SP;IGV;TM	No
TMEM126B	55863	complex I assembly factor TMEM126B, mitochondrial isoform a	NP_060950.3	1	1	1	2	0.82	0.69					1	1	13715	55863	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No
FZD6	8323	frizzled-6 isoform a precursor	NP_003497.2	2	1	1	6	0.82	0.69					1	1	4559	8323	frizzled homolog 6 (Drosophila)	G-protein coupled receptor activity	Plasma membrane	G protein coupled receptor	Cell communication;Signal transduction	FZ;TM;SP	Yes
DENND6A	201627	protein DENND6A	NP_689891.1	1	2	2	4	0.82	0.69	3.25	2.87	3.8	2.8	2	2									
GPX1	2876	glutathione peroxidase 1 isoform 1	NP_000572.2	2	7	7	16	0.82	0.69	10.65	26.02	28.2	61.3	10	10	11749	2876	glutathione peroxidase 1	Peroxidase activity	Cytosol	Enzyme: Peroxidase	Anti-apoptosis	-	Yes
LMF2	91289	lipase maturation factor 2	NP_149977.2	1	1	1	2	0.82	0.69					1	1	12519	91289	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
PLK3	1263	serine/threonine-protein kinase PLK3	NP_004064.2	1	1	1	1	0.82	0.68					1	1	4222	1263	polo-like kinase 3 (Drosophila)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
POM121	9883	nuclear envelope pore membrane protein POM 121 isoform 1	NP_001244119.1	3	1	1	2	0.82	0.68					1	1	11448	9883	POM121 membrane glycoprotein (rat)	Structural constituent of nuclear pore	Nucleus	Integral membrane protein	Transport	-	No
VAMP7	6845	vesicle-associated membrane protein 7 isoform 3	NP_001172112.1	3	2	2	5	0.82	0.66	30.85	22.64	37.1	21.4	2	2	2084	6845	synaptobrevin-like 1	Transporter activity	Plasma membrane;Cell surface;Lysosome	Transport/cargo protein	Transport	TM;SP	No
VPS36	51028	vacuolar protein-sorting-associated protein 36 isoform 1	NP_057159.2	3	3	3	5	0.82	0.64	14.66	28.27	17.1	26.1	2	2	12620	51028	chromosome 13 open reading frame 9	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
DCN	1634	decorin isoform a preproprotein	NP_001911.1	2	1	1	17	0.82	0.61	5.17	8.07	16.5	19.1	15	15	501	1634	decorin	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	SP;LRR;CC	Yes
ALS2CL	259173	ALS2 C-terminal-like protein isoform 1	NP_667340.2	1	1	1	1	0.82	0.61					1	1	10643	259173	ALS2 C-terminal like	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	MORN;VPS9;PH	Yes
AFAP1L2	84632	actin filament-associated protein 1-like 2 isoform 3	NP_001274753.1	3	3	3	9	0.82	0.59	19.42	22.09	36.6	29.6	5	5	13902	84632	KIAA1914	Transcription regulator activity	Cytoplasm	Adapter molecule	Signal transduction	PH;CC	No
CHD1	1105	chromodomain-helicase-DNA-binding protein 1	NP_001261.2	1	2	4	7	0.81	1.56	21.42	14.96	24.8	34	2	2	3668	1105	chromodomain helicase DNA binding protein 1	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CHROMO;DEXDc;HELIC;CC	Yes
MYLK	4638	myosin light chain kinase, smooth muscle isoform 1	NP_444253.3	9	1	2	4	0.81	1.38					1	1	2952	4638	myosin, light polypeptide kinase	Protein serine/threonine kinase activity	Plasma membrane	Serine/threonine kinase	Cell communication;Signal transduction	IGC2;FN3;S_T_kinase;S_T_Y_Kinase	Yes
C11orf68	83638	UPF0696 protein C11orf68 isoform 1	NP_001129107.1	2	2	2	3	0.81	1.34					1	1	12553	83638	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
CLASP2	23122	CLIP-associating protein 2 isoform 2	NP_001193973.1	1	1	6	20	0.81	1.27					1	1	12054	23122	cytoplasmic linker associated protein 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	-	No
SCAP	22937	sterol regulatory element-binding protein cleavage-activating protein	NP_036367.2	1	1	1	2	0.81	1.13					1	1	3300	22937	None	Chaperone activity	Endoplasmic reticulum	Chaperone	Metabolism;Energy pathways	WD40;TM	Yes
HMGN2	3151	non-histone chromosomal protein HMG-17	NP_005508.1	1	4	4	20	0.81	1.12	10.19	13.29	27.9	52.5	11	11	1230	3151	high-mobility group nucleosomal binding domain2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
PCYOX1	51449	prenylcysteine oxidase 1 precursor	NP_057381.3	1	10	10	32	0.81	1.08	5.78	7.45	21.8	38.2	21	21	11422	51449	prenylcysteine oxidase 1	Catalytic activity	Lysosome	Enzyme: Oxidase	Metabolism;Energy pathways	-	Yes
NCK1	4690	cytoplasmic protein NCK1 isoform 1	NP_006144.1	3	2	2	3	0.81	1.07	22.81	11.03	26.5	16.9	2	2	2740	4690	NCK adaptor protein 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	SH3;SH2	Yes
TXNRD2	10587	thioredoxin reductase 2, mitochondrial isoform 1 precursor	NP_006431.2	1	1	1	2	0.81	1.07					1	1	18519	10587	thioredoxin reductase 2	Catalytic activity	Mitochondrion	Enzyme: Reductase	Cell death;Cell proliferation	-	Yes
BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	NP_061330.2	1	4	4	8	0.81	1.06	12	10.02	22	24	5	5	11270	55971	BAI1-associated protein 2-like 1	Molecular function unknown	-	Unclassified	Biological_process unknown	SH3;CC	No
ARL6IP4	51329	ADP-ribosylation factor-like protein 6-interacting protein 4 isoform 3	NP_001002251.2	4	2	6	11	0.81	1.06					1	1	9640	51329	ADP-ribosylation-like factor 6 interactingprotein 4	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	No
GNAQ	2776	guanine nucleotide-binding protein G(q) subunit alpha	NP_002063.2	1	5	8	18	0.81	1.06	12.68	6.51	23.4	15.6	5	5	2998	2776	guanine nucleotide binding protein (G protein),q polypeptide	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	CC	Yes
POP4	10775	ribonuclease P protein subunit p29	NP_006618.1	1	1	1	2	0.81	1.05					1	1	9358	10775	processing of precursor 4, ribonuclease P/MRPsubunit (S. cerevisiae)	Ribonuclease activity	Nucleolus	Ribonuclease	Protein metabolism	-	No
CPSF6	11052	cleavage and polyadenylation specificity factor subunit 6 isoform 2	NP_001287876.1	2	12	12	24	0.81	1.05	10.69	6.79	31.8	26.1	13	13	5401	11052	cleavage and polyadenylation specific factor 6,68kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
TUBA4A	7277	tubulin alpha-4A chain isoform 1	NP_005991.1	4	8	28	418	0.81	1.05	5.62	4.94	27.7	31.9	36	36	1851	7277	tubulin, alpha 1 (testis specific)	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	TUBULIN	Yes
CREBBP	1387	CREB-binding protein isoform a	NP_004371.2	3	1	1	2	0.81	1.04					1	1	2534	1387	CREB binding protein (Rubinstein-Taybisyndrome)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BROMO;ZnF_ZZ;CC	Yes
ALG3	10195	dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase isoform a	NP_005778.1	1	1	1	2	0.81	1.03					1	1	3067	10195	asparagine-linked glycosylation 3 homolog(yeast, alpha-1,3-mannosyltransferase)	Transferase activity	Endoplasmic reticulum membrane	Enzyme: Mannosyltransferase	Metabolism;Energy pathways	TM	Yes
LPXN	9404	leupaxin isoform 1	NP_001137467.1	3	2	2	6	0.81	1	5.32	9.59	7.5	16.7	3	3	5651	9404	leupaxin	Receptor signaling complex scaffold activity	Cytoplasm;Nucleus	Adapter molecule	Cell communication;Signal transduction	LIM	Yes
TNPO2	30000	transportin-2 isoform 2	NP_038461.2	2	5	9	33	0.81	0.99	8.74	12.71	16	28.7	5	5	4301	30000	transportin 2 (importin 3, karyopherin beta 2b)	Transporter activity	Nucleoplasm	Transport/cargo protein	Transport	IBN_NT;HEAT;ARM	Yes

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GPAA1	8733	glycosylphosphatidylinositol anchor attachment 1 protein	NP_003792.1	1	2	2	2	0.81	0.99	20.82	9.34	24.3	13.1	2	2	4334	8733	GPAA1P anchor attachment protein 1 homolog(yeast)	Cytoskeletal anchoring activity	Endoplasmic reticulum	Anchor protein	Protein metabolism	TM	Yes
ARPC2	10109	actin-related protein 2/3 complex subunit 2	NP_005722.1	1	12	12	33	0.81	0.99	6.44	7.27	24.3	34.1	21	21	10367	10109	actin related protein 2/3 complex, subunit 2,34kDa	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance;Cytoskeleton organization and biogenesis	-	Yes
GLB1	2720	beta-galactosidase isoform a preproprotein	NP_000395.2	5	10	10	42	0.81	0.96	5.22	10.2	20.5	49.4	23	23	1975	2720	galactosidase, beta 1	Catalytic activity	Lysosome	Enzyme: Hydroxylase	Metabolism;Energy pathways	SP	Yes
RAB5C	5878	ras-related protein Rab-5C isoform b	NP_001238968.1	2	8	11	74	0.81	0.95	15.02	17.54	70.4	105.3	27	27	4947	5878	RAB5C, member RAS oncogene family	GTPase activity	Endosome	GTPase	Cell communication;Signal transduction	RAB	Yes
IDH1	3417	isocitrate dehydrogenase [NADP] cytoplasmic	NP_005887.2	1	22	23	82	0.81	0.94	5.25	7.61	27.9	48.1	41	41	984	3417	isocitrate dehydrogenase 1 (NADP+), soluble	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
CD46	4179	membrane cofactor protein isoform 2 precursor	NP_758869.1	8	4	4	9	0.81	0.94	7.38	2.59	14.7	6	6	6	406	4179	membrane cofactor protein (CD46,trophoblast-lymphocyte cross-reactive antigen)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;SUSHI;SP	Yes
MVP	9961	major vault protein isoform 1	NP_005106.2	3	40	40	194	0.81	0.93	3.67	3.57	28.8	32.7	91	92	5475	9961	major vault protein	Nucleocytoplasmic transporter activity	Cytoplasm	Transport/cargo protein	Cell growth and/or maintenance	CC	Yes
ZWILCH	55055	protein zwilch homolog isoform 1	NP_060445.3	2	2	2	5	0.81	0.93	0.65	10.87	0.9	17.6	3	3	7640	55055	None	Molecular function unknown	Kinetochore	Unclassified	Biological_process unknown	-	No
WLS	79971	protein wntless homolog isoform 2	NP_001002292.3	3	1	1	1	0.81	0.92					1	1									
PKM	5315	pyruvate kinase PKM isoform a	NP_002645.3	5	5	41	641	0.81	0.91	5.28	5.37	28	32.2	41	41									
GLOD4	51031	glyoxalase domain-containing protein 4	NP_057164.3	1	10	10	34	0.81	0.9	7.95	5.12	27.7	19.7	18	18	12678	51031	chromosome 17 open reading frame 25	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	Yes
KIF11	3832	kinesin-like protein KIF11	NP_004514.2	1	2	2	3	0.81	0.89	6.95	29.6	8	38.6	2	2	1023	3832	kinesin family member 11	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	KISC;CC	Yes
PPA2	27068	inorganic pyrophosphatase 2, mitochondrial isoform 1 precursor	NP_789845.1	4	13	14	38	0.81	0.89	8.68	6.98	29.7	26.1	17	17	18494	27068	None	Catalytic activity	Mitochondrion;Cytoplasm	Enzyme: Phosphatase	Metabolism;Energy pathways	SP	Yes
DCTPP1	79077	dCTP pyrophosphatase 1	NP_077001.1	1	4	4	7	0.81	0.88	6.89	2.83	11.2	5	4	4	18310	79077	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
DHRS7	51635	dehydrogenase/reductase SDR family member 7 precursor	NP_057113.1	1	9	9	27	0.81	0.87	4.69	12.14	12.6	36.3	11	11	16802	51635	dehydrogenase/reductase (SDR family) member 7	Catalytic activity	-	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	Yes
MACROD1	28992	O-acetyl-ADP-ribose deacetylase MACROD1	NP_054786.2	1	3	3	4	0.81	0.86	22.5	0.38	32.3	0.6	3	3	17448	28992	None	Molecular function unknown	Mitochondrion	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	A1pp	Yes
TRIM14	9830	tripartite motif-containing protein 14	NP_055603.2	1	2	2	5	0.81	0.84	14.93	2.8	17.3	3.3	2	2	5948	9830	tripartite motif-containing 14	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	BBOX;PRY;SPRY	Yes
AKR7A2	8574	aflatoxin B1 aldehyde reductase member 2	NP_003680.2	2	6	6	21	0.81	0.83	6.42	9.02	17.5	25.3	11	11	4567	8574	aldo-keto reductase family 7, member A2(aflatoxin aldehyde reductase)	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	ALDKR	Yes
HADHA	3030	trifunctional enzyme subunit alpha, mitochondrial precursor	NP_000173.2	1	40	40	197	0.81	0.83	4.04	4.63	35.8	42.6	113	112	2934	3030	hydroxyacyl-Coenzyme Adehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase(trifunctional protein), alpha subunit	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	CC	Yes
PTGES3L-AARSD1	100885850	PTGES3L-AARSD1 protein isoform 1	NP_001129514.2	3	2	2	8	0.81	0.83	16.09	1.94	26.5	3.2	4	4									
SLC9A1	6548	sodium/hydrogen exchanger 1	NP_003038.2	1	6	6	10	0.81	0.83	19.56	16.43	40.5	34.3	6	6	123	6548	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	CC;TM;SP	Yes
VIM	7431	vimentin	NP_003371.2	8	44	52	371	0.81	0.81	3.03	3.91	34	44.8	182	181	1899	7431	vimentin	Structural constituent of cytoskeleton	Intermediate filament	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
EFS	10278	embryonal Fyn-associated substrate isoform 1	NP_005855.1	3	1	1	1	0.81	0.8					1	1	9932	10278	embryonal Fyn-associated substrate	Molecular function unknown	Cytoplasm	Unclassified	Signal transduction	SH3	Yes
MCM2	4171	DNA replication licensing factor MCM2	NP_004517.2	1	15	15	37	0.81	0.79	4.84	10.7	17.2	38.3	19	19	303	4171	MCM2 minichromosome maintenance deficient 2,mitotin (S. cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MCM;CC	Yes
TMEM11	8834	transmembrane protein 11, mitochondrial	NP_003867.1	1	2	2	4	0.81	0.78	10.81	9.86	12.4	10.9	2	2	12680	8834	chromosome 17 open reading frame 35	Molecular function unknown	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	TM	No
MVK	4598	mevalonate kinase isoform a	NP_000422.1	2	7	7	19	0.81	0.78	10.12	10.54	27.6	27.8	11	11	2015	4598	mevalonate kinase (mevalonic aciduria)	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes

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SP3	6670	transcription factor Sp3 isoform 1	NP_003102.1	3	1	1	2	0.81	0.77					1	1	3483	6670	Sp3 transcription factor	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	Yes
RNF123	63891	E3 ubiquitin-protein ligase RNF123	NP_071347.2	1	2	2	2	0.81	0.77					1	1	11499	63891	ring finger protein 123	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	SPRY;CC;RING	No
UBN2	254048	ubinuclein-2	NP_775840.3	1	1	1	3	0.81	0.77					1	1	19387	254048	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
DPM1	8813	dolichol-phosphate mannosyltransferase subunit 1	NP_003850.1	1	6	6	14	0.81	0.76	8.16	8.43	16.3	15.8	6	6	4613	8813	dolichyl-phosphate mannosyltransferasepolypeptide 1, catalytic subunit	Mannosyltransferase activity	Plasma membrane	Enzyme: Synthase	Metabolism;Energy pathways	-	Yes
C20orf27	54976	UPF0687 protein C20orf27 isoform 1	NP_001034229.1	2	1	1	7	0.81	0.74	7.37	8.97	12	13.3	4	4	16648	54976	chromosome 20 open reading frame 27	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
RNPEP	6051	aminopeptidase B	NP_064601.3	1	24	24	79	0.81	0.74	4.8	4.83	26.8	24.6	46	46	4055	6051	arginyl aminopeptidase (aminopeptidase B)	Aminopeptidase activity	Golgi apparatus	Aminopeptidase	Protein metabolism	-	Yes
ACTG1	71	actin, cytoplasmic 2	NP_001186883.1	2	12	34	1614	0.81	0.74	1.92	4.83	33.9	87.1	452	443	17	71	actin, gamma 1	Structural constituent of cytoskeleton	Cytoplasm	Structural protein	Cell growth and/or maintenance	ACTIN	Yes
CHMP6	79643	charged multivesicular body protein 6	NP_078867.2	1	1	1	2	0.81	0.7					1	1	8564	79643	chromatin modifying protein 6	Molecular function unknown	-	Unclassified	Transport	CC	No
C9orf41	138199	UPF0586 protein C9orf41	NP_689633.1	1	1	1	2	0.81	0.68					1	1	12958	138199	chromosome 9 open reading frame 41	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
CMPK1	51727	UMP-CMP kinase isoform a	NP_057392.1	1	2	2	3	0.81	0.64	33.59	84.64	39.9	89.4	2	2	18258	51727	cytidylate kinase	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP	Yes
KRT75	9119	keratin, type II cytoskeletal 75	NP_004684.2	2	1	18	202	0.81	0.6					1	1	11057	9119	None	Structural molecule activity	-	Structural protein	Cell growth and/or maintenance	CC	Yes
RBM47	54502	RNA-binding protein 47 isoform a	NP_001092104.1	2	1	1	4	0.81	0.57	1.68	2.61	1.9	2.1	2	2	13373	54502	None	RNA binding	-	RNA binding protein	Regulation of gene expression, epigenetic	RRM	No
MST1R	4486	macrophage-stimulating protein receptor isoform 1 preproprotein	NP_002438.2	2	3	3	4	0.81	0.57	4.99	12.05	7	12	3	3	2545	4486	macrophage stimulating 1 receptor(c-met-related tyrosine kinase)	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	TM;SEMA;PSI;IPT;Tyr_Kinase;SP	Yes
MTMR1	8776	myotubularin-related protein 1 isoform 1	NP_001293073.1	2	2	2	3	0.81	0.54	11.06	60.28	12.7	49	2	2	2163	8776	myotubularin related protein 1	Protein tyrosine/serine/threonine phosphatase activity;Lipid phosphatase activity	-	Lipid phosphatase;Dual specificity phosphatase	Cell communication;Signal transduction	GRAM;CC	Yes
TRIM16	10626	tripartite motif-containing protein 16	NP_006461.3	1	1	1	2	0.81	0.51					1	1	15552	10626	tripartite motif-containing 16	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	BBOX;CC;PRY;SPRY	Yes
POLR2E	5434	DNA-directed RNA polymerases I, II, and III subunit RPABC1	NP_002686.2	1	1	1	2	0.8	1.83					1	1	15946	5434	polymerase (RNA) II (DNA directed) polypeptideE, 25kDa	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
MED25	81857	mediator of RNA polymerase II transcription subunit 25	NP_112235.2	1	1	1	2	0.8	1.81					1	1	14380	81857	mediator of RNA polymerase II transcription,subunit 25 homolog (yeast)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
CPSF4	10898	cleavage and polyadenylation specificity factor subunit 4 isoform 1	NP_006684.1	2	1	1	2	0.8	1.76					1	1	4338	10898	cleavage and polyadenylation specific factor 4,30kDa	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C2HC;ZnF_C3H1	Yes
KLHL24	54800	kelch-like protein 24	NP_060114.2	1	1	1	1	0.8	1.69					1	1	16838	54800	None	Molecular function unknown	-	Unclassified	Biological_process unknown	BTB;KELCH	Yes
C19orf25	148223	UPF0449 protein C19orf25	NP_689695.2	1	1	1	1	0.8	1.5					1	1	12703	148223	chromosome 19 open reading frame 25	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
NAB2	4665	NGFI-A-binding protein 2	NP_005958.1	1	1	1	2	0.8	1.44					1	1	3854	4665	NGFI-A binding protein 2 (EGR1 binding protein2)	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS	Yes
SAMD1	90378	atherin	NP_612361.1	1	1	1	1	0.8	1.39					1	1	18011	90378	sterile alpha motif domain containing 1	Molecular function unknown	-	Unclassified	Biological_process unknown	SAM	No
TBP	6908	TATA-box-binding protein isoform 1	NP_003185.1	2	1	1	2	0.8	1.37					1	1	2511	6908	TATA box binding protein	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	No
TBL1XR1	79718	F-box-like/WD repeat-containing protein TBL1XR1	NP_078941.2	1	3	3	4	0.8	1.3	0.92	12.5	1.3	28.7	3	3	15476	79718	transducin (beta)-like 1X-linked receptor 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LISH;WD40	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
JTB	10899	protein JTB precursor	NP_006685.1	1	1	1	2	0.8	1.28					1	1	5240	10899	jumping translocation breakpoint	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	TM;SP	Yes
VDAC1	7416	voltage-dependent anion-selective channel protein 1	NP_003365.1	1	15	16	112	0.8	1.26	5.13	2.84	28.5	24.6	46	46	5137	7416	voltage-dependent anion channel 1	Voltage-gated ion channel activity	Mitochondrion	Voltage gated channel	Transport	-	Yes
ELP2	55250	elongator complex protein 2 isoform 1	NP_001229804.1	6	4	4	6	0.8	1.26	8.42	9.69	11.6	21.3	3	3	15443	55250	signal transducer and activator oftranscription 3 interacting protein 1	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Cell communication;Signal transduction	WD40	No
MRPL38	64978	39S ribosomal protein L38, mitochondrial	NP_115867.2	1	5	5	10	0.8	1.24	20.88	7.62	42.5	23.5	6	6	14758	64978	mitochondrial ribosomal protein L38	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
ADAM9	8754	disintegrin and metalloproteinase domain-containing protein 9 precursor	NP_003807.1	1	10	10	16	0.8	1.22	5.68	9.2	13.7	34.7	9	9	4091	8754	a disintegrin and metalloproteinase domain 9(meltrin gamma)	Metallopeptidase activity	Plasma membrane;Nucleus;Cytoplasm	Metallo protease	Protein metabolism	TM;REP;DISINT;ACR;SP;EGFL	Yes
MGST3	4259	microsomal glutathione S-transferase 3	NP_004519.1	1	4	4	13	0.8	1.19	18.71	43.61	41	236.5	7	7	5192	4259	microsomal glutathione S-transferase 3	Glutathione transferase activity	Endoplasmic reticulum	Enzyme: Glutathione transferase	Metabolism;Energy pathways	TM	Yes
C1orf35	79169	multiple myeloma tumor-associated protein 2	NP_077295.1	1	1	1	4	0.8	1.15	20.02	20.68	22.9	34.8	2	2	10090	79169	chromosome 1 open reading frame 35	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
TMEM199	147007	transmembrane protein 199	NP_689677.1	1	2	2	3	0.8	1.13	1.99	7.96	2.3	12.8	2	2	12679	147007	chromosome 17 open reading frame 32	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	Yes
MDH2	4191	malate dehydrogenase, mitochondrial isoform 1 precursor	NP_005909.2	4	20	20	122	0.8	1.09	3.07	2.74	19.3	23.5	60	60	1099	4191	malate dehydrogenase 2, NAD (mitochondrial)	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
HTRA2	27429	serine protease HTRA2, mitochondrial isoform 1 preproprotein	NP_037379.1	4	3	3	6	0.8	1.09	1.06	1.74	1.2	3.3	2	3	5919	27429	protease, serine, 25	Serine-type peptidase activity	Mitochondrion	Serine protease	Protein metabolism	TM;TRYPSIN;PDZ	Yes
CLIP4	79745	CAP-Gly domain-containing linker protein 4 isoform 1	NP_078968.3	2	1	1	1	0.8	1.06					1	1	8634	79745	restin-like 2	Cytoskeletal protein binding	-	Cytoskeletal associated protein	Cell growth and/or maintenance	ANK	Yes
PSMB1	5689	proteasome subunit beta type-1	NP_002784.1	1	11	11	42	0.8	1.04	10.28	4.59	40.1	22.7	22	22	3603	5689	proteasome (prosome, macropain) subunit, betatype, 1	Ubiquitin-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	-	Yes
BRE	9577	BRCA1-A complex subunit BRE isoform 2	NP_954661.1	4	4	4	12	0.8	1.04	10.61	8.71	19.2	20.5	5	5	8498	9577	brain and reproductive organ-expressed (TNFRSF1Amodulator)	Binding	Cytosol	Unclassified	Cell proliferation;Regulation of signal transduction	-	No
HACD3	51495	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	NP_057479.2	1	4	4	12	0.8	1.01	8.36	1.28	16.4	3.2	6	6									
PDLIM5	10611	PDZ and LIM domain protein 5 isoform a	NP_006448.4	8	18	18	55	0.8	1.01	6.53	6.35	28.2	35	28	28	5799	10611	PDZ and LIM domain 5	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PDZ;LIM	Yes
SEC13	6396	protein SEC13 homolog isoform 3	NP_001129498.1	5	8	8	22	0.8	1.01	15.82	3.65	48.4	13.3	13	13	2538	6396	SEC13-like 1 (S. cerevisiae)	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	WD40	Yes
NT5C1B-RDH14	100526794	NT5C1B-RDH14 protein isoform 1	NP_001186032.1	2	1	1	1	0.8	0.99					1	1									
UBE3A	7337	ubiquitin-protein ligase E3A isoform 2	NP_000453.2	3	7	7	21	0.8	0.95	6.72	4.97	17.1	15	10	10	3375	7337	ubiquitin protein ligase E3A (human papillomavirus E6-associated protein, Angelman syndrome)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Metabolism;Energy pathways	HECT;CC	Yes
BCL2L13	23786	bcl-2-like protein 13 isoform b	NP_001257655.1	8	7	7	12	0.8	0.95	9.08	8.13	20.7	22	8	8	9822	23786	BCL2-like 13 (apoptosis facilitator)	Molecular function unknown	Mitochondrion	Integral membrane protein	Apoptosis	CC;BCL;TM	Yes
GNAI3	2773	guanine nucleotide-binding protein G(k) subunit alpha	NP_006487.1	8	6	10	73	0.8	0.95	16.5	7.46	54.3	27.9	15	15	765	2773	guanine nucleotide binding protein (G protein),alpha inhibiting activity polypeptide 3	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	-	Yes
ELMO3	79767	engulfment and cell motility protein 3	NP_078988.2	1	9	9	19	0.8	0.93	11.55	6.19	26.5	17.4	8	9	12104	79767	engulfment and cell motility 3 (ced-12 homolog,C. elegans)	Motor activity	-	Motor protein	Cell growth and/or maintenance	-	Yes
EMC4	51234	ER membrane protein complex subunit 4 isoform a	NP_057538.1	2	3	3	4	0.8	0.93	18.92	3.59	21.8	4.7	2	2									
PLEC	5339	plectin isoform 1c	NP_000436.2	16	1	345	1366	0.8	0.92					1	1									
ATP1B1	481	sodium/potassium-transporting ATPase subunit beta-1	NP_001668.1	1	7	7	25	0.8	0.91	5.58	4.58	16.9	15.7	14	14	1663	481	ATPase, Na+/K+ transporting, beta 1polypeptide	ATPase activity	Plasma membrane	ATPase	Transport	TM	No
GALNT3	2591	polypeptide N-acetylgalactosaminyltransferase 3	NP_004473.2	2	8	8	12	0.8	0.91	12.74	14.3	29.5	38	8	8	3453	2591	UDP-N-acetyl-alpha-D-galactosamine:polypeptideN-acetylgalactosaminyltransferase 3 (GalNAc-T3)	Galactosyltransferase activity	Golgi apparatus	Enzyme: Galactosyltransferase	Protein metabolism	TM;CC	Yes
LTA4H	4048	leukotriene A-4 hydrolase isoform 1	NP_000886.1	3	28	28	92	0.8	0.89	5.34	5.52	30.6	35.5	49	49	1056	4048	leukotriene A4 hydrolase	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Protein metabolism	-	Yes
PTRF	284119	polymerase I and transcript release factor	NP_036364.2	1	17	17	110	0.8	0.89	7.4	7.76	46.5	55.1	56	56	4433	284119	polymerase I and transcript release factor	Transcription regulator activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NLS;CC	Yes
FAM49B	51571	protein FAM49B	NP_001243692.1	2	10	10	33	0.8	0.88	4.21	3.68	14	13.4	17	17	13313	51571	family with sequence similarity 49, member B	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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SLC25A11	8402	mitochondrial 2-oxoglutarate/malate carrier protein isoform 1	NP_003553.2	3	10	10	23	0.8	0.88	9.61	6.49	28.2	20.8	13	13	5003	8402	solute carrier family 25 (mitochondrialcarrier; oxoglutarate carrier), member 11	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	TM	Yes
TKFC	26007	bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	NP_056348.2	2	7	7	11	0.8	0.86	11.75	5.07	23.2	10.6	6	6									
CHD1L	9557	chromodomain-helicase-DNA-binding protein 1-like isoform 1	NP_004275.4	5	1	1	1	0.8	0.86					1	1	9880	9557	chromodomain helicase DNA binding protein1-like	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HELIC;DEXDc;CC;A1pp	Yes
PRIM2	5558	DNA primase large subunit isoform a	NP_000938.2	1	2	2	3	0.8	0.86					1	1	8900	5558	primase, polypeptide 2A, 58kDa	DNA-directed RNA polymerase activity	Nucleus	RNA polymerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
UBXN6	80700	UBX domain-containing protein 6 isoform 1	NP_079517.1	2	3	3	7	0.8	0.84	21.15	8.03	29.8	11.7	3	3	18253	80700	UBX domain containing 1	Molecular function unknown	Cytoplasm;Membrane fraction	Unclassified	Biological_process unknown	PUG;UBX	Yes
PML	5371	protein PML isoform 1	NP_150241.2	9	24	24	55	0.8	0.83	4.45	5.03	20.5	23.9	32	32	23	5371	promyelocytic leukemia	Transcription regulator activity;Transporter activity	Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of gene expression, epigenetic	RING;BBOX;CC;NLS;LZ	Yes
PLOD1	5351	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor	NP_000293.2	1	16	17	58	0.8	0.78	3.58	6.62	13.5	24.7	22	22	1086	5351	procollagen-lysine 1, 2-oxoglutarate5-dioxygenase 1	Catalytic activity	Endoplasmic reticulum	Enzyme: Hydroxylase	Metabolism;Energy pathways	P4HC;SP	Yes
BLVRA	644	biliverdin reductase A precursor	NP_001240752.1	1	11	11	30	0.8	0.76	4.15	7.19	14.9	24.9	20	20	11229	644	biliverdin reductase A	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
PARP4	143	poly [ADP-ribose] polymerase 4	NP_006428.2	1	15	15	32	0.8	0.73	4.94	10.17	16	30.6	16	16	9598	143	poly (ADP-ribose) polymerase family, member 4	Catalytic activity	Nucleus	Enzyme: Ribosyltransferase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRCT;VIT;VWA	Yes
YWHAZ	7534	14-3-3 protein zeta/delta	NP_003397.1	1	15	19	196	0.8	0.69	4.22	7.15	29.6	44.1	73	73	3183	7534	tyrosine 3-monooxygenase/tryptophan5-monooxygenase activation protein, zeta polypeptide	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Regulation of cell cycle	CC	Yes
CDH13	1012	cadherin-13 isoform 2	NP_001207417.1	5	3	3	5	0.8	0.66	31.93	36.42	46.4	43.5	3	3	3219	1012	cadherin 13, H-cadherin (heart)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	SP;Cadherin;GPI	Yes
TACC2	10579	transforming acidic coiled-coil-containing protein 2 isoform a	NP_996744.3	8	1	1	2	0.8	0.66					1	1	5600	10579	transforming, acidic coiled-coil containingprotein 2	Molecular function unknown	Centrosome	Cell cycle control protein	Cell growth and/or maintenance	CC	Yes
S100A6	6277	protein S100-A6	NP_055439.1	1	4	4	12	0.8	0.64	42.36	25.21	87.5	37.6	5	5	237	6277	S100 calcium binding protein A6 (calcyclin)	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF;S_100	Yes
S100A9	6280	protein S100-A9	NP_002956.1	1	6	6	15	0.8	0.62	5.79	27.11	13.1	50.2	8	8	472	6280	S100 calcium binding protein A9 (calgranulinB)	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
NDUFB4	4710	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 isoform 1	NP_004538.2	2	4	4	12	0.8	0.61	2.04	17.3	4.3	28.3	7	7	11955	4710	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 4, 15kDa	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
LSR	51599	lipolysis-stimulated lipoprotein receptor isoform 2	NP_991403.1	5	3	3	5	0.8	0.56	3.79	67.84	5.3	72.8	3	3	17283	51599	None	Receptor activity	Plasma membrane	Integral membrane protein	Lipoprotein metabolism	IG;TM	No
PLSCR3	57048	phospholipid scramblase 3	NP_065093.2	1	1	1	3	0.79	1.88					1	1	7400	57048	phospholipid scramblase 3	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	-	Yes
PCBP2	5094	poly(rC)-binding protein 2 isoform b	NP_114366.1	8	1	11	75	0.79	1.7					1	1	3129	5094	poly(rC) binding protein 2	RNA binding;DNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes
HERC5	51191	E3 ISG15--protein ligase HERC5	NP_057407.2	1	1	1	2	0.79	1.69					1	1	10502	51191	hect domain and RLD 5	Ligase activity	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	HECT	Yes
NAA35	60560	N-alpha-acetyltransferase 35, NatC auxiliary subunit	NP_078911.3	1	4	4	6	0.79	1.27	6.66	8.94	9.2	19.9	3	3	11291	60560	MAK10 homolog, amino-acid N-acetyltransferasesubunit, (S. cerevisiae)	Molecular function unknown	-	Unclassified	Cell growth and/or maintenance	-	Yes
SF3B6	51639	splicing factor 3B subunit 6	NP_057131.1	1	3	3	3	0.79	1.2					1	1									
GM2A	2760	ganglioside GM2 activator isoform 1 precursor	NP_000396.2	2	4	4	12	0.79	1.17	6.01	2.21	11.7	6.4	6	6	2034	2760	GM2 ganglioside activator	Transporter activity	Lysosome	Transport/cargo protein	Metabolism;Energy pathways	SP	Yes
SAR1B	51128	GTP-binding protein SAR1b	NP_057187.1	1	3	7	38	0.79	1.15	7.97	19.92	14.2	48.3	5	4	9647	51128	SAR1a gene homolog 2 (S. cerevisiae)	GTPase activity	Endoplasmic reticulum	GTPase	Cell communication;Signal transduction	-	Yes
ZNF207	7756	BUB3-interacting and GLEBS motif-containing protein ZNF207 isoform c	NP_001091977.1	3	2	2	3	0.79	1.14	4.91	17.59	5.5	29	2	2	4576	7756	zinc finger protein 207	DNA binding;Transcription factor activity	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism;Transcription	ZNFC2;NLS	Yes
GPX8	493869	probable glutathione peroxidase 8 isoform a	NP_001008398.2	4	2	2	4	0.79	1.12	17.68	16.8	19.9	27.2	2	2	17416	493869	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No

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OSBPL6	114880	oxysterol-binding protein-related protein 6 isoform c	NP_001188409.1	5	1	2	3	0.79	1.09					1	1	9476	114880	oxysterol binding protein-like 6	Transporter activity;Lipid binding	Cytoplasm	Transport/cargo protein	Transport;Lipid metabolism	PH;CC	Yes
GPAM	57678	glycerol-3-phosphate acyltransferase 1, mitochondrial precursor	NP_065969.3	1	1	1	2	0.79	1.08					1	1	3865	57678	glycerol-3-phosphate acyltransferase,mitochondrial	Acyltransferase activity	Mitochondrion	Enzyme: Acyltransferase	Metabolism;Energy pathways	PISC	Yes
GPR108	56927	protein GPR108 precursor	NP_001073921.1	1	1	1	2	0.79	1.07					1	1	18896	56927	G protein-coupled receptor 108	G-protein coupled receptor activity	Integral to membrane	G protein coupled receptor	Signal transduction	TM	Yes
NEK7	140609	serine/threonine-protein kinase Nek7	NP_598001.1	1	1	1	3	0.79	1.07					1	1	6027	140609	NIMA (never in mitosis gene a)-related kinase 7	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
PIK3CA	5290	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform	NP_006209.2	1	1	1	2	0.79	1.05					1	1	1382	5290	phosphoinositide-3-kinase, catalytic, alphapolypeptide	Lipid kinase activity	Plasma membrane	Lipid Kinase	Cell communication;Signal transduction	C2;PI3KA;PI3KC;CC	Yes
RPS16	6217	40S ribosomal protein S16	NP_001011.1	1	15	15	58	0.79	1.05	9.99	4.34	44.7	24.8	29	29	4724	6217	ribosomal protein S16	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
MICAL1	64780	protein-methionine sulfoxide oxidase MICAL1 isoform 3	NP_001273542.1	3	5	5	8	0.79	1	1.69	24.93	2.7	53.1	4	4	6183	64780	microtubule associated monoxygenase, calponinand LIM domain containing 1	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CH;LIM;CC	Yes
NT5C2	22978	cytosolic purine 5'-nucleotidase	NP_036361.1	1	5	5	7	0.79	0.99	22.43	12.04	41.2	27.3	5	5	2686	22978	5`-nucleotidase, cytosolic II	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
ELP3	55140	elongator complex protein 3 isoform 1	NP_060561.3	5	5	5	12	0.79	0.99	1.05	1.83	1.9	4.1	5	5	10936	55140	elongation protein 3 homolog (S. cerevisiae)	Acyltransferase activity	Nucleus	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
WDR75	84128	WD repeat-containing protein 75 isoform 1	NP_115544.1	2	7	7	11	0.79	0.99	9.12	13.03	17.7	32.5	6	6	7775	84128	WD repeat domain 75	Molecular function unknown	-	Unclassified	Cell communication	WD40	No
TFCP2	7024	alpha-globin transcription factor CP2 isoform 1	NP_005644.2	3	3	5	10	0.79	0.93	7.52	5.78	10.3	9.3	3	3	1790	7024	transcription factor CP2	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PPP2R5E	5529	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform isoform a	NP_006237.1	3	5	6	12	0.79	0.93	14.94	12.76	26.9	27.1	5	5	9040	5529	protein phosphatase 2, regulatory subunit B(B56), epsilon isoform	Molecular function unknown	Cytoplasm	Regulatory/other subunit	Cell communication;Signal transduction	-	No
FAM208A	23272	protein FAM208A isoform a	NP_001106207.1	2	2	2	4	0.79	0.92	29.9	16.34	34.3	21.5	2	2									
AGK	55750	acylglycerol kinase, mitochondrial precursor	NP_060708.1	1	8	8	16	0.79	0.92	8.01	8.19	19.1	23	9	9	8554	55750	multiple substrate lipid kinase	Lipid kinase activity	Integral to membrane	Lipid Kinase	Cell communication;Signal transduction	DAGKC	No
HSDL1	83693	inactive hydroxysteroid dehydrogenase-like protein 1 isoform a	NP_113651.4	2	2	2	3	0.79	0.9	18.83	3.62	21.4	4.6	2	2	17117	83693	hydroxysteroid dehydrogenase like 1	Catalytic activity	-	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	No
NBEAL2	23218	neurobeachin-like protein 2	NP_055990.1	1	8	8	15	0.79	0.9	6.89	9.21	16.4	25.4	9	9	11789	23218	neurobeachin-like 2	Molecular function unknown	-	Unclassified	Biological_process unknown;Signal transduction	WD40	No
MAP2	4133	microtubule-associated protein 2 isoform 1	NP_002365.3	4	4	4	6	0.79	0.9	9.75	1.17	15.5	2.1	4	4	1140	4133	microtubule-associated protein 2	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
PRKCZ	5590	protein kinase C zeta type isoform 1	NP_002735.3	3	1	1	2	0.79	0.89					1	1	1504	5590	protein kinase C, zeta	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Anti-apoptosis;Signal transduction;Negative regulation of enzyme activity;Inflammatory response	PB1;C1;S_T_kinase;Tyr_Kinase	Yes
PTPN11	5781	tyrosine-protein phosphatase non-receptor type 11 isoform 1	NP_002825.3	2	18	18	32	0.79	0.88	6.66	12.5	22	47.8	17	17	1470	5781	protein tyrosine phosphatase, non-receptortype 11 (Noonan syndrome 1)	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	SH2;Tyr_Phos	Yes
LGALS1	3956	galectin-1	NP_002296.1	1	9	9	50	0.79	0.86	4.25	8.48	17	37.9	25	25	1040	3956	lectin, galactoside-binding, soluble, 1(galectin 1)	Receptor binding	Extracellular	Ligand	Immune response	-	Yes
NAPRT	93100	nicotinate phosphoribosyltransferase isoform 1	NP_660202.3	2	9	9	27	0.79	0.83	12.14	17.21	38.4	60.1	15	15									
PIGO	84720	GPI ethanolamine phosphate transferase 3 isoform 1	NP_116023.2	2	3	3	6	0.79	0.83	9.24	35.77	12.7	55.2	3	3	15134	84720	phosphatidylinositol glycan, class O	Molecular function unknown	Endoplasmic reticulum	Unclassified	Biological_process unknown	SP;TM	Yes
PGGT1B	5229	geranylgeranyl transferase type-1 subunit beta	NP_005014.2	1	2	2	3	0.79	0.83	11.64	10.33	13.1	12.2	2	2	3612	5229	protein geranylgeranyltransferase type I, betasubunit	Transferase activity	-	Enzyme: Prenyltransferase	Metabolism;Energy pathways	-	Yes
AKAP1	8165	A-kinase anchor protein 1, mitochondrial precursor	NP_003479.1	1	2	2	3	0.79	0.83	16.47	15.03	18.7	17.8	2	2	3905	8165	A kinase (PRKA) anchor protein 1	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein	Cell growth and/or maintenance	TM;KH;TUDOR	Yes
PRRC2B	84726	protein PRRC2B	NP_037450.2	1	6	8	13	0.79	0.8	14.36	10.26	25.9	18.6	5	5									
LRP1	4035	prolow-density lipoprotein receptor-related protein 1 precursor	NP_002323.2	1	10	10	21	0.79	0.77	11.79	13.14	31.5	34.7	11	11	138	4035	low density lipoprotein-related protein 1(alpha-2-macroglobulin receptor)	Receptor activity	Endoplasmic reticulum	Cell surface receptor	Cell communication;Signal transduction	LDLRB;EGF;EGFL;EGFCA;SP;TM;LDLA	Yes
MYO1C	4641	unconventional myosin-Ic isoform a	NP_001074248.1	3	30	30	109	0.79	0.76	3.74	3.84	23.1	22.8	59	59	9411	4641	myosin IC	Motor activity	Plasma membrane	Motor protein	Cell growth and/or maintenance	MYOSIN;IQ	Yes

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MCM6	4175	DNA replication licensing factor MCM6	NP_005906.2	1	19	19	36	0.79	0.76	8.69	8.79	27.2	26.4	15	15	3485	4175	MCM6 minichromosome maintenance deficient 6(MIS5 homolog, S. pombe) (S. cerevisiae)	Protein binding	Nucleus	Cell cycle control protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MCM	Yes
LLGL1	3996	lethal(2) giant larvae protein homolog 1	NP_004131.3	1	8	8	14	0.79	0.74	7.5	12.78	17.8	29.1	9	9	2982	3996	lethal giant larvae homolog 1 (Drosophila)	Structural constituent of cytoskeleton	Cytoplasm;Plasma membrane;Cell junction	Cytoskeletal protein	Cell growth and/or maintenance	WD40	No
STAT2	6773	signal transducer and activator of transcription 2 isoform 1	NP_005410.1	4	5	5	17	0.79	0.74	6.86	10.15	14.4	20.2	7	7	2778	6773	signal transducer and activator oftranscription 2, 113kDa	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SH2;CC	Yes
IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	NP_892017.2	2	2	2	3	0.79	0.74	28.36	22.53	32.6	23.9	2	2	17160	359948	interferon regulatory factor 2 bindingprotein 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZFC3	No
CMBL	134147	carboxymethylenebutenolidase homolog	NP_620164.1	1	2	2	6	0.79	0.73	1.64	9.74	2.2	12.4	3	3	14055	134147	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PVRL1	5818	nectin-1 isoform 1 precursor	NP_002846.3	3	6	6	7	0.79	0.72	1.44	5.96	2.3	8.6	4	4	7200	5818	poliovirus receptor-related 1 (herpesvirusentry mediator C; nectin)	Cell adhesion molecule activity	Cell junction	Immunoglobulin;Adhesion molecule	Immune response;Cell adhesion	IGV;SP;TM;Ig_LIKE	Yes
ERAP1	51752	endoplasmic reticulum aminopeptidase 1 isoform a precursor	NP_057526.3	2	10	10	25	0.79	0.72	7.59	9.22	21.9	24.4	13	13	6015	51752	None	Aminopeptidase activity	Endoplasmic reticulum	Aminopeptidase	Protein metabolism	SP	Yes
HIBCH	26275	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial isoform 1 precursor	NP_055177.2	2	3	3	3	0.79	0.71	18.61	12.4	21.1	12.6	2	2	11023	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase	Hydrolase activity	Mitochondrion	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
HADH	3033	hydroxyacyl-coenzyme A dehydrogenase, mitochondrial isoform 1 precursor	NP_001171634.2	2	6	7	18	0.79	0.67	11.32	21.27	30.1	50.1	11	11	8372	3033	L-3-hydroxyacyl-Coenzyme A dehydrogenase,short chain	Molecular function unknown	Mitochondrion	Enzyme: Dehydrogenase	Biological_process unknown	SP	Yes
C1orf123	54987	UPF0587 protein C1orf123 isoform 1	NP_060357.1	2	2	2	2	0.79	0.65					1	1	7929	54987	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
SNCA	6622	alpha-synuclein isoform NACP140	NP_000336.1	3	7	7	13	0.79	0.63	4.22	12.69	9.5	23	8	8	1227	6622	synuclein, alpha (non A4 component of amyloidprecursor)	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	SYNUC	Yes
SH3BGRL3	83442	SH3 domain-binding glutamic acid-rich-like protein 3	NP_112576.1	1	3	3	6	0.79	0.62	12.2	6.31	19.5	7.8	4	4	15332	83442	SH3 domain binding glutamic acid-richprotein like 3	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
PPP3R1	5534	calcineurin subunit B type 1	NP_000936.1	1	2	2	3	0.79	0.57	52.57	116.3	63.9	117.2	2	2	3195	5534	protein phosphatase 3 (formerly 2B),regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)	Phosphatase regulator activity	Cytoplasm	Regulatory/other subunit	Cell communication;Signal transduction	EF	Yes
SFT2D2	375035	vesicle transport protein SFT2B	NP_955376.1	1	2	2	3	0.79	0.51	6.46	90.44	7.2	73	2	2	14192	375035	None	Molecular function unknown	-	Unclassified	Biological_process unknown	TM	No
ISOC2	79763	isochorismatase domain-containing protein 2, mitochondrial isoform 2	NP_078986.1	3	5	5	13	0.78	1.52	16.53	13.72	32.5	54.7	6	6	8030	79763	isochorismatase domain containing 2	Molecular function unknown	-	Unclassified	Metabolism;Energy pathways	-	Yes
CD81	975	CD81 antigen isoform 1	NP_004347.1	2	3	3	9	0.78	1.44	21.58	11.74	38.9	39.1	5	5	8924	975	CD81 antigen (target of antiproliferativeantibody 1)	Catalytic activity	Plasma membrane	Enzyme: Oxidase	Metabolism;Energy pathways	TM	Yes
MTMR14	64419	myotubularin-related protein 14 isoform 2	NP_001070993.1	3	1	1	3	0.78	1.37					1	1	8654	64419	None	Lipid phosphatase activity	Cytoplasm	Lipid phosphatase	Phosphoinositide-mediated signaling;Lipid metabolism;Endosome transport;Vesicle-mediated transport	-	No
ADAM10	102	disintegrin and metalloproteinase domain-containing protein 10 precursor	NP_001101.1	1	4	4	5	0.78	1.32	0.85	9.38	1.2	21.6	3	3	3723	102	a disintegrin and metalloproteinase domain 10	Metallopeptidase activity	Plasma membrane	Metallo protease	Protein metabolism	TM;REP;DISINT;SP	Yes
DYNLL1	8655	dynein light chain 1, cytoplasmic	NP_003737.1	1	4	5	25	0.78	1.25	19.78	26.6	52.2	141.3	10	10	3334	8655	dynein, cytoplasmic, light polypeptide 1	Motor activity	Cytoplasm	Motor protein	Cell growth and/or maintenance	-	Yes
ABCB4	5244	multidrug resistance protein 3 isoform B	NP_061337.1	3	1	1	1	0.78	1.15					1	1	1371	5244	ATP-binding cassette, sub-family B (MDR/TAP),member 4	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM;AAA	Yes
TMED1	11018	transmembrane emp24 domain-containing protein 1 precursor	NP_006849.1	1	2	2	4	0.78	1.14	18.88	4.9	21.1	7.9	2	2	5653	11018	transmembrane emp24 domain containing 1	Receptor binding	Plasma membrane	Ligand	Cell communication;Signal transduction	TM	No
LRWD1	222229	leucine-rich repeat and WD repeat-containing protein 1	NP_690852.1	1	1	1	2	0.78	1.11					1	1	10904	222229	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	LRR;WD40	No
RPS27A	6233	ubiquitin-40S ribosomal protein S27a precursor	NP_001129064.1	3	4	11	86	0.78	1.09	11	35.33	26.3	167.5	9	9	1878	6233	ribosomal protein S27a	Ubiquitin-specific protease activity	Ribosome	Ubiquitin proteasome system protein	Protein metabolism	UBQ	No
ZNF330	27309	zinc finger protein 330 isoform 1	NP_055302.1	1	1	1	2	0.78	1.09					1	1	15775	27309	zinc finger protein 330	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	NLS;CXXC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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TMEM141	85014	transmembrane protein 141	NP_116317.1	1	1	1	1	0.78	1.05					1	1	17490	85014	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No
TBK1	29110	serine/threonine-protein kinase TBK1	NP_037386.1	1	1	1	2	0.78	1.05					1	1	5322	29110	TANK-binding kinase 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	No
FLRT3	23767	leucine-rich repeat transmembrane protein FLRT3 precursor	NP_938205.1	1	5	5	7	0.78	1.04	26.43	14.34	43.1	30.4	4	4	5313	23767	fibronectin leucine rich transmembrane protein3	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;LRR;TM	Yes
MCM3AP	8888	germinal-center associated nuclear protein	NP_003897.2	1	3	3	4	0.78	1.04	67.56	5.53	86.1	8.1	2	2	4483	8888	MCM3 minichromosome maintenance deficient 3(S. cerevisiae) associated protein	Chromatin binding	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	CC	Yes
AAK1	22848	AP2-associated protein kinase 1	NP_055726.3	1	6	6	10	0.78	1	12.97	17.07	25.3	43.9	6	6	10620	22848	AP2 associated kinase 1	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein	Transport	S_T_Y_Kinase	No
CDC42BPA	8476	serine/threonine-protein kinase MRCK alpha isoform B	NP_003598.2	9	1	3	6	0.78	0.96					1	1	4562	8476	CDC42 binding protein kinase alpha(DMPK-like)	Protein serine/threonine kinase activity	Cell junction	Serine/threonine kinase	Cell communication;Signal transduction;Cytoskeleton organization and biogenesis	S_T_kinase;CC;C1;PH;CNH;PBD	Yes
HS1BP3	64342	HCLS1-binding protein 3	NP_071905.3	1	4	4	12	0.78	0.95	27.33	31.05	55.7	83	6	6	13357	64342	None	Molecular function unknown	-	Unclassified	Biological_process unknown	PX	No
FLNA	2316	filamin-A isoform 2	NP_001104026.1	2	126	138	957	0.78	0.94	2.1	1.59	34.8	31.5	421	422	2060	2316	filamin A, alpha (actin binding protein 280)	Cytoskeletal anchoring activity	Cytoplasm	Anchor protein;Structural protein	Cell growth and/or maintenance	CH;IGFLMN	Yes
FAF1	11124	FAS-associated factor 1	NP_008982.1	1	6	6	11	0.78	0.94	19.94	9.97	35.6	21.1	5	5	5124	11124	Fas (TNFRSF6) associated factor 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Apoptosis	UBX;CC	Yes
SIRPA	140885	tyrosine-protein phosphatase non-receptor type substrate 1 precursor	NP_001035111.1	2	1	1	1	0.78	0.94					1	1	3912	140885	protein tyrosine phosphatase, non-receptortype substrate 1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SP;TM;IGC;Ig_LIKE	Yes
MRPL18	29074	39S ribosomal protein L18, mitochondrial	NP_054880.2	1	1	1	1	0.78	0.94					1	1	14744	29074	mitochondrial ribosomal protein L18	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
TAPBP	6892	tapasin isoform 2 precursor	NP_757345.2	2	3	3	7	0.78	0.93	14.1	23.31	22.2	45.5	4	4	9061	6892	TAP binding protein (tapasin)	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein folding	Ig_LIKE;TM;SP	Yes
RTKN	6242	rhotekin isoform a	NP_001015055.1	3	8	8	21	0.78	0.93	19.06	8.06	52.3	24	11	10	3795	6242	rhotekin	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Cell communication;Signal transduction	HR1;PH	No
SH3BP4	23677	SH3 domain-binding protein 4	NP_055336.1	1	4	4	6	0.78	0.91	7.98	21.36	12.5	40.5	4	4	9285	23677	SH3-domain binding protein 4	Receptor signaling complex scaffold activity	-	Adapter molecule	Cell communication;Signal transduction	SH3	No
ZNF385A	25946	zinc finger protein 385A isoform a	NP_001124439.1	4	1	1	1	0.78	0.88					1	1	16448	25946	zinc finger protein 385	Transcription factor activity	Nucleolus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2;NLS	Yes
IFI35	3430	interferon-induced 35 kDa protein	NP_005524.2	1	1	1	1	0.78	0.87					1	1	2844	3430	interferon-induced protein 35	Molecular function unknown	Cytoplasm	Unclassified	Immune response	LZ	Yes
TBPL1	9519	TATA box-binding protein-like protein 1	NP_001240605.1	1	1	1	1	0.78	0.86					1	1	9272	9519	TBP-like 1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
TRIM26	7726	tripartite motif-containing protein 26	NP_003440.1	1	2	2	6	0.78	0.85	6.21	0.65	6.9	0.8	2	2	2901	7726	tripartite motif-containing 26	DNA binding	Nucleus	DNA binding protein	Biological_process unknown	RING;BBOX;PRY;SPRY;CC	Yes
SLC12A4	6560	solute carrier family 12 member 4 isoform a	NP_005063.1	10	4	4	12	0.78	0.85	8.37	15.97	14.6	31	5	5	4987	6560	solute carrier family 12 (potassium/chloridetransporters), member 4	Ion transporter activity	Plasma membrane	Integral membrane protein	Transport	TM	Yes
PARL	55486	presenilins-associated rhomboid-like protein, mitochondrial isoform 1 preproprotein	NP_061092.3	2	1	1	1	0.78	0.85					1	1	8484	55486	presenilin associated, rhomboid-like	Metallopeptidase activity	Mitochondrion	Metallo protease	Protein metabolism	TM	No
SLFN5	162394	schlafen family member 5	NP_659412.3	3	12	14	26	0.78	0.84	6.12	3.85	17.3	11.8	13	13	17519	162394	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
FAM83H	286077	protein FAM83H	NP_940890.3	1	26	26	56	0.78	0.83	7.7	10.73	33.2	49.6	29	28	13521	286077	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	No
KDM5B	10765	lysine-specific demethylase 5B	NP_006609.3	1	4	4	5	0.78	0.82	20.17	57.81	27.9	97.5	3	3	9251	10765	Jumonji, AT rich interactive domain 1B(RBP2-like)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BRIGHT;PHD;JMJC;JmjN	Yes
PDCD6IP	10015	programmed cell death 6-interacting protein isoform 1	NP_037506.2	3	36	36	128	0.78	0.8	3.55	3.37	22.8	21.9	66	65	6425	10015	programmed cell death 6 interacting protein	Molecular function unknown	Cytoplasm	Unclassified	Apoptosis	CC	Yes
KIAA1033	23325	WASH complex subunit 7 isoform 1	NP_001280569.1	2	8	9	17	0.78	0.8	6.96	14.46	16.5	35.6	9	9	13829	23325	KIAA1033	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
CPT2	1376	carnitine O-palmitoyltransferase 2, mitochondrial precursor	NP_000089.1	1	7	7	16	0.78	0.77	7.96	13.32	17.7	29.7	8	8	2802	1376	carnitine palmitoyltransferase II	Palmitoyltransferase activity	Mitochondrion	Enzyme: Palmitoyltransferase	Metabolism;Energy pathways	-	Yes

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
BASP1	10409	brain acid soluble protein 1	NP_006308.3	1	15	15	61	0.78	0.76	6.19	6.15	28.3	27.2	33	33	8389	10409	brain abundant, membrane attached signalprotein 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
NID2	22795	nidogen-2 precursor	NP_031387.3	2	1	1	2	0.78	0.75					1	1	5654	22795	nidogen 2 (osteonidogen)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	NIDO;G2F;EGFCA;THYRO;LDLRB;SP	Yes
DPM3	54344	dolichol-phosphate mannosyltransferase subunit 3 isoform 1	NP_061846.2	2	1	1	4	0.78	0.73	24.07	7.14	26.9	7.3	2	2	16179	54344	dolichyl-phosphate mannosyltransferasepolypeptide 3	Catalytic activity	Endoplasmic reticulum	Enzyme: Synthase	Metabolism	TM	No
SEC14L1	6397	SEC14-like protein 1 isoform b	NP_001191337.1	3	1	1	2	0.78	0.71					1	1	3295	6397	SEC14-like 1 (S. cerevisiae)	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	SEC14	Yes
STX7	8417	syntaxin-7	NP_003560.2	1	7	7	27	0.78	0.71	12.41	6.18	33.1	14.7	11	11	4449	8417	syntaxin 7	Protein binding	Endosome	Integral membrane protein	Transport	SynN;TM;CC	Yes
COQ6	51004	ubiquinone biosynthesis monooxygenase COQ6, mitochondrial isoform a	NP_872282.1	2	1	1	1	0.78	0.69					1	1	16742	51004	coenzyme Q6 homolog (yeast)	FAD binding	-	Unclassified	Metabolism	-	Yes
ATL3	25923	atlastin-3 isoform 1	NP_056274.3	2	15	15	42	0.78	0.68	5.42	7.94	20.5	26.2	23	23	13170	25923	None	Molecular function unknown	Mitochondrion	Unclassified	Immune response	-	No
ANTXR2	118429	anthrax toxin receptor 2 isoform 2 precursor	NP_001139266.1	3	1	1	1	0.78	0.66					1	1	7452	118429	anthrax toxin receptor 2	Cytoskeletal protein binding	Endoplasmic reticulum	Cytoskeletal associated protein	Cell growth and/or maintenance	SP;VWA;TM	Yes
DEF6	50619	differentially expressed in FDCP 6 homolog	NP_071330.3	1	2	2	3	0.78	0.63	20.4	42.29	22.8	38.8	2	2	10869	50619	differentially expressed in FDCP 6 homolog(mouse)	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	PH;CC	No
ENDOD1	23052	endonuclease domain-containing 1 protein precursor	NP_055851.1	1	8	8	22	0.78	0.63	9.01	33.9	20	65.8	8	8	13819	23052	None	Molecular function unknown	-	Unclassified	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	SP;Endonuclease;TM	Yes
LCLAT1	253558	lysocardiolipin acyltransferase 1 isoform 1	NP_872357.2	3	1	1	1	0.78	0.61					1	1	17458	253558	lysocardiolipin acyltransferase	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Metabolism	TM;PISC;SP	No
CLN5	1203	ceroid-lipofuscinosis neuronal protein 5	NP_006484.1	1	3	3	5	0.78	0.6	24.82	10.87	34.4	11.4	3	3	7619	1203	ceroid-lipofuscinosis, neuronal 5	Molecular function unknown	Lysosome	Unclassified	Biological_process unknown	TM	Yes
EGLN1	54583	egl nine homolog 1	NP_071334.1	3	1	1	2	0.77	1.43					1	1	6971	54583	egl nine homolog 1 (C. elegans)	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	P4HC	Yes
EPN3	55040	epsin-3	NP_060427.2	1	2	4	6	0.77	1.17					1	1	6272	55040	epsin 3	Molecular function unknown	Extracellular	Unclassified	Biological_process unknown	UIM	Yes
DGAT1	8694	diacylglycerol O-acyltransferase 1	NP_036211.2	1	2	2	4	0.77	1.12	10.41	3.85	14	7.5	3	3	5360	8694	diacylglycerol O-acyltransferase homolog 1(mouse)	Acyltransferase activity	Endoplasmic reticulum	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM	Yes
SRPX	8406	sushi repeat-containing protein SRPX isoform 1 precursor	NP_006298.1	4	3	3	3	0.77	1.08	3.94	12.9	5.2	24.4	3	3	2175	8406	sushi-repeat-containing protein, X-linked	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	SP;SUSHI	Yes
CDS2	8760	phosphatidate cytidylyltransferase 2	NP_003809.1	1	1	1	2	0.77	1.08					1	1	9150	8760	CDP-diacylglycerol synthase (phosphatidatecytidylyltransferase) 2	Nucleotidyltransferase activity	Mitochondrion;Nucleus;Cytoplasm	Enzyme: Nucleotidyltransferase	Metabolism;Energy pathways	TM	Yes
TAGLN2	8407	transgelin-2 isoform a	NP_001264153.1	3	11	11	51	0.77	1.07	5.14	7.21	20.4	40.9	26	26	6864	8407	transgelin 2	Molecular function unknown	-	Unclassified	Biological_process unknown	CH	Yes
YWHAQ	10971	14-3-3 protein theta	NP_006817.1	1	11	16	150	0.77	1.03	10.99	7.58	54	48.8	36	35	886	10971	tyrosine 3-monooxygenase/tryptophan5-monooxygenase activation protein, theta polypeptide	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	-	Yes
VPS51	738	vacuolar protein sorting-associated protein 51 homolog	NP_037397.2	1	5	5	10	0.77	1	17.64	6.53	27.8	13.1	4	4									
MCM4	4173	DNA replication licensing factor MCM4	NP_005905.2	1	17	17	39	0.77	1	6.21	8.14	21.7	37.7	20	20	9094	4173	MCM4 minichromosome maintenance deficient 4 (S.cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MCM	Yes
GPR89B	51463	Golgi pH regulator B	NP_057418.1	2	3	3	9	0.77	0.99	12.75	13.69	22.2	30.9	5	5	13604	51463	G protein-coupled receptor 89	G-protein coupled receptor activity	Integral to membrane	G protein coupled receptor	Cell communication;Signal transduction	TM	No
ARSA	410	arylsulfatase A isoform a precursor	NP_001078896.2	2	2	2	4	0.77	0.99	29.7	20.47	33.3	29.4	2	2	9617	410	arylsulfatase A	Catalytic activity	Lysosome	Enzyme: Sulphatase	Metabolism;Energy pathways	SULF;SP	Yes
TBC1D2	55357	TBC1 domain family member 2A isoform 1	NP_001254500.1	3	14	14	35	0.77	0.97	9.24	8.73	31.6	37.2	19	18	11624	55357	TBC1 domain family, member 2	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction;Regulation of cell growth	PH;CC;TBC	Yes
NDUFS8	4728	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor	NP_002487.1	1	4	4	7	0.77	0.91	11.99	37.29	18.5	76.9	4	4	3683	4728	NADH dehydrogenase (ubiquinone) Fe-S protein8, 23kDa (NADH-coenzyme Q reductase)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP	Yes
RASA1	5921	ras GTPase-activating protein 1 isoform 1	NP_002881.1	2	7	7	15	0.77	0.91	11.2	11.47	24.9	30.2	8	8	745	5921	RAS p21 protein activator (GTPase activatingprotein) 1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	SH2;SH3;PH;C2;RASGAP	Yes

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PDLIM7	9260	PDZ and LIM domain protein 7 isoform 1	NP_005442.2	3	14	14	52	0.77	0.91	6.51	10.04	25	47.2	24	24	10436	9260	PDZ and LIM domain 7 (enigma)	Receptor signaling complex scaffold activity	Cytoskeleton	Adapter molecule	Cell communication;Signal transduction	PDZ;LIM	Yes
RDH10	157506	retinol dehydrogenase 10	NP_742034.1	1	1	1	1	0.77	0.89					1	1	7605	157506	retinol dehydrogenase 10 (all-trans)	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM	No
TTC38	55020	tetratricopeptide repeat protein 38	NP_060401.2	1	2	2	2	0.77	0.83					1	1	7943	55020	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ARL6IP5	10550	PRA1 family protein 3	NP_006398.1	1	4	4	23	0.77	0.83	10.12	7.64	28.6	23.3	13	13	9303	10550	ADP-ribosylation-like factor 6 interactingprotein 5	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	TM	No
VARS	7407	valine--tRNA ligase	NP_006286.1	6	35	35	116	0.77	0.78	4.44	4.1	26.3	24.4	57	57	10362	7407	valyl-tRNA synthetase 2	Ligase activity	-	Enzyme: Ligase	Metabolism;Energy pathways	CC	Yes
HSD17B7	51478	3-keto-steroid reductase isoform 1	NP_057455.1	1	2	2	3	0.77	0.78	19.75	9.46	21.7	10.5	2	2	5996	51478	hydroxysteroid (17-beta) dehydrogenase 7	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM	Yes
PARP14	54625	poly [ADP-ribose] polymerase 14	NP_060024.2	1	21	21	53	0.77	0.75	7.7	4.59	30.4	17.4	25	25	11421	54625	poly (ADP-ribose) polymerase family, member 14	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
MCL1	4170	induced myeloid leukemia cell differentiation protein Mcl-1 isoform 1	NP_068779.1	2	2	2	3	0.77	0.74					1	1	8870	4170	myeloid cell leukemia sequence 1 (BCL2-related)	Protein binding;Chaperone activity	Mitochondrial membrane	Chaperone	Anti-apoptosis;Apoptosis;Signal transduction	BCL;TM	Yes
ERLIN1	10613	erlin-1	NP_006450.2	1	11	14	48	0.77	0.73	8.41	9.17	28.6	29.8	19	19	8502	10613	SPFH domain family, member 1	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM;PHB	No
CA2	760	carbonic anhydrase 2 isoform 1	NP_000058.1	2	7	7	45	0.77	0.73	5.04	5.6	17.6	18.4	20	20	2023	760	carbonic anhydrase II	Catalytic activity	Cytoplasm	Enzyme: Carbonic anhydrase	Metabolism;Energy pathways	-	Yes
XDH	7498	xanthine dehydrogenase/oxidase	NP_000370.2	2	17	17	51	0.77	0.72	4.63	11.36	17.5	41.7	24	24	6363	7498	xanthine dehydrogenase	Catalytic activity	Peroxisome	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
SSH1	54434	protein phosphatase Slingshot homolog 1 isoform 1	NP_061857.3	3	2	2	2	0.77	0.71	48.08	68.63	56.1	77.3	2	2	9486	54434	slingshot homolog 1 (Drosophila)	Protein tyrosine/serine/threonine phosphatase activity	Cytoplasm	Dual specificity phosphatase	Cell growth and/or maintenance	DSPC	Yes
MYO18A	399687	unconventional myosin-XVIIIa isoform a	NP_510880.2	2	16	16	26	0.77	0.7	8.34	7.27	25.2	19.9	15	15	10106	399687	myosin XVIIIA	Structural molecule activity	Endoplasmic reticulum;Nucleus	Structural protein	Cell growth and/or maintenance	PDZ;MYOSIN;IQ;CC	Yes
SPATS2L	26010	SPATS2-like protein isoform b	NP_001093894.1	1	1	15	33	0.77	0.7					1	1	10916	26010	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC	Yes
HN1	51155	hematological and neurological expressed 1 protein isoform 2	NP_001002032.1	4	3	3	4	0.77	0.67	28.6	2.22	32.1	2.1	2	2	13665	51155	hematological and neurological expressed 1	Molecular function unknown	Nucleus;Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
IQGAP1	8826	ras GTPase-activating-like protein IQGAP1	NP_003861.1	3	59	63	278	0.77	0.65	4.15	4.96	37.7	38.2	129	130	4541	8826	IQ motif containing GTPase activating protein1	GTPase activator activity	Cytoplasm	GTPase activating protein	Cytoskeleton organization and biogenesis	CH;CC;WW;IQ;RASGAP	Yes
EFR3A	23167	protein EFR3 homolog A	NP_055952.2	1	3	3	5	0.77	0.64	8.71	25.33	11.7	23.4	3	2	17179	23167	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
RBM17	84991	splicing factor 45	NP_116294.1	1	2	2	5	0.76	1.89	32.79	24.39	36.5	73	2	2	9501	84991	RNA binding motif protein 17	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC;G_PATCH;RRM	Yes
TM9SF1	10548	transmembrane 9 superfamily member 1 isoform a precursor	NP_006396.2	2	1	1	2	0.76	1.6					1	1	9987	10548	transmembrane 9 superfamily member 1	Receptor activity	Plasma membrane	Integral membrane protein	Signal transduction	SP;TM	Yes
MRPS34	65993	28S ribosomal protein S34, mitochondrial isoform 1	NP_001287829.1	2	2	2	7	0.76	1.52	15.27	4.75	23.4	14.5	4	4	17599	65993	mitochondrial ribosomal protein S34	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	Yes
SOS1	6654	son of sevenless homolog 1	NP_005624.2	1	1	1	1	0.76	1.49					1	1	1681	6654	son of sevenless homolog 1 (Drosophila)	Guanyl-nucleotide exchange factor activity	Cytoplasm	Guanine nucleotide exchange factor	Cell communication;Signal transduction	RHOGEF;PH;RasGEFN;RasGEF;CC;SP	Yes
QRSL1	55278	glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	NP_060762.3	1	1	1	2	0.76	1.42					1	1	15199	55278	glutaminyl-tRNA synthase(glutamine-hydrolyzing)-like 1	Amidinotransferase activity	-	Enzyme: Amidinotransferase	Metabolism;Energy pathways	-	No
EI24	9538	etoposide-induced protein 2.4 homolog isoform 1	NP_004870.3	1	1	1	3	0.76	1.3	22.7	4.07	24.8	7.5	2	2	5526	9538	etoposide induced 2.4 mRNA	Signal transducer activity	Integral to membrane	Integral membrane protein	Cell communication;Signal transduction	SP;TM	No
PHF6	84295	PHD finger protein 6 isoform 1	NP_001015877.1	2	5	5	12	0.76	1.13	20.99	12.15	40.3	34.5	6	6	2330	84295	PHD finger protein 6	Transcription regulator activity	Nucleolus;Nucleus;Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PHD;NLS	Yes
KIAA1671	85379	uncharacterized protein KIAA1671	NP_001138678.1	1	3	3	5	0.76	1.11	14.07	4.87	15.1	7.7	2	2	19693	85379	KIAA1671	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
SIPA1L3	23094	signal-induced proliferation-associated 1-like protein 3	NP_055888.1	1	3	4	6	0.76	1.09	3.87	0.03	5.1	0.1	3	3	18755	23094	Signal-induced proliferation-associated 1 like 3	Peptide binding	-	Unclassified	Biological_process unknown	PDZ;CC	Yes
SUCLG2	8801	succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial isoform 2 precursor	NP_003839.2	2	13	13	38	0.76	1.08	5.32	1.99	17.4	9.2	18	18	6799	8801	succinate-CoA ligase, GDP-forming, betasubunit	Ligase activity	Mitochondrion	Enzyme: Ligase	Metabolism;Energy pathways	-	Yes
CYB5B	80777	cytochrome b5 type B	NP_085056.2	1	2	2	3	0.76	1.06	69.7	8.61	86.7	13	2	2	13106	80777	None	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	TM	Yes
EEF1A1	1915	elongation factor 1-alpha 1	NP_001393.1	1	14	25	353	0.76	1.04	9.2	11.99	83.3	212.6	108	109	559	1915	eukaryotic translation elongation factor 1alpha 1	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of cell cycle	-	Yes

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MPHOSPH8	54737	M-phase phosphoprotein 8	NP_059990.2	1	2	2	4	0.76	1.02	15.53	15.26	16.9	22.3	2	2	13682	54737	None	Molecular function unknown	Nucleus	Cell cycle control protein	Cell growth and/or maintenance	CHROMO;ANK;CC	Yes
TOMM70A	9868	mitochondrial import receptor subunit TOM70	NP_055635.3	1	15	15	41	0.76	0.93	8.4	6.08	28.3	25	19	19	16194	9868	translocase of outer mitochondrial membrane70 homolog A (yeast)	Auxiliary transport protein activity	Mitochondrion	Membrane transport protein	Transport	SP;TM;TPR	Yes
CCDC53	51019	WASH complex subunit CCDC53 isoform 1	NP_057137.1	2	1	1	4	0.76	0.92	19.47	40.31	21.1	56.1	2	2	13031	51019	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	Yes
APMAP	57136	adipocyte plasma membrane-associated protein	NP_065392.1	1	15	15	48	0.76	0.89	6.47	8.5	25.1	39.3	25	25									
EPHX1	2052	epoxide hydrolase 1	NP_001129490.1	1	8	8	22	0.76	0.87	7.96	8.67	21.1	26.5	12	12	581	2052	epoxide hydrolase 1, microsomal (xenobiotic)	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase	Metabolism;Energy pathways	ABH	No
HSPA4L	22824	heat shock 70 kDa protein 4L	NP_055093.2	1	23	28	86	0.76	0.85	6.77	9.27	28.8	45.1	30	30	7137	22824	heat shock 70kDa protein 4-like	Heat shock protein activity	Cytoplasm	Heat shock protein	Protein metabolism	-	Yes
ERP29	10961	endoplasmic reticulum resident protein 29 isoform 1 precursor	NP_006808.1	2	8	8	37	0.76	0.83	6.49	6.55	21.1	23.3	18	18	3794	10961	chromosome 12 open reading frame 8	Chaperone activity	Endoplasmic reticulum	Chaperone	Protein folding	SP;TM	Yes
VDAC3	7419	voltage-dependent anion-selective channel protein 3 isoform 1	NP_005653.3	2	11	12	78	0.76	0.83	5.2	5.69	21.8	26.4	30	30	6750	7419	voltage-dependent anion channel 3	Voltage-gated ion channel activity	Mitochondrion	Voltage gated channel	Transport	LZ	Yes
ATP13A1	57130	manganese-transporting ATPase 13A1	NP_065143.2	1	8	8	17	0.76	0.82	2.92	5.44	7	14.1	10	10	12501	57130	ATPase type 13A1	ATPase activity	Integral to membrane	ATPase	Metabolism;Energy pathways	TM	Yes
ICMT	23463	protein-S-isoprenylcysteine O-methyltransferase	NP_036537.1	1	1	1	1	0.76	0.8					1	1	9321	23463	isoprenylcysteine carboxyl methyltransferase	Methyltransferase activity	Endoplasmic reticulum	Enzyme: Methyltransferase	Protein modification	TM	Yes
RAB4B	53916	ras-related protein Rab-4B	NP_057238.3	10	2	4	37	0.76	0.78	38.13	48.02	42.5	57.3	2	2	11473	53916	RAB4B, member RAS oncogene family	GTPase activity	-	GTPase	Cell communication;Signal transduction	RAB	Yes
RALB	5899	ras-related protein Ral-B	NP_002872.1	1	2	3	7	0.76	0.77	16.91	3.41	18.4	3.7	2	2	1550	5899	v-ral simian leukemia viral oncogene homolog B(ras related; GTP binding protein)	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	RAS	No
CAST	831	calpastatin isoform f	NP_001035905.1	2	4	27	136	0.76	0.77	13.37	3.27	29.3	7.1	8	8	233	831	calpastatin	Protease inhibitor activity	Nucleus;Cytoplasm;Perinuclear region	Protease inhibitor	Protein metabolism	CC	Yes
ARMCX3	51566	armadillo repeat-containing X-linked protein 3	NP_057691.1	1	3	3	5	0.76	0.77	9.26	14.06	12.2	19	3	3	2294	51566	armadillo repeat containing, X-linked 3	Molecular function unknown	Plasma membrane	Unclassified	Immune response;Embryonic development	ARM;TM	Yes
MICAL2	9645	protein-methionine sulfoxide oxidase MICAL2 isoform a	NP_055447.1	5	2	3	5	0.76	0.77					1	1	10085	9645	microtubule associated monoxygenase, calponinand LIM domain containing 2	Cytoskeletal protein binding	-	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;LIM	Yes
HSD17B11	51170	estradiol 17-beta-dehydrogenase 11 precursor	NP_057329.3	1	1	1	2	0.76	0.7					1	1	10881	51170	dehydrogenase/reductase (SDR family) member 8	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	SP	No
PLEK2	26499	pleckstrin-2	NP_057529.1	1	3	3	7	0.76	0.68	9.61	10.45	14.7	14.3	4	4	12151	26499	pleckstrin 2	Cytoskeletal protein binding	Plasma membrane	Cytoskeletal associated protein	Cell growth and/or maintenance	PH;DSH	Yes
LAMTOR1	55004	ragulator complex protein LAMTOR1	NP_060377.1	1	5	5	15	0.76	0.68	8.14	6.68	17.6	12.9	8	8									
NCOA2	10499	nuclear receptor coactivator 2	NP_006531.1	1	1	1	2	0.76	0.65					1	1	9066	10499	nuclear receptor coactivator 2	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HLH;PAS	Yes
HLA-A	3105	HLA class I histocompatibility antigen, A-1 alpha chain precursor	NP_001229687.1	1	1	6	26	0.76	0.64	6.52	4.68	7.1	4.3	2	2	826	3105	major histocompatibility complex, class I, A	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein	Immune response	IGC;SP;TM	Yes
VPS29	51699	vacuolar protein sorting-associated protein 29 isoform 3	NP_001269079.1	4	4	4	14	0.76	0.63	3.68	11.11	7.9	20.1	8	8	9499	51699	vacuolar protein sorting 29 (yeast)	Hydrolase activity;Protein binding	Endosome	Transport/cargo protein;Enzyme: Hydrolase	Protein metabolism;Protein targeting	-	Yes
LGALS3	3958	galectin-3 isoform 1	NP_002297.2	2	4	4	8	0.76	0.61	27.39	9.63	54.5	14.4	6	6	1090	3958	lectin, galactoside-binding, soluble, 3(galectin 3)	Transcription regulator activity	Cytoplasm	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	GLECT	Yes
C14orf159	80017	UPF0317 protein C14orf159, mitochondrial isoform b precursor	NP_001273399.1	5	4	4	8	0.76	0.55	42.69	31.56	72.1	35.5	4	4	16612	80017	chromosome 14 open reading frame 159	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
BCAM	4059	basal cell adhesion molecule isoform 1 precursor	NP_005572.2	2	7	7	15	0.76	0.55	24.76	10.02	57.1	15.7	8	8	197	4059	Lutheran blood group (Auberger b antigen included)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction;Cell-cell adhesion;Cell-matrix adhesion;Cell adhesion	TM;IG;IGC2;SP	Yes
INPP5K	51763	inositol polyphosphate 5-phosphatase K isoform 1	NP_057616.2	2	1	1	2	0.76	0.54					1	1	8489	51763	None	Lipid phosphatase activity	Golgi apparatus;Endoplasmic reticulum	Lipid phosphatase	Regulation of signal transduction	I_Phosphatase	Yes
PCBP2	5094	poly(rC)-binding protein 2 isoform a	NP_005007.2	6	1	11	78	0.75	1.49	29.84	45.18	32.4	121	2	2	3129	5094	poly(rC) binding protein 2	RNA binding;DNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	KH	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
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ARMC8	25852	armadillo repeat-containing protein 8 isoform 2	NP_056211.2	5	3	3	7	0.75	1.39	7.41	10.04	9.7	24.4	3	3	9992	25852	armadillo repeat containing 8	Molecular function unknown	-	Unclassified	Biological_process unknown	ARM	No
DEFA6	1671	defensin-6 preproprotein	NP_001917.1	1	1	1	2	0.75	1.23					1	1	2719	1671	defensin, alpha 6, Paneth cell-specific	Defense/immunity protein activity	Secretory granule	Defensin	Immune response	SP	Yes
URB1	9875	nucleolar pre-ribosomal-associated protein 1	NP_055640.2	1	5	5	8	0.75	1.23	41.05	7.1	78.4	19.7	5	5	19701	9875	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	Protein binding	-	Unclassified	Biological_process unknown	-	Yes
IRF6	3664	interferon regulatory factor 6 isoform 1	NP_006138.1	2	13	13	38	0.75	1.21	9.79	10.44	34.4	63.4	21	21	6227	3664	interferon regulatory factor 6	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	IRF	Yes
CIRBP	1153	cold-inducible RNA-binding protein isoform 1	NP_001271.1	3	6	6	11	0.75	1.16	14.34	18.15	24.3	49.6	5	5	8375	1153	cold inducible RNA binding protein	RNA binding	Nucleus	RNA binding protein	Cell communication;Signal transduction	RRM	Yes
ZZEF1	23140	zinc finger ZZ-type and EF-hand domain-containing protein 1	NP_055928.3	1	1	1	1	0.75	1.16					1	1	15906	23140	zinc finger, ZZ-type with EF hand domain 1	Molecular function unknown	-	Unclassified	Biological_process unknown	EF;F58C;ZnF_ZZ	Yes
CNN2	1265	calponin-2 isoform d	NP_001290430.1	4	12	13	46	0.75	1.15	10.99	9.94	38	54.5	20	20	3847	1265	calponin 2	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CH	Yes
FBLIM1	54751	filamin-binding LIM protein 1 isoform a	NP_060026.2	3	7	7	12	0.75	1.07	7.71	13.4	14.2	36.2	6	6	9669	54751	None	Cytoskeletal protein binding	Actin cytoskeleton	Cytoskeletal associated protein	Regulation of cell shape	LIM;NES	No
NR2F1	7025	COUP transcription factor 1	NP_005645.1	4	1	1	1	0.75	1.05					1	1	584	7025	nuclear receptor subfamily 2, group F, member 1	Ligand-dependent nuclear receptor activity	Nucleus	Nuclear receptor	Cell communication;Signal transduction	ZnF_C4;HOLI	Yes
GOLGA7	51125	Golgin subfamily A member 7 isoform a	NP_057183.2	2	1	1	10	0.75	1.05	20.99	21.94	36.2	55	5	5	13595	51125	golgi autoantigen, golgin subfamily a, 7	Transporter activity	Golgi apparatus	Integral membrane protein	Transport	CC	No
XPO4	64328	exportin-4	NP_071904.4	1	5	6	14	0.75	1.04	29.02	4.02	57.4	10.2	6	6	18307	64328	exportin 4	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	Yes
STBD1	8987	starch-binding domain-containing protein 1	NP_003934.1	1	2	2	3	0.75	1.03	0.94	8.63	1	12.6	2	2	8460	8987	None	Molecular function unknown	Plasma membrane	Integral membrane protein	Biological_process unknown	TM	Yes
HIP1R	9026	huntingtin-interacting protein 1-related protein isoform 1	NP_003950.1	3	3	4	6	0.75	0.99	0.5	7.3	0.6	12.6	3	3	10412	9026	None	Cytoskeletal protein binding	Cytoplasmic vesicle	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
SEC11A	23478	signal peptidase complex catalytic subunit SEC11A isoform 3	NP_001258851.1	6	5	5	11	0.75	0.99	16	22.71	32.4	65.3	7	7	7503	23478	SEC11-like 1 (S. cerevisiae)	Aminopeptidase activity	-	Aminopeptidase	Protein metabolism	TM	Yes
NPC2	10577	epididymal secretory protein E1 precursor	NP_006423.1	1	1	1	2	0.75	0.99					1	1	3008	10577	Niemann-Pick disease, type C2	Transporter activity	Lysosome	Transport/cargo protein	Metabolism;Energy pathways	SP	Yes
ZNF414	84330	zinc finger protein 414 isoform 1	NP_001139647.1	1	1	1	2	0.75	0.98					1	1	17511	84330	zinc finger protein 414	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZNFC2	No
NAGK	55577	N-acetyl-D-glucosamine kinase	NP_060037.3	1	7	7	18	0.75	0.94	11.64	11.82	26.5	34.1	9	9	8441	55577	N-acetylglucosamine kinase	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
UBLCP1	134510	ubiquitin-like domain-containing CTD phosphatase 1	NP_659486.2	1	3	3	4	0.75	0.9	25.4	16.83	33.8	26.7	3	3	8318	134510	None	Hydrolase activity	Nucleus	Enzyme: Phosphatase	RNA metabolism	UBQ;CC;CPDc	No
ITPA	3704	inosine triphosphate pyrophosphatase isoform a	NP_258412.1	3	2	2	5	0.75	0.86	5.08	2.86	6.6	4.3	3	3	8856	3704	inosine triphosphatase (nucleoside triphosphatepyrophosphatase)	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	-	Yes
ARL3	403	ADP-ribosylation factor-like protein 3	NP_004302.1	1	8	8	16	0.75	0.84	5.36	4.28	12.1	10.8	9	9	5260	403	ADP-ribosylation factor-like 3	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	ARF	Yes
RDH11	51109	retinol dehydrogenase 11 isoform 1 precursor	NP_057110.3	2	6	6	16	0.75	0.84	11.13	13.06	25.3	33.7	9	9	9707	51109	retinol dehydrogenase 11 (all-trans and 9-cis)	Catalytic activity	Endoplasmic reticulum	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM	Yes
GNPAT	8443	dihydroxyacetone phosphate acyltransferase	NP_055051.1	1	3	3	5	0.75	0.83	1.61	22.41	2.1	33.2	3	3	4120	8443	glyceronephosphate O-acyltransferase	Acyltransferase activity	Peroxisome	Enzyme: Acyltransferase	Metabolism;Energy pathways	PISC	No
RIN1	9610	ras and Rab interactor 1	NP_004283.2	1	7	7	15	0.75	0.8	6.49	3.46	13.9	7.8	8	8	5813	9610	Ras and Rab interactor 1	Molecular function unknown	Plasma membrane	Unclassified	Cell communication;Signal transduction	SH2;VPS9;RA	Yes
STX17	55014	syntaxin-17	NP_060389.2	1	2	2	3	0.75	0.79	1.31	40.99	1.4	48.2	2	2	5013	55014	syntaxin 17	Auxiliary transport protein activity	Endoplasmic reticulum	Membrane transport protein	Transport	CC;TM;t_SNARE	Yes
IAH1	285148	isoamyl acetate-hydrolyzing esterase 1 homolog precursor	NP_001034702.1	1	4	4	6	0.75	0.77	28.96	8.36	38.8	11.1	3	3	19064	285148	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	Hydrolase activity	-	Enzyme: Esterase	Energy pathways;Metabolism	-	No
TACO1	51204	translational activator of cytochrome c oxidase 1	NP_057444.2	1	3	3	6	0.75	0.73	21.61	9.46	28.8	12	3	3	17421	51204	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	Yes
EHD2	30846	EH domain-containing protein 2	NP_055416.2	1	13	15	46	0.75	0.73	8.52	14.8	32.8	58.4	25	25	10434	30846	EH-domain containing 2	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	EH;NLS	Yes
HSPB1	3315	heat shock protein beta-1	NP_001531.1	1	12	12	252	0.75	0.72	4.89	4.58	43.8	39.3	132	131	9076	3315	heat shock 27kDa protein 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	Yes
TMPO	7112	thymopoietin isoform beta	NP_001027454.1	3	8	15	44	0.75	0.72	8.55	13.47	21.5	33.1	11	11	1777	7112	thymopoietin	Molecular function unknown	Nucleus;Nuclear membrane;Mitochondrion;Cytoplasm	Peptide hormone	Nuclear organization and biogenesis;Regulation of cell cycle	TM	Yes
RAP1A	5906	ras-related protein Rap-1A precursor	NP_001010935.1	1	2	9	22	0.75	0.72	42.33	31.75	47.1	33.3	2	2	1545	5906	RAP1A, member of RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAS	No

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PHAX	51808	phosphorylated adapter RNA export protein	NP_115553.2	1	3	3	5	0.75	0.71	22.89	32.52	24.6	33.7	2	2	15122	51808	None	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	NES	No
VEZT	55591	vezatin	NP_060069.3	1	2	2	3	0.75	0.63	39.22	146.24	43.2	209.4	2	2	11671	55591	None	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	TM;CC	Yes
ARPP19	10776	cAMP-regulated phosphoprotein 19 isoform 1	NP_001293120.1	9	3	3	4	0.75	0.62	21.02	20.52	22.5	18.2	2	2	9264	10776	None	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	-	Yes
FIS1	51024	mitochondrial fission 1 protein	NP_057152.2	1	4	4	16	0.75	0.6	16.94	10.28	37.1	17.6	8	8	12352	51024	tetratricopeptide repeat domain 11	Molecular function unknown	Mitochondrion	Unclassified	Apoptosis	TM;LZ;CC;TPR	Yes
C16orf62	57020	UPF0505 protein C16orf62 isoform 1	NP_064710.4	2	1	1	2	0.75	0.55					1	1	14455	57020	None	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	No
GBP6	163351	guanylate-binding protein 6	NP_940862.2	1	5	5	8	0.75	0.55	5.6	75.5	8.4	100.1	4	4	13572	163351	guanylate binding protein family, member 6	GTPase activity	-	GTPase	Cell communication;Signal transduction	CC	No
CNNM3	26505	metal transporter CNNM3 isoform 1 precursor	NP_060093.3	2	1	1	2	0.74	1.42					1	1	7419	26505	cyclin M3	Molecular function unknown	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	TM	No
VIL1	7429	villin-1	NP_009058.2	1	1	1	2	0.74	1.33					1	1	1898	7429	villin 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	GEL;VHP	Yes
RTN3	10313	reticulon-3 isoform d	NP_958833.1	9	3	3	7	0.74	1.21	27.95	16.22	29.9	28.3	2	2	18516	10313	reticulon 3	Molecular function unknown	Endoplasmic reticulum	Integral membrane protein	Biological_process unknown	TM	Yes
PCDH1	5097	protocadherin-1 isoform 2 precursor	NP_115796.2	4	1	1	1	0.74	1.2					1	1	4692	5097	protocadherin 1 (cadherin-like 1)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell adhesion	SP;Cadherin;TM	Yes
HSPE1-MOB4	100529241	HSPE1-MOB4 protein	NP_001189414.1	4	4	5	19	0.74	1.17	4.31	15.18	8.5	49.5	7	7									
GNB2	2783	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	NP_005264.2	3	4	10	49	0.74	1.17	15.07	7.32	36.4	27.5	10	10	11820	2783	guanine nucleotide binding protein (G protein),beta polypeptide 2	GTPase activity	Cytoplasm	G protein	Cell communication;Signal transduction	CC;WD40	Yes
SPG20	23111	spartin	NP_001135766.1	1	2	2	3	0.74	1.15	19.08	42.76	20.2	78.9	2	2	6170	23111	spastic paraplegia 20, spartin (Troyersyndrome)	Molecular function unknown	Cytoplasm	Unclassified	Transport	CC	Yes
PIR	8544	pirin	NP_001018119.1	1	1	1	2	0.74	1.12					1	1	4510	8544	pirin (iron-binding nuclear protein)	Transcription regulator activity;Transcription cofactor activity	Nuclear matrix	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CMPK2	129607	UMP-CMP kinase 2, mitochondrial isoform 1 precursor	NP_997198.2	3	2	2	4	0.74	1.07	3.81	12.86	4	19.6	2	2	11233	129607	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
VKORC1L1	154807	vitamin K epoxide reductase complex subunit 1-like protein 1 isoform 2	NP_001271271.1	2	2	2	3	0.74	1.06					1	1	12312	154807	vitamin K epoxide reductase complex, subunit1-like 1	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
AK2	204	adenylate kinase 2, mitochondrial isoform a	NP_001616.1	3	7	7	24	0.74	1.01	15.83	9.35	38.5	30.5	10	10	47	204	adenylate kinase 2	Catalytic activity	Mitochondrion	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
RBFOX2	23543	RNA binding protein fox-1 homolog 2 isoform 5	NP_001076047.1	12	1	1	1	0.74	1					1	1									
HMGCL	3155	hydroxymethylglutaryl-CoA lyase, mitochondrial isoform 1 precursor	NP_000182.2	1	1	1	2	0.74	0.96					1	1	2003	3155	3-hydroxymethyl-3-methylglutaryl-Coenzyme Alyase (hydroxymethylglutaricaciduria)	Lyase activity	Mitochondrion	Enzyme: Lyase	Metabolism;Energy pathways	SP	Yes
NDUFS7	374291	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NP_077718.3	1	4	4	8	0.74	0.88	8.14	4.62	13.4	9.1	5	5	3491	374291	NADH dehydrogenase (ubiquinone) Fe-S protein7, 20kDa (NADH-coenzyme Q reductase)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
GLO1	2739	lactoylglutathione lyase	NP_006699.2	1	7	7	13	0.74	0.87	13.62	14.54	32.7	41.7	10	10	730	2739	glyoxalase I	Lyase activity	Cytoplasm	Enzyme: Lyase	Metabolism;Energy pathways	-	Yes
HOOK2	29911	protein Hook homolog 2 isoform 1	NP_037444.2	2	1	1	2	0.74	0.87					1	1	9698	29911	hook homolog 2 (Drosophila)	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC;TM	Yes
POGLUT1	56983	protein O-glucosyltransferase 1 precursor	NP_689518.1	1	4	4	12	0.74	0.85	14.25	7.92	26.4	16.5	6	6									
CCDC50	152137	coiled-coil domain-containing protein 50 long isoform	NP_848018.1	2	1	1	2	0.74	0.83					1	1	6463	152137	chromosome 3 open reading frame 6	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	CC	Yes
ITGB4	3691	integrin beta-4 isoform 1 precursor	NP_000204.3	1	1	65	204	0.74	0.82					1	1	946	3691	integrin, beta 4	Cell adhesion molecule activity	Integral to membrane;Nucleus	Adhesion molecule	Cell communication;Signal transduction;Cell migration;Cell adhesion;Wound healing	PSI;VWA;CALXB;FN3;TM;EGF;SP	Yes
PLP2	5355	proteolipid protein 2	NP_002659.1	1	2	2	8	0.74	0.78	14.46	16.6	21.5	26.4	4	4	2121	5355	proteolipid protein 2 (colonicepithelium-enriched)	Ion channel activity	Endoplasmic reticulum	Ion channel	Transport	TM;SP	No
HOMER3	9454	homer protein homolog 3 isoform 1	NP_004829.3	3	5	5	8	0.74	0.76	14.2	17.8	23.8	31	5	5	7270	9454	homer homolog 3 (Drosophila)	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	WH1;SPECTRIN;CC	Yes
CSNK1D	1453	casein kinase I isoform delta isoform 1	NP_001884.2	2	1	4	6	0.74	0.74					1	1	2920	1453	casein kinase 1, delta	Protein serine/threonine kinase activity	Cytoplasm;Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes

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MCM5	4174	DNA replication licensing factor MCM5	NP_006730.2	1	14	14	31	0.74	0.73	11.99	8.52	37.8	26	17	17	4075	4174	MCM5 minichromosome maintenance deficient 5,cell division cycle 46 (S. cerevisiae)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	MCM	Yes
PALLD	23022	palladin isoform 4	NP_001159582.1	6	19	19	37	0.74	0.72	9.59	12.4	32.4	40.5	20	19	9731	23022	None	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	IGC2	No
SAMD9	54809	sterile alpha motif domain-containing protein 9	NP_060124.2	2	16	17	38	0.74	0.72	6.31	8.95	20	27.9	18	18	11531	54809	sterile alpha motif domain containing 9	Molecular function unknown	-	Unclassified	Biological_process unknown	SAM	Yes
HEBP1	50865	heme-binding protein 1	NP_057071.2	1	1	1	2	0.74	0.72					1	1	16162	50865	heme binding protein 1	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
PLIN3	10226	perilipin-3 isoform 1	NP_005808.3	3	18	18	74	0.74	0.7	11.51	8.56	56.1	38.3	38	38	4080	10226	mannose-6-phosphate receptor binding protein1	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
AIM1	202	absent in melanoma 1 protein	NP_001615.2	1	30	30	79	0.74	0.69	8.1	8.11	40.7	38.1	43	43	18576	202	absent in melanoma 1	Calcium ion binding	Cytoskeleton	Calcium binding protein	Cell communication;Regulation of cell proliferation;Signal transduction	XTAL	Yes
PKP2	5318	plakophilin-2 isoform 2b	NP_004563.2	6	21	22	52	0.74	0.68	8.05	12.3	30	41.8	24	23	4177	5318	plakophilin 2	Molecular function unknown	Nucleus	Unclassified	Cell adhesion	ARM	Yes
AGO4	192670	protein argonaute-4	NP_060099.2	4	2	2	2	0.74	0.67	8.38	11.04	8.8	10.5	2	2									
PRDX3	10935	thioredoxin-dependent peroxide reductase, mitochondrial isoform a precursor	NP_006784.1	2	8	8	45	0.74	0.66	5.18	11.03	18.9	36.7	24	24	5305	10935	peroxiredoxin 3	Peroxidase activity	Mitochondrion	Enzyme: Peroxidase	Metabolism;Energy pathways	-	Yes
LAMP1	3916	lysosome-associated membrane glycoprotein 1 precursor	NP_005552.3	1	5	5	29	0.74	0.64	12.74	15.36	36.4	37.8	14	14	1076	3916	lysosomal-associated membrane protein 1	Molecular function unknown	Lysosome	Integral membrane protein	Biological_process unknown	SP;TM	Yes
EFNB2	1948	ephrin-B2 precursor	NP_004084.1	1	1	1	2	0.74	0.61					1	1	2754	1948	ephrin-B2	Receptor binding	Plasma membrane	Membrane bound ligand	Cell communication;Signal transduction	SP;TM	Yes
FAM83A	84985	protein FAM83A isoform a	NP_116288.2	3	2	2	3	0.74	0.57	18.61	44.3	19.8	37.1	2	2	17489	84985	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PHPT1	29085	14 kDa phosphohistidine phosphatase isoform 4	NP_001274271.1	4	2	2	3	0.73	1.73					1	1	17849	29085	phosphohistidine phosphatase 1	Phosphoprotein phosphatase activity	Cytoplasm	Enzyme: Phosphatase	Biological_process unknown	-	No
MFN1	55669	mitofusin-1	NP_284941.2	1	1	2	4	0.73	1.34					1	1	16344	55669	mitofusin 1	GTPase activity	Mitochondrion	GTPase	Mitochondrion organization and biogenesis	CC;TM	Yes
DNAJB1	3337	dnaJ homolog subfamily B member 1 isoform 1	NP_006136.1	2	12	13	39	0.73	1.19	12.4	6.32	37.7	30.9	16	16	5198	3337	DnaJ (Hsp40) homolog, subfamily B, member 1	Heat shock protein activity	Cytoplasm	Heat shock protein	Protein metabolism	DNAJ	Yes
PPP6C	5537	serine/threonine-protein phosphatase 6 catalytic subunit isoform a	NP_001116827.1	3	5	5	8	0.73	1.13	4.19	25.18	4.4	42	2	2	2141	5537	protein phosphatase 6, catalytic subunit	Protein serine/threonine phosphatase activity	Nucleus	Serine/threonine phosphatase	Cell communication;Signal transduction	PP2A	Yes
CSRP1	1465	cysteine and glycine-rich protein 1 isoform 1	NP_004069.1	2	4	4	12	0.73	1.13	14.2	3.7	28.1	11.1	7	7	470	1465	cysteine and glycine-rich protein 1	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	LIM;NLS	Yes
TELO2	9894	telomere length regulation protein TEL2 homolog	NP_057195.2	1	7	7	13	0.73	1.06	7.6	12.85	14.7	37.4	7	7	10016	9894	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
PARVA	55742	alpha-parvin	NP_060692.2	1	3	4	15	0.73	1.06	8.65	8.57	14.3	20.5	5	5	16283	55742	parvin, alpha	Cytoskeletal protein binding	Plasma membrane;Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	CH;NLS	Yes
ARMT1	79624	protein-glutamate O-methyltransferase isoform a	NP_078849.1	2	4	4	8	0.73	1.06	4.78	3.03	7	6.4	4	4									
SNX3	8724	sorting nexin-3 isoform a	NP_003786.1	4	2	3	4	0.73	1.04					1	1	9333	8724	sorting nexin 3	Protein transporter activity	Endosome	Transport/cargo protein	Intracellular signaling cascade;Protein transport	PX	Yes
ABI1	10006	abl interactor 1 isoform a	NP_005461.2	12	6	7	11	0.73	1.01	12.32	15.94	22.4	41	6	6	4336	10006	abl-interactor 1	Binding	Cytosol	Adapter molecule	Regulation of cell growth;Signal transduction	SH3;PEST	Yes
ERH	2079	enhancer of rudimentary homolog	NP_004441.1	1	2	2	6	0.73	1	9.35	8.06	11.9	14	3	3	9026	2079	enhancer of rudimentary homolog (Drosophila)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
HEATR6	63897	HEAT repeat-containing protein 6	NP_071353.4	1	4	4	8	0.73	0.96	7.3	15.18	10.7	29.8	4	4	12399	63897	None	Molecular function unknown	-	Unclassified	Biological_process unknown	HEAT	No
TFDP1	7027	transcription factor Dp-1	NP_009042.1	1	1	1	2	0.73	0.96					1	1	1792	7027	transcription factor Dp-1	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
SLMAP	7871	sarcolemmal membrane-associated protein isoform a	NP_001291349.1	5	4	4	16	0.73	0.96	19.46	19.62	44.5	61.6	9	9	4079	7871	sarcolemma associated protein	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM;FHA;CC	Yes
SLC12A9	56996	solute carrier family 12 member 9 isoform 1	NP_064631.2	3	3	3	6	0.73	0.89	16.8	11.31	21.5	17.5	3	3	11564	56996	solute carrier family 12 (potassium/chloridetransporters), member 9	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	-	No
TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	NP_110382.3	1	7	7	14	0.73	0.85	10.58	8.35	23.6	21.5	9	9	15590	81542	thioredoxin domain containing	Oxidoreductase activity	Endoplasmic reticulum	Enzyme: Oxidoreductase	Metabolism;Energy pathways	SP;TM	No
GSTZ1	2954	maleylacetoacetate isomerase isoform 1	NP_665877.1	3	2	2	7	0.73	0.85	59.4	60.09	86.4	109.6	3	3	4785	2954	glutathione transferase zeta 1(maleylacetoacetate isomerase)	Glutathione transferase activity	-	Enzyme: Glutathione transferase	Metabolism;Energy pathways	-	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

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C1orf116	79098	specifically androgen-regulated gene protein isoform 1	NP_076427.2	2	15	15	34	0.73	0.8	8.14	7.56	26.5	27	19	19	15294	79098	None	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
CEPT1	10390	choline/ethanolaminephosphotransferase 1	NP_001007795.1	1	1	1	4	0.73	0.79	7.69	26.24	8	30	2	2	13024	10390	choline/ethanolamine phosphotransferase 1	Catalytic activity	Integral to membrane	Enzyme: Phosphotransferase	Metabolism;Energy pathways	TM	Yes
CAPG	822	macrophage-capping protein isoform 1	NP_001738.2	2	12	12	49	0.73	0.77	7.88	8.81	29.2	35.1	25	25	1088	822	capping protein (actin filament), gelsolin-like	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	GEL	Yes
TXNIP	10628	thioredoxin-interacting protein	NP_006463.3	1	2	2	6	0.73	0.77	25.6	16.4	33.1	22.1	3	3	5964	10628	thioredoxin interacting protein	Molecular function unknown	Cytoplasm	Cell cycle control protein	Cell communication;Signal transduction	-	Yes
MTX3	345778	metaxin-3 isoform 1	NP_001161213.1	2	1	1	2	0.73	0.77					1	1	17614	345778	metaxin 3	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
GABARAP	11337	gamma-aminobutyric acid receptor-associated protein	NP_009209.1	1	1	1	1	0.73	0.73					1	1	5496	11337	GABA(A) receptor-associated protein	Molecular function unknown	Cytoplasm	Unclassified	Transport	-	No
ITGA3	3675	integrin alpha-3 isoform a precursor	NP_002195.1	2	18	18	51	0.73	0.71	7.8	10.72	31.2	42.8	29	29	5431	3675	integrin, alpha 3 (antigen CD49C, alpha 3subunit of VLA-3 receptor)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;INTA;SP	Yes
DPP7	29952	dipeptidyl peptidase 2 preproprotein	NP_037511.2	1	3	3	6	0.73	0.7	12.27	68.55	15.7	100.7	3	3	7634	29952	dipeptidylpeptidase 7	Serine-type peptidase activity	Lysosome	Serine protease	Protein metabolism	SP	Yes
NDUFA13	51079	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NP_057049.5	1	4	4	16	0.73	0.66	7.65	11.7	16.8	23.4	9	9	9452	51079	None	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
GSTK1	373156	glutathione S-transferase kappa 1 isoform a	NP_057001.1	4	7	7	27	0.73	0.57	9.63	12.78	27.7	29	15	15	13613	373156	glutathione S-transferase kappa 1	Glutathione transferase activity	Peroxisome;Mitochondrion	Enzyme: Glutathione transferase	Metabolism	-	Yes
XPNPEP3	63929	probable Xaa-Pro aminopeptidase 3 isoform 1	NP_071381.1	1	3	4	11	0.72	1.69	23.75	26.25	24.6	69.3	2	2	10052	63929	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ND2	4536	NADH dehydrogenase subunit 2	YP_003024027.1	1	1	1	4	0.72	1.53	33.84	3.84	35.7	8.3	2	2									
PSEN1	5663	presenilin-1 isoform I-467	NP_000012.1	2	1	1	4	0.72	1.25	41.3	2.76	44.1	4.9	2	2	87	5663	presenilin 1 (Alzheimer disease 3)	Cell adhesion molecule activity	Endoplasmic reticulum;Nucleus;Cytoplasm	Integral membrane protein	Cell-cell adhesion	PSN;TM	Yes
H2AFZ	3015	histone H2A.Z	NP_002097.1	6	3	5	23	0.72	1.19	12.77	16.31	24.8	54.9	7	7	823	3015	H2A histone family, member Z	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
ADH5	128	alcohol dehydrogenase class-3	NP_000662.3	1	12	12	49	0.72	1.15	9.16	4.88	35.8	30.4	28	28	64	128	alcohol dehydrogenase 5 (class III), chipolypeptide	Oxidoreductase activity	Cytoplasm	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
ORC1	4998	origin recognition complex subunit 1 isoform 1	NP_004144.2	2	1	1	2	0.72	1.11					1	1									
RPF2	84154	ribosome production factor 2 homolog isoform 1	NP_115570.1	2	3	3	7	0.72	1.11	13.23	6.81	21.7	17.1	5	5	12552	84154	brix domain containing 1	Molecular function unknown	Nucleolus	Unclassified	Biological_process unknown	-	No
YES1	7525	tyrosine-protein kinase Yes	NP_005424.1	50	2	6	26	0.72	1.07	1.5	14.79	1.5	22.6	2	2	1285	7525	v-yes-1 Yamaguchi sarcoma viral oncogene homolog1	Protein-tyrosine kinase activity	Cytoplasm	Tyrosine kinase	Cell communication;Signal transduction	SH3;SH2;Tyr_Kinase	Yes
CSNK1E	1454	casein kinase I isoform epsilon	NP_001885.1	1	1	4	6	0.72	1.03					1	1	2919	1454	casein kinase 1, epsilon	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	DNA repair;Signal transduction	S_T_kinase;NLS	Yes
AURKA	6790	aurora kinase A	NP_003591.2	1	1	1	2	0.72	1.01					1	1	4066	6790	serine/threonine kinase 6	Protein serine/threonine kinase activity	Centrosome	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase	Yes
GGH	8836	gamma-glutamyl hydrolase precursor	NP_003869.1	1	5	5	16	0.72	1	12.29	11.18	25.4	32.3	8	8	3299	8836	gamma-glutamyl hydrolase (conjugase,folylpolygammaglutamyl hydrolase)	Hydrolase activity	Lysosome	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
TANC1	85461	protein TANC1 isoform 1	NP_203752.2	1	1	1	2	0.72	1					1	1	18146	85461	None	Molecular function unknown	Extracellular	Unclassified	Biological_process unknown	ANK;TPR;CC	No
PRPF38A	84950	pre-mRNA-splicing factor 38A	NP_116253.2	1	1	1	1	0.72	0.97					1	1	10972	84950	PRP38 pre-mRNA processing factor 38 (yeast)domain containing A	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
MRPL17	63875	39S ribosomal protein L17, mitochondrial	NP_071344.1	1	4	4	9	0.72	0.97	6.52	17.03	8.2	29.3	3	3	10096	63875	mitochondrial ribosomal protein L17	Structural constituent of ribosome	Mitochondrion	Ribosomal subunit	Protein metabolism	-	No
SYNPO	11346	synaptopodin isoform C	NP_001159681.1	2	1	6	12	0.72	0.91					1	1	12179	11346	synaptopodin	Cytoskeletal protein binding	Cytoskeleton;Nucleus;Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
RTN4	57142	reticulon-4 isoform A	NP_065393.1	5	7	7	91	0.72	0.91	6.97	5.76	35	36.2	46	45	7259	57142	reticulon 4	Protein binding	Endoplasmic reticulum membrane;Nucleus;Cytoplasm	Integral membrane protein	Regulation of cell growth	TM;CC	Yes
NEDD4	4734	E3 ubiquitin-protein ligase NEDD4 isoform 3	NP_001271267.1	5	4	5	12	0.72	0.89	8.43	3.13	10.6	4.8	3	3	3786	4734	neural precursor cell expressed,developmentally down-regulated 4	Ubiquitin-specific protease activity	Cytoplasm	Ubiquitin proteasome system protein	Protein metabolism	WW;HECT;C2	Yes
CLIC4	25932	chloride intracellular channel protein 4	NP_039234.1	2	10	11	40	0.72	0.89	10.46	15.66	38.2	76.6	24	24	5943	25932	chloride intracellular channel 4	Intracellular ligand-gated ion channel activity	Cytoplasm	Intracellular ligand gated channel	Transport	-	Yes
MYO1D	4642	unconventional myosin-Id isoform 1	NP_056009.1	3	10	10	17	0.72	0.89	18.52	4.66	46.8	13.8	11	11	7581	4642	myosin ID	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	IQ	Yes

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PARP12	64761	poly [ADP-ribose] polymerase 12	NP_073587.1	1	1	1	1	0.72	0.87					1	1	15696	64761	poly (ADP-ribose) polymerase family, member 12	DNA binding	-	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C3H1	Yes
SLC25A6	293	ADP/ATP translocase 3	NP_001627.2	2	1	13	152	0.72	0.86	4.51	4.71	9.2	11.4	8	8	2461	293	solute carrier family 25 (mitochondrialcarrier; adenine nucleotide translocator), member 6	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	TM	Yes
RUFY1	80230	RUN and FYVE domain-containing protein 1 isoform a	NP_079434.3	10	13	13	26	0.72	0.83	11.21	8.45	32.3	27.8	15	15	15282	80230	RUN and FYVE domain containing 1	Ubiquitin-specific protease activity	Endosome	Ubiquitin proteasome system protein	Cell communication;Signal transduction	CC;FYVE	Yes
ALDH3A1	218	aldehyde dehydrogenase, dimeric NADP-preferring	NP_000682.3	5	1	2	4	0.72	0.82					1	1	4	218	aldehyde dehydrogenase 3 family, memberA1	Catalytic activity	Cytoplasm	Enzyme: Dehydrogenase	Metabolism;Energy pathways	CC	Yes
ACAP2	23527	arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	NP_036419.3	1	6	6	11	0.72	0.81	10.85	10.53	22.3	24.4	8	8	9681	23527	centaurin, beta 2	GTPase activator activity	Cytoplasm	GTPase activating protein	Cell communication;Signal transduction	ANK;CC;ARFGAP	Yes
TECR	9524	very-long-chain enoyl-CoA reductase	NP_612510.1	1	6	6	12	0.72	0.81	21.32	4.65	42.3	9.9	7	7	17076	9524	glycoprotein, synaptic 2	Catalytic activity	Endoplasmic reticulum	Enzyme: Reductase	Metabolism;Energy pathways	TM	No
NEDD8-MDP1	100528064	NEDD8-MDP1 protein	NP_001186752.1	2	1	1	4	0.72	0.8	10.94	6.02	13.6	8.3	3	3									
ELMOD2	255520	ELMO domain-containing protein 2	NP_714913.1	1	2	2	3	0.72	0.78	7.82	4.85	8	5.3	2	2	13267	255520	ELMO domain containing 2	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
ANXA2	302	annexin A2 isoform 1	NP_001002858.1	2	31	31	528	0.72	0.78	2.29	2.38	28.4	32.3	285	284	1061	302	annexin A2	Calcium ion binding	Nucleus	Calcium binding protein	Cell communication;Signal transduction	ANX	Yes
KIAA1715	80856	protein lunapark isoform 1 precursor	NP_001291937.1	5	4	4	7	0.72	0.74	23.07	24.13	34.1	36.9	4	4	13886	80856	KIAA1715	Protein binding	Integral to membrane	Integral membrane protein	Biological_process unknown	TM;CC	No
ACSF2	80221	acyl-CoA synthetase family member 2, mitochondrial isoform 1	NP_001275897.1	5	8	8	14	0.72	0.74	4.11	17.08	7.3	31.7	6	6	13380	80221	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
TMEM245	23731	transmembrane protein 245	NP_114401.2	1	1	1	2	0.72	0.72					1	1									
RAB9A	9367	ras-related protein Rab-9A	NP_004242.1	2	1	1	2	0.72	0.71					1	1	2236	9367	RAB9A, member RAS oncogene family	Molecular function unknown	Endosome	Unclassified	Cell communication;Signal transduction	RAB	No
RAC2	5880	ras-related C3 botulinum toxin substrate 2	NP_002863.1	3	4	7	14	0.72	0.71	14.13	13.85	20.5	19.9	4	4	3628	5880	ras-related C3 botulinum toxin substrate 2 (rhofamily, small GTP binding protein Rac2)	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RHO	Yes
ARHGAP21	57584	rho GTPase-activating protein 21	NP_065875.3	1	1	1	2	0.72	0.68					1	1	6445	57584	Rho GTPase activating protein 21	GTPase activator activity	Golgi apparatus	GTPase activating protein	Cell communication;Signal transduction	PDZ;RHOGAP;PH	Yes
MRC2	9902	C-type mannose receptor 2 precursor	NP_006030.2	1	4	4	5	0.72	0.65	29.76	14.86	38.2	17	3	3	10094	9902	mannose receptor, C type 2	Receptor activity	Plasma membrane	Cell surface receptor	Biological_process unknown	SP;FN2;LECTIN_C;TM;RICIN	Yes
SERPINA1	5265	alpha-1-antitrypsin precursor	NP_000286.3	1	1	1	2	0.72	0.64					1	1	2463	5265	serine (or cysteine) proteinase inhibitor,clade A (alpha-1 antiproteinase, antitrypsin), member 1	Protease inhibitor activity	Extracellular	Protease inhibitor	Protein metabolism	SP;SERPIN	Yes
AHNAK2	113146	protein AHNAK2	NP_612429.2	1	89	89	213	0.72	0.61	4.15	5.47	32.6	36.9	114	114	12261	113146	chromosome 14 open reading frame 78	Molecular function unknown	Nucleus	Unclassified	Transport	PDZ	No
MSRA	4482	mitochondrial peptide methionine sulfoxide reductase isoform a precursor	NP_036463.1	4	1	1	2	0.72	0.6					1	1	3152	4482	methionine sulfoxide reductase A	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	SP	Yes
SUN2	25777	SUN domain-containing protein 2 isoform b	NP_056189.1	2	13	14	31	0.72	0.6	12.56	15.52	36.3	37.5	15	15	15611	25777	unc-84 homolog B (C. elegans)	Molecular function unknown	Integral to membrane	Unclassified	Cell organization and biogenesis	TM;CC	Yes
SET	6418	protein SET isoform 2	NP_003002.2	5	2	13	47	0.71	1.74	11.65	11.46	11.7	28.8	2	2	9023	6418	SET translocation (myeloid leukemia-associated)	MHC class I receptor activity;MHC class II receptor activity	Nucleus	MHC complex protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
ERICH1	157697	glutamate-rich protein 1 isoform 1	NP_997215.1	2	1	1	3	0.71	1.74	30.41	15.12	31.1	38.6	2	2	14105	157697	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
SLC30A1	7779	zinc transporter 1	NP_067017.2	1	4	4	6	0.71	1.32	35.75	3.11	46.1	7.1	3	3	15366	7779	solute carrier family 30 (zinc transporter),member 1	Auxiliary transport protein activity	Integral to membrane	Membrane transport protein	Transport	TM	Yes
ARL1	400	ADP-ribosylation factor-like protein 1 isoform 1	NP_001168.1	2	6	6	21	0.71	1.25	14.89	15.18	34.4	66	10	10	4574	400	ADP-ribosylation factor-like 1	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	ARF	Yes
NPC1	4864	Niemann-Pick C1 protein precursor	NP_000262.2	1	8	8	28	0.71	1.12	9.18	7.98	24.9	34.4	14	14	9622	4864	Niemann-Pick disease, type C1	Receptor activity	Cytoplasm	Cell surface receptor	Cell communication;Signal transduction	SP;TM	Yes
NDUFV1	4723	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial isoform 1 precursor	NP_009034.2	2	11	11	20	0.71	1.08	17.49	11.25	45.3	43.9	12	12	1191	4723	NADH dehydrogenase (ubiquinone) flavoprotein1, 51kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
ALDH6A1	4329	methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial isoform 1 precursor	NP_005580.1	3	3	3	6	0.71	1.05	11.25	17.66	13.9	33.1	3	3	4416	4329	aldehyde dehydrogenase 6 family, member A1	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	TM	Yes

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Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

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PIH1D1	55011	PIH1 domain-containing protein 1	NP_060386.1	1	1	1	2	0.71	1.04					1	1	7938	55011	None	Molecular function unknown	-	Unclassified	Biological_process unknown	CC	No
CD58	965	lymphocyte function-associated antigen 3 isoform 1	NP_001770.1	2	1	1	1	0.71	0.99					1	1	1081	965	CD58 antigen, (lymphocyte function-associatedantigen 3)	Molecular function unknown	Plasma membrane	Unclassified	Immune response	SP;IG;GPI;TM	No
CORO1C	23603	coronin-1C isoform a	NP_001098707.1	3	16	17	81	0.71	0.94	6.59	2.36	31.3	14.6	43	43	9244	23603	coronin, actin binding protein, 1C	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	WD40	Yes
TAOK1	57551	serine/threonine-protein kinase TAO1 isoform 1	NP_065842.1	5	1	3	6	0.71	0.89					1	1	15467	57551	TAO kinase 1	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC	No
PPIC	5480	peptidyl-prolyl cis-trans isomerase C precursor	NP_000934.1	1	3	3	11	0.71	0.84	7.91	3.3	12.6	6.2	5	5	459	5480	peptidylprolyl isomerase C (cyclophilin C)	Chaperone activity	-	Chaperone	Protein metabolism	SP	Yes
ANXA4	307	annexin A4	NP_001144.1	1	21	22	61	0.71	0.8	10.27	3.33	42.9	15.1	32	32	112	307	annexin A4	Calcium ion binding	Nucleus	Calcium binding protein	Cell communication;Signal transduction	ANX	Yes
NUP62	23636	nuclear pore glycoprotein p62	NP_057637.2	1	1	1	2	0.71	0.77					1	1	5782	23636	nucleoporin 62kDa	Transporter activity	Nuclear membrane	Transport/cargo protein	Transport	CC	No
NDUFA9	4704	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor	NP_004993.1	1	10	10	32	0.71	0.76	18.04	15.15	60.1	53.6	19	19	4832	4704	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 9, 39kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
TRIM25	7706	E3 ubiquitin/ISG15 ligase TRIM25	NP_005073.2	1	21	21	63	0.71	0.74	5.61	4.75	22.8	20	32	32	2711	7706	tripartite motif-containing 25	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RING;CC;PRY;SPRY	Yes
TOP2A	7153	DNA topoisomerase 2-alpha	NP_001058.2	1	4	11	30	0.71	0.71	9.94	5.51	14.3	7.8	4	4	536	7153	topoisomerase (DNA) II alpha 170kDa	DNA topoisomerase activity	Nucleus	Enzyme: Topoisomerase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
LEMD2	221496	LEM domain-containing protein 2 isoform 1	NP_851853.1	1	4	4	6	0.71	0.71	22.23	5.69	32.6	8.1	4	4	13984	221496	LEM domain containing 2	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
MOV10	4343	putative helicase MOV-10 isoform 1	NP_001123551.1	2	9	9	14	0.71	0.7	10.96	8.87	22.2	17.8	8	8	14732	4343	Mov10, Moloney leukemia virus 10, homolog(mouse)	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Biological_process unknown	-	Yes
DDX60	55601	probable ATP-dependent RNA helicase DDX60	NP_060101.3	3	21	21	40	0.71	0.7	3.45	7.75	10.7	23.9	19	19	7877	55601	None	DNA binding	-	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC	Yes
FLRT2	23768	leucine-rich repeat transmembrane protein FLRT2 precursor	NP_037363.1	1	3	3	5	0.71	0.68	9	5.02	9.1	4.8	2	2	5312	23768	fibronectin leucine rich transmembrane protein2	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	SP;LRR;TM	Yes
PYGL	5836	glycogen phosphorylase, liver form isoform 1	NP_002854.3	2	36	37	148	0.71	0.68	6.46	6.98	39.7	41	70	70	1987	5836	phosphorylase, glycogen; liver (Hers disease,glycogen storage disease type VI)	Phosphorylase activity	-	Enzyme: Phosphorylase	Metabolism;Energy pathways	-	Yes
REL	5966	proto-oncogene c-Rel isoform 1	NP_002899.1	2	1	1	1	0.71	0.67					1	1	1286	5966	v-rel reticuloendotheliosis viral oncogenehomolog (avian)	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	IPT;RHD	Yes
DTX3L	151636	E3 ubiquitin-protein ligase DTX3L	NP_612144.1	1	9	9	14	0.71	0.65	14.48	25.86	25.5	42.6	6	6	16843	151636	deltex 3-like (Drosophila)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	RING;NLS;NES	Yes
NDUFA6	4700	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NP_002481.2	1	2	2	5	0.71	0.63	8.89	15.24	10.9	16.8	3	3	11884	4700	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 6, 14kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
ADIRF	10974	adipogenesis regulatory factor	NP_006820.1	1	1	1	2	0.71	0.58					1	1									
RAB1B	81876	ras-related protein Rab-1B	NP_112243.1	12	6	14	143	0.7	1.51	17.82	11.2	67.7	96.6	24	23	11469	81876	RAB1B, member RAS oncogene family	GTPase activity	Golgi apparatus	GTPase	Cell communication;Signal transduction	RAB	Yes
ADGRE5	976	CD97 antigen isoform 1 preproprotein	NP_510966.1	3	1	1	2	0.7	1.39					1	1									
CAST	831	calpastatin isoform m	NP_001177371.1	4	2	25	127	0.7	1.37	33.53	2.42	42.2	5.8	3	3	233	831	calpastatin	Protease inhibitor activity	Nucleus;Cytoplasm;Perinuclear region	Protease inhibitor	Protein metabolism	CC	Yes
ESRP1	54845	epithelial splicing regulatory protein 1 isoform 1	NP_060167.2	5	3	3	10	0.7	1.08	0.9	2.19	1.3	4.7	4	4	7881	54845	None	RNA binding	Nucleus	RNA binding protein	Biological_process unknown	RRM;SP	No
COPS7B	64708	COP9 signalosome complex subunit 7b isoform b	NP_073567.1	6	3	3	4	0.7	1.07	28.28	36.59	28.7	59.7	2	2	9889	64708	COP9 constitutive photomorphogenic homologsubunit 7B (Arabidopsis)	Molecular function unknown	Cytoplasm	Unclassified	Cell communication;Signal transduction	PINT;CC	No
ADO	84890	2-aminoethanethiol dioxygenase	NP_116193.2	1	3	3	4	0.7	1.06	1.71	12.33	2.1	22.9	3	3	12566	84890	chromosome 10 open reading frame 22	Molecular function unknown	-	Unclassified	Biological_process unknown	-	No
COMT	1312	catechol O-methyltransferase isoform MB-COMT	NP_000745.1	2	7	7	32	0.7	1.05	12.02	7.52	34.5	32.5	16	16	284	1312	catechol-O-methyltransferase	Acyltransferase activity	Endoplasmic reticulum;Cytoplasm	Enzyme: Acyltransferase	Metabolism;Energy pathways	TM	Yes
RAB12	201475	ras-related protein Rab-12	NP_001020471.2	10	1	2	35	0.7	1					1	1	18749	201475	RAB12, member RAS oncogene family	GTP binding	-	G protein	Signal transduction	RAB	No

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CALD1	800	caldesmon isoform 1	NP_149129.2	5	18	18	206	0.7	0.99	3.97	3.06	26.7	28.4	90	84	251	800	caldesmon 1	Cytoskeletal protein binding	Cytoplasm;Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
NBAS	51594	neuroblastoma-amplified sequence	NP_056993.2	1	6	6	11	0.7	0.92	2.21	15.02	2.7	28.3	3	4	10473	51594	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	CC	No
GNAI1	2770	guanine nucleotide-binding protein G(i) subunit alpha-1 isoform 1	NP_002060.4	9	5	9	60	0.7	0.89	13.65	15.04	29.4	41.9	9	9	756	2770	guanine nucleotide binding protein (G protein),alpha inhibiting activity polypeptide 1	GTPase activity	Plasma membrane	G protein	Cell communication;Signal transduction	GALP	Yes
MFI2	4241	melanotransferrin isoform 1 precursor	NP_005920.2	2	4	4	9	0.7	0.86	19.85	15.44	31.9	30.2	5	5	1122	4241	antigen p97 (melanoma associated) identified bymonoclonal antibodies 133.2 and 96.5	Molecular function unknown	Plasma membrane	Unclassified	Immune response	SP;TR_FER	Yes
TGFBRAP1	9392	transforming growth factor-beta receptor-associated protein 1	NP_004248.2	1	1	1	2	0.7	0.84					1	1	6948	9392	transforming growth factor, beta receptorassociated protein 1	Chaperone activity	Cytoplasm	Chaperone	Protein metabolism	-	No
CRIP2	1397	cysteine-rich protein 2 isoform 2	NP_001257766.1	3	4	4	10	0.7	0.83	10.66	17.88	16.7	34	5	5	3113	1397	cysteine-rich protein 2	Receptor signaling complex scaffold activity	Nucleus	Adapter molecule	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	LIM	Yes
EXOC5	10640	exocyst complex component 5	NP_006535.1	1	2	2	4	0.7	0.82	9.97	47.14	9.9	58.8	2	2	7258	10640	SEC10-like 1 (S. cerevisiae)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	CC	Yes
RRM2	6241	ribonucleoside-diphosphate reductase subunit M2 isoform 1	NP_001159403.1	2	2	3	10	0.7	0.82	3.02	16.4	4.2	27.3	4	4	1587	6241	ribonucleotide reductase M2 polypeptide	Oxidoreductase activity	Nucleus	Cell cycle control protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
CKMT1A	548596	creatine kinase U-type, mitochondrial precursor	NP_001015001.1	2	22	23	68	0.7	0.81	11.62	8.25	51.1	41.4	35	35	18683	548596	creatine kinase, mitochondrial 1A	Transferase activity	Mitochondrion	Enzyme: Phosphotransferase	Energy pathways	SP	Yes
DSTN	11034	destrin isoform a	NP_006861.1	2	5	5	11	0.7	0.79	11.98	3.43	22.4	7.1	7	7	16446	11034	destrin (actin depolymerizing factor)	Cytoskeletal protein binding	Nucleus	Cytoskeletal associated protein	Cell growth and/or maintenance	ADF	Yes
PARP9	83666	poly [ADP-ribose] polymerase 9 isoform b	NP_001139575.1	3	12	12	23	0.7	0.78	14.26	14.36	35.8	40.2	12	12	10686	83666	poly (ADP-ribose) polymerase family, member 9	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
GBAS	2631	protein NipSnap homolog 2 isoform 1	NP_001474.1	2	3	3	3	0.7	0.75	1.46	19.62	1.4	21	2	2	4302	2631	glioblastoma amplified sequence	Molecular function unknown	Plasma membrane	Unclassified	Cell communication;Signal transduction	SP;TM	Yes
FERMT1	55612	fermitin family homolog 1	NP_060141.3	1	11	12	36	0.7	0.75	12.73	8.36	37.8	26.1	17	17	6388	55612	chromosome 20 open reading frame 42	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	PH	Yes
ALDH4A1	8659	delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial isoform a precursor	NP_003739.2	2	13	13	30	0.7	0.72	7.68	5.12	22.4	15.4	17	17	6009	8659	aldehyde dehydrogenase 4 family, member A1	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
PNPLA2	57104	patatin-like phospholipase domain-containing protein 2	NP_065109.1	1	1	1	2	0.7	0.71					1	1	11443	57104	patatin-like phospholipase domain containing 2	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism;Energy pathways	TM	No
IL1RAP	3556	interleukin-1 receptor accessory protein isoform 3 precursor	NP_001161403.1	3	2	2	5	0.7	0.71	8.94	10.78	10.8	13.3	3	3	4021	3556	interleukin 1 receptor accessory protein	Receptor activity	Plasma membrane;Soluble fraction	Cell surface receptor	Immune response	TM;IG;TIR;SP	Yes
TEP1	7011	telomerase protein component 1	NP_009041.2	1	2	2	4	0.7	0.68	23.86	47.25	23.8	48.2	2	2	3404	7011	telomerase-associated protein 1	RNA binding	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	WD40	Yes
COL7A1	1294	collagen alpha-1(VII) chain precursor	NP_000085.1	1	14	14	28	0.7	0.66	10.84	12.47	26.9	29.2	12	12	358	1294	collagen, type VII, alpha 1 (epidermolysisbullosa, dystrophic, dominant and recessive)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	VWA;FN3;COLL;KUNITZ;SP	Yes
TRIP10	9322	cdc42-interacting protein 4 isoform 1	NP_001275891.1	1	1	19	46	0.7	0.57					1	1	5142	9322	thyroid hormone receptor interactor 10	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell growth and/or maintenance	FES;CC;SH3	Yes
FAT2	2196	protocadherin Fat 2 precursor	NP_001438.1	1	22	22	39	0.7	0.57	17.56	15.83	65.9	46.3	24	24	5041	2196	FAT tumor suppressor homolog 2 (Drosophila)	Cell adhesion molecule activity	-	Adhesion molecule	Cell communication;Signal transduction	Cadherin;LAMG;EGF;TM	Yes
ITGA5	3678	integrin alpha-5 precursor	NP_002196.2	1	4	4	8	0.7	0.57	10.9	11.13	17.1	14.3	5	5	627	3678	integrin, alpha 5 (fibronectin receptor, alphapolypeptide)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	INTA;SP;TM	Yes
MAP6	4135	microtubule-associated protein 6 isoform 1	NP_149052.1	1	1	1	1	0.69	1.63					1	1	15989	4135	microtubule-associated protein 6	Cytoskeletal protein binding	Cytoskeleton	Cytoskeletal associated protein	Cell growth and/or maintenance	-	No
CIC	23152	protein capicua homolog isoform CIC-L	NP_001291744.1	2	2	2	4	0.69	1.31	42.1	30.68	42.6	61.5	2	2	10831	23152	capicua homolog (Drosophila)	Transcription factor activity	Nucleus;Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	HMG	No
RSU1	6251	ras suppressor protein 1 isoform 1	NP_036557.1	2	5	5	14	0.69	0.94	7.54	5.29	14.7	14.1	8	8	1551	6251	Ras suppressor protein 1	Molecular function unknown	-	Unclassified	Cell adhesion;Signal transduction	LRR	Yes

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ACTN1	87	alpha-actinin-1 isoform b	NP_001093.1	3	36	59	412	0.69	0.9	4.5	5.74	34.6	60.6	118	118	20	87	actinin, alpha 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein;Structural protein	Cell growth and/or maintenance	CH;SPECTRIN;EF	Yes
PKM	5315	pyruvate kinase PKM isoform c	NP_001193725.1	5	6	42	578	0.69	0.82	6.03	22.49	13.2	63.4	10	10									
PSMB9	5698	proteasome subunit beta type-9 proprotein	NP_002791.1	1	2	2	2	0.69	0.8	108.61	63.78	144.8	83.3	2	2	1514	5698	proteasome (prosome, macropain) subunit, betatype, 9 (large multifunctional protease 2)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Cell cycle	-	Yes
TBC1D10B	26000	TBC1 domain family member 10B	NP_056342.3	1	2	2	3	0.69	0.76	55.58	21.54	58.7	23.5	2	2	10892	26000	TBC1 domain family, member 10B	GTPase activator activity	-	GTPase activating protein	Cell communication;Signal transduction	TBC;CC	No
DCAKD	79877	dephospho-CoA kinase domain-containing protein	NP_001275583.1	1	3	3	6	0.69	0.74	2.87	5.99	3.4	7.7	3	3	8012	79877	None	Kinase activity	-	Enzyme: Phosphorylase	Biological_process unknown	TM	No
PTK7	5754	inactive tyrosine-protein kinase 7 isoform e	NP_001257327.1	5	5	5	6	0.69	0.74	10.82	19.5	16.9	33.1	5	5	3534	5754	PTK7 protein tyrosine kinase 7	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	IGC2;Ig_LIKE;Tyr_Kinase;TM;SP	Yes
SLC25A20	788	mitochondrial carnitine/acylcarnitine carrier protein	NP_000378.1	1	1	1	3	0.69	0.71					1	1	1953	788	solute carrier family 25(carnitine/acylcarnitine translocase), member 20	Catalytic activity	Mitochondrion	Enzyme: Translocase	Metabolism;Energy pathways	TM	Yes
SLC39A10	57181	zinc transporter ZIP10 precursor	NP_065075.1	1	1	1	2	0.69	0.71					1	1	10572	57181	solute carrier family 39 (zinc transporter),member 10	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	No
MAPKAPK3	7867	MAP kinase-activated protein kinase 3	NP_004626.1	4	4	5	8	0.69	0.71	48.83	35.67	64	37	3	2	3678	7867	mitogen-activated protein kinase-activatedprotein kinase 3	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;NLS	No
MAOA	4128	amine oxidase [flavin-containing] A isoform 1	NP_000231.1	3	11	11	21	0.69	0.7	5.59	11.82	13.3	29.5	12	12	2400	4128	monoamine oxidase A	Catalytic activity	Mitochondrion	Enzyme: Oxidase	Metabolism;Energy pathways	-	Yes
HLA-C	3107	HLA class I histocompatibility antigen, Cw-1 alpha chain precursor	NP_001229971.1	2	8	12	35	0.69	0.69	12.13	12.88	28.3	30.2	11	11	829	3107	major histocompatibility complex, class I, C	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein	Immune response	SP;IGC;TM	Yes
F11R	50848	junctional adhesion molecule A precursor	NP_058642.1	1	10	10	25	0.69	0.67	9.65	5.92	25.1	14.8	14	14	12038	50848	F11 receptor	Cell adhesion molecule activity	Cell junction	Adhesion molecule	Cell communication;Signal transduction	IGV;Ig_LIKE;TM;SP	Yes
GLUL	2752	glutamine synthetase	NP_002056.2	1	4	4	10	0.69	0.67	32.52	22.93	53.4	35.3	5	5	701	2752	glutamate-ammonia ligase (glutamine synthase)	Transaminase activity	Cytosol	Enzyme: Aminotransferase	Metabolism;Energy pathways	-	Yes
FAM83B	222584	protein FAM83B	NP_001010872.1	1	10	10	15	0.69	0.65	7.8	7.46	16.2	14.7	9	9	10158	222584	chromosome 6 open reading frame 143	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ABHD14B	84836	alpha/beta hydrolase domain-containing protein 14B isoform 1	NP_116139.1	2	3	3	7	0.69	0.65	24.46	26.83	34.8	36.2	4	4	17504	84836	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
IMPACT	55364	protein IMPACT	NP_060909.1	1	1	1	2	0.69	0.58					1	1	13739	55364	None	Molecular function unknown	-	Unclassified	Biological_process unknown	RWD	No
GANAB	23193	neutral alpha-glucosidase AB isoform 3 precursor	NP_938149.2	2	1	36	142	0.68	1.43	1.53	4.69	1.5	9.5	2	2	3516	23193	glucosidase, alpha; neutral AB	Hydrolase activity	Endoplasmic reticulum	Enzyme: Hydrolase	Carbohydrate metabolism	SP	Yes
C2CD5	9847	C2 domain-containing protein 5 isoform b	NP_001273104.1	5	1	1	2	0.68	1.3					1	1									
FRMD6	122786	FERM domain-containing protein 6 isoform 2	NP_001253975.1	2	1	1	2	0.68	1.07					1	1	12646	122786	chromosome 14 open reading frame 31	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	B41	Yes
PTPN6	5777	tyrosine-protein phosphatase non-receptor type 6 isoform 3	NP_536859.1	3	2	2	4	0.68	1.04	56.2	5.89	58.4	8.7	2	2	1475	5777	protein tyrosine phosphatase, non-receptor type6	Protein tyrosine phosphatase activity	Cytoplasm	Tyrosine phosphatase	Cell communication;Signal transduction	SH2;Tyr_Phos	Yes
PDCD4	27250	programmed cell death protein 4 isoform 1	NP_055271.2	3	12	12	31	0.68	0.82	13.26	9.89	37.2	33.3	16	16	10549	27250	programmed cell death 4 (neoplastictransformation inhibitor)	Molecular function unknown	Nucleus;Cytoplasm	Unclassified	Apoptosis	MA3	Yes
PRDX5	25824	peroxiredoxin-5, mitochondrial isoform a precursor	NP_036226.1	3	12	12	66	0.68	0.8	9.84	10.16	38.5	47.9	31	31	5958	25824	peroxiredoxin 5	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
REXO2	25996	oligoribonuclease, mitochondrial precursor	NP_056338.2	1	1	1	1	0.68	0.8					1	1	6192	25996	None	Ribonuclease activity	Mitochondrion	Ribonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	EXOIII	Yes
NUB1	51667	NEDD8 ultimate buster 1 isoform 1	NP_001230280.1	2	2	2	4	0.68	0.76	51.06	22.37	52.6	24.3	2	2	7450	51667	None	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	CC;UBA;NLS	Yes
MGST2	4258	microsomal glutathione S-transferase 2 isoform 1 precursor	NP_002404.1	2	2	2	5	0.68	0.75	1.91	11.61	2.3	15.2	3	3	3436	4258	microsomal glutathione S-transferase 2	Glutathione transferase activity	Endoplasmic reticulum	Enzyme: Glutathione transferase	Metabolism;Energy pathways	SP;TM	Yes
ANO1	55107	anoctamin-1	NP_060513.5	1	1	1	1	0.68	0.73					1	1	18202	55107	transmembrane protein 16A	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
SUB1	10923	activated RNA polymerase II transcriptional coactivator p15	NP_006704.3	1	6	6	17	0.68	0.72	6.14	10.94	11.1	21.2	7	7	2737	10923	None	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
PI4KA	5297	phosphatidylinositol 4-kinase alpha	NP_477352.3	1	2	2	4	0.68	0.7					1	1	8972	5297	phosphatidylinositol 4-kinase, catalytic,alpha polypeptide	Lipid kinase activity	Golgi apparatus	Lipid Kinase	Cell communication;Signal transduction	PI3KA;PI3KC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al*., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
CADM2	253559	cell adhesion molecule 2 isoform 3 precursor	NP_694854.2	5	1	1	2	0.68	0.66					1	1	11046	253559	immunoglobulin superfamily, member 4D	Cell adhesion molecule activity	-	Adhesion molecule	Cell communication;Signal transduction	SP;Ig_LIKE;IGC2;Band 4.1;TM;IG	Yes
ARL4C	10123	ADP-ribosylation factor-like protein 4C isoform 1	NP_001269360.1	2	1	1	2	0.68	0.64					1	1	11988	10123	ADP-ribosylation factor-like 7	GTPase activity	Nucleus	GTPase	Cell communication;Signal transduction	ARF	Yes
ITGB4	3691	integrin beta-4 isoform 3 precursor	NP_001005731.1	2	1	65	203	0.68	0.63					1	1	946	3691	integrin, beta 4	Cell adhesion molecule activity	Integral to membrane;Nucleus	Adhesion molecule	Cell communication;Signal transduction;Cell migration;Cell adhesion;Wound healing	PSI;VWA;CALXB;FN3;TM;EGF;SP	Yes
MYO5A	4644	unconventional myosin-Va isoform 1	NP_000250.3	2	4	4	9	0.68	0.63	13.23	13.43	18.1	17.1	4	4	1179	4644	myosin VA (heavy polypeptide 12, myoxin)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	MYOSIN;IQ;CC	Yes
ADAM15	8751	disintegrin and metalloproteinase domain-containing protein 15 isoform 6 preproprotein	NP_997080.1	6	1	1	1	0.68	0.63					1	1	5674	8751	a disintegrin and metalloproteinase domain 15(metargidin)	Metallopeptidase activity	Plasma membrane	Metallo protease	Cell adhesion;Protein metabolism	TM;REP;DISINT;RGD;SP;ACR	Yes
PLEC	5339	plectin isoform 1a	NP_958786.1	16	1	345	1368	0.68	0.61	28.22	21.28	27.7	18.4	2	2									
ITPR3	3710	inositol 1,4,5-trisphosphate receptor type 3	NP_002215.2	1	23	29	58	0.68	0.61	10.01	9.71	33.7	29.1	23	23	926	3710	inositol 1,4,5-triphosphate receptor, type 3	Intracellular ligand-gated ion channel activity	Plasma membrane	Intracellular ligand gated channel	Cell communication;Signal transduction	MIR;RYDR;TM;CC	Yes
FLOT2	2319	flotillin-2	NP_004466.2	1	14	14	41	0.68	0.61	3.89	14.19	12.2	41.4	21	21	580	2319	flotillin 2	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	PHB;CC	Yes
RAB10	10890	ras-related protein Rab-10	NP_057215.3	12	6	8	78	0.68	0.6	6.18	7.75	13.4	14.9	10	10	6692	10890	RAB10, member RAS oncogene family	GTPase activity	Nucleus;Golgi vesicle	GTPase	Cell communication;Signal transduction	RAB	Yes
TBC1D5	9779	TBC1 domain family member 5 isoform a	NP_001127853.1	2	4	4	8	0.68	0.6	8.24	56.41	12.6	87	5	5	10262	9779	TBC1 domain family, member 5	Molecular function unknown	-	Unclassified	Biological_process unknown	TBC	Yes
ARF6	382	ADP-ribosylation factor 6	NP_001654.1	4	5	5	27	0.67	1.36	9.16	11.08	21.5	55.9	12	12	2714	382	ADP-ribosylation factor 6	Transporter activity	Cytosol	Transport/cargo protein	Transport	ARF	Yes
KRT81	3887	keratin, type II cuticular Hb1	NP_002272.2	4	2	3	7	0.67	1.26					1	1	3691	3887	keratin, hair, basic, 1	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	CC	Yes
FBXW9	84261	F-box/WD repeat-containing protein 9	NP_115677.2	1	1	1	1	0.67	1.19					1	1	12361	84261	F-box and WD-40 domain protein 9	Molecular function unknown	-	Unclassified	Biological_process unknown	F_BOX;WD40	No
NXT1	29107	NTF2-related export protein 1	NP_037380.1	1	1	1	3	0.67	1.09					1	1	16159	29107	NTF2-like export factor 1	Transporter activity	Nucleus	Transport/cargo protein	Transport	-	No
CHMP1A	5119	charged multivesicular body protein 1a isoform 2	NP_002759.2	1	1	1	2	0.67	1.06					1	1	1237	5119	procollagen (type III) N-endopeptidase	Metallopeptidase activity	-	Metallo protease	Protein metabolism	CC	No
TMED2	10959	transmembrane emp24 domain-containing protein 2 precursor	NP_006806.1	1	6	6	16	0.67	1.05	30.03	11.47	57.5	32.7	7	7	17984	10959	None	Transporter activity	Golgi apparatus	Transport/cargo protein	Transport	SP;CC;TM	Yes
MON2	23041	protein MON2 homolog isoform 1	NP_055841.2	5	2	2	3	0.67	1.05					1	1	11123	23041	None	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
ATP6V1G1	9550	V-type proton ATPase subunit G 1	NP_004879.1	1	4	4	5	0.67	0.99	8.37	6.05	9.7	10.4	3	3	6294	9550	ATPase, H+ transporting, lysosomal 13kDa, V1subunit G isoform 1	Transporter activity	Lysosome	Transport/cargo protein	Metabolism;Energy pathways	CC	Yes
NDUFA11	126328	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 isoform 2	NP_001180304.1	2	2	2	8	0.67	0.98	7.83	2.35	10.5	4.6	4	4	14818	126328	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 11, 14.7kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	Yes
RBKS	64080	ribokinase isoform 1	NP_071411.1	1	1	1	2	0.67	0.98					1	1	15222	64080	ribokinase	Catalytic activity	-	Enzyme: Phosphotransferase	Metabolism;Energy pathways	-	Yes
SLC25A4	291	ADP/ATP translocase 1	NP_001142.2	2	1	10	29	0.67	0.87					1	1	58	291	solute carrier family 25 (mitochondrialcarrier; adenine nucleotide translocator), member 4	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	TM	Yes
NDUFB1	4707	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	NP_004536.2	1	1	1	2	0.67	0.87					1	1	11952	4707	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 1, 7kDa	Oxidoreductase activity	Integral to membrane	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
BCAP31	10134	B-cell receptor-associated protein 31 isoform a	NP_001132929.1	2	8	8	18	0.67	0.84	10.55	3.19	22.7	8.5	10	10	2319	10134	B-cell receptor-associated protein 31	Transporter activity	Endoplasmic reticulum	Transport/cargo protein	Transport	SP;TM;CC	Yes
TCHH	7062	trichohyalin	NP_009044.2	1	1	1	1	0.67	0.8					1	1	19269	7062	trichohyalin	Calcium ion binding	-	Calcium binding protein	Calcium-mediated signaling	S_100;EF;CC	Yes
SYNPO	11346	synaptopodin isoform A	NP_009217.3	2	1	6	11	0.67	0.8					1	1	12179	11346	synaptopodin	Cytoskeletal protein binding	Cytoskeleton;Nucleus;Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	-	Yes
ERMP1	79956	endoplasmic reticulum metallopeptidase 1	NP_079172.2	1	8	8	20	0.67	0.78	8.88	10.34	20	27.4	11	11	17227	79956	KIAA1815	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
ENO3	2027	beta-enolase isoform 1	NP_001967.3	2	1	4	65	0.67	0.76					1	1	11746	2027	enolase 3 (beta, muscle)	Catalytic activity	Extracellular	Enzyme: Hydratase	Metabolism;Energy pathways	-	Yes
RAC1	5879	ras-related C3 botulinum toxin substrate 1 isoform Rac1b	NP_061485.1	5	5	8	25	0.67	0.76	19.77	9.1	45.9	23.2	11	11	3627	5879	ras-related C3 botulinum toxin substrate 1 (rhofamily, small GTP binding protein Rac1)	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	RHO	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells
Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
ATP2B4	493	plasma membrane calcium-transporting ATPase 4 isoform 4b	NP_001675.3	3	13	19	48	0.67	0.73	14.11	7.99	36.7	22.2	14	14	159	493	ATPase, Ca++ transporting, plasma membrane 4	ATPase activity	Plasma membrane	ATPase	Transport	TM	Yes
JUP	3728	junction plakoglobin	NP_068831.1	1	30	34	129	0.67	0.7	6.84	9.35	35.2	52.5	56	56	1414	3728	junction plakoglobin	Cell adhesion molecule activity	Cytoplasm	Adhesion molecule	Cell communication;Signal transduction	ARM	Yes
DFNA5	1687	non-syndromic hearing impairment protein 5 isoform a	NP_001120925.1	2	10	10	24	0.67	0.69	8.71	11.7	21.2	29.7	13	13	2996	1687	deafness, autosomal dominant 5	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
GUSB	2990	beta-glucuronidase isoform 1 precursor	NP_000172.2	5	3	3	6	0.67	0.68	6.79	12.65	10.2	19.5	5	5	2018	2990	glucuronidase, beta	Hydrolase activity	Lysosome	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
NDUFB5	4711	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial isoform 1 precursor	NP_002483.1	2	2	2	4	0.67	0.64	36.77	11.9	44.5	13.3	3	3	11956	4711	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 5, 16kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM;CC	Yes
ITGA6	3655	integrin alpha-6 isoform b precursor	NP_000201.2	2	38	38	123	0.67	0.63	5.63	9.65	31.3	52.9	66	66	945	3655	integrin, alpha 6	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	TM;INTA;SP	Yes
SCAF4	57466	splicing factor, arginine/serine-rich 15 isoform 1	NP_065757.1	3	2	2	4	0.67	0.55	54.05	73.24	54.8	61.6	2	2									
DNAJB2	3300	dnaJ homolog subfamily B member 2 isoform b	NP_006727.2	4	2	3	6	0.67	0.51	22.43	20.07	21.4	14.6	2	2	7249	3300	DnaJ (Hsp40) homolog, subfamily B, member 2	Heat shock protein activity	Cytoplasm	Heat shock protein	Protein metabolism	DNAJ;UIM	Yes
MGST1	4257	microsomal glutathione S-transferase 1 isoform a	NP_665735.1	3	1	1	4	0.66	1.31	46.41	23.65	45.8	45.8	2	2	705	4257	microsomal glutathione S-transferase 1	Glutathione transferase activity	Microsome	Enzyme: Glutathione transferase	Metabolism;Energy pathways;Xenobiotic metabolism	SP	Yes
PTTG1IP	754	pituitary tumor-transforming gene 1 protein-interacting protein isoform 1 precursor	NP_004330.1	1	1	1	8	0.66	1.26	18.1	4.79	24.4	12.1	4	4	4807	754	pituitary tumor-transforming 1 interactingprotein	Transporter activity	Nucleus	Transport/cargo protein	Transport	NLS;TM;CC;PSI	No
C14orf169	79697	bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	NP_078920.2	1	2	2	3	0.66	1.26					1	1	12641	79697	chromosome 14 open reading frame 169	Transcription regulator activity	Nucleolus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	JMJC	No
ATP5J2-PTCD1	100526740	ATP5J2-PTCD1 fusion protein	NP_001185808.1	6	4	4	19	0.66	1.19	10.97	13.02	21.8	49.2	9	9									
ESRRA	2101	steroid hormone receptor ERR1 isoform 1	NP_004442.3	3	2	2	2	0.66	1.04					1	1	7210	2101	estrogen-related receptor alpha	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ZnF_C4;HOLI	Yes
DES	1674	desmin	NP_001918.3	5	2	8	38	0.66	1.03	3.09	10.44	4.6	24.4	5	5	514	1674	desmin	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	CC	Yes
CAV2	858	caveolin-2 isoform a	NP_001224.1	3	1	1	3	0.66	1.03	70.88	14.05	74.8	20.8	2	2	3029	858	caveolin 2	Protein binding	Plasma membrane	Integral membrane protein	Cell communication;Signal transduction	TM	Yes
AKR1C2	1646	aldo-keto reductase family 1 member C2 isoform 1	NP_995317.1	2	3	14	53	0.66	0.98	24.14	31.7	32.8	68.3	4	4	11857	1646	aldo-keto reductase family 1, member C2(dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroiddehydrogenase, type III)	Oxidoreductase activity;Transporter activity	Cytosol	Enzyme: Dehydrogenase	Metabolism;Transport	-	No
RAB32	10981	ras-related protein Rab-32	NP_006825.1	1	5	7	20	0.66	0.91	28.48	5.86	43.6	12	5	5	6700	10981	RAB32, member RAS oncogene family	GTPase activity	Mitochondrion	GTPase	Cell communication;Signal transduction	RAB	Yes
RHOC	389	rho-related GTP-binding protein RhoC precursor	NP_786886.1	2	4	11	47	0.66	0.83	3.73	4.4	4.9	7.3	4	4	1322	389	ras homolog gene family, member C	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	RHO	Yes
SLC25A1	6576	tricarboxylate transport protein, mitochondrial isoform b	NP_001243463.1	3	9	9	37	0.66	0.77	15.1	7.85	45.8	26.9	19	19	1832	6576	solute carrier family 25 (mitochondrialcarrier; citrate transporter), member 1	Transporter activity	Mitochondrion	Transport/cargo protein	Transport	TM	Yes
ANXA3	306	annexin A3	NP_005130.1	1	18	18	67	0.66	0.72	5.92	5.87	23.4	25.5	35	35	111	306	annexin A3	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	ANX	Yes
HSPA12A	259217	heat shock 70 kDa protein 12A	NP_079291.2	1	1	1	2	0.66	0.63					1	1	19074	259217	heat shock 70kDa protein 12A	Heat shock protein activity	-	Heat shock protein	Protein folding	-	Yes
TOR4A	54863	torsin-4A	NP_060193.2	1	2	2	3	0.66	0.56					1	1									
TAMM41	132001	phosphatidate cytidylyltransferase, mitochondrial isoform a	NP_001271330.1	2	2	2	4	0.65	1.83	80.07	46.25	111.6	277	3	3									
ENOSF1	55556	mitochondrial enolase superfamily member 1 isoform rTSbeta	NP_059982.2	2	1	1	1	0.65	1.81					1	1	9590	55556	enolase superfamily member 1	Ligase activity	-	Enzyme: Ligase	Metabolism;Energy pathways	-	No
PDXP	57026	pyridoxal phosphate phosphatase	NP_064711.1	1	1	1	1	0.65	1.21					1	1	16468	57026	pyridoxal (pyridoxine, vitamin B6) phosphatase	Acid phosphatase activity	-	Enzyme: Phosphatase	Metabolism;Energy pathways	-	Yes
PSD3	23362	PH and SEC7 domain-containing protein 3 isoform a	NP_056125.3	2	1	1	2	0.65	1.07					1	1	11462	23362	pleckstrin and Sec7 domain containing 3	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	Sec7;PH;CC	Yes

Supplementary Table S1. List of quantified proteins in OKF6/TERT1-Smoke cells

Rajagopalan *et al* ., 2017. Role of protein kinase N2 (PKN2) in cigarette smoke-mediated oncogenic transformation of oral cells

Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
HIST1H1C	3006	histone H1.2	NP_005310.1	3	2	11	72	0.65	1.07	28.97	4.19	38.9	8.9	4	4	7514	3006	histone 1, H1c	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H15	Yes
RAB27B	5874	ras-related protein Rab-27B	NP_004154.2	1	2	2	3	0.65	1.02					1	1	4846	5874	RAB27B, member RAS oncogene family	GTPase activity	Plasma membrane	GTPase	Cell communication;Signal transduction	RAB	Yes
NDUFB10	4716	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NP_004539.1	1	6	6	12	0.65	0.97	12.4	3.89	22.9	10.7	8	8	11958	4716	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 10, 22kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
CSNK1A1	1452	casein kinase I isoform alpha isoform 2	NP_001883.4	5	8	9	15	0.65	0.95	21.45	11.45	41	31.4	8	8	2739	1452	casein kinase 1, alpha 1	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell cycle	S_T_kinase;NLS;S_T_Y_Kinase	Yes
DHCR24	1718	delta(24)-sterol reductase precursor	NP_055577.1	1	5	5	8	0.65	0.94	16.06	9.39	23.6	19.9	5	5	5916	1718	24-dehydrocholesterol reductase	Catalytic activity	Plasma membrane	Enzyme: Reductase	Metabolism;Energy pathways	TM;SP	No
HIST1H2AE	3012	histone H2A type 1-B/E	NP_066390.1	3	1	7	165	0.65	0.87	34.82	30.91	33	39.7	2	2	4152	3012	histone 1, H2ae	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H2A	No
IGF1R	3480	insulin-like growth factor 1 receptor isoform 1 precursor	NP_000866.1	2	1	1	2	0.65	0.83					1	1	932	3480	insulin-like growth factor 1 receptor	Transmembrane receptor protein tyrosine kinase activity	Plasma membrane	Receptor tyrosine kinase	Cell communication;Signal transduction	TM;REC;FU;FN3;Tyr_Kinase;SP	Yes
NDUFB3	4709	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NP_001244031.1	1	1	1	2	0.65	0.81					1	1	11954	4709	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 3, 12kDa	Oxidoreductase activity	-	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	No
MINPP1	9562	multiple inositol polyphosphate phosphatase 1 isoform 1 precursor	NP_004888.2	3	3	3	4	0.65	0.8	15.47	9.57	17.6	13.4	3	3	5652	9562	multiple inositol polyphosphate histidinephosphatase, 1	Lipid phosphatase activity	Endoplasmic reticulum	Lipid phosphatase	Cell communication;Signal transduction	SP	Yes
SNX8	29886	sorting nexin-8	NP_037453.1	1	1	1	5	0.65	0.79	4.46	4.54	4.1	5.1	2	2	11592	29886	sorting nexin 8	Transporter activity	-	Transport/cargo protein	Transport	PX	Yes
CDC42BPG	55561	serine/threonine-protein kinase MRCK gamma	NP_059995.2	1	2	2	4	0.65	0.77	4.82	2.94	4.4	3.2	2	2	13013	55561	CDC42 binding protein kinase gamma(DMPK-like)	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Cell communication;Signal transduction	S_T_kinase;CC;C1;PH;CNH;PBD	Yes
FXYD3	5349	FXYD domain-containing ion transport regulator 3 isoform 3	NP_001129479.1	3	1	1	2	0.65	0.75	14.75	22.24	13.7	23.8	2	2	5410	5349	FXYD domain containing ion transport regulator3	Ion channel activity	Plasma membrane	Ion channel	Transport	SP;TM	Yes
CISD2	493856	CDGSH iron-sulfur domain-containing protein 2	NP_001008389.1	1	1	1	4	0.65	0.75	0.09	9.24	0.1	9.8	2	2	17413	493856	None	Molecular function unknown	Integral to membrane	Unclassified	Biological_process unknown	TM	No
GNG12	55970	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 precursor	NP_061329.3	1	4	4	15	0.65	0.71	17.1	14.26	32	29.1	8	8	13592	55970	guanine nucleotide binding protein (G protein),gamma 12	GTPase activity	Cytoplasm	G protein	Cell communication;Signal transduction	CC	Yes
HPX	3263	hemopexin precursor	NP_000604.1	1	5	5	10	0.65	0.67	9.23	8.68	14.8	14.4	6	6	793	3263	hemopexin	Transporter activity	Extracellular	Transport/cargo protein	Transport	SP;HX	Yes
NDUFAB1	4706	acyl carrier protein, mitochondrial precursor	NP_004994.1	1	2	2	4	0.65	0.58	22.54	9.77	20.8	8	2	2	11951	4706	NADH dehydrogenase (ubiquinone) 1, alpha/betasubcomplex, 1, 8kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	No
GET4	51608	Golgi to ER traffic protein 4 homolog	NP_057033.2	1	4	4	12	0.64	1.51	5.85	2.75	8.4	9.3	5	5									
SMARCA1	6594	probable global transcription activator SNF2L1 isoform d	NP_001269803.1	3	1	8	11	0.64	1.06					1	1	2055	6594	SWI/SNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DEXDc;HELIC;SANT	Yes
DNAJB14	79982	dnaJ homolog subfamily B member 14 isoform 1	NP_001026893.1	2	1	1	4	0.64	1.05	10.7	32.28	9.7	51.1	2	2	7013	79982	None	Chaperone activity	-	Chaperone	Protein metabolism;Protein folding	DNAJ	Yes
UBE2N	7334	ubiquitin-conjugating enzyme E2 N	NP_003339.1	2	7	7	24	0.64	1.05	17.59	9.55	42.1	37.5	13	13	4725	7334	ubiquitin-conjugating enzyme E2N (UBC13homolog, yeast)	Ubiquitin-specific protease activity	Nucleus	Ubiquitin proteasome system protein	Protein metabolism	UBC	Yes
ZAK	51776	mitogen-activated protein kinase kinase kinase MLT isoform 1	NP_057737.2	1	1	4	7	0.64	1.03					1	1									
EXD2	55218	exonuclease 3'-5' domain-containing protein 2 isoform 1	NP_001180289.1	2	1	1	2	0.64	0.99					1	1	16592	55218	chromosome 14 open reading frame 114	Exonuclease activity	-	DNA exonuclease	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	35EXO	Yes
DOCK6	57572	dedicator of cytokinesis protein 6	NP_065863.2	1	4	4	11	0.64	0.91	18.25	15.97	23.9	29.8	4	4	13243	57572	dedicator of cytokinesis 6	Guanyl-nucleotide exchange factor activity	-	Guanine nucleotide exchange factor	Cell communication;Signal transduction	-	Yes
ITGB1	3688	integrin beta-1 isoform 1A precursor	NP_002202.2	2	23	23	129	0.64	0.79	7.03	6.28	38.5	42.3	67	67	628	3688	integrin, beta 1 (fibronectin receptor, betapolypeptide, antigen CD29 includes MDF2, MSK12)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Immune cell migration	PSI;VWA;TM;SP;INTB	Yes

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SLC25A5	292	ADP/ATP translocase 2	NP_001143.2	2	5	14	167	0.64	0.77	6.7	9.73	19.5	34.4	20	20	2147	292	solute carrier family 25 (mitochondrialcarrier; adenine nucleotide translocator), member 5	ATP binding	Mitochondrion	Integral membrane protein	Metabolism;Energy pathways	TM	Yes
HEBP2	23593	heme-binding protein 2	NP_055135.1	1	3	3	9	0.64	0.7	14.41	28.61	20.8	47.4	5	5	9316	23593	heme binding protein 2	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	No
EPPK1	83481	epiplakin	NP_112598.3	1	21	28	74	0.64	0.69	10.94	6.82	38.3	25.4	28	28	6500	83481	epiplakin 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	PLEC	Yes
CA3	761	carbonic anhydrase 3	NP_005172.1	1	1	1	2	0.64	0.69					1	1	260	761	carbonic anhydrase III, muscle specific	Catalytic activity	Cytoplasm	Enzyme: Carbonic anhydrase	Metabolism;Energy pathways	-	Yes
SF3B4	10262	splicing factor 3B subunit 4	NP_005841.1	1	1	1	4	0.63	1.7	8.65	5.79	7.7	14	2	2	12028	10262	splicing factor 3b, subunit 4, 49kDa	Ribonucleoprotein	Nucleus	RNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	RRM	Yes
NUBP1	4682	cytosolic Fe-S cluster assembly factor NUBP1 isoform 1	NP_002475.2	2	3	3	5	0.63	1.47	60.89	11.03	58.7	23.2	2	2	2611	4682	nucleotide binding protein 1 (MinD homolog, E.coli)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	AAA	No
STON2	85439	stonin-2 isoform 2	NP_001243359.1	2	4	4	10	0.63	1.41	7	33.9	10.9	171.5	6	6	10531	85439	None	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	-	Yes
MED18	54797	mediator of RNA polymerase II transcription subunit 18	NP_060108.2	1	1	1	1	0.63	1.26					1	1	17476	54797	mediator of RNA polymerase II transcription,subunit 18 homolog (yeast)	Transcription regulator activity	-	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
SNAPIN	23557	SNARE-associated protein Snapin	NP_036569.1	1	1	1	2	0.63	1.15					1	1	6111	23557	SNAP-associated protein	Auxiliary transport protein activity	Cytoplasm	Membrane transport protein	Transport	CC	Yes
PDPR	55066	pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial precursor	NP_060460.4	1	3	3	11	0.63	1.12	16.68	3.49	23.9	8.7	5	5									
OSBPL10	114884	oxysterol-binding protein-related protein 10 isoform 1	NP_060254.2	2	3	4	7	0.63	0.88	23.44	25.25	21.1	32.3	2	2	9480	114884	oxysterol binding protein-like 10	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	PH	Yes
ACOT13	55856	acyl-coenzyme A thioesterase 13 isoform 1	NP_060943.1	2	3	3	11	0.63	0.87	1.05	5.4	1.5	10.6	5	5	7158	55856	thioesterase superfamily member 2	Hydrolase activity	-	Enzyme: Hydrolase	Metabolism;Energy pathways	-	No
OAS1	4938	2'-5'-oligoadenylate synthase 1 isoform 3	NP_001027581.1	3	3	3	5	0.63	0.85	16.55	25.17	14.9	31	2	2	8879	4938	2`,5`-oligoadenylate synthetase 1, 40/46kDa	Ligase activity	Cytoplasm	Enzyme: Ligase	Immune response	-	Yes
VRK2	7444	serine/threonine-protein kinase VRK2 isoform 1	NP_001123953.1	4	1	1	2	0.63	0.84					1	1	3702	7444	vaccinia related kinase 2	Protein serine/threonine kinase activity	Nucleus	Serine/threonine kinase	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	S_T_kinase;TM;S_T_Y_Kinase	Yes
MMS19	64210	MMS19 nucleotide excision repair protein homolog isoform 1	NP_071757.4	3	5	5	16	0.63	0.83	16.21	29.86	25.6	66.7	6	6	17579	64210	MMS19-like (MET18 homolog, S. cerevisiae)	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
CNTN1	1272	contactin-1 isoform 1 precursor	NP_001834.2	2	1	1	2	0.63	0.79	4.84	30.74	4.4	35.4	2	2	7189	1272	contactin 1	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell growth and/or maintenance	IGC2;FN3;SP;Ig_LIKE	Yes
USMG5	84833	up-regulated during skeletal muscle growth protein 5	NP_116136.1	1	3	3	6	0.63	0.73					1	1	18277	84833	upregulated during skeletal muscle growth 5	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes
NMI	9111	N-myc-interactor	NP_004679.2	1	3	3	4	0.63	0.73	48.25	4.57	45.2	4.7	2	2	4632	9111	N-myc (and STAT) interactor	Transcription factor activity	Cytoplasm	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CC	Yes
SPPL2A	84888	signal peptide peptidase-like 2A precursor	NP_116191.2	1	2	2	3	0.63	0.7					1	1									
GALE	2582	UDP-glucose 4-epimerase	NP_001121093.1	1	14	14	46	0.63	0.69	15.91	13.38	44.8	40.4	18	18	6092	2582	UDP-galactose-4-epimerase	Racemase and epimerase activity	-	Enzyme: Epimerase	Metabolism	-	No
DECR1	1666	2,4-dienoyl-CoA reductase, mitochondrial precursor	NP_001350.1	1	7	7	31	0.63	0.64	16.38	17.6	43.2	47.5	16	16	1959	1666	2,4-dienoyl CoA reductase 1, mitochondrial	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	-	Yes
WDR81	124997	WD repeat-containing protein 81 isoform 1	NP_001157281.1	1	2	2	5	0.63	0.64	69.07	23.19	67.8	21.2	2	2	8748	124997	None	Molecular function unknown	-	Unclassified	Cell communication;Signal transduction	WD40	No
SPG11	80208	spatacsin isoform 1	NP_079413.3	2	1	1	2	0.63	0.62					1	1	7963	80208	None	Molecular function unknown	Cytosol	Unclassified	Biological_process unknown	CC	Yes
PYGB	5834	glycogen phosphorylase, brain form	NP_002853.2	1	33	34	135	0.63	0.59	12.41	10.37	63.7	47.5	55	55	720	5834	phosphorylase, glycogen; brain	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase	Metabolism;Energy pathways	-	Yes
DDX19B	11269	ATP-dependent RNA helicase DDX19B isoform 1	NP_009173.1	5	1	15	47	0.62	1.82	49.93	23.18	58	83.9	3	3	5781	11269	DEAD (Asp-Glu-Ala-As) box polypeptide 19	ATPase activity	Cytoplasm;Nucleus	ATPase	Metabolism	DEXDc;HELIC	Yes
TBC1D24	57465	TBC1 domain family member 24 isoform 1	NP_001186036.1	2	1	1	2	0.62	1.31					1	1	18938	57465	TBC1 domain family, member 24	Molecular function unknown	-	Unclassified	Cell-cell signaling	TBC	No
MTFR1	9650	mitochondrial fission regulator 1 isoform 3	NP_001139311.1	3	1	1	2	0.62	1.12					1	1	12389	9650	None	Molecular function unknown	Mitochondrion	Unclassified	Biological_process unknown	-	Yes
ANXA8	653145	annexin A8 isoform 2	NP_001035173.1	4	2	23	121	0.62	1.1	20.26	11.75	43.2	44.9	11	11	18906	653145	annexin A8-like 1	Calcium ion binding	-	Calcium binding protein	Signal transduction	ANX	Yes
DCTD	1635	deoxycytidylate deaminase isoform a	NP_001012750.1	2	1	1	2	0.62	1					1	1	9623	1635	dCMP deaminase	Deaminase activity	-	Enzyme: Deaminase	Metabolism;Energy pathways	-	No

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VPS28	51160	vacuolar protein sorting-associated protein 28 homolog isoform 2	NP_898880.1	2	1	1	2	0.62	0.95					1	1	11675	51160	vacuolar protein sorting 28 (yeast)	Transporter activity	Cytoplasm	Transport/cargo protein	Transport	-	Yes
PHF3	23469	PHD finger protein 3 isoform 1	NP_055968.1	2	1	1	2	0.62	0.92					1	1	8477	23469	PHD finger protein 3	Transcription factor activity	Nucleus	Transcription factor	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	PHD;NLS	Yes
ERAP2	64167	endoplasmic reticulum aminopeptidase 2	NP_071745.1	1	7	7	17	0.62	0.9	12.24	16.95	21.9	45.1	8	8	14306	64167	None	Aminopeptidase activity	Endoplasmic reticulum	Aminopeptidase	Protein metabolism	-	Yes
SSBP1	6742	single-stranded DNA-binding protein, mitochondrial precursor	NP_001243439.1	1	3	3	10	0.62	0.82	24.96	16.92	35.6	31.9	5	5	2703	6742	single-stranded DNA binding protein 1	DNA binding	Mitochondrion	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	Yes
UQCRB	7381	cytochrome b-c1 complex subunit 7 isoform 3	NP_001241681.1	3	1	1	2	0.62	0.8					1	1	11770	7381	ubiquinol-cytochrome c reductase bindingprotein	Catalytic activity	Mitochondrion	Enzyme: Reductase	Metabolism;Energy pathways	-	Yes
HLA-B	3106	major histocompatibility complex, class I, B precursor	NP_005505.2	1	3	6	24	0.62	0.79	33.71	6.39	44	11.3	4	5	828	3106	major histocompatibility complex, class I, B	MHC class I receptor activity;MHC class II receptor activity	Plasma membrane	MHC complex protein	Immune response	SP;IGC;TM	Yes
HEXB	3074	beta-hexosaminidase subunit beta isoform 1 preproprotein	NP_000512.1	2	9	10	22	0.62	0.79	14.25	7.53	30	19.8	11	11	6043	3074	hexosaminidase B (beta polypeptide)	Hydrolase activity	Lysosome	Enzyme: Hydrolase	Metabolism;Energy pathways	SP	Yes
PPP1R13B	23368	apoptosis-stimulating of p53 protein 1	NP_056131.2	1	1	1	2	0.62	0.77					1	1	7345	23368	protein phosphatase 1, regulatory(inhibitor) subunit 13B	Protein binding	Cytoplasm	Regulatory/other subunit	Apoptosis	CC;ANK;SH3	Yes
TMBIM6	7009	bax inhibitor 1 isoform 2	NP_001092046.1	2	2	2	4	0.62	0.73	19.94	12.38	17.5	12.8	2	2	2851	7009	testis enhanced gene transcript (BAX inhibitor1)	Molecular function unknown	Integral to membrane	Integral membrane protein	Apoptosis	TM	Yes
NFU1	27247	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial isoform 2	NP_001002755.1	2	1	1	3	0.61	1.9					1	1	12163	27247	HIRA interacting protein 5	Molecular function unknown	Mitochondrion;Cytosol	Unclassified	Biological_process unknown	-	Yes
DCAF11	80344	DDB1- and CUL4-associated factor 11 isoform 1	NP_079506.3	2	1	1	1	0.61	1.76					1	1	18297	80344	WD repeat domain 23	Molecular function unknown	-	Unclassified	Biological_process unknown	WD40	Yes
NUDT2	318	bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]	NP_001152.1	1	2	2	3	0.61	1.55					1	1	4168	318	nudix (nucleoside diphosphate linked moietyX)-type motif 2	Hydrolase activity	Cytoplasm	Enzyme: Hydrolase	Metabolism	-	Yes
CCDC109B	55013	calcium uniporter regulatory subunit MCUb, mitochondrial	NP_060388.2	1	1	1	2	0.61	1.48					1	1	7939	55013	None	Molecular function unknown	Plasma membrane	Unclassified	Biological_process unknown	TM;CC	No
CFDP1	10428	craniofacial development protein 1	NP_006315.1	1	2	2	3	0.61	1.38					1	1	16282	10428	craniofacial development protein 1	Molecular function unknown	Cytoplasm	Unclassified	Cell growth and/or maintenance	-	No
MRPS28	28957	28S ribosomal protein S28, mitochondrial	NP_054737.1	1	1	1	6	0.61	1.36	10.49	19.17	11	47.6	3	3	10097	28957	mitochondrial ribosomal protein S28	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	S1	No
JAGN1	84522	protein jagunal homolog 1	NP_115881.3	1	2	2	6	0.61	1.34	14.47	33.61	15.3	91.8	3	3	13749	84522	jagunal homolog 1 (Drosophila)	Molecular function unknown	-	Integral membrane protein	Biological_process unknown	TM	No
COX20	116228	cytochrome c oxidase protein 20 homolog	NP_932342.1	1	1	1	5	0.61	1.2	20.75	8.5	22.1	17.8	3	3									
MTCH1	23787	mitochondrial carrier homolog 1 PSAP-LL	NP_001258570.1	2	1	1	3	0.61	1.11					1	1	14787	23787	mitochondrial carrier homolog 1 (C. elegans)	Caspase activator activity	Mitochondrion	Unclassified	Apoptosis	TM	No
TMOD1	7111	tropomodulin-1	NP_003266.1	1	1	2	6	0.61	1	60.47	4.59	55.8	6.5	2	2	1838	7111	tropomodulin 1	Cytoskeletal protein binding	Cytoplasm	Cytoskeletal associated protein	Cell growth and/or maintenance	CC	Yes
SCFD2	152579	sec1 family domain-containing protein 2	NP_689753.2	1	2	2	5	0.61	0.98	13.34	17.12	11.6	24	2	2	15300	152579	sec1 family domain containing 2	Transporter activity	-	Transport/cargo protein	Transport	-	Yes
PRKAB2	5565	5'-AMP-activated protein kinase subunit beta-2	NP_005390.1	2	1	1	1	0.61	0.93					1	1	4117	5565	protein kinase, AMP-activated, beta 2non-catalytic subunit	Molecular function unknown	Cytoplasm	Regulatory/other subunit	Cell communication;Signal transduction	-	Yes
MAEA	10296	macrophage erythroblast attacher isoform 1	NP_001017405.1	6	3	3	4	0.61	0.88	54.38	32.38	62.9	52.6	3	3	8427	10296	macrophage erythroblast attacher	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell adhesion	CTLH;TM;LISH	No
SPINT1	6692	kunitz-type protease inhibitor 1 isoform 2 precursor	NP_003701.1	2	5	5	7	0.61	0.85	22.19	0.35	27.7	0.6	4	4	5494	6692	serine protease inhibitor, Kunitz type 1	Protease inhibitor activity	Membrane fraction	Protease inhibitor	Protein metabolism	SP;KUNITZ;LDLA;TM	Yes
PLS3	5358	plastin-3 isoform 1	NP_005023.2	4	21	27	95	0.61	0.77	8.64	16.31	32.7	88.8	37	37	2133	5358	plastin 3 (T isoform)	Structural molecule activity	Cytoplasm	Structural protein	Cell growth and/or maintenance	EF;CH	Yes
TNS4	84951	tensin-4 precursor	NP_116254.4	1	6	6	9	0.61	0.74	7.78	11.94	11.7	21.9	6	6	12223	84951	tensin 4	Molecular function unknown	Plasma membrane	Unclassified	Cell communication;Signal transduction	SP;SH2	No
NAV1	89796	neuron navigator 1 isoform 1	NP_065176.3	2	6	6	7	0.61	0.72	33.1	29.29	47.4	49.8	5	5	10113	89796	neuron navigator 1	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	CC;AAA	No
HSPE1	3336	10 kDa heat shock protein, mitochondrial	NP_002148.1	1	4	5	10	0.61	0.72	8.09	14.14	12.1	25.5	6	6	2535	3336	heat shock 10kDa protein 1 (chaperonin 10)	Heat shock protein activity	Mitochondrion	Heat shock protein	Protein metabolism	-	Yes
SLC1A4	6509	neutral amino acid transporter A isoform 1	NP_003029.2	2	1	1	2	0.61	0.7					1	1	2576	6509	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	Yes
CYP2S1	29785	cytochrome P450 2S1 precursor	NP_085125.1	1	2	2	7	0.61	0.69	33.48	54.8	36.5	72.9	3	3	7481	29785	cytochrome P450, family 2, subfamily S,polypeptide 1	Catalytic activity	Endoplasmic reticulum	Enzyme: Oxygenase	Metabolism;Energy pathways	SP;TM	Yes
SFXN3	81855	sideroflexin-3	NP_112233.2	1	9	11	33	0.61	0.68	13.03	9.93	30.3	25.6	14	14	15329	81855	sideroflexin 3	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	Yes

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NDUFC2	4718	NADH dehydrogenase [ubiquinone] 1 subunit C2 isoform 1	NP_004540.1	2	1	1	1	0.61	0.68					1	1	11960	4718	NADH dehydrogenase (ubiquinone) 1, subcomplexunknown, 2, 14.5kDa	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	TM	Yes
SERPINB5	5268	serpin B5	NP_002630.2	1	26	26	165	0.61	0.58	5.95	6.63	32.6	34.9	78	78	1111	5268	serine (or cysteine) proteinase inhibitor,clade B (ovalbumin), member 5	Protease inhibitor activity	Cytoplasm	Protease inhibitor	Protein metabolism	SERPIN	Yes
GJB3	2707	gap junction beta-3 protein	NP_076872.1	1	1	1	2	0.6	1.29					1	1	4505	2707	gap junction protein, beta 3, 31kDa (connexin31)	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport;Cell communication	TM	No
PLEKHA1	59338	pleckstrin homology domain-containing family A member 1 isoform 1	NP_001001974.1	2	1	1	2	0.6	0.81					1	1	9686	59338	pleckstrin homology domain containing, familyA (phosphoinositide binding specific) member 1	Receptor signaling complex scaffold activity;Signal transducer activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	PH	Yes
LMNA	4000	lamin isoform A	NP_733821.1	6	56	59	262	0.6	0.78	5.32	3.88	39.5	37.1	143	141	1035	4000	lamin A/C	Structural molecule activity	Nucleus;Cytoplasm	Structural protein	Cell growth and/or maintenance	CC;NLS	Yes
CAV1	857	caveolin-1 isoform alpha	NP_001744.2	3	9	9	32	0.6	0.77	16.47	14.85	42.7	50.1	17	17	3028	857	caveolin 1, caveolae protein, 22kDa	Structural molecule activity	Plasma membrane	Structural protein	Cell growth and/or maintenance	TM	Yes
BACH1	571	transcription regulator protein BACH1	NP_001177.1	1	1	1	2	0.6	0.76					1	1	4127	571	BTB and CNC homology 1, basic leucine zippertranscription factor 1	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BTB;BRLZ;CC	Yes
GBP1	2633	interferon-induced guanylate-binding protein 1	NP_002044.2	3	13	13	26	0.6	0.52	8.74	16.64	21.1	35.9	16	16	2681	2633	guanylate binding protein 1,interferon-inducible, 67kDa	GTPase activity	Cytoplasm	GTPase	Cell communication;Signal transduction	CC	Yes
EMILIN1	11117	EMILIN-1 precursor	NP_008977.1	1	1	1	1	0.59	1.36					1	1	563	11117	elastin microfibril interfacer 1	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	SP;CC;COLL;C1Q	Yes
HIST1H1D	3007	histone H1.3	NP_005311.1	3	1	10	70	0.59	1.25	1.46	2.76	1.2	4.9	2	2	6764	3007	histone 1, H1d	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	H15	No
B2M	567	beta-2-microglobulin precursor	NP_004039.1	1	1	1	1	0.59	1.2					1	1	189	567	beta-2-microglobulin	MHC class I receptor activity;MHC class II receptor activity	Extracellular	MHC complex protein	Immune response	SP;IGC	Yes
DIRC2	84925	disrupted in renal carcinoma protein 2	NP_116228.1	1	1	1	1	0.59	1.17					1	1	4142	84925	disrupted in renal carcinoma 2	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	TM	No
IFI44	10561	interferon-induced protein 44	NP_006408.3	1	1	1	2	0.59	0.95					1	1	9998	10561	interferon-induced protein 44	Molecular function unknown	Cytoplasm	Unclassified	Biological_process unknown	-	Yes
ZC2HC1A	51101	zinc finger C2HC domain-containing protein 1A	NP_057094.2	1	1	1	2	0.59	0.91					1	1									
STEAP3	55240	metalloreductase STEAP3 isoform a	NP_878919.2	2	2	2	3	0.59	0.9	14.62	2.1	12.3	2.7	2	2	10285	55240	None	Molecular function unknown	Nucleus	Cell cycle control protein	Cell communication;Signal transduction	TM	No
ENAH	55740	protein enabled homolog isoform a	NP_001008493.1	2	5	5	13	0.59	0.85	26.57	12.8	35.9	24.6	5	5	12360	55740	enabled homolog (Drosophila)	Structural constituent of cytoskeleton	Cytoplasm;Nucleus	Cytoskeletal protein	Cell growth and/or maintenance	WH1;ERM;CC	Yes
NDUFB7	4713	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	NP_004137.2	1	2	2	3	0.59	0.77	23.69	17.64	20	19.3	2	2	11957	4713	NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 7, 18kDa	Cell adhesion molecule activity	Mitochondrion	Adhesion molecule	Metabolism;Energy pathways	CC	No
EXOC6B	23233	exocyst complex component 6B	NP_056004.1	1	6	6	15	0.59	0.68	6.35	20.37	9.2	35.1	6	6	19418	23233	exocyst complex component 6B	Molecular function unknown	-	Unclassified	Cell-cell signaling	CC	Yes
FPGT	8790	fucose-1-phosphate guanylyltransferase isoform 1	NP_003829.3	2	1	1	2	0.59	0.66					1	1	6790	8790	fucose-1-phosphate guanylyltransferase	Phosphorylase activity	Cytoplasm	Enzyme: Phosphorylase	Metabolism;Energy pathways	-	Yes
ACTR1B	10120	beta-centractin	NP_005726.1	1	2	6	25	0.59	0.57	11.43	31.67	9.6	25.8	2	2	5508	10120	ARP1 actin-related protein 1 homolog B,centractin beta (yeast)	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	ACTIN	Yes
COL6A2	1292	collagen alpha-2(VI) chain isoform 2C2 precursor	NP_001840.3	3	1	1	2	0.58	1.1	0.86	7.06	0.7	11.1	2	2	2110	1292	collagen, type VI, alpha 2	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	SP;VWA;COLL	Yes
CYP20A1	57404	cytochrome P450 20A1	NP_803882.1	1	1	1	2	0.58	0.97					1	1	7100	57404	cytochrome P450, family 20, subfamily A,polypeptide 1	Catalytic activity	-	Enzyme: Oxygenase	Metabolism;Energy pathways	TM;CC	No
MIF	4282	macrophage migration inhibitory factor	NP_002406.1	1	2	2	7	0.58	0.94	4.76	9.14	3.9	12.1	2	2	1091	4282	macrophage migration inhibitory factor(glycosylation-inhibiting factor)	Cytokine activity	Extracellular	Cytokine	Cell communication;Signal transduction	-	Yes
MSLN	10232	mesothelin isoform 2 preproprotein	NP_037536.2	2	1	1	1	0.58	0.89					1	1	3030	10232	mesothelin	Cell adhesion molecule activity	Membrane fraction	Adhesion molecule	Cell adhesion;Immune response	SP	Yes
LAMB2	3913	laminin subunit beta-2 precursor	NP_002283.3	1	3	3	10	0.58	0.85	27.43	20.49	40.6	44.5	6	6	1034	3913	laminin, beta 2 (laminin S)	Extracellular matrix structural constituent	Extracellular	Extracellular matrix protein	Cell growth and/or maintenance	EGFLAM;SP;CC;LAMNT	Yes

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SLC25A3	5250	phosphate carrier protein, mitochondrial isoform b precursor	NP_998776.1	2	8	8	28	0.58	0.82	20.29	7.76	48.1	25.1	15	15	2654	5250	solute carrier family 25 (mitochondrialcarrier; phosphate carrier), member 3	Transporter activity	Mitochondrial membrane	Transport/cargo protein	Transport	TM	Yes
P3H2	55214	prolyl 3-hydroxylase 2 isoform a precursor	NP_060662.2	2	1	1	2	0.58	0.75					1	1									
BMP1	649	bone morphogenetic protein 1 isoform 3 precursor	NP_006120.1	2	1	1	2	0.58	0.66					1	1	209	649	bone morphogenetic protein 1	Metallopeptidase activity	Extracellular;Nucleus	Metallo protease	Protein metabolism	CUB;EGFCA;SP;ZnMc	Yes
IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	NP_005522.2	8	26	26	78	0.58	0.64	8.34	8.73	30.9	36.1	39	39	969	3428	interferon, gamma-inducible protein 16	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of cell growth	HIN	Yes
CAMK2D	817	calcium/calmodulin-dependent protein kinase type II subunit delta isoform 5	NP_742112.1	15	5	7	15	0.58	0.56	26.17	18.55	35.2	23.7	5	5	9653	817	calcium/calmodulin-dependent protein kinase(CaM kinase) II delta	Protein serine/threonine kinase activity	Cytoplasm	Serine/threonine kinase	Regulation of cell growth	S_T_kinase	Yes
KIRREL3	84623	kin of IRRE-like protein 3 isoform 1 precursor	NP_115920.1	3	1	1	1	0.58	0.56					1	1	9679	84623	kin of IRRE like 3 (Drosophila)	Antigen binding	Extracellular	Immunoglobulin	Cell communication;Signal transduction	SP;Ig_LIKE;IGC2;TM	Yes
S100A8	6279	protein S100-A8	NP_002955.2	1	6	6	14	0.58	0.55	25.89	14.84	41.7	21.9	7	7	471	6279	S100 calcium binding protein A8 (calgranulinA)	Calcium ion binding	Cytoplasm	Calcium binding protein	Cell communication;Signal transduction	EF	Yes
CBX5	23468	chromobox protein homolog 5	NP_036249.1	1	2	2	3	0.58	0.55	13.99	14.21	11.6	11.1	2	2	5131	23468	chromobox homolog 5 (HP1 alpha homolog,Drosophila)	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	CHROMO	No
PPL	5493	periplakin	NP_002696.3	1	28	28	55	0.58	0.53	9.84	16.04	33.2	50.9	32	32	4187	5493	periplakin	Structural constituent of cytoskeleton	Plasma membrane	Cytoskeletal protein	Cell growth and/or maintenance	PLEC;CC;SPECTRIN	Yes
TMEM192	201931	transmembrane protein 192	NP_001093859.1	1	2	2	3	0.58	0.52	22.93	2.79	18.9	2.1	2	2	8787	201931	None	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
SLC38A5	92745	sodium-coupled neutral amino acid transporter 5	NP_277053.2	1	1	1	2	0.57	1.67					1	1	6718	92745	solute carrier family 38, member 5	Transporter activity	Plasma membrane	Transport/cargo protein	Transport	TM	No
F3	2152	tissue factor isoform 1 precursor	NP_001984.1	2	1	1	2	0.57	1.49					1	1	603	2152	coagulation factor III (thromboplastin, tissuefactor)	Cofactor binding	Plasma membrane	Coagulation factor	Protein metabolism	SP;TM	Yes
DTNBP1	84062	dysbindin isoform a	NP_115498.2	4	1	1	2	0.57	1.35					1	1	6190	84062	dystrobrevin binding protein 1	Protein binding	Cytoplasm	Unclassified	Cell organization and biogenesis	CC	Yes
RMDN2	151393	regulator of microtubule dynamics protein 2 isoform 1	NP_653314.3	3	1	1	2	0.57	1.22					1	1									
EOGT	285203	EGF domain-specific O-linked N-acetylglucosamine transferase isoform a precursor	NP_001265618.1	2	5	5	8	0.57	0.85	14.9	20.26	14.7	30.5	3	3									
NDUFS5	4725	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	NP_004543.1	1	1	1	3	0.57	0.68					1	1	11961	4725	NADH dehydrogenase (ubiquinone) Fe-S protein5, 15kDa (NADH-coenzyme Q reductase)	Oxidoreductase activity	Mitochondrion	Enzyme: Oxidoreductase	Metabolism;Energy pathways	-	Yes
LYPD3	27076	ly6/PLAUR domain-containing protein 3 precursor	NP_055215.2	1	4	4	6	0.57	0.64	18.05	22.73	20.7	29.8	4	4	10783	27076	None	Molecular function unknown	-	Unclassified	Biological_process unknown	LU;SP	Yes
TOR2A	27433	prosalusin isoform a precursor	NP_001078816.1	2	1	1	2	0.57	0.6					1	1	16271	27433	torsin family 2, member A	Molecular function unknown	Extracellular	Unclassified	Biological_process unknown	SP;TM	No
TRPC4AP	26133	short transient receptor potential channel 4-associated protein isoform a	NP_056453.1	2	1	1	4	0.56	1.31					1	1	9238	26133	transient receptor potential cation channel,subfamily C, member 4 associated protein	Structural molecule activity;Peptide transporter activity	Cytoplasm	Transport/cargo protein;Structural protein	Cell communication;Signal transduction;Antigen receptor-mediated signaling pathway;Transport	-	Yes
PCYOX1L	78991	prenylcysteine oxidase-like isoform 1 precursor	NP_076933.3	2	1	1	3	0.56	0.97					1	1	14552	78991	None	Molecular function unknown	-	Unclassified	Biological_process unknown	SP	No
MMAB	326625	cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial precursor	NP_443077.1	1	2	2	5	0.56	0.74	4.91	3.27	4.8	4.2	3	3	7398	326625	methylmalonic aciduria (cobalamin deficiency)type B	Catalytic activity	Mitochondrion	Enzyme: Adenosyltransferase	Metabolism;Energy pathways	-	Yes
PTGFRN	5738	prostaglandin F2 receptor negative regulator precursor	NP_065173.2	1	14	14	26	0.56	0.65	8.91	11.63	18.2	27.7	13	13	3124	5738	prostaglandin F2 receptor negative regulator	Protein binding	Golgi apparatus	Integral membrane protein	Cell communication;Signal transduction	SP;IG;TM	Yes
TRIM65	201292	tripartite motif-containing protein 65 isoform 1	NP_775818.2	2	1	1	1	0.56	0.58					1	1	15569	201292	tripartite motif-containing 65	Molecular function unknown	-	Unclassified	Biological_process unknown	RING;BBOX;SPRY;CC	No
RPS28	6234	40S ribosomal protein S28	NP_001022.1	1	2	2	6	0.55	1.34	22.61	4.82	21.7	11.3	3	3	4731	6234	ribosomal protein S28	Structural constituent of ribosome	Ribosome	Ribosomal subunit	Protein metabolism	-	Yes
ZNF860	344787	zinc finger protein 860	NP_001131146.2	1	1	1	1	0.55	1.19					1	1									
TRAPPC8	22878	trafficking protein particle complex subunit 8	NP_055754.2	1	2	2	5	0.55	1.18	8.52	6.77	8.1	13.9	3	3									
UBL7	84993	ubiquitin-like protein 7 isoform b	NP_001273670.1	2	1	1	2	0.55	0.99					1	1	16556	84993	ubiquitin-like 7 (bone marrow stromalcell-derived)	Ubiquitin-like-protein-specific protease activity	-	Ubiquitin proteasome system protein	Protein metabolism	UBA	Yes
ITGB5	3693	integrin beta-5 precursor	NP_002204.2	1	2	2	3	0.55	0.98	0.14	43.2	0.1	65.7	2	2	949	3693	integrin, beta 5	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	PSI;VWA;TM;SP	Yes

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Gene Symbol	Gene ID	Protein Description	Protein Accession	# Proteins	# Unique Peptides	# Peptides	# PSMs	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Standard Errors [%]: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Variabilities [%]: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (130/126) R1	Ratio Counts: F13: OKF6/TERT1-Smoke/ OKF6/TERT1-Parental (128/127) R2	HPRD ID	Entrez Gene Id	Gene Name	Molecular Function	Primary Localization	Molecular Class	Biological Process	Domains	Plasma Proteome Database
PROCR	10544	endothelial protein C receptor precursor	NP_006395.2	1	2	2	6	0.55	0.8	8.84	14.49	8.4	20.2	3	3	2801	10544	protein C receptor, endothelial (EPCR)	Antigen binding	Plasma membrane	Immunoglobulin	Immune response	SP;TM	Yes
SFN	2810	14-3-3 protein sigma	NP_006133.1	1	16	19	205	0.55	0.79	14.29	17.88	80.2	199.4	81	81	3185	2810	stratifin	Receptor signaling complex scaffold activity	Cytoplasm	Adapter molecule	Cell communication;Signal transduction	CC	Yes
CD109	135228	CD109 antigen isoform 1 preproprotein	NP_598000.2	3	14	14	31	0.55	0.75	15.54	13.85	34	41.8	15	15	10590	135228	CD109 antigen (Gov platelet alloantigens)	Molecular function unknown	Plasma membrane	Unclassified	Immune response	A2M;SP;GPI	Yes
FLOT1	10211	flotillin-1	NP_005794.1	1	8	8	18	0.55	0.61	5.78	27.04	9.6	52.6	9	9	6105	10211	flotillin 1	Molecular function unknown	Plasma membrane	Unclassified	Cell growth and/or maintenance	PHB;CC	Yes
FKBP5	2289	peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1	NP_001139248.1	2	19	19	40	0.55	0.52	17.25	16.11	48.4	42.1	23	23	4019	2289	FK506 binding protein 5	Isomerase activity	Cytoplasm	Enzyme: Isomerase	Metabolism;Energy pathways	TPR	Yes
ZNHIT2	741	zinc finger HIT domain-containing protein 2	NP_055020.1	1	1	1	2	0.54	1.23					1	1	5200	741	zinc finger, HIT domain containing 2	Molecular function unknown	Nucleus	Unclassified	Biological_process unknown	-	Yes
LYPLA2	11313	acyl-protein thioesterase 2	NP_009191.1	1	2	2	2	0.54	0.93					1	1	7127	11313	lysophospholipase II	Phospholipase activity	-	Enzyme: Phospholipase	Metabolism;Energy pathways	SP	No
DSCR3	10311	Down syndrome critical region protein 3	NP_006043.1	1	2	2	4	0.54	0.77	35.41	7.35	27.7	8	2	2	10390	10311	Down syndrome critical region gene 3	Molecular function unknown	-	Unclassified	Biological_process unknown	-	Yes
PLXNB1	5364	plexin-B1 precursor	NP_002664.2	1	1	1	1	0.54	0.75					1	1	3032	5364	plexin B1	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction	SEMA;PSI;IPT;CC;SP	Yes
ADH1B	125	alcohol dehydrogenase 1B isoform 1	NP_000659.2	1	1	1	3	0.54	0.66	26.32	4.79	20.3	4.5	2	2	65	125	alcohol dehydrogenase IB (class I), betapolypeptide	Catalytic activity	Mitochondrion	Enzyme: Dehydrogenase	Metabolism;Energy pathways	-	Yes
DGKA	1606	diacylglycerol kinase alpha	NP_001336.2	3	13	13	36	0.54	0.57	14.72	14.37	32.6	33.6	16	16	517	1606	diacylglycerol kinase, alpha 80kDa	Catalytic activity	Cytoplasm	Enzyme: Phosphotransferase	Cell communication;Signal transduction	C1;DAGKC;EF;DAGKa	Yes
TCAF1	9747	protein FAM115A isoform 1	NP_055534.1	3	1	1	2	0.53	1.31					1	1									
ANXA8L1	728113	annexin A8-like protein 1 isoform 1	NP_001092315.2	3	2	23	105	0.53	1.26	20.18	8.75	21.8	22.3	4	4	19373	728113	None	Calcium ion binding	-	Calcium binding protein	Signal transduction	ANX	No
SNAP29	9342	synaptosomal-associated protein 29	NP_004773.1	1	1	1	2	0.53	0.73					1	1	11968	9342	synaptosomal-associated protein, 29kDa	Auxiliary transport protein activity	Plasma membrane	Membrane transport protein	Transport	t_SNARE	Yes
HIST1H3F	8968	histone H3.1	NP_066298.1	4	3	8	37	0.53	0.71	8.99	14.96	10.7	24.1	5	5	11910	8968	histone 1, H3f	DNA binding	Nucleus	DNA binding protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	-	No
S100A16	140576	protein S100-A16	NP_525127.1	1	5	5	18	0.53	0.65	6.57	26.2	9.8	50.9	8	8	11529	140576	S100 calcium binding protein A16	Calcium ion binding	Nucleolus	Calcium binding protein	Cell communication;Signal transduction	EF	No
TNC	3371	tenascin precursor	NP_002151.2	1	36	36	100	0.53	0.61	15.44	8.04	66.5	37.3	54	54	1756	3371	tenascin C (hexabrachion)	Cell adhesion molecule activity	Extracellular	Adhesion molecule	Cell communication;Signal transduction	EGF;FN3;FBG;RGD;SP	Yes
S100A13	6284	protein S100-A13	NP_005970.1	1	4	4	9	0.53	0.57	13.6	27.33	17.9	39.2	6	6	3586	6284	S100 calcium binding protein A13	Calcium ion binding	Nucleus	Calcium binding protein	Cell communication;Signal transduction	S_100	Yes
SUN1	23353	SUN domain-containing protein 1 isoform a	NP_001124437.1	5	8	9	19	0.53	0.57	17.69	24	25.1	37.5	7	7	16257	23353	unc-84 homolog A (C. elegans)	Intracellular transporter activity	Nucleus	Integral membrane protein	Cell growth and/or maintenance	TM;CC	Yes
CD14	929	monocyte differentiation antigen CD14 precursor	NP_000582.1	1	4	4	9	0.53	0.57	12.53	12.48	13.3	14.3	4	4	1151	929	CD14 antigen	Receptor activity	Cell surface	Cell surface receptor	Immune response	LRR;SP	Yes
IFIT1	3434	interferon-induced protein with tetratricopeptide repeats 1 isoform 1	NP_001539.3	4	18	19	41	0.53	0.55	11.4	9.7	28.3	25	21	21	983	3434	interferon-induced protein withtetratricopeptide repeats 1	Nucleic acid binding;Protein binding	Cytoplasm	DNA binding protein;RNA binding protein	Biological_process unknown	TPR	Yes
ITGAV	3685	integrin alpha-V isoform 1 precursor	NP_002201.1	3	26	26	63	0.53	0.51	13.14	17.26	42.6	54.8	34	34	1903	3685	integrin, alpha V (vitronectin receptor, alphapolypeptide, antigen CD51)	Receptor activity	Plasma membrane	Cell surface receptor	Cell communication;Signal transduction;Cell adhesion	TM;INTA;SP	Yes
PYCARD	29108	apoptosis-associated speck-like protein containing a CARD isoform a	NP_037390.2	2	4	4	12	0.52	0.91	36.62	10.91	49	24.8	6	6	6020	29108	PYD and CARD domain containing	Caspase activator activity	Cytoplasm	Adapter molecule	Apoptosis	CARD	No
NDOR1	27158	NADPH-dependent diflavin oxidoreductase 1 isoform a	NP_001137498.1	4	1	1	2	0.52	0.9					1	1	10444	27158	NADPH dependent diflavin oxidoreductase 1	Catalytic activity	Cytoplasm	Enzyme: Reductase	Metabolism;Energy pathways	-	No
C14orf1	11161	probable ergosterol biosynthetic protein 28	NP_009107.1	1	2	2	3	0.52	0.73	18.89	16.67	13.9	17.4	2	2	5201	11161	chromosome 14 open reading frame 1	Molecular function unknown	Plasma membrane	Unclassified	Metabolism;Energy pathways	TM	Yes
NDUFA7	4701	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NP_004992.2	1	3	3	4	0.52	0.63	20.01	35.97	18.2	40.8	3	3	11885	4701	NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 7, 14.5kDa	Molecular function unknown	Mitochondrion	Unclassified	Metabolism;Energy pathways	-	Yes
PPP1R14C	81706	protein phosphatase 1 regulatory subunit 14C	NP_112211.1	1	3	3	7	0.52	0.59	49.91	24.63	55.5	29.5	4	4	17890	81706	protein phosphatase 1, regulatory(inhibitor) subunit 14C	Molecular function unknown	Integral to membrane	Regulatory/other subunit	Cell communication;Signal transduction	-	Yes
LIMA1	51474	LIM domain and actin-binding protein 1 isoform 2	NP_057441.1	2	2	38	104	0.51	1.37	13.77	2.54	12.2	6	3	3	9755	51474	None	Structural constituent of cytoskeleton	Cytoplasm	Cytoskeletal protein	Cell growth and/or maintenance	LIM	Yes
CELSR1	9620	cadherin EGF LAG seven-pass G-type receptor 1 precursor	NP_055061.1	1	1	1	1	0.51	1.19					1	1	5160	9620	cadherin, EGF LAG seven-pass G-type receptor 1(flamingo homolog, Drosophila)	G-protein coupled receptor activity	Plasma membrane;Nucleus	G protein coupled receptor	Cell communication;Signal transduction	SP;Cadherin;EGFL;LAMG;HRM;GPS;TM	Yes
LAMP2	3920	lysosome-associated membrane glycoprotein 2 isoform C precursor	NP_001116078.1	3	1	1	2	0.51	1.08					1	1	2396	3920	lysosomal-associated membrane protein 2	Cell adhesion molecule activity	Lysosome	Adhesion molecule	Cell growth and/or maintenance	TM;SP	Yes

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ANO6	196527	anoctamin-6 isoform d	NP_001191732.1	4	3	3	6	0.51	0.75	22.31	7.2	19.9	9.4	3	3	18746	196527	Transmembrane protein 16F	Molecular function unknown	Integral to membrane	Integral membrane protein	Biological_process unknown	TM	No
CROT	54677	peroxisomal carnitine O-octanoyltransferase isoform 1	NP_001137407.1	2	4	4	9	0.51	0.58	30.63	14.94	31.9	17.4	4	4	12081	54677	carnitine O-octanoyltransferase	Acyltransferase activity	Peroxisome	Enzyme: Acyltransferase	Metabolism;Energy pathways	-	Yes
DSG3	1830	desmoglein-3 preproprotein	NP_001935.2	1	16	16	38	0.51	0.52	11.49	26.54	25.4	63.7	18	18	1355	1830	desmoglein 3 (pemphigus vulgaris antigen)	Cell adhesion molecule activity	Plasma membrane	Adhesion molecule	Cell communication;Signal transduction	Cadherin;SP;TM	Yes
NFKBIE	4794	NF-kappa-B inhibitor epsilon	NP_004547.2	1	1	1	2		1.78						1	5181	4794	nuclear factor of kappa light polypeptide geneenhancer in B-cells inhibitor, epsilon	Transcription regulator activity	Nucleus	Transcription regulatory protein	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	ANK	Yes