

**Supplementary Table 3: List of total proteins identified in microalbuminuriaMiA group by LC-MS/MS using orbitrap**

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100001593	P42785	MTOR	Lysosomal Pro-X carboxypeptidase	10.89	2	3	3	6	9.30	496	55.8	7.21	Lysosome	Proteolysis	Carboxypeptidase activity	Yes 1
IP100001952	O94919		Endonuclease domain-containing 1 protein	18.20	1	6	6	12	16.64	500	55.0	5.71	Extracellular region		Nuclease activity	Yes 3
IP100002745	Q9UIBR2	MYB	Cathepsin Z	9.57	1	2	2	2	6.26	303	33.8	7.11	Lysosome	Proteolysis	Endopeptidase activity	Yes 1
IP100003362	P11021		HSPA5 protein	5.04	10	1	2	4	5.04	655	72.4	5.16	ER lumen	Anti-apoptosis	Nucleotide binding	Yes
IP100003437	Q16661	GUCA2B	Guanylate cyclase activator 2B	11.61	1	1	1	1	2.46	112	12.1	6.48	Extracellular region	Circulatory system process	Enzyme activator activity	Yes 1
IP100003919	Q53TR4	GAPD	Isoform 1 of glutamyl-peptide cyclotransferase	11.08	4	3	3	9	11.65	361	40.9	6.61	Extracellular region	Proteolysis	Peptidase activity	Yes
IP100004573	P01833	PIGR	Polymorphic immunoglobulin receptor	18.72	1	11	11	50	85.90	764	83.2	5.74	Extracellular region			Yes 1
IP100004656	P61769	LYZ	Beta-2-microglobulin	40.34	4	5	5	47	88.15	119	13.7	6.52	Golgi membrane	Regulation of leukocyte mediated cytotoxicity		Yes
IP100005038	P52758	HRSP12	Ribonuclease UK114	25.55	3	2	2	2	5.62	137	14.5	8.68	Cytoplasm. Nucleus. Note: Mostly cytoplasmic but, in less differentiated cells occasionally nuclear	Regulation of translation	Nuclease activity	No
IP100005126	P52799	EFNB2	Ephrin-B2	4.80	1	1	1	1	3.61	333	36.9	8.85	Plasma membrane	Vasculature development	Ephrin receptor binding	Yes 1
IP100006114	P36955	CD14	Pigment epithelium-derived factor	41.39	3	13	13	143	218.37	418	46.3	6.38	Extracellular region	Cell proliferation	Enzyme inhibitor activity	Yes
IP100006662	P05090	APOD	Apolipoprotein D	25.93	5	4	4	45	38.28	189	21.3	5.15	Extracellular region	Lipid metabolic process	Lipid transporter activity	Yes
IP100006705	P11684	CETP	Uteroglobin	41.76	1	3	3	5	8.38	91	10.0	5.06	Extracellular region	Negative regulation of transcription from RNA polymerase II promoter	Enzyme inhibitor activity	Yes
IP100007047	P05109	S100A8	Protein S100-A8	60.22	1	5	5	14	15.54	93	10.8	7.03	Nucleolus	Defense response	Calcium ion binding	No
IP100007221	P05154		Plasma serine protease inhibitor	32.27	2	10	10	62	40.10	406	45.7	9.26	Extracellular region	Membrane fusion	Pattern binding	Yes
IP100007664			Plasma glutamate carboxypeptidase	21.40	4	7	7	16	23.46	472	51.9	6.18	Cell fraction	Proteolysis	Carboxypeptidase activity	

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IP100007752	P68371	TUBB2C	Tubulin beta-2C chain	24.49	9	1	7	16	27.70	445	49.8	4.89	Cytosol	Cell killing	Nucleotide binding	No	
IP100007778	Q8TC97		Di-N-acetylchitinase	16.10	2	4	4	11	16.47	385	43.7	6.64	Lysosome	Polysaccharide catabolic process	Chitinase activity	Yes	
IP100007800	Q9UKU9		Angiopoietin-related protein 2	9.74	2	3	3	3	5.88	493	57.1	7.53	Extracellular region	Signal transduction; multicellular organismal development	Receptor binding	Yes	
IP100008787	P54802		Alpha-N-acetylglucosaminidase	25.57	3	11	11	115	160.22	743	82.1	6.54	Lysosome	Involved in the degradation of heparan sulfate	Alpha-N-acetylglucosaminidase activity	Yes	
IP100009027	Q4ZG28	REG1A	Lithostathine-1-alpha	33.73	3	4	4	19	19.59	166	18.7	5.94	Extracellular region	Positive regulation of cell proliferation	Sugar binding	Yes	
IP100009028	P05452	CLEC3B	Tetranectin	23.27	2	3	3	9	8.62	202	22.6	5.67	Extracellular region	Skeletal system development	Sugar binding	Yes	
IP100009030	P13473	CDH1	Isoform LAMP-2A of lysosome-associated membrane glycoprotein 2	2.93	3	1	1	2	4.96	410	44.9	5.63	Cell membrane	Platelet activation		Yes	1
IP100009276	Q9UNN8	beta-globin	Endothelial protein C receptor precursor	14.55	1	3	3	41	46.01	275	30.7	8.48	Centrosome	Immune response		Yes	1
IP100009653	Q9H756	REG1A	Leucine-rich repeat-containing protein 19	3.51	1	1	1	3	5.38	370	42.3	5.12	Integral to membrane			Yes	1
IP100009823	P15085	CPA1	Carboxypeptidase A1	12.65	5	4	4	9	13.78	419	47.1	5.76	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes	
IP100009865	P13645	KRT10	Keratin, type I cytoskeletal 10	41.78	7	23	24	1492	871.02	584	58.8	5.21	Cytoskeleton	Ectoderm development	Structural molecule activity	No	
IP100009901	P61970	NUTF2	Nuclear transport factor 2	33.86	1	2	2	4	12.67	127	14.5	5.38	Nuclear envelope	Protein targeting	Protein transporter activity	No	
IP100010105	P56537	eIF-6	Eukaryotic translation initiation factor 6	13.06	3	2	2	3	6.10	245	26.6	4.68	Cytoplasm. Nucleus	Mature ribosome assembly	Protein binding	No	
IP100010182	P07108	C4A	Isoform 1 of acyl-CoA-binding protein	18.39	7	1	1	1	2.55	87	10.0	6.57	Cell fraction	Transport	Acyl-CoA binding	No	
IP100010290	P07148	DBI	FABP1 protein (fragment)	42.54	3	3	3	10	16.81	134	15.1	9.51	Cytoplasm	Lipid transport	Chromatin binding	No	
IP100010471	Q59GX5		Plastin-2	8.45	2	3	3	7	13.83	627	70.2	5.43	Cell fraction	Cell activation	Actin binding	No	
IP100010675	Q03403	TFF2	Trefoil factor 2	21.71	1	2	2	4	7.97	129	14.3	5.81	Extracellular region	Digestion	Protein binding	Yes	
IP100010949	Q9HAT2		Isoform 1 of sialate O-acetyltransferase	7.65	3	3	3	10	8.32	523	58.3	7.33	Plasma membrane		Sialate O-acetyltransferase activity		

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IP100011229	P07339	CTSD	Cathepsin D	23.54	6	6	24	24.61	412	44.5	6.54	Lysosome.	Autophagic vacuole formation	Endopeptidase activity	Yes
IP100011261	P07360	C8B	Complement component C8 gamma chain	34.16	2	4	15	50.01	202	22.3	8.31	Melanosome Extracellular region	Adaptive immune response	Retinoid binding	Yes
IP100011302	P13987	C6	CD59 glycoprotein	25.00	1	4	30	25.78	128	14.2	6.48	Cell fraction	Cell surface receptor linked signal transduction	Protein binding	Yes
IP100011564	P31431	MAPK4	Syndecan-4	13.13	1	2	4	5.14	198	21.6	4.50	Golgi apparatus	Regulation of muscle contraction	Cytoskeletal protein binding	Yes 1
IP100011604	P23434	GCSH	Glycine cleavage system H protein, mitochondrial	11.56	2	1	1	3.85	173	18.9	4.88	Mitochondrion	Glycine metabolic process	Aminomethyl transferase activity	Yes
IP100011685	Q03692	COL10A1	Collagen alpha-1(X) chain	4.71	1	1	1	2.60	680	66.1	9.67	Extracellular region	Skeletal system development	Calcium ion binding	Yes
IP100012102	P15586		N-acetylglucosamine-6-sulfatase	18.48	3	7	43	17.58	552	62.0	8.31	Lysosome	Polysaccharide catabolic process	Calcium ion binding	Yes 1
IP100012503	P07602	IVL	Isoform Sap-mu-0 of proactivator polypeptide	9.35	5	3	62	49.86	524	58.1	5.17	Lysosome	Membrane lipid metabolic process	Enzyme activator activity	Yes
IP100013179	P41222	LEP	Prostaglandin-H2 D-isomerase	42.63	4	4	623	837.21	190	21.0	7.80	Rough ER	Prostaglandin biosynthetic process	Prostaglandin-D synthase activity	Yes
IP100013303	Q13449	LSAMP	Limbic system-associated membrane protein	4.73	2	1	2	3.99	338	37.4	6.98	Plasma membrane	Cell adhesion	Protein binding	Yes 1
IP100013382	P09228	GSTP1	Cystatin-SA	10.64	1	1	2	3.15	141	16.4	4.93	Extracellular region		Enzyme inhibitor activity	Yes
IP100013885	P31944	OBSCN	Caspase-14	25.62	1	5	9	9.40	242	27.7	5.58	Lysosome	Proteolysis	Endopeptidase activity	No
IP100013895	P31949	S100A11	Protein S100-A11	29.52	1	1	3	6.13	105	11.7	7.12	Nucleus	Regulation of DNA replication	Calcium ion binding	No
IP100013933	P15924		Isoform DPl of desmoplakin	7.18	3	13	43	27.91	2871	331.6	6.81	Cell junction , desmosome	Ectoderm development	Structural molecule activity	No
IP100014048	P07998	THBS1	Ribonuclease pancreatic	50.64	1	4	134	90.90	156	17.6	8.79	Extracellular region		Nuclease activity	Yes 1
IP100014375	Q07075	ENPEP	Glutamyl aminopeptidase	2.61	1	2	5	2.37	109.2	109.2	5.47	Plasma membrane	Angiogenesis	Aminopeptidase activity	No 1
IP100015681	P09603		Isoform 1 of macrophage colony-stimulating factor 1	9.75	4	4	20	22.29	554	60.1	5.29	Extracellular region	Cell activation	Cytokine activity	No

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IP100016334	P43121	MCAM	Isoform 1 of cell surface glycoprotein MUC18	9.60	2	3	3	5.33	646	71.6	5.76	Plasma membrane	Cell adhesion		Yes
IP100016645	Q15375	EPHA7	Isoform 1 of ephrin type-A receptor 7	3.01	6	2	2	8.17	998	112.0	5.80	Plasma membrane	Cell morphogenesis	Nucleotide binding	Yes
IP100016915	Q16270		Insulin-like growth factor-binding protein 7	29.08	1	5	9	7.64	282	29.1	7.90	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes
IP100017601	Q1L857	CP	Ceruloplasmin	35.68	8	30	335	435.83	1065	122.1	5.72	Extracellular region	Transition metal ion transport	Ferroxidase activity	Yes
IP100017951	Q9H5H6	CD44	cDNA: FLJ23429 fis, clone HRC10578	18.46	1	1	1	2.92	195	21.1	9.47				No
IP100017987	P35321	SPRR1A	Cornifin-A	19.10	2	1	1	5.79	89	9.9	8.48	Cytoplasm	Ectoderm development	Structural molecule activity	No
IP100018236	Q6LBL5	GM2A	Ganglioside GM2 activator	15.54	1	2	18	29.08	193	20.8	5.31	Lysosome	Ganglioside metabolic process	Beta-N-acetylhexosaminidase activity	Yes
IP100018953	P27487	DPP4	Dipeptidyl peptidase 4	10.70	2	6	27	34.35	766	88.2	6.04	Cell membrane	Response to hypoxia	Endopeptidase activity	Yes
IP100019359	P35527	THBS4	Keratin, type I cytoskeletal 9	54.09	1	23	23	318.70	623	62.0	5.24	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IP100019449	P10153	RNASE2	Non-secretory ribonuclease	19.88	2	3	76	36.18	161	18.3	8.73	Lysosome	RNA catabolic process	Nuclease activity	Yes
IP100019943	P43652	MCAM	Afamin	25.71	1	13	61	55.38	599	69.0	5.90	Extracellular region	Vitamin transport	Vitamin E binding	Yes
IP100019954	Q6BD2	CST6	Cystatin-M	48.32	1	4	14	51.72	149	16.5	8.09	Cornified envelope	Ectoderm development	Enzyme inhibitor activity	Yes
IP100019988	Q53GP1		N-sulphoglucosamine sulphohydrolase	4.98	1	2	2	5.07	502	56.7	6.95	Lysosome	Proteoglycan metabolic process	Calcium ion binding	Yes
IP100020019	Q15848	ADIPOQ	Adiponectin	6.15	1	1	2	3.77	244	26.4	5.74	Extracellular region	Response to hypoxia	Cytokine activity	Yes
IP100020091	P19652	ORM2	Alpha-1-acid glycoprotein 2	55.72	1	6	11	241.26	201	23.6	5.11	Extracellular region	Acute-phase response	Binding	Yes
IP100020599	Q53G71		Calreticulin	6.47	1	2	2	4.72	417	48.1	4.44	Cell fraction	Negative regulation of transcription from RNA polymerase II promoter	Opsonin binding	No
IP100020986	P51884	PSMD7	Lumican	35.21	3	9	9	73.39	338	38.4	6.61	Extracellular	Sensory perception	Structural molecule activity	Yes
IP100021085	O75594	CALB1	Peptidoglycan recognition protein 1	37.24	1	4	4	31.90	196	21.7	8.59	Extracellular region	Peptidoglycan metabolic process	Pattern binding	Yes

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IP100021263	P63104	LU	14-3-3 protein zeta/delta	13.47	4	2	2	5	11.93	245	27.7	4.79	Cell fraction	Cell activation	Transcription factor binding	No
IP100021304	P35908	KRT2	Keratin, type II cytoskeletal 2	69.61	3	28	34	530	375.67	645	65.8	8.00	Cytoskeleton	Cell activation	Structural molecule activity	No
IP100021439	P60709	ACTB	Actin, cytoplasmic 1	20.00	23	2	4	20	11.77	375	41.7	5.48	Histone acetyltransferase complex	Cell	Nucleotide binding	No
IP100021794	P10619		Lysosomal protective protein	7.50	3	2	2	5	6.41	480	54.4	6.61	Lysosome	Proteolysis	Carboxypeptidase activity	Yes
IP100021828	P04080	VTN	Cystatin-B	45.92	1	3	3	5	11.62	98	11.1	7.56	Nucleolus	Behavior	Protease binding	No
IP100021841	P02647	APOA1	Apolipoprotein A-I	43.82	2	13	134	240.11	267	267	30.8	5.76	Extracellular region	Regulation of cytokine production	Beta-amyloid binding	Yes
IP100021854	P02652	APOA2	Apolipoprotein A-II	43.00	1	3	3	16	43.06	100	11.2	6.62	Extracellular region	Regulation of cytokine production	Enzyme inhibitor activity	Yes
IP100021857	P02656	APOC3	Apolipoprotein C-III	16.16	2	1	1	5	16.59	99	10.8	5.41	Extracellular region	Neutral lipid metabolic process	Enzyme inhibitor activity	Yes
IP100021885	P02671	FGA	Isoform 1 of fibrinogen alpha chain	28.52	4	15	15	148	142.01	866	94.9	6.01	Cell fraction	Cell activation	Protein binding	Yes
IP100022204	P29508		Isoform 1 of serpin B3	31.28	5	4	10	68	34.80	390	44.5	6.81	Cytoplasm	Immune response	Enzyme inhibitor activity	No
IP100022213	P20142	PGC	Gastricin	3.09	1	1	1	1	2.35	388	42.4	4.46	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP100022331	P04180	ANXA1	Phosphatidylcholine-sterol acyltransferase	13.86	1	3	3	5	10.33	440	49.5	6.11	Extracellular region	Cellular amino acid derivative metabolic process	Carboxylesterase activity	Yes 2
IP100022371	Q68DR3	HRG	Histidine-rich glycoprotein	28.19	1	11	11	99	88.18	525	59.5	7.50	Extracellular region	Regulation of blood coagulation	Pattern binding	Yes
IP100022391	P02743	APCS	Serum amyloid P-component	11.21	1	2	2	4	13.17	223	25.4	6.54	Extracellular region	Acute inflammatory response	Calcium ion binding	Yes
IP100022395	P02748	C9	Complement component C9	27.73	1	11	11	44	57.91	559	63.1	5.59	Extracellular region	Cytolysis by symbiont of host cells		Yes
IP100022417	P02750	LRG1	Leucine-rich alpha-2-glycoprotein	36.02	1	7	7	68	66.93	347	38.2	6.95	Extracellular region	Fat cell differentiation		Yes
IP100022426	P02760	AMBIP	Protein AMBP	54.55	2	17	17	2239	1665.87	352	39.0	6.25	Cell fraction	Negative regulation of immune system process	Enzyme inhibitor activity	Yes

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IP100022429	P02763	ORM1	Alpha-1-acid glycoprotein 1	53.23	2	7	10	298	201	23.5	5.02	Extracellular region	Acute-phase response	Protein binding	Yes
IP100022432	P02766		Transferrin	65.31	4	8	8	428	147	15.9	5.76	Extracellular region	Transport	Hormone activity	Yes
IP100022449	Q92608	DOCK2	Isoform 1 of dedicator of cytokinesis protein 2	0.87	1	1	1	2.42	1830	211.8	6.87	Cytosol	Cell morphogenesis	Small GTPase regulator activity	No
IP100022488	P02790	PPBP	Hemopexin	44.37	1	12	12	596	462	51.6	7.02	Extracellular region	Regulation of protein amino acid phosphorylation	Iron ion binding	Yes
IP100022810	P53634		Isoform 1 of dipeptidyl peptidase 1	12.53	1	3	3	36	463	51.8	6.99	Lysosome	Proteolysis	Endopeptidase activity	No
IP100022895	Q7Z3U3		Alpha-1B-glycoprotein	42.42	4	11	11	329.07	495	54.2	5.87	Extracellular region			Yes
IP100022974	P12273	PIP	Prolactin-inducible protein	32.19	1	3	3	142.89	146	16.6	8.05	Extracellular region		Actin binding	Yes
IP100023673	Q08380	LGALS3BP	Galectin-3-binding protein	11.45	5	5	5	7.91	585	65.3	5.27	Extracellular region	Defense response	Scavenger receptor activity	Yes
IP100023728	Q92820	GGH	Gamma-glutamyl hydrolase	32.39	1	7	7	23.51	318	35.9	7.11	Lysosome	Glutamine metabolic process	Peptidase activity	Yes
IP100024046	B7Z9B1		cDNA FLJ52398, highly similar to cadherin-13	11.84	3	6	6	45.14	760	83.4	5.12	Plasma membrane	Angiogenesis	Calcium ion binding	No
IP100024292	P98164	HSPG2	Low-density lipoprotein receptor-related protein 2	2.77	2	9	9	27.72	4655	521.6	5.08	Cell fraction	Generation of a signal involved in cell-cell signaling	Calcium ion binding	Yes 1
IP100024307	P98172	EFNB1	Ephrin-B1	7.23	1	2	2	4.66	346	38.0	8.94	Cell fraction	Cell morphogenesis	Ephrin receptor binding	Yes 1
IP100025204	O43866	ZFP161	CD5 antigen-like	6.34	1	1	1	2.52	347	38.1	5.47	Extracellular region	Apoptosis	Scavenger receptor activity	Yes
IP100025318	O75368		SH3 domain-binding glutamic acid-rich-like protein	37.72	1	3	3	10.79	114	12.8	5.25	Cytoplasm		SH3 domain binding	No
IP100025476	P04746	AMY1A	Pancreatic alpha-amylase	28.77	8	2	10	75	511	57.7	7.05	Extracellular region	Carbohydrate metabolism	Alpha-amylase activity	Yes
IP100025753	Q02413		Desmoglein-1	6.48	1	4	4	23.58	1049	113.7	5.03	Cytosol	Cell-cell junction assembly	Calcium ion binding	Yes
IP100025861	P12830	CDH1	Cadherin-1	17.35	4	8	8	56.05	882	97.4	4.73	Plasma membrane	<i>In utero</i> embryonic development	Calcium ion binding	Yes 1
IP100026050	B3KQK7		Ceroid-lipofuscinosis neuronal protein 5	2.70	1	1	1	2.41	407	46.3	8.38	Lysosome	Cellular ion homeostasis	Protein binding	Yes 1

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IP 00026926	Q02747	SEMG2	Guanylin	9.57	1	1	1	3	10.30	115	12.4	4.59	Extracellular region	Signal transduction	Hormone activity	Yes 1
IP 00027444	P30740	SERPINB1	Leukocyte elastase inhibitor	18.47	1	5	5	20	28.47	379	42.7	6.28	Cytoplasm	Regulation of proteolysis	Enzyme inhibitor activity	No
IP 00027462	P06702	S100A9	Protein S100-A9	74.56	2	6	6	58	73.70	114	13.2	6.13	Cytoplasm	Cell motion	Calcium ion binding	No
IP 00027482	P08185		Corticosteroid-binding globulin	13.58	1	4	4	14	27.69	405	45.1	6.04	Extracellular region	Steroid metabolic process	Enzyme inhibitor activity	Yes
IP 00027493	P08195	CD55	Isoform 2 of 4F2 cell-surface antigen heavy chain	2.27	6	1	1	2	4.56	529	57.9	5.35	Apical plasma membrane	Ion transport	Amine transporter activity	No 1
IP 00027547	P81605	DLK1	Dermcidin	32.73	2	3	3	7	9.65	110	11.3	6.54	Extracellular region	Cell killing	Manganese ion binding	Yes
IP 00027827	Q16867		Extracellular superoxide dismutase (Cu-Zn)	12.08	1	2	2	4	4.74	240	25.8	6.61	Cell fraction	Response to hypoxia	Pattern binding	Yes
IP 00027851	Q9BVJ8	HEXA	cDNA FLJ53927, highly similar to beta-hexosaminidase alpha chain	9.81	4	4	4	5	7.89	540	62.0	5.26	Membrane	Skeletal system development	Beta-N-acetylhexosaminidase activity	No
IP 00028931	Q14126	DSG2	Desmoglein-2	1.25	1	1	1	2	3.31	1118	122.2	5.24	Plasma membrane	Cell adhesion	Calcium ion binding	Yes 2
IP 00029260	P08571		Monocyte differentiation antigen CD14	27.20	2	7	7	111	98.17	375	40.1	6.23	Cell membrane	Regulation of cytokine production	Lipopolysaccharide binding	Yes
IP 00030871	O95497	VNN1	Pantetheinase	15.01	4	5	5	6	7.63	513	57.0	5.55	Plasma membrane	Acute inflammatory response	Phospholipid binding	Yes
IP 00031065	P24855	DNASE1	Deoxyribonuclease-1	37.23	1	4	4	54	51.23	282	31.4	4.91	Extracellular region	DNA metabolic process	Actin binding	Yes 1
IP 00031121	P16870		Carboxypeptidase E precursor	10.84	4	4	4	5	7.48	572	63.6	6.49	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes
IP 00032179	P01008	SERPINC1	Antithrombin-III	51.94	2	18	18	292	395.11	464	52.6	6.71	Extracellular region	Response to nutrient	Pattern binding	Yes
IP 00032220	Q86U78	AGT	Angiotensinogen	33.40	2	11	11	187	258.02	485	53.1	6.32	Extracellular region	Ovulation from ovarian follicle	Enzyme inhibitor activity	Yes
IP 00032293	P01034	CFL1	Cystatin-C	41.10	1	4	4	202	429.30	146	15.8	8.75	Extracellular region	Defense response	Beta-amylloid binding	Yes 1
IP 00032294	P01036	CST3	Cystatin-S	20.57	2	2	2	6	10.24	141	16.2	5.02	Extracellular region	Enzyme inhibitor activity	Enzyme inhibitor activity	Yes
IP 00032311	P18428	LBP	Lipopolysaccharide-binding protein	14.97	1	6	6	34	49.55	481	53.3	6.70	Cell activation	Cell activation	Lipopolysaccharide binding	Yes

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100032325	P01040	CSTA	Cystatin-A	53.06	2	3	3	22	31.18	98	11.0	5.50	Cytoplasm	Ectoderm development	Protease binding	No
IP100056357	Q969H8	BHMT	UPF0556 protein C19orf10	8.67	1	1	1	1	2.38	173	18.8	6.68	Extracellular region	Positive regulation of cell proliferation	Growth factor activity	Yes
IP100059263	Q96A54	KLK3	Adiponectin receptor protein 1	3.47	1	1	1	1	2.43	375	42.6	7.02	Integral to membrane	Regulation of cell growth	Hormone binding	No
IP100059476	P16444	TCF9	Dipeptidase 1	8.03	1	2	2	3	5.22	411	45.6	6.15	Plasma membrane	Proteolysis	Peptidase activity	Yes
IP100060800	Q96DA0	CD44	Zymogen granule protein 16 homolog B	32.21	1	3	3	21	37.80	208	22.7	7.39	Extracellular region		Sugar binding	Yes
IP100072918	E7ENL6	MMRN2	322 kDa protein	2.25	9	5	5	9	7.61	2976	322.0	6.90		Cell adhesion	Enzyme inhibitor activity	Yes
IP100073772	Q2TU34		Fructose-1,6-bisphosphatase 1	15.09	1	3	3	10	10.36	338	36.8	6.99	Cell fraction	Monosaccharide metabolic process	Magnesium ion binding	No
IP100082931	Q9UBC9	SPRR3	Small proline-rich protein 3	28.40	2	3	3	14	13.11	169	18.1	8.57	Cytoplasm	Ectoderm development	Structural molecule activity	No
IP100098827	Q9Y547	HSPB11	Heat shock protein beta-11	17.36	1	1	1	1	2.53	144	16.3	5.03		Cell adhesion		No
IP100099883			Isoform 1 of G-protein coupled receptor family C group 5 member C	3.40	4	1	1	1	2.57	441	48.2	8.43	Mitochondrion	Cell surface receptor linked signal transduction		Yes
IP100103423	P78310	HBA1;	Isoform 4 of coxsackievirus and adenovirus receptor	5.00	6	1	1	1	2.39	200	22.4	8.43	Extracellular region	Mitochondrion organization		Yes
IP100103636	Q14508		Isoform 2 of WAP four-disulfide core domain protein 2	43.84	3	2	2	12	17.88	73	8.1	7.50	Extracellular region	Proteolysis	Enzyme inhibitor activity	Yes
IP100106494	B7Z416	RDHL	cDNA FLJ55219, highly similar to Dehydrogenase/reductase SDR family member 9	4.75	1	1	1	1	2.88	379	41.9	8.90	Cell fraction	Retinoid metabolic process	Alcohol dehydrogenase (NAD) activity	Yes
IP100107731	Q81YS5	OSCAR	Isoform 6 of osteoclast-associated immunoglobulin-like receptor	11.90	9	2	2	10	12.15	252	27.6	8.59	Plasma membrane			Yes
IP100154366	Q5JWF2	F10	Isoform XLas-3 of guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	3.19	3	1	1	1	2.63	752	77.6	5.03	Golgi membrane	Skeletal system development	Nucleotide binding	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100154742	P0CG05	IGLC2	IGL@ protein	40.60	16	3	6	70	50.80	234	24.8	6.37	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100160130	Q7LC53	CUBN	Cubilin	3.09	1	7	7	16	27.00	3623	398.5	5.35	Cell fraction	<i>In utero</i> embryonic development	Calcium ion binding	Yes
IP100163074	Q9HCN6		Isoform 2 of platelet glycoprotein VI	12.46	5	3	3	13	16.73	321	35.1	9.39	Cell membrane	Cell activation	Collagen binding	Yes
IP100163119	P51161	FABP6	Isoform 1 of gastrotropin	14.06	2	1	1	2	3.09	128	14.4	6.80	Cytosol	Steroid metabolic process	Fatty acid binding	No
IP100163207	Q96PD5	PGLYRP	Isoform 1 of N-acetylmuramoyl-L-alanine amidase	32.81	2	9	9	42	75.26	576	62.2	7.55	Extracellular region	Peptidoglycan metabolic process	Pattern binding	Yes
IP100163563	Q96S96	PEBP4	Phosphatidyethanolamine-binding protein 4	31.28	1	3	3	6	16.30	227	25.7	6.54	Lysosome			Yes
IP100165972	Q6FWH3		Complement factor D preproprotein	43.46	1	7	7	45	93.02	260	27.8	7.25	Extracellular region	Immune effector process	Endopeptidase activity	Yes
IP100166205	Q8N1N4		Isoform 2 of keratin, type II cytoskeletal 78	5.85	2	2	2	4	2.46	410	45.0	5.20	Cytoskeleton		Structural molecule activity	
IP100166729	P25311	AZGP1	Zinc-alpha-2-glycoprotein	41.61	6	11	11	173	106.95	298	34.2	6.05	Extracellular region	Immune response	Nuclease activity	Yes
IP100170635	Q8WVN6	SECTM1	Secreted and transmembrane protein 1	20.97	1	3	3	114	178.65	248	27.0	7.43	Extracellular region	Immune response	Cytokine activity	Yes
IP100174541	P18510	IL1RN	Isoform 4 of interleukin-1 receptor antagonist protein	23.78	5	2	2	5	8.80	143	16.1	4.88	Extracellular region	Defense response	Fibroblast growth factor receptor binding	Yes
IP100176427	Q8NFW8	KRTHB6	Cell adhesion molecule 4	14.69	1	4	4	33	42.33	388	42.8	6.30	Integral to membrane	Cell adhesion		Yes
IP100178015	Q16820	MEP1B	Meprin A subunit beta	4.28	1	1	1	1	2.66	701	79.5	5.74	Cell fraction	Proteolysis	Endopeptidase activity	Yes
IP100180408	Q9Y2K3		Myosin-15	0.92	1	1	1	1	2.52	1946	224.5	5.85	Cytoskeleton		Nucleotide binding	No
IP100180675	Q9UQM3		Tubulin alpha-1A chain	25.72	16	1	7	25	38.17	451	50.1	5.06	Cytosol	Protein complex assembly	Nucleotide binding	No
IP100186736	Q969P0	IGSF8	Isoform 3 of immunoglobulin superfamily member 8	3.61	2	1	1	1	3.03	526	55.8	8.78	Integral to membrane	Cell motion		Yes
IP100215746	P15090	FABP4	Fatty acid-binding protein, adipocyte	25.00	3	3	3	16	42.50	132	14.7	7.14	Cell fraction	Cytokine production	Fatty acid binding	No
IP100215894	P01042		Isoform LMW of kininogen-1	32.55	5	2	13	63	54.73	427	47.9	6.65	Extracellular region , extracellular space	Muscle system process	Pattern binding	Yes

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Supplementary Table 3: Contd...

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IP100215980	Q9UEI6	PVRL2	Isoform alpha of poliovirus receptor-related protein 2	7.31	2	2	2	4	7.23	479	51.3	5.11	Plasma membrane	Regulation of leukocyte mediated cytotoxicity	Coreceptor activity	Yes 1
IP100215983	P00915	PLAU	Carbonic anhydrase 1	41.00	4	6	6	18	26.26	261	28.9	7.12	Golgi apparatus	One-carbon metabolic process	Carbonate dehydratase activity	No
IP100216107	P32418	S100A11	Isoform 3 of sodium/calcium exchanger 1	2.45	5	1	1	3	5.95	937	104.6	4.97	Cell fraction	Response to reactive oxygen species	Calcium:sodium antiporter activity	Yes 11
IP100216641	Q12860		Isoform 2 of contactin-1	4.57	3	3	3	8	10.19	1007	111.8	5.77	Cell membrane	Cell adhesion	Anchored to membrane	No
IP100216691	P07737	PFN1	Profilin-1	31.43	1	3	3	9	20.28	140	15.0	8.27	Cytoskeleton	Embryonic epithelial tube formation	Actin binding	No
IP100216773	Q8IUK7		ALB protein	8.08	10	3	3	46	21.14	396	45.1	6.10	Extracellular space	Cytolysis by symbiont of host cells	DNA binding	Yes
IP100217291	Q92859	NEO1	Isoform 2 of neogenin	1.07	4	1	1	1	2.19	1408	154.2	6.37	Plasma membrane	Syncytium formation by plasma membrane fusion	Transcription regulator activity	Yes 1
IP100217963	P08779	KRT16	Keratin, type I cytoskeletal 16	43.13	22	13	18	159	88.62	473	51.2	5.05	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IP100218413	P43251		Biotinidase	15.10	5	6	6	22	40.32	543	61.1	6.25	Golgi apparatus	Ectoderm development	Biotin carboxylase activity	Yes
IP100218733	P00441	SOD1	Superoxide dismutase (Cu-Zn)	53.90	2	5	5	14	25.57	154	15.9	6.13	Cytoplasm	MAPKKK cascade	Superoxide dismutase activity	No
IP100218918	Q5TZZ9	ANXA1	Annexin A1	36.71	4	9	9	44	40.74	346	38.7	7.02	Nucleus, cytoplasm	Lipid transport	Enzyme inhibitor activity	No
IP100218949	P36980	SERPINF1	Isoform short of complement factor H-related protein 2	9.88	4	2	2	3	5.08	243	27.9	6.92	Extracellular region	Involved in complement regulation. Can associate with lipoproteins and may play a role in lipid metabolism		Yes
IP100219025	P35754	SAA4	Glutaredoxin-1	47.17	1	2	2	6	15.55	106	11.8	8.09	Cytosol	Generation of precursor metabolites and energy	Electron carrier activity	No
IP100219131	O75144	ICOSLG	Isoform 1 of ICOS ligand	9.27	4	2	2	2	5.86	302	33.3	5.31	Membrane	Cell activation	Receptor binding	Yes 1

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100219426	P15151	FABP4	Isoform gamma of poliovirus receptor	9.62	4	2	2	17	32.33	364	39.3	6.21	Extracellular region	Regulation of leukocyte mediated cytotoxicity	Viral receptor activity	Yes
IP100219619	Q9H6X2	FLJ22002	Isoform 3 of anthrax toxin receptor 1	14.48	8	2	2	14	20.38	297	33.3	6.68	Cell membrane	Actin cytoskeleton reorganization	Actin filament binding	Yes
IP100219684	P05413	FABP3	Fatty acid-binding protein, heart	10.53	1	2	2	3	10.39	133	14.8	6.80	Cytosol	Cellular amino acid derivative metabolic process	Lipid transporter activity	No
IP100219713	P02679	FGB	Isoform gamma-A of fibrinogen gamma chain	32.72	6	10	10	73	54.69	437	49.5	6.09	Extracellular region	Cell activation	Calcium ion binding	Yes
IP100219806	P31151	S100A7	Protein S100-A7	42.57	2	5	5	26	36.50	101	11.5	6.77	Extracellular region	Response to reactive oxygen species	Calcium ion binding	No
IP100219827	Q86SR0	SLURP2	Secreted Ly-6/uPAR-related protein 2	13.40	2	1	1	2	5.86	97	10.2	6.62	Extracellular region			Yes
IP100220146	Q02487	DSC2	Isoform 2B of desmocollin-2	10.51	3	5	5	12	14.37	847	93.7	5.47	Plasma membrane	Cell adhesion	Calcium ion binding	Yes
IP100220216	P24821	TNC	Isoform 6 of tenascin	0.96	7	1	1	4	5.13	1564	171.2	5.10	Extracellular region	Cell adhesion	Cell adhesion	Yes
IP100220281	Q8N619		Isoform alpha-1 of guanine nucleotide-binding protein G(o) subunit alpha	7.91	2	2	2	3	5.26	354	40.0	5.53	Cell fraction	Response to reactive oxygen species	Nucleotide binding	No
IP100220327	P04264	KRT1	Keratin, type II cytoskeletal 1	60.87	12	32	36	575	340.04	644	66.0	8.12	Cytoskeleton	Complement activation, lectin pathway	Structural molecule activity	No
IP100220361	P05937	CALB1	Calbindin	6.13	1	1	1	1	2.58	261	30.0	4.83	Cytosol	Behavior	Steroid binding	No
IP100221224	Q81VL7		Aminopeptidase N	26.06	1	18	18	156	268.89	967	109.5	5.48	Cell fraction	Angiogenesis	Aminopeptidase activity	No
IP100247063	P08473	MME	Nephrilysin	3.33	1	2	2	2	2.94	750	85.5	5.73	Cell fraction	Proteolysis	Endopeptidase activity	No
IP100247167	Q6ZVX7		Nonspecific cytotoxic cell receptor protein 1 homolog	4.00	1	1	1	2	2.48	275	30.8	6.62		Macromolecule catabolic process		No
IP100289275	O75339	ICOSLG	Cartilage intermediate layer protein 1	2.79	2	2	2	4	5.73	1184	132.5	8.38	Extracellular region	Negative regulation of signal transduction	Alkaline phosphatase activity	Yes
IP100289933	Q13477	LSAMP	Isoform 2 of mucosal addressin cell adhesion molecule 1	5.54	3	1	1	9	14.17	271	28.7	5.80	Membrane	Cell adhesion,immune response	Cell adhesion,immune response	Yes

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Supplementary Table 3: Contd...

Accession	Accession	ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM	
IP100290085	P19022	KRT4		Cadherin-2	5.41	7	5	5	7	22.56	906	99.7	4.81	Membrane	Blood vessel development	Calcium ion binding	Yes	1
IP100290856	Q8Y5Y7	XLKD1		Lymphatic vessel endothelial hyalurononic acid receptor 1	3.42	1	1	1	5	5.13	322	35.2	8.28	Cell fraction	Polysaccharide catabolic process	Pattern binding	Yes	1
IP100291136	P12109	COL6A1		Collagen alpha-1 (VI) chain	15.66	2	10	10	50	51.32	1028	108.5	5.43	Extracellular region	Cell adhesion	Growth factor binding	Yes	
IP100291866	P05155	GAPDH		Plasma protease C1 inhibitor	26.20	3	12	12	125	183.04	500	55.1	6.55	Extracellular region	Regulation of complement activation	Complement binding	Yes	
IP100292069	Q14UF5	DAF		Isoform 2 of complement decay-accelerating factor	5.51	9	2	2	3	4.68	381	41.4	7.59	Cell membrane	Adaptive immune response	Blood group antigen	Yes	
IP100292130	Q07507	TRAMP		Dermatopontin	8.46	1	1	1	4	6.37	201	24.0	4.82	Extracellular region	Cell adhesion		Yes	
IP100292150	Q6AZ94	ITIH4		Latent-transforming growth factor beta-binding protein 2	1.04	1	1	1	2	3.20	1821	194.9	5.19	Extracellular region	Protein targeting	Calcium ion binding	Yes	
IP100292946	P05543	REG1A		Thyroxine-binding globulin	40.00	1	11	11	54	78.48	415	46.3	6.30	Extracellular region	Aging	Enzyme inhibitor activity	Yes	
IP100293088	P10253			Lysosomal alpha-glucosidase	20.90	2	1	11	57	38.34	952	105.3	5.99	Lysosome	Maltose metabolic process	Alpha-glucosidase activity	Yes	
IP100293275	Q8NHS7	PTPRS		Protein tyrosine phosphatase, receptor type, sigma isoform 3 precursor	2.40	7	2	2	3	4.69	1501	168.3	6.54	Plasma membrane	Protein amino acid dephosphorylation activity	Phosphoprotein phosphatase	Yes	1
IP100295414	P39059	TGFBR2		Collagen alpha-1 (XV) chain	2.31	1	2	2	4	16.88	1388	141.6	5.00	Extracellular region	Angiogenesis	Structural molecule activity	Yes	
IP100296099	Q7KYY3	THBS1		Thrombospondin-1	1.03	1	1	1	1	2.56	1170	129.3	4.94	Extracellular region	MAPKK cascade	Pattern binding	Yes	
IP100296141	Q9UHL4	DPP7		Dipeptidyl peptidase 2	6.50	2	2	2	6	11.04	492	54.3	6.32	Lysosome	Proteolysis	Aminopeptidase activity	Yes	
IP100296537	P23142	FBLN1		Isoform C of fibulin-1	7.76	8	3	3	8	14.54	683	74.4	5.24	Extracellular region	Interspecies interaction between organisms	Structural molecule activity	Yes	
IP100296589	Q8N3Y0	ITPK1		ITPK1 protein (fragment)	4.73	1	1	1	1	2.61	444	48.6	5.19	Intracellular	Inositol metabolic process	Nucleotide binding	No	
IP100296608	P10643			Complement component C7	11.98	1	4	7	21	36.70	843	93.5	6.48	Extracellular region	Adaptive immune response		Yes	
IP100296777	Q8N4S1			SPARC-like protein 1	16.87	4	2	6	13	9.68	664	75.2	4.81	Extracellular region	Signal transduction	Calcium ion binding	Yes	

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IP100297056	Q9UBG3	CRNN	Comulin	24.44	2	5	5	8	12.64	495	53.5	6.10	Cell fraction	Cell adhesion	Calcium ion binding	No
IP100298793	O00462	MANBA	Beta-mannosidase	8.53	2	5	5	8	11.00	879	100.8	5.52	Cell fraction	Glycoprotein catabolic process	Beta-mannosidase activity	Yes
IP100299547	P80188	LCN2	Isoform 1 of neutrophil gelatinase-associated lipocalin	40.91	2	5	5	13	42.01	198	22.6	8.91	Extracellular region	Response to virus		Yes
IP100300786	Q53F26	AMY1A	Alpha-amylase 1	30.53	3	1	9	185	235.13	511	57.7	6.93	Extracellular region	Digestion	Alpha-amylase activity	Yes
IP100301364	P63208	YWHAZ	Isoform 1 of S-phase kinase-associated protein 1	7.36	1	1	1	1	2.51	163	18.6	4.54	Mitotic cell cycle	Mitotic cell cycle		No
IP100304273	P06727	GSN	Apolipoprotein A-IV	49.24	2	15	15	171	196.77	396	45.4	5.38	Extracellular region	Response to reactive oxygen species	Lipid transporter activity	Yes
IP100306378	O00187	MASP2	Isoform 2 of MANNAN-binding lectin serine protease 2	35.68	3	4	4	22	23.39	185	20.6	5.96	Extracellular region	Complement activation, lectin pathway	Endopeptidase activity	Yes
IP100306543	Q99988	RARRES2	Growth/differentiation factor 15	5.19	1	1	1	1	2.81	308	34.1	9.66	Extracellular region	Cell surface receptor linked signal transduction	Cytokine activity	Yes
IP100328113	Q9NP01		Fibrillin-1	0.45	1	1	1	2	5.12	2871	312.0	4.93	Microfibril	Skeletal system development	Structural molecule activity	Yes
IP100328243	Q8IV08	PLD3	Phospholipase D3	2.04	1	1	1	2	2.58	490	54.7	6.47	ER	Lipid catabolic process	Phospholipase activity	No
IP100329771	Q9P2N4	ADAMTS9	Isoform 2 of A disintegrin and metalloproteinase with thrombospondin motifs 9	1.84	3	1	1	1	2.80	1629	182.6	7.68	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP100332887			Signal-regulatory protein alpha precursor	9.52	5	3	3	4	5.95	504	54.9	6.98	Plasma membrane	Cell adhesion	SH3 domain binding	
IP100334282	Q92520	FAM3C	Protein FAM3C	28.63	3	4	4	21	75.86	227	24.7	8.29	Extracellular	Ion transport	Cytokine activity	Yes
IP100337399	P57103	SLC8A3	Isoform 4 of sodium/calcium exchanger 3	3.06	5	1	1	1	2.49	620	68.9	5.14	Integral to membrane		Calcium:sodium antiporter activity	Yes
IP100374563	Q5XG79	MANBA	Aggrin	4.11	2	6	6	16	22.37	2045	214.7	6.40	Extracellular region	Regulation of transcription, DNA-dependent	Structural molecule activity	Yes
IP100375426	Q6LAF8	HBA2	Cathepsin H	8.05	2	2	2	4	10.32	323	36.2	8.10	Lysosome	Proteolysis	Endopeptidase activity	Yes

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IP100376379	Q7Z794	DLK1	Keratin, type II cytoskeletal 1b	12.28	1	5	6	37	35.07	578	61.9	5.99	Cytoskeleton		Structural molecule activity	No
IP100376436	Q9BQ83	A2M	Isoform 4 of vacuolar protein sorting-associated protein 13B	2.20	5	1	1	1	2.80	863	97.3	5.16	Nuclear chromosome	Double-strand break repair via homologous recombination	Nuclease activity	No
IP100383486			22 kDa protein	10.88	3	1	1	1	2.77	193	22.0	5.69	ER	RNA processing	RNA binding	Yes
IP100383615	Q8N126		Isoform 3 of cell adhesion molecule 3	8.24	3	2	2	2	4.46	352	38.3	5.96	Plasma membrane	Cell adhesion	Calcium ion binding	Yes
IP100383975	Q86T07		Full-length cDNA clone CS0DN001YP04 of Adult brain of Homo sapiens (Fragment)	5.18	2	1	1	4	5.90	367	40.4	5.30	Extracellular region	Circulatory system process	Calcium ion binding	No
IP100384067	Q8N2R4	ICAM1	cDNA FLJ90027 fis, clone HEMBA1001228, highly similar to human germline oligomeric matrix protein (COMP) mRNA	9.92	4	1	1	2	2.96	131	13.9	8.59	Extracellular region	Skeletal system development	Pattern binding	Yes
IP100384282	Q9UJU1		Cytovillin 2 (fragment)	7.09	7	1	1	1	2.54	141	16.2	9.31	Cytoplasm		Cytoskeletal protein binding	No
IP100384401	Q9JUL85		Myosin-reactive immunoglobulin kappa chain variable region (fragment)	16.51	1	1	1	15	22.77	109	11.8	8.51				No
IP100384444	P02533	KRT14	Keratin, type I cytoskeletal 14	41.95	23	8	18	116	100.61	472	51.5	5.16	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IP100385005	Q7Z3M0	CDK5RAP2	Putative uncharacterized protein	0.75	5	1	1	1	2.27	1607	183.2	5.53	Centrosome	Regulation of neuron differentiation	Microtubule binding	No
IP100385252	P04206	HRG	DKFZp686M1993 Ig kappa chain V-III region GOL	31.19	13	2	2	36	40.50	109	11.8	9.25	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100385253	P04207		Ig kappa chain V-III region CLL	12.40	1	1	1	8	9.68	129	14.3	8.51	Extracellular region	Complement activation, classical pathway	Antigen binding	Yes
IP100385696	P10451	SPP1	Isoform D of osteopontin	42.81	6	1	9	41	25.70	292	33.0	4.74	Extracellular region	Skeletal system development	Cytokine activity	Yes
IP100386209	Q96A30	KLK3	Putative preproPSA-RP2	43.89	7	5	5	30	32.15	180	19.7	6.11	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP100386324			Seven transmembrane helix receptor	1.50	1	1	1	1	2.55	1465	156.5	10.83	Cytoskeleton	Microtubule-based process	Nucleotide binding	

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IPi00386621	Q9BRL5		CALM3 protein	18.92	7	2	2	3	5.37	148	16.6	4.44	Cell cycle	Calcium ion binding	No
IPi00386975	Q9HB00	DSC1	Isoform 1B of desmocollin-1	8.93	2	5	5	11	8.25	840	93.8	5.53	Cell adhesion	Calcium ion binding	Yes 1
IPi00387024	P01596		Ig kappa chain V-I region CAR	16.82	3	1	1	12	20.48	107	11.7	9.41	Complement activation, classical pathway	Antigen binding	No
IPi00387098	P01606		Ig kappa chain V-I region OU	16.67	1	1	1	42	44.58	108	11.8	9.91	Complement activation, classical pathway	Antigen binding	No
IPi00387105	P01612		Ig kappa chain V-I region Mev	16.51	1	1	1	1	2.79	109	11.9	6.57	Complement activation, classical pathway	Antigen binding	No
IPi00387106	P01613		Ig kappa chain V-I region Ni	30.36	2	2	2	19	21.11	112	12.2	5.36	Complement activation, classical pathway	Antigen binding	No
IPi00387120	P01625		Ig kappa chain V-IV region Len	28.95	4	2	2	15	16.42	114	12.6	7.93	Complement activation, classical pathway	Antigen binding	No
IPi00395488	Q6EMK4	VASN	Vasorin	20.21	1	7	7	75	127.25	673	71.7	7.39	Extracellular region		Yes 1
IPi00396004	Q6ZRU0		cDNA FLJ46111 fis, clone TEST12034913, moderately similar to Keratin, type II cytoskeletal 8	6.09	1	1	1	3	6.64	197	22.3	4.84	Keratin filament	Structural molecule activity	No
IPi00396056	P36639	NUDT1	Isoform p18 of 7,8-dihydro-8-oxoguanine triphosphatase	15.38	5	2	2	2	4.77	156	17.9	5.08	Cytoplasm	Purine nucleotide metabolic process	No
IPi00397361	P30530	AXL	Isoform short of tyrosine-protein kinase receptor UFO	6.10	2	4	4	48	68.00	885	97.3	5.39	Plasma membrane	Protein amino acid phosphorylation	Yes 1
IPi00397579	O75335		Isoform 2 of liprin-alpha-4	3.18	5	1	1	1	2.65	692	77.0	7.77	Cell surface		No
IPi00397801	Q5D862	FLG2	Filaggrin-2	6.32	1	6	6	19	14.63	2391	247.9	8.31	Extracellular region	Structural molecule activity	No
IPi00398625	Q86YZ3	HRNR	Hormerin	17.93	1	15	15	82	32.61	2850	282.2	10.04	Cornified envelope	Calcium ion binding	No
IPi00401212			GPM6A protein	17.95	4	1	1	1	2.55	78	8.9	6.51	Cell surface	Ion channel activity	Yes 1
IPi00402215	Q05707	COL14A1	Isoform 3 of collagen alpha-1 (XIV) chain	1.18	3	1	1	3	5.08	1701	183.0	5.29	Extracellular region	Structural molecule activity	Yes 1

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular function	Signal TM
IP100410360	Q8NEJ9	NGDN	Isoform 2 of neuroguidin	9.00	3	1	1	1	2.50	311	35.2	9.33	Filopodium	Regulation of translation		No
IP100411592	Q12873	CHD3	Isoform 2 of chromodomain-helicase-DNA-binding protein 3	0.51	4	1	1	1	2.34	1966	222.7	7.52	Histone deacetylase complex	Chromatin organization	Nucleotide binding	No
IP100412771	Q9Y5K6	PCDHB4	CD2-associated protein	2.97	1	1	1	1	2.50	639	71.4	6.40	Ruffle	M phase of mitotic cell cycle	Structural molecule activity	No
IP100413773	O75129		Isoform 6 of astroactin-2	4.81	1	1	1	1	2.39	395	44.5	5.86	Integral to membrane			Yes 2
IP100413958	Q14315	CDH1	Isoform 2 of filamin-C	3.23	2	5	5	8	16.56	2692	287.1	5.97	Cytoskeleton		Actin binding	No
IP100414684	Q6Y808	FBXO11	Isoform 2 of semenogelin-1	5.47	2	1	1	1	3.65	402	45.3	9.38	Extracellular region	Insemination	Structural molecule activity	Yes
IP100414694	P39060	COL18A1	Isoform 3 of collagen alpha-1 (XVIII) chain	4.56	3	2	2	5	6.86	1339	135.7	6.47	Extracellular region	Cell morphogenesis	Structural molecule activity	Yes
IP100414784	Q9UGN4	C9	Isoform 1 of CMRF35-like molecule 8	6.02	1	1	1	3	3.11	299	33.2	5.49	Plasma membrane	Immune response		Yes 1
IP100418145	Q8WZ75	ROBO4	Isoform 3 of roundabout homolog 4	6.41	4	3	3	6	8.24	702	75.2	7.18	Integral to membrane	Angiogenesis		Yes
IP100418163	Q6U2E9	ACTB	Component 4B preproprotein	35.26	6	1	37	279	281.76	1744	192.6	7.27	Extracellular space	Complement activation	Endopeptidase inhibitor activity	Yes
IP100418446	Q13510	ASAH1	Isoform 2 of acid ceramidase	10.95	4	3	3	15	20.31	411	46.5	7.85	Lysosome	Membrane lipid metabolic process	Hydrolase activity	Yes
IP100418676	Q0P6H9	TMEM62	Transmembrane protein 62	5.75	1	1	1	2	3.25	643	73.1	9.26	Integral to membrane			Yes 6
IP100428511	P58400	NRXN1	Neurexin-1-beta	5.66	1	1	1	1	2.30	442	46.6	7.80	Plasma membrane	Cell morphogenesis	Calcium channel regulator activity	Yes 2
IP100441094	Q5ZPR3		Isoform 3 of CD276 antigen	3.65	4	1	1	6	12.09	493	52.7	5.52	Plasma membrane	Cell activation		Yes 1
IP100443913	Q6ZRJ0	WDR87	cDNA FLJ46325 fis, clone TEST14043371	19.25	1	1	1	1	2.52	161	18.7	9.11				Yes 4
IP100450768	Q14666		Keratin, type I cytoskeletal 17	21.06	18	4	11	54	29.95	432	48.1	5.02	Cytoplasm	Epidermis development	Protein binding	No
IP100455173	Q8WZ42		Titin isoform N2-B	0.18	14	3	3	4	8.35	26926	2991.1	6.74				No
IP100455315	P07355	ANXA2	Isoform 1 of annexin A2	31.27	7	7	7	28	28.83	339	38.6	7.75	Cell fraction	Skeletal system development	Enzyme inhibitor activity	No
IP100465016	O00391	QSOX1	Isoform 2 of sulfhydryl oxidase 1	7.62	4	3	3	10	18.63	604	66.8	8.56	Golgi membrane	Protein folding	Oxidoreductase activity	Yes 1
IP100465436	Q8TAK2		Catalase	2.85	1	1	1	2	3.31	527	59.7	7.39	Lysosome	Response to reactive oxygen species	Nucleotide binding	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular function	Signal TM
IP100478003	P01023	AGT	Alpha-2-macroglobulin	40.71	7	38	38	232	361.38	1474	163.2	6.46	Extracellular region	Regulation of complement activation , lectin pathway	Enzyme inhibitor activity	Yes
IP100478209	A4D1S5	RAB19	Isoform 1 of Ras-related protein Rab-19	6.69	1	1	1	1	2.51	284	31.8	8.00	Plasma membrane	Intracellular signaling cascade	Nucleotide binding	No
IP100479027			Blood coagulation inhibitor, disintegrin domain containing protein	6.74	1	1	1	1	2.78	356	39.2	6.89				
IP100479116	P22792	CPN2	Carboxypeptidase N subunit 2	7.89	1	2	2	10	10.00	545	60.6	5.99	Extracellular region	Posttranscriptional regulation of gene expression		Yes
IP100479723	P02751	FN1	Isoform 10 of fibronectin	9.42	18	11	11	35	26.04	2176	239.5	5.88	ER-Golgi intermediate compartment	Cell morphogenesis	Pattern binding	No
IP100480192	Q5VY30	CTBS	Retinol binding protein 4, plasma	62.81	3	8	8	1015	1970.87	199	22.9	6.09	Extracellular region	Skeletal system development	Retinoid binding	No
IP100514530	Q5T8M8	ACTA1	Uncharacterized protein	14.88	23	1	3	17	12.02	289	32.3	5.31	Stress fiber	Muscle system process	Nucleotide binding	No
IP100514669	Q5T123	PPT1	SH3 domain binding glutamic acid-rich protein like 3	32.95	4	3	3	21	36.27	88	9.4	9.36	Extracellular region	Cellular homeostasis	Electron carrier activity	No
IP100514908	Q5T749	KPRP	Keratinocyte proline-rich protein	1.55	1	1	1	1	2.34	579	64.1	8.27	Extracellular region			No
IP100550731	Q8TCD0		Putative uncharacterized protein	41.00	19	1	6	255	233.21	239	26.2	8.06				Yes
IP100550936	Q6P2N0	DPEP1	Myosin light chain kinase, smooth muscle isoform 7	15.69	11	2	2	3	4.83	153	16.8	4.28	Protein amino acid phosphorylation	Protein amino acid phosphorylation	Nucleotide binding	No
IP100552768	O60744	TXN	Thioredoxin, isoform CRA_b	15.29	2	1	1	10	7.30	85	9.4	6.04	Mitochondrion	Generation of precursor metabolites and energy		No
IP100552937	Q5JJS37		NHL repeat-containing protein 3	19.02	3	3	3	5	10.25	347	38.3	6.43	Extracellular region			Yes
IP100554538			Uncharacterized protein	15.14	7	4	4	19	23.10	555	60.3	6.39	Cytosol	Tissue homeostasis	Endopeptidase activity	
IP100554556	O60888	CUTA	Isoform C of protein CutA	17.31	3	1	1	2	4.18	156	16.8	5.21	Cornified envelope	Protein complex assembly	Retinoic acid receptor activity	Yes
IP100554618	D0AB07		Basal cell adhesion molecule isoform 2 precursor	4.42	2	2	2	3	5.26	588	63.7	6.10	Plasma membrane	Cell adhesion	Laminin receptor activity	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IP100554711	P14923	JUP	Junction plakoglobin	12.48	4	6	6	24	10.90	745	81.7	6.14	Cell junction	Protein complex assembly	Structural molecule activity	No	No
IP100555577	Q59GA0		Thy-1 cell surface antigen variant (fragment)	20.00	2	2	2	4	5.11	145	15.9	9.00	Membrane	T cell receptor signaling pathway	GPI anchor binding	Yes	Yes
IP100555789	Q59G69		Glia maturation factor, beta variant (fragment)	20.54	3	1	1	1	2.65	112	12.9	5.17	Intracellular	Actin binding	Actin binding	No	No
IP100555812	P02774	GC	Vitamin D-binding protein precursor	57.38	5	19	19	321	352.35	474	52.9	5.45	Extracellular region	Vitamin metabolic process	Actin binding	Yes	Yes
IP100556658	Q59HE4		Putative uncharacterized protein (fragment)	11.65	3	1	1	3	5.33	103	11.7	7.84		Transport	Lipid binding	No	No
IP100604401	Q9Y2E5		Isoform 2 of epididymis-specific alpha-mannosidase	4.51	3	3	3	4	5.31	954	107.6	7.05	Extracellular region	Monosaccharide metabolic process	Alpha-mannosidase activity	Yes	Yes
IP100607744	Q9NVH1		Isoform 2 of DNAJ homolog subfamily C member 11	3.84	1	1	1	1	2.50	521	58.9	7.61		Protein folding	Heat shock protein binding	No	No
IP100607763	Q9UNW1	MINPP1	Isoform 3 of multiple inositol polyphosphate phosphatase 1	7.75	3	1	1	28	14.47	284	31.5	8.92	ER	Skeletal system development	Acid phosphatase activity	Yes	Yes
IP100639961	C9JFK9	BAG3	Uncharacterized protein	5.23	1	1	1	2	4.48	325	34.7	9.39	Cytosol	Protein folding		No	No
IP100640115	Q9BV28	hCG_1983504	cDNA FLJ77784	17.20	4	1	4	10	18.44	378	42.4	4.96	Cytoskeleton	M phase of mitotic cell cycle	Nucleotide binding	No	No
IP100641481	Q9H4L8		Isoform 2 of cholesterol ester transfer protein	6.47	2	2	2	6	8.61	433	47.8	6.01	Extracellular region	Cellular amino acid derivative metabolic process	Lipid transporter activity	Yes	Yes
IP100642882			31 kDa protein	4.32	3	1	1	1	2.56	278	30.7	9.09	Plasma membrane	Cell adhesion	Sugar binding		
IP100642936	Q5TA02		Glutathione S-transferase omega 1	5.00	2	1	1	1	2.36	200	23.3	7.21	Cytoplasm	Vitamin metabolic process	Glutathione transferase activity	No	No
IP100643158			43 kDa protein	11.29	10	2	3	7	12.13	381	42.5	4.83	Cytoskeleton	Protein complex assembly	Nucleotide binding		
IP100643462			27 kDa protein	18.14	1	1	1	1	2.67	226	26.6	6.54					
IP100643490	Q68DC4	MDH2	Putative uncharacterized protein DKFZp779G2333	10.74	4	4	4	20	21.11	540	59.2	5.63	Membrane	Cell activation	Integrin binding	Yes	1
IP100644296	Q66K77	DKFZp666N164	456 kDa protein	0.78	17	2	2	2	2.46	4222	455.9	5.20	Plasma membrane	Protein amino acid phosphorylation	Nucleotide binding	Yes	Yes

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100644497			Conserved hypothetical protein	5.80	16	1	1	3	5.54	293	31.8	5.62		Immune response	Antigen binding	
IP100644576	Q96C61	FLNA	Filamin A, alpha	6.14	8	10	10	20	30.97	2607	276.4	6.05	Extracellular region	Regulation of nucleotide metabolic process	Glycoprotein binding	No
IP100644697	Q9Y5Z4	C7	HEBP2 protein (fragment)	13.08	3	2	2	3	7.31	214	24.0	5.38	Cytosol			No
IP100644930	Q9UIB8	CD84	Isoform 6 of SLAM family member 5	12.45	6	2	2	11	15.59	241	26.9	5.39	Plasma membrane	Defense response		Yes
IP100644990	Q8N7G9	RALGPS2	cDNA FLJ25604 fis, clone JTH14207	6.39	2	1	1	1	2.73	548	61.3	8.94	Plasma membrane	Intracellular signaling cascade	Guanyl-nucleotide exchange factor activity	No
IP100645038	Q5T985	ACTA1	Inter-alpha (globulin) inhibitor H2	24.81	4	13	13	61	96.58	935	105.2	7.03		Polysaccharide metabolic process	Enzyme inhibitor activity	Yes
IP100645213	Q5SRP4	APOM	Apolipoprotein M, isoform CRA_a	11.21	3	1	1	2	6.94	116	13.0	7.75	Extracellular region	Lipid transport	Lipid transporter activity	No
IP100645710	Q8N440	NEGR1	cDNA FLJ59691, highly similar to neuronal growth regulator 1	5.75	2	1	1	3	4.64	226	24.7	6.76	Plasma membrane	Cell adhesion		Yes
IP100646555	Q6R2W3		SCAN domain-containing protein 3	1.28	1	1	1	1	2.39	1325	151.6	6.73	Nucleus	DNA integration	DNA binding	No
IP100647896	Q9BUU9	TUBB	Tubulin, beta	33.33	12	2	8	15	24.24	372	41.7	4.91	Cytosol	M phase of mitotic cell cycle	Nucleotide binding	No
IP100654673	Q7L7X3	TAOK1	TAOK1 protein	3.05	2	1	1	1	3.57	853	97.5	6.93	Cytoplasm	Mitotic prometaphase	ATP binding	No
IP100658202	A8MWWK3	CDH2	cDNA FLJ53252, highly similar to cadherin-2	13.37	5	5	5	32	52.50	875	97.0	4.84	Membrane	Blood vessel development	Calcium ion binding	No
IP100738216	Q9Y2F5	KIAA0947	Uncharacterized protein KIAA0947	1.72	1	1	1	1	3.08	2266	247.7	5.48		Positive regulation of immune system process		Yes
IP100741107	Q5JRA6	MIA3	Isoform 3 of melanoma inhibitory activity protein 3	2.00	3	1	1	1	2.46	500	56.5	4.45	ER			No
IP100746718			Profilaggrin	1.82	3	2	2	4	2.45	1212	132.0	9.63		Ectoderm development	Structural molecule activity	
IP100748955	Q06AK0	GP1BA	Platelet glycoprotein Ib alpha chain	10.54	2	3	3	11	18.84	626	68.9	6.68	Cell fraction	Cell morphogenesis	Peptide receptor activity	Yes
IP100749485	O95460		Isoform 3 of matrilin-4	4.17	5	1	1	1	2.70	432	47.5	5.92	Extracellular region			Yes

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Supplementary Table 3: Contd...

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IP100759659	Q8NBJ4	GOLM1	Isoform 2 of Golgi membrane protein 1	12.53	6	3	3	10	11.05	391	44.2	4.91	Golgi apparatus			Yes	1
IP100783665	O75079	LAMA5	Laminin subunit alpha-5	0.51	1	1	1	1	2.35	3695	399.5	6.99	Extracellular region	Cell morphogenesis	Integrin binding	Yes	
IP100783862	P30043	SERPINA4	Flavin reductase	6.80	2	1	1	1	3.02	206	22.1	7.65	Extracellular region	Oxidation reduction	Bilirubin reductase activity	Yes	
IP100783987	P01024	C3	Complement C3 (fragment)	49.55	3	56	56	596	655.99	1663	187.0	6.40	Extracellular region	Regulation of type IIa hypersensitivity	Enzyme inhibitor activity	Yes	
IP100784865	Q6P5S8	IGK@	IGK@ protein	47.03	6	10	10	671	811.31	236	25.8	6.33		Cell morphogenesis		Yes	
IP100787628	Q0GGW3	RTN4RL2	RTN4RL2	7.25	2	1	1	2	3.37	193	21.4	8.51	Plasma membrane	Cell morphogenesis		Yes	
IP100788236	Q6GTX8	Em:AF200455.10	Isoform 4 of leukocyte-associated immunoglobulin-like receptor 1	12.44	7	2	2	19	25.46	209	23.0	5.76	Plasma membrane	Immune response		Yes	1
IP100788674	F2Z2H7		13 kDa protein	13.45	13	1	1	1	2.84	119	13.0	6.76	Extracellular region	Positive regulation of signal transduction	Sugar binding	No	
IP100788781			Uncharacterized protein	15.84	2	1	1	1	3.79	101	11.2	6.07		Ectoderm development	Fatty acid binding	No	
IP100788877	Q8WXG6	CFI	Isoform 6 of MAP kinase-activating death domain protein	1.56	10	1	1	1	2.59	1479	163.9	6.32	Plasma membrane	MAPKKK cascade	Small GTPase regulator activity	No	
IP100789077			12 kDa protein	15.60	2	1	1	16	16.30	109	11.7	4.97	Extracellular region	Gamete generation	Structural molecule activity	No	
IP100789150	C9JDD2	CD300E	Uncharacterized protein	11.48	3	1	1	1	2.50	122	13.7	5.25	Plasma membrane	Immune response		No	
IP100789477	B7Z4X2		cDNA FLJ58679, highly similar to Lactoferrin	18.77	8	9	9	71	110.13	666	73.1	7.85	Extracellular region	Transition metal ion transport	Endopeptidase activity		
IP100790819			14 kDa protein	21.54	2	1	1	2	3.90	130	13.6	9.45	Cell fraction	Renal system process involved in regulation of blood volume	Actin binding		
IP100790892			6 kDa protein	35.29	8	1	1	1	3.85	51	5.6	4.89	Phosphopyruvate hydratase complex	Monosaccharide metabolic process	Magnesium ion binding		
IP100792087			Uncharacterized protein	5.13	3	1	1	1	3.14	234	26.3	4.54	Protein complex assembly				

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100793097			8 kDa protein	23.88	2	1	1	3	6.07	67	7.8	6.52	Cell fraction	Regulation of neurotransmitter levels	Enzyme inhibitor activity	
IP100793420	Q13161	PLA2G7	Bone morphogenic protein type II receptor	2.45	2	1	1	1	2.65	530	59.9	5.66	Plasma membrane	Formation of primary germ layer	Nucleotide binding	Yes 1
IP100793930	Q8WU19	ZNF384	TUBA1B protein	34.63	24	1	7	19	30.21	335	37.2	4.98	Microtubule	Microtubule-based movement	GTP binding	No
IP100794777	A6NIW5	PRDX2	Uncharacterized protein	12.50	3	1	1	4	5.45	136	15.1	6.13		MAPKKK cascade	Peroxidase activity	No
IP100794822			23 kDa protein	11.34	1	1	1	1	2.58	194	22.7	9.52	Nuclear envelope	RNA localization	Peptidase activity	
IP100795527			21 kDa protein	76.22	26	5	5	22	27.79	185	20.8	7.40	Nucleoplasm	Mitotic cell cycle	Structural constituent of ribosome	
IP100795633			CLU	17.86	5	8	8	34	51.99	448	52.3	6.38	Extracellular region	Cell morphogenesis		
IP100796137			38 kDa protein	6.55	11	2	2	27	16.06	336	37.8	5.48				
IP100796316	Q5T0H8		cDNA FLJ53327, highly similar to Gelsolin	22.70	6	8	8	157	137.16	705	77.7	5.69			Actin binding	No
IP100796776	E7EU87		cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5	26.63	8	8	14	135	55.47	567	60.1	6.19	Cytoskeleton	Ectoderm development	Structural molecule activity	No
IP100797221	P04406		Glyceraldehyde-3-phosphate dehydrogenase	8.99	5	1	1	7	9.12	267	28.6	9.09		Monosaccharide metabolic process	Nucleotide binding	
IP100797471			42 kDa protein	13.66	11	3	4	77	50.05	366	41.6	5.53	Cytoskeleton		Structural molecule activity	
IP100798210	Q13421	NMI	Isoform 4 of mesothelin	8.53	6	3	3	5	10.80	621	67.9	6.20	Extracellular region	Cell adhesion	Antigen binding	Yes 1
IP100815674	A0PJG2	LPHN1	LPHN1 protein (fragment)	3.61	3	1	1	1	2.50	388	43.9	8.28	Plasma membrane	Cell surface receptor linked signal transduction	Sugar binding	Yes 1
IP100828108	P16070	DSP	Isoform 15 of CD44 antigen	15.65	19	3	3	19	14.65	294	32.1	5.21	Cell fraction	Syncytium formation	Pattern binding	Yes 1
IP100830092	Q9GZX9	KRT23	Isoform 2 of twisted gastrulation protein homolog 1	10.14	2	1	1	1	2.70	148	16.8	5.62	Extracellular region	membrane fusion Skeletal system development		Yes

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP 00844132			43 kDa protein	8.56	6	2	3	11	397	43.0	6.39	Regulation of type IIa hypersensitivity	Cell surface receptor linked signal transduction		
IP 00845506	Q6UXB8	LYPD2	Isoform 2 of peptidase inhibitor 16	22.22	2	5	5	24	270	29.7	5.71	Membrane	Putative serine protease inhibitor activity	Peptidase inhibitor activity	Yes
IP 00847635	P01011	SERPINA3	Isoform 1 of alpha-1-antichymotrypsin	57.68	3	17	17	2197	2756.94	423	5.52	Extracellular region	Tissue homeostasis	DNA binding	Yes
IP 00852577	Q6DHW4	LTBP2	HCG2040025	65.09	4	1	4	79	106	11.4	7.87				Yes
IP 00853068	P78461		Hemoglobin alpha-2	14.55	2	1	1	1	110	11.9	8.76	Cytosol	Gas transport	Oxygen transporter activity	No
IP 00853468	Q32KK2		Arylsulfatase A isoform b	23.17	4	6	6	43	423	44.9	5.87	Cell fraction	Autophagy	Arylsulfatase activity	No
IP 00855846	Q9P1F3	C6orf115	UPF0727 protein C6orf115	16.05	1	1	1	5	81	9.1	6.29				
IP 00855927	A6ZIE2	MUC1	MUC1 isoform M8	15.81	24	2	2	3	215	22.9	7.46	Extracellular region	Female pregnancy		Yes
IP 00868965	Q149M9	ufHSD2	Isoform 2 of NACHT and WD repeat domain-containing protein 1	1.33	3	1	1	1	1358	150.7	7.05			Nucleotide binding	No
IP 00869004	P01009		Isoform 3 of alpha-1-antitrypsin	15.03	3	3	3	11	306	34.7	5.19	Extracellular region	Response to hypoxia	Protease binding	Yes
IP 00871227	Q96RW7	AGRN	Isoform 1 of hemicentin-1	0.59	2	2	2	8	5635	613.0	6.49	Extracellular region	Blood coagulation	Calcium ion binding	Yes
IP 00871537	Q9JUP8	HBB	Gamma-interferon-inducible lysosomal thiol reductase preproprotein	4.40	2	1	1	1	250	27.9	4.88	Lysosome	Antigen processing and presentation of exogenous peptide antigen		Yes
IP 00872788	Q14195		Dihydropyrimidinase-related protein 3	2.81	7	1	1	1	570	61.9	6.49	Cytoskeleton		Dihydro pyrimidinase activity	No
IP 00873341			155 kDa protein	3.90	3	3	3	10	1383	154.7	6.21	Plasma membrane	Protein amino acid dephosphorylation activity	Phosphoprotein phosphatase	
IP 00873419			38 kDa protein	9.68	3	1	1	1	341	37.7	5.20	Integral to membrane			
IP 00873761	Q2I377		Small proline rich protein	23.29	2	1	1	4	73	8.1	8.72	Cytoplasm	Ectoderm development	Structural molecule activity	No
IP 00873924	Q9UNH2	IL18BP	Isoform A of Interleukin-18-binding protein	6.19	1	1	1	5	194	21.1	7.39	Extracellular region	Adaptive immune response	Cytokine binding	Yes

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IP100874274	Q6AWA4	DKFZp686O0870	Uncharacterized protein	1.13	3	1	1	1	2.53	1685	191.7	8.66	Transcription factor TFIIIC complex	Transcription	DNA binding	No	No
IP100877884			17 kDa protein	12.42	2	1	1	1	2.31	153	17.0	4.92	Extracellular region	Single fertilization			
IP100877925	C9JPV4	SERPINF2	Uncharacterized protein	20.45	5	3	3	4	8.81	264	29.5	6.93	Extracellular region	Acute inflammatory response	Protease binding	Yes	Yes
IP100878470			8 kDa protein	33.33	1	1	1	2	2.81	78	8.3	7.34					
IP100878551	B4DUA5	P4HB	cDNA FLJ59430, highly similar to protein disulfide-isomerase	2.65	2	1	1	1	2.64	452	51.2	4.88	Extracellular region	Cellular amino acid derivative metabolic process	Protein disulfide isomerase activity	Yes	Yes
IP100879368	Q8TCZ8	APOE	Apolipoprotein E	13.89	4	2	2	2	3.87	216	24.6	5.85	Extracellular region	Response to reactive oxygen species	Beta-amyloid binding	No	No
IP100879709	P13671		Complement component 6 precursor	11.35	1	9	9	36	57.13	943	105.7	6.79	Extracellular region	<i>In utero</i> embryonic development		Yes	Yes
IP100883772	P10253		Lysosomal alpha-glucosidase preproprotein	20.80	1	1	11	54	37.61	952	105.3	6.00	Lysosome	Maltose metabolic process	Alpha-glucosidase activity		
IP100888683	Q13835		Similar to plakophilin 1, partial	2.40	3	1	1	2	3.56	625	69.2	8.81	Cytoskeleton	Cell adhesion	Structural molecule activity		
IP100889133	Q8NDA2		hemimentin 2	0.37	4	1	1	1	2.31	3783	405.3	5.67					
IP100890703	B1N7B8	ASAH1	Cryocrystatglobulin CC1 kappa light chain variable region (fragment)	16.82	2	1	1	8	13.92	107	11.8	7.99					No
IP100892671			32 kDa protein	5.76	13	1	1	5	7.35	295	32.0	8.03		Immune response	Antigen binding		
IP100892870			Protein	2.55	3	1	1	2	2.48	470	51.5	6.46	Integral to membrane	Immune response	Antigen binding		
IP100892879			27 kDa protein	12.65	3	2	2	11	12.21	245	26.7	8.56	Plasma membrane	Cell adhesion			
IP100892906			18 kDa protein	6.67	7	1	1	1	2.25	165	18.0	8.12	Cytosol	Protein localization	Selenium binding		
IP100893223	C9JMK5	PIK3IP1	Uncharacterized protein	17.93	5	2	2	7	10.52	145	16.0	7.90	Integral to membrane			Yes	Yes
IP100893243	E7ENY2	GBP1	22 kDa protein	8.95	6	1	1	1	3.43	190	21.9	7.27		Intracellular signaling cascade	Zinc ion binding	No	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100893273	E7EV71		Latent-transforming growth factor beta-binding protein 1 isoform 5 precursor	1.46	9	1	1	1	3.18	1300	142.6	4.93	Extracellular region		Protein kinase activity	Yes
IP100893517	E7EP88		Putative uncharacterized protein EFEMP1	9.49	12	3	3	4	2.94	411	46.4	4.92	Ubiquitin ligase complex	Proteolysis	Ubiquitin-protein ligase activity	No
IP100895917	FCGR3A	FCGR3A	Low affinity immunoglobulin gamma Fc region receptor III-A isoform d precursor	4.74	4	1	1	1	2.71	253	28.9	8.29	Immune response	Immune response	IgG binding	Yes
IP100895943			Serum amyloid A2 isoform b	16.87	3	1	1	13	28.02	83	9.2	7.18	Extracellular region	Cell activation		
IP100896413	E9PGN5	HEXA	Inter-alpha (globulin) inhibitor H4 isoform 2 precursor	39.33	8	22	22	216	207.36	900	99.8	6.47		Acute inflammatory response	Enzyme inhibitor activity	Yes
IP100902623	B3KQX7		Major prion protein	7.36	5	1	1	7	11.37	163	18.2	5.76	ER	Protein complex assembly	Copper ion binding	Yes 2
IP100902750	B3KTX0		cDNA FLJ38893 fis, clone NOVAR1000091, highly similar to colorectal mutant cancer protein	7.30	3	1	1	1	2.85	411	46.1	5.05				No
IP100908532	B4DWL3	LAMP1	cDNA FLJ57633, highly similar to lysosome-associated membrane glycoprotein 1	4.40	2	1	1	1	2.90	364	39.0	8.87	Autophagy	Autophagy		Yes 2
IP100908562	B4DLI3		cDNA FLJ51237, moderately similar to Carcinoembryonic antigen-related cell adhesion molecule 8	13.28	2	2	2	7	11.96	256	27.8	8.44				Yes
IP100908698	B5A966	EPHA1	Soluble EPHA1 variant 1	3.80	3	1	1	2	3.31	474	51.0	7.61	Plasma membrane	Protein amino acid phosphorylation	Nucleotide binding	Yes
IP100908730	B4DRJ4		cDNA FLJ55126, highly similar to procollagen C-endopeptidase enhancer 1	19.34	2	2	2	8	5.57	181	19.5	7.02	Extracellular region			Yes

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	# number of proteins	# number of unique peptides	# number of peptides	# number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular function	Signal TM
IP100908746	B4DRT4	PEBP1	cDNA FLJ51535, highly similar to Phosphatidylinositol-3-OH kinase class I domain containing protein 1	60.65	4	5	5	16	21.33	155	17.3	6.00		Regulation of neurotransmitter levels	Nucleotide binding	No
IP100908953	E7EN39		cDNA FLJ54049, highly similar to Multimerin-2	3.58	2	2	2	7	10.36	727	80.0	5.74	Extracellular region			Yes
IP100908954	B4DKK0		cDNA FLJ52511, highly similar to abhydrolase domain-containing protein 14B	16.92	5	1	1	1	3.13	130	13.9	6.11	Lysosome			Yes
IP100909048	B5A971	EPHB4	Soluble EPHB4 variant 2	3.59	3	1	1	2	2.60	306	33.3	6.95	Plasma membrane	Protein amino acid phosphorylation	Nucleotide binding	Yes
IP100909103	B4E2S6		cDNA FLJ51462, highly similar to TGF-beta receptor type-2	2.77	3	1	1	3	5.72	542	61.4	5.40	Cytosol	Skeletal system development	Nucleotide binding	No
IP100909283	B4DMA7		cDNA FLJ58514, highly similar to cadherin-11	13.74	3	6	6	10	13.96	779	85.5	4.83	Plasma membrane	Skeletal system development	Calcium ion binding	No
IP100909303	Q5HYG5		cDNA FLJ58073, moderately similar to Cathepsin B	24.36	3	4	4	13	20.83	275	31.0	6.77	Cell fraction	Proteolysis	Endopeptidase activity	Yes
IP100909555	E7ENW3		cDNA FLJ51602, highly similar to interferon-induced guanylate-binding protein 1	3.36	2	1	1	26	9.82	357	41.2	6.73	Plasma membrane	Immune response	Nucleotide binding	No
IP100909967	B5A957	PDGFRB	Soluble PDGFRB variant 1	4.17	2	1	1	1	2.87	336	37.4	4.87	Skeletal system development	Skeletal system development	Nucleotide binding	Yes
IP100910380	D6RA29		cDNA FLJ54278, highly similar to SPARC-like protein 1	16.38	3	1	5	12	10.28	519	58.5	4.94	Extracellular space	Calcium ion binding	Calcium ion binding	Yes
IP100910395	O95206	CABYR	cDNA FLJ56819, highly similar to Protocadherin-8	2.85	4	1	1	1	2.30	596	63.1	7.09	Plasma membrane	Somitogenesis	Calcium ion binding	Yes
IP100910597	E7ERY7		cDNA FLJ56823, highly similar to protein-glutamine gamma-glutamyltransferase E	2.44	2	1	1	1	2.38	533	58.8	7.15		Hair follicle development	Nucleotide binding	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100910625	P02749		cDNA FLJ51265, moderately similar to beta-2-glycoprotein 1	42.70	2	10	10	86	86.72	274	30.3	7.85	Extracellular region	Negative regulation of angiogenesis	Eukaryotic cell surface binding	Yes
IP100910734	E9PER2		cDNA FLJ53641, highly similar to intercellular adhesion molecule 1	10.59	4	3	3	3	7.72	444	48.1	8.16	Membrane	Cell activation	Integrin binding	Yes 1
IP100910738	B4DKV4		cDNA FLJ60647, highly similar to keratin, type II cytoskeletal 6B	31.94	3	1	14	105	44.87	526	55.7	8.43	Keratin filament		Structural molecule activity	No
IP100910803	B4DNW9		cDNA FLJ57491, moderately similar to T-cell antigen CD7	13.25	2	1	1	4	5.57	166	17.7	8.21				Yes
IP100910870	B4DXT2		cDNA FLJ59163, highly similar to heat shock cognate 71 kDa protein	14.76	13	1	2	4	7.57	210	23.1	8.50	Cytosol	Protein folding	Nucleotide binding	No
IP100910975	B4DNY5		CMRF35-like molecule 9 isoform 3 precursor	22.34	5	3	3	4	6.67	273	29.9	6.54		Immune response		Yes 1
IP100917198	B8ZZ35	NAGA	N-acetylgalactosaminidase, alpha-	13.21	3	2	2	5	5.94	212	23.7	5.54	Lysosome		Alpha-N-acetylgalactosaminidase activity	No
IP100917285	B4DFW2	TIMP2	cDNA FLJ57920, highly similar to metalloproteinase inhibitor 2	7.91	3	1	1	2	6.40	177	20.0	7.17	Extracellular region	Regulation of nucleotide metabolic process	Enzyme inhibitor activity	No
IP100917449			Protein	10.92	3	1	1	2	5.35	119	13.2	6.54	Extracellular region	Release of cytochrome c from mitochondria	Gamma-glutamyl cyclotransferase activity	No
IP100917696	Q8WY28	DSP	Candidate tumor suppressor protein	3.01	2	1	1	2	2.38	798	89.1	6.27	Cell fraction	Endocytosis	Low-density lipoprotein receptor activity	No
IP100921523	P00751	BF	Isoform 1 of complement factor B (fragment)	16.88	11	8	8	28	15.26	764	85.5	7.06	Extracellular region	Complement activation, alternative pathway	Complement binding	Yes
IP100922193	B4DJZ2		cDNA FLJ59705, highly similar to transcription factor 7-like 2	5.01	1	1	1	5	7.01	339	38.0	9.31			DNA binding	No
IP100922213	Q9H382		cDNA FLJ53292, highly similar to hom sapiens FN1, transcript variant 5, mRNA	8.19	2	1	5	24	20.83	1014	111.2	6.21	Extracellular region	Cell morphogenesis	Pattern binding	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100924548	C9JNR0	IL1R2	Uncharacterized protein	8.30	3	1	1	1	2.58	229	26.3	7.40	Integral to membrane	Immune response	Cytokine receptor activity	Yes
IP100924656			228 kDa protein	1.18	1	1	1	1	2.60	2115	227.8	7.93				
IP100925319	C9JYS1	DAG1	Uncharacterized protein	16.67	4	1	1	1	2.99	96	10.3	5.29		Morphogenesis of an epithelium	Calcium ion binding	Yes
IP100926178	C9JL85	JUP	Uncharacterized protein	32.69	3	1	1	1	3.41	52	5.7	4.78	Axon	Regulation of translation		No
IP100928622	Q53QL7	PLGLB2	Putative uncharacterized protein PLGL	11.83	5	1	1	3	4.67	93	10.6	5.21	Extracellular region			No
IP100927191	P16278		Isoform 3 of beta-galactosidase	15.30	8	7	7	19	27.17	647	72.7	6.25	Cytosol		Beta-galactosidase activity	Yes
IP100927883	E9PCV0		cDNA FLJ53268, highly similar to beta-glucuronidase	6.53	4	2	2	7	11.98	505	58.3	6.99	Lysosome	Polysaccharide catabolic process	Beta-glucuronidase activity	Yes 1
IP100929685	P04278		sex hormone-binding globulin isoform 2 precursor	6.25	2	1	1	1	2.37	384	41.7	6.71	Extracellular region	Reproductive developmental process	Steroid binding	
IP100930404	P06870	ENO1	Isoform 2 of kallikrein-1	12.50	2	2	2	13	7.09	216	23.8	4.65	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP100936444	B4E1L4		cDNA FLJ59081, highly similar to Mucin-5B	0.74	3	1	1	1	3.32	5706	590.4	6.67	Extracellular region	Cell adhesion	Enzyme inhibitor activity	
IP100939169	O75882	CREG1	Isoform 3 of attraction	1.67	5	2	2	2	3.16	1198	133.6	6.98	Extracellular region	Defense response	Sugar binding	Yes 1
IP100939281	Q7Z4R8	PVRL2	UPF0669 protein C6orf120	10.99	1	1	1	5	5.85	191	20.8	4.84	Extracellular region			Yes
IP100939624	P40189	COL18A1	Isoform 2 of interleukin-6 receptor subunit beta	9.12	5	2	2	7	8.51	329	37.5	5.67	Cell membrane	Regulation of cytokine production	Cytokine receptor activity	Yes 1
IP100939673	B4DS15		cDNA FLJ51061, highly similar to opioid-binding protein/cell adhesion molecule	9.29	3	2	2	7	11.44	312	34.3	6.40	Plasma membrane	Cell adhesion	Peptide receptor activity	
IP100940517	C9J1L3	VSIG4	Uncharacterized protein	16.74	7	2	2	9	16.40	227	25.4	7.14		Regulation of cytokine production		Yes 1
IP100941565	A2A2K4	COL12A1	Uncharacterized protein	1.87	5	2	2	3	6.67	1874	203.0	6.07	Cell activation	Skeletal system development	Structural molecule activity	No

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Supplementary Table 3: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM	
IP100942625	Q96FE7		phosphoinositide-3-kinase-interacting protein 1 isoform 2	15.03	5	2	2	4	5.57	173	18.5	4.91	Integral to membrane			
IP100943326	P98160		Basement membrane-specific heparan sulfate proteoglycan core protein variant	5.17	3	16	16	155	163.25	4374	466.8	6.49	Lysosome	Skeletal system development		
IP100943343	Q9NPR5		PTPRJ, protein tyrosine phosphatase receptor J, eta	5.76	3	2	2	3	4.94	538	57.1	5.60	Plasma membrane	Blood vessel development	Phosphoprotein phosphatase activity	Yes
IP100945229	E7ER45	MGAM	312 kDa protein	5.59	3	7	7	13	16.59	2754	311.9	5.41	Plasma membrane	Polysaccharide catabolic process	Glucan 1	No
IP100945626	E9PDZ3	ATP11B	Uncharacterized protein	8.21	2	1	1	1	2.28	134	14.7	7.14	Nuclear envelope	Purine nucleotide metabolic process	Nucleotide binding	No
IP100946705	Q6UX73		Isoform 2 of UPF0764 protein C16orf89	3.60	6	1	1	5	7.44	361	40.6	5.87	Extracellular region			
IP100946754	Q86W20	LPPR4	Protease serine 1	14.08	8	1	1	6	10.51	142	15.4	7.27		Proteolysis	Endopeptidase activity	No
IP100946889	C9J795	PVRL3	Uncharacterized protein	17.69	6	1	1	3	7.35	130	13.9	7.93	Plasma membrane	Eye development	Identical protein binding	Yes
IP100946958			23 kDa protein	6.47	7	1	1	1	2.31	201	22.7	6.14				No
IP100947275	C9JNC3	BTN2A1	Uncharacterized protein	12.79	10	1	1	1	2.31	86	9.9	7.34	Plasma membrane			No
IP100947285	E9PBV3	SBSN	suprabasin isoform 1 precursor	26.27	3	6	6	36	26.48	590	60.5	7.01				Yes
IP100952944			Uncharacterized protein	10.65	4	4	4	13	20.31	676	70.8	5.07	Extracellular region	Fatty acid metabolic process	Pattern binding	
IP100953689	P02765	AHSG	Alpha-2-HS-glycoprotein	44.14	4	8	8	128	184.29	367	39.3	5.72	Extracellular region	Skeletal system development	Enzyme inhibitor activity	Yes
IP100956045	D3DU30		Intercellular adhesion molecule 2, isoform CRA_b	12.16	2	2	2	19	27.60	255	27.8	6.89				
IP1009566313			58 kDa protein	37.27	14	4	19	130	51.17	542	58.3	8.00				
IP100956475	B7Z553		cDNA FLJ51266, highly similar to vitronectin	17.29	2	3	3	8	8.56	214	23.6	4.64				
IP100964180			Protein	8.11	6	1	1	1	3.88	185	21.9	5.77				No
IP100964934	B4E096	NGFR	cDNA FLJ51424, highly similar to tumor necrosis factor receptor superfamily member 16	4.50	2	1	1	1	2.46	333	35.7	4.70		Receptor		No

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Supplementary Table 3: Contd...

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IP100965713	D6REL8		Uncharacterized protein	5.15	2	1	1	1	2.54	272	31.2	7.25	Fibrinogen complex	Platelet activation	Protein binding, bridging	Yes	
IP100966295			Light chain of factor I	19.97	5	8	8	45	63.11	576	65.0	7.50					
IP100966346	E7ESB3	KRT7	23 kDa protein	14.85	9	2	2	2	2.45	202	23.2	7.53		Protein ADP-ribosylation	NAD(P)+-protein-arginine ADP-ribosyltransferase activity	Yes	
IP100966568			Protein	18.55	8	1	1	1	2.48	124	13.2	9.67					
IP100966681	D6R978	TNFAIP3	Uncharacterized protein	20.20	1	1	1	1	2.67	99	11.0	5.17				No	
IP100966866	Q6QBS2	DMD	Epidermal growth factor	5.24	3	3	3	5	8.63	1165	129.2	5.73				No	
IP100967014	D6RBV2	LMAN2	Uncharacterized protein	32.31	5	6	6	44	59.81	325	36.5	6.65	Membrane			Yes	
IP100967451	D6RHJ3	CANX	Uncharacterized protein	20.25	11	1	1	2	5.91	79	8.6	4.16			Calcium ion binding	Yes	
IP100967837	E7EPG1	MMRN1	111 kDa protein	1.55	2	1	1	1	2.28	970	110.7	7.02				No	
IP100968042	D6RBG2		Uncharacterized protein	27.33	6	2	2	3	10.11	150	16.3	4.77	Membrane	Homophilic cell adhesion	Calcium ion binding	Yes	
IP100968044	D6RBG3	PCDH1	Uncharacterized protein	44.87	6	1	1	1	2.73	78	8.8	8.18				No	
IP100969595	D6W5J8	hCG_1639753	Uncharacterized protein	29.87	1	1	1	9	26.45	77	8.3	6.24			Binding	No	
IP100973362	B7Z6J1		cDNA FLJ55035, highly similar to Dihydrolysoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	8.43	3	1	1	5	7.92	166	17.9	8.06					

ER: Endoplasmic reticulum, LC-MS/MS: Liquid chromatography-tandem mass spectrometry, FN1: Fibronectin 1, TGF-beta: Transforming growth factor-beta, LMW: Low molecular weight, COMP: Cartilage oligomeric matrix protein, MAP: Mitogen-activated protein, PTPRJ: Protein tyrosine phosphatase receptor J, GPI: Glycosylphosphatidylinositol, MW: Molecular weight, MiA: Microalbuminuria, CLL: Chronic lymphocytic leukemia, PSM: Peptide spectrum match, AA: Amino acids, TM: Transmembrane domain