

**Supplementary Table 2: List of total proteins identified in NA group by LC-MS/MS using orbitrap**

Accession	Accession	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
IP100001429	Q9Y5E5	PCDHB4	Protocadherin beta-4	1.51	1	1	1	1	2.47	795	87.2	5.20	Plasma membrane	Cell adhesion	Calcium ion binding	Yes 1
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	Blood vessel development	Nuclease activity	Yes 3
IP100002188	Q96PQ9	LOX	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	0.76	1	1	1	1	2.30	1849	208.6	5.85	Extracellular region		Protein-lysine 6-oxidase activity	Yes
IP100002745	Q9JUBR2	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
IP100003470	P01611		Ig kappa chain V-J region Wes	16.67	1	1	1	2	2.87	108	11.6	7.28	Extracellular region	Complement activation	Antigen binding	No
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
IP100004101	Q93088	BHMT	Betaine--homocysteine S-methyltransferase 1	11.08	3	3	3	10	15.05	406	45.0	7.03	Cytoplasm	Sulfur amino acid metabolic process	S-methyl transferase activity	No
IP100004573	P01833	PIGR	Polymeric 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
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

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IP100006971	Q9HCU0	GP6	Isoform 1 of endosialin	1.59	1	1	1	1	2.52	757	80.8	5.35	Endosome		Calcium ion binding	Yes 1
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	Yes
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
IP100007983	Q96JY6	PDLIM2	Isoform 3 of PDZ and LIM domain protein 2	8.47	1	1	1	1	2.86	366	39.2	8.90	Cytoskeleton		Zinc ion binding	No
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
IP100009650	P31025	LCN1	Lipocalin-1	6.25	1	1	1	1	2.28	176	19.2	5.58	Cell fraction	Proteolysis	Enzyme inhibitor activity	Yes
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

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IP100009997	O43505		N-acetyllactosaminide beta-1,3-N-acetylglucosaminyl transferase	3.86	1	1	1	4	5.41	415	47.1	7.20	Golgi membrane	Polysaccharide biosynthetic process	Acetylglucosaminyltransferase activity	Yes
IP100010156	Q0VG04	MAPK4	Mitogen-activated protein kinase 4	6.47	1	1	1	1	2.85	587	65.9	5.45	Nucleus	Protein amino acid phosphorylation	Nucleotide 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	
IP100011302	P13987	C6	CD59 glycoprotein	25.00	1	4	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	2	4	5.14	198	21.6	4.50	Golgi apparatus	Regulation of muscle contraction	Cytoskeletal protein binding	Yes
IP100011692	P07476		Involucrin	6.39	1	3	3	6	7.04	595	69.6	4.60	Cornified envelope	Ectoderm development	Structural molecule activity	No
IP100012102	P15586		N-acetylglucosamine-6-sulfatase	18.48	3	7	7	43	17.58	552	62.0	8.31	Lysosome	Polysaccharide catabolic process	Calcium ion binding	Yes
IP100012503	P07602	IVL	Isoform Sap-mu-0 of Proactivator polypeptide	9.35	5	3	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	4	623	837.21	190	21.0	7.80	Rough ER	Prostaglandin biosynthetic process	Prostaglandin-D synthase activity	Yes
IP100013382	P09228	GSTP1	Cystatin-SA	10.64	1	1	1	2	3.15	141	16.4	4.93	Extracellular region	Immune response	Enzyme inhibitor activity	Yes
IP100013438	P15814	ACPP	Immunoglobulin lambda-like polypeptide 1	14.08	2	2	2	4	5.37	213	22.9	10.07	Extracellular region			Yes
IP100013885	P31944	OBSCN	Caspase-14	25.62	1	5	5	9	9.40	242	27.7	5.58	Lysosome	Proteolysis	Endopeptidase activity	No
IP100013890	P31947	SFN	Isoform 1 of 14-3-3 protein sigma	9.68	1	1	1	1	3.59	248	27.8	4.74	Extracellular region	Regulation of cyclin-dependent protein kinase activity	Enzyme inhibitor activity	No
IP100014048	P07998	THBS1	Ribonuclease pancreatic	50.64	1	4	4	134	90.90	156	17.6	8.79	Extracellular region	Nuclease activity		Yes
IP100014375	Q07075	ENPEP	Glutamyl aminopeptidase	2.61	1	2	2	5	2.37	957	109.2	5.47	Plasma membrane	Angiogenesis	Aminopeptidase activity	No

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IPi00016287	Q9H6P9	PROS1	Threonine synthase-like 1	2.42	1	1	1	1	2.51	743	83.0	7.12		Threonine metabolic process	Nucleotide binding	No
IPi00016915	Q16270		Insulin-like growth factor-binding protein 7	29.08	1	5	5	9	7.64	282	29.1	7.90	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes
IPi00017601	Q1L857	CP	Ceruloplasmin	35.68	8	30	30	335	435.83	1065	122.1	5.72	Extracellular region	Transition metal ion transport	Ferroxidase activity	Yes
IPi00017987	P35321	SPRR1A	Cornifin-A	19.10	2	1	1	3	5.79	89	9.9	8.48	Cytoplasm	Ectoderm development	Structural molecule activity	No
IPi00018236	Q6LBL5	GM2A	Ganglioside GM2 activator	15.54	1	2	2	18	29.08	193	20.8	5.31	Lysosome	Ganglioside metabolic process	Beta-N-acetylhexosaminidase activity	Yes
IPi00018840	Q15650	TRIP11	Activating signal cointegrator 1	2.93	1	1	1	1	2.21	581	66.1	7.85	Nucleolus	Transcription	Transcription cofactor activity	No
IPi00018953	P27487	DPP4	Dipeptidyl peptidase 4	10.70	2	6	6	27	34.35	766	88.2	6.04	Cell membrane	Response to hypoxia	Endopeptidase activity	Yes 1
IPi00019038	P61626	LYZ	Lysozyme C	8.11	1	1	1	1	2.25	148	16.5	9.16	Extracellular region	Defense response	Lysozyme activity	Yes
IPi00019157	Q6UVK1	C4B	Chondroitin sulfate proteoglycan 4	0.65	1	1	1	1	2.96	2322	250.4	5.47	Plasma membrane	Angiogenesis	Collagen binding	Yes 1
IPi00019359	P35527	THBS4	Keratin, type I cytoskeletal 9	54.09	1	23	23	561	318.70	623	62.0	5.24	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IPi00019449	P10153	RNASE2	Non-secretory ribonuclease	19.88	2	3	3	76	36.18	161	18.3	8.73	Lysosome	RNA catabolic process	Nuclease activity	Yes
IPi00019907	P51654	GPC3	Glypican-3	6.72	4	2	2	2	6.42	580	65.5	6.37	Extracellular region	Urogenital system development	Glycoprotein binding	Yes
IPi00019943	P43652	MCAM	Afamin	25.71	1	13	13	61	55.38	599	69.0	5.90	Extracellular region	Vitamin transport	Vitamin E binding	Yes
IPi00019954	Q6IBD2	CST6	Cystatin-M	48.32	1	4	4	14	51.72	149	16.5	8.09	Cornified envelope	Ectoderm development	Enzyme inhibitor activity	Yes
IPi00019988	Q53GP1		N-sulphoglucosamine sulphohydrolase	4.98	1	2	2	2	5.07	502	56.7	6.95	Lysosome	Proteoglycan metabolic process	Calcium ion binding	Yes
IPi00020019	Q15848	ADIPOQ	Adiponectin	6.15	1	1	1	2	3.77	244	26.4	5.74	Extracellular region	Response to hypoxia	Cytokine activity	Yes
IPi00020091	P19652	ORM2	Alpha-1-acid glycoprotein 2	55.72	1	6	11	179	241.26	201	23.6	5.11	Extracellular region	Acute-phase response	Binding	Yes
IPi00020986	P51884	PSMD7	Lumican	35.21	3	9	9	78	73.39	338	38.4	6.61	Extracellular	Sensory perception	Structural molecule activity	Yes
IPi00020990	Q99983	OMD	Osteomodulin	5.46	1	1	1	1	3.37	421	49.5	5.59	Extracellular region	Cell adhesion		Yes
IPi00021085	O75594	CALB1	Peptidoglycan recognition protein 1	37.24	1	4	4	24	31.90	196	21.7	8.59	Extracellular region	Peptidoglycan metabolic process	Pattern binding	Yes

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IP100021302	Q9UGT4	SUSD2	Sushi domain-containing protein 2	1.70	1	1	2	2	2.41	822	90.1	6.28	Plasma membrane	Immune response	Pattern binding	Yes
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
IP100021447	P19961	ITIH1	Alpha-amylase 2B epidermal	24.27	1	1	8	179	227.33	511	57.7	7.09	Extracellular region	Carbohydrate metabolic process	Alpha-amylase activity	Yes
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-1	43.82	2	13	13	134	240.11	267	30.8	5.76	Extracellular region	Regulation of cytokine production	Beta-amylloid binding	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
IP100022255	Q6UX06	OLFM4	Olfactomedin-4	5.29	1	2	2	3	7.86	510	57.2	5.69	Extracellular region	Cell adhesion		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
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
IP100022432	P02766		Transferrin	65.31	4	8	8	428	1055.42	147	15.9	5.76	Extracellular region	Transport	Hormone activity	Yes
IP100022488	P02790	PPBP	Hemopexin	44.37	1	12	12	596	812.66	462	51.6	7.02	Extracellular region	Regulation of protein amino acid phosphorylation	Iron ion binding	Yes

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IP100022810	P53634		Isoform 1 of dipeptidyl peptidase 1	12.53	1	3	3	36	34.72	463	51.8	6.99	Lysosome	Proteolysis	Endopeptidase activity		
IP100022895	Q7Z3U3		Alpha-1B-glycoprotein	42.42	4	11	11	181	329.07	495	54.2	5.87	Extracellular region		Actin binding	No	
IP100022974	P12273	PIP	Prolactin-inducible protein	32.19	1	3	3	57	142.89	146	16.6	8.05	Extracellular region	Insemination	Structural molecule activity	Yes	
IP100023020	P04279	SEMG1	Isoform 1 of Semenogelin-1	44.59	2	15	18	210	419.77	462	52.1	9.29	Extracellular region	Cell adhesion		Yes	
IP100023648	O14498	ISLR	Immunoglobulin superfamily containing leucine-rich repeat protein	3.27	1	1	1	4	3.01	428	46.0	5.15	Extracellular region			Yes	
IP100023728	Q92820	GGH	Gamma-glutamyl hydrolase	32.39	1	7	7	27	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	54	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	20	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	3	4.66	346	38.0	8.94	Cell fraction	Cell morphogenesis	Ephrin receptor binding	Yes	1
IP100025415	Q6IRW3	SEMG2	Semenogelin-2	52.06	1	20	23	180	244.86	582	65.4	9.07	Extracellular region	Sexual reproduction	Structural molecule activity	Yes	
IP100025476	P04746	AMY1A	Pancreatic alpha-amylase	28.77	8	2	10	75	92.36	511	57.7	7.05	Extracellular region	Carbohydrate metabolism	Alpha-amylase activity	Yes	
IP100025753	Q02413		Desmoglein-1	6.48	1	4	4	26	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	86	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	1	2.41	407	46.3	8.38	Lysosome	Cellular ion homeostasis	Protein binding	Yes	1
IP100026199	P22352	COL5A1	Glutathione peroxidase 3	19.47	1	3	3	4	12.79	226	25.5	8.05	Cell fraction	Response to reactive oxygen species	Peroxidase activity	Yes	
IP100027412	P40199	CEACAM6	Carcinoembryonic antigen-related cell adhesion molecule 6	3.78	1	1	1	1	2.26	344	37.2	5.82	Plasma membrane	Cell-cell signaling	Protein binding	Yes	
IP100027444	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	

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IP 00027462	P06702	S100A9	Protein S100-A9	74.56	2	6	6	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	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	2	4.56	529	57.9	5.35	Apical plasma membrane	Ion transport	Amine transmembrane transporter activity	No
IP 00027547	P81605	DLK1	Dermcidin	32.73	2	3	3	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	4.74	240	25.8	6.61	Cell fraction	Response to hypoxia	Pattern binding	Yes
IP 00029168	P08519	SOD3	Apolipoprotein (a)	6.82	1	1	1	2.32	4548	501.0	5.88	Extracellular region	Circulatory system process	Endopeptidase activity	Yes
IP 00029260	P08571		Monocyte differentiation antigen CD14	27.20	2	7	7	98.17	375	40.1	6.23	Cell membrane	Regulation of cytokine production	Lipopolysaccharide binding	Yes
IP 00029997	O95336	PGLS	6-phosphoglucono lactonase	10.08	1	1	1	5.52	258	27.5	6.05	Cytoplasm	Monosaccharide metabolic process	Carboxylesterase activity	Yes
IP 00030602	Q9NXV9	EIF2C4	Protein argonaute-4	1.74	2	1	1	2.24	861	97.0	9.06	Cytoplasmic mRNA processing body membrane	RNA catabolic process	RNA binding	No
IP 00030871	O95497	VNN1	Pantetheinase	15.01	4	5	5	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	51.23	282	31.4	4.91	Extracellular region	DNA metabolic process	Actin binding	Yes
IP 00031121	P16870		Carboxypeptidase E precursor	10.84	4	4	4	7.48	572	63.6	6.49	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes
IP 00031410	Q96QW8		Serine/threonine-protein kinase mTOR	1.18	1	1	1	2.85	2549	288.7	7.17	Extracellular region	Response to acid	Nucleotide binding	No
IP 00031661	Q9BV14	ENO1	Nucleolar complex protein 4 homolog	7.95	1	1	1	2.59	516	58.4	7.49	Nucleus membrane	rRNA processing	Protein binding	No
IP 00032179	P01008	SERPINC1	Antithrombin-III	51.94	2	18	18	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	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	429.30	146	15.8	8.75	Extracellular region	Defense response	Beta-amyloid binding	Yes
IP 00032294	P01036	CST3	Cystatin-S	20.57	2	2	2	10.24	141	16.2	5.02	Extracellular region	Enzyme inhibitor activity	Enzyme inhibitor activity	Yes
IP 00032325	P01040	CSTA	Cystatin-A	53.06	2	3	3	31.18	98	11.0	5.50	Cytoplasm	Epidermal development	Protease binding	No

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Supplementary Table 2: 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
IP100032404	O60882	TXN	Matrix metalloproteinase-20 c receptor protein 1	8.28	1	1	1	1	3.28	483	54.3	8.76	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP100059263	Q96A54	KLK3		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
IP100061507	Q9H0W9	C11orf54	Isoform 3 of Ester hydrolase C11orf54	6.42	3	1	1	1	2.61	265	29.5	5.58	Nucleus	Exhibits ester hydrolase activity on the substrate p-nitrophenyl acetate	Zinc ion binding	No
IP100064377	Q969Z4	KRT8	Tumor necrosis factor receptor superfamily member 19L	2.56	1	1	1	1	2.26	430	46.1	8.35	Plasma membrane			Yes
IP100066856	Q6UXB3	LYPD2	Ly6/PLAUR domain-containing protein 2	11.20	1	1	1	1	2.40	125	13.1	5.96	Plasma membrane			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
IP100102821	Q8WU39		Isoform 1 of plasma cell-induced resident ER protein	6.88	1	1	1	2	2.59	189	20.7	5.57	Extracellular region	Apoptosis		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
IP100107731	Q8IYS5	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
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
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

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Supplementary Table 2: 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
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
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
IP100169285	Q8NHP8	PLBD2	Putative phospholipase B-like 2	2.89	1	1	1	7	5.56	589	65.4	6.80	Lysosome	Lipid catabolic process		Yes 1
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 1
IP100171768	Q8NI77	KIF18A	Kinesin-like protein KIF18A	2.56	1	1	1	1	2.84	898	102.2	8.91	Ruffle	Mitotic sister chromatid segregation	Nucleotide binding	No
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	Q8NFZ8	KRTHB6	Cell adhesion molecule 4	14.69	1	4	4	33	42.33	388	42.8	6.30	Integral to membrane	Cell adhesion		Yes 1
IP100215794	Q9H324	HBB	A disintegrin and metalloproteinase with thrombospondin motifs 10	1.54	1	1	1	1	2.42	1103	120.8	7.94	Extracellular region	Proteolysis	Endopeptidase activity	Yes
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
IP100215980	Q9JUE6	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
IP100216984	P27482	PON1	Calmodulin-like protein 3	8.05	1	1	1	1	2.36	149	16.9	4.42		Calcium ion binding	Calcium ion binding	No

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**Supplementary Table 2: 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
IP100217182	Q4LE79		Isoform DP11 of desmoplakin	2.02	3	3	3	6	8.93	2272	260.0	6.96	Cornified envelope	Ectoderm development	Structural molecule activity	No
IP100217291	Q92859	NEO1	Isoform 2 of neogenin	1.07	4	1	1	1	2.19	1408	154.2	6.37	Plasma membrane	Synctium formation by plasma membrane fusion	Transcription regulator activity	Yes 1
IP100217775	P04233	CD74	Isoform 2 of HLA class II histocompatibility antigen gamma chain	5.60	2	1	1	1	2.70	232	26.4	9.14	Lysosome	MAPKKK cascade	Cytokine binding	No 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
IP100218202	P09603	FBP1	Isoform 3 of macrophage colony-stimulating factor 1	21.88	4	4	4	27	27.52	256	29.2	5.35	Cell activation	Cell activation	Cytokine activity	Yes 1
IP100218407	P05062		Fructose-bisphosphate aldolase B	8.79	3	2	2	6	11.51	364	39.4	7.87	Lysosome	Monosaccharide metabolic process	Fructose-bisphosphate aldolase 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
IP100218414	P00918	CA2	Carbonic anhydrase 2	6.15	1	1	1	3	5.69	260	29.2	7.40	Cell fraction	Urogenital system development	Carbonate dehydratase 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	Enzyme inhibitor activity	No
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
IP100219221	P47929	PPIC	Galectin-7	8.09	1	1	1	1	2.24	136	15.1	7.62	Extracellular region	Apoptosis	Sugar binding	No
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 1

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Supplementary Table 2: 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
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
IP100219625	P17813	CPE	Isoform short of endoglin	2.88	2	1	1	2	3.47	625	67.5	6.57	Cell fraction	Negative regulation of transcription from RNA polymerase II promoter	Pattern binding	Yes
IP100219757	P09211	GSTP1	Glutathione S-transferase P	18.57	2	2	2	5	9.26	210	23.3	5.64	Cytoplasm	Anti-apoptosis	Glutathione transferase activity	No
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		Yes
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
IP100220339	P35228	NOS2	Isoform 2 of nitric oxide synthase, inducible	1.53	2	1	1	2	4.30	1114	126.7	7.96	Blood vessel development	Blood vessel development	Nucleotide binding	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
IP100236554	P05164	MPO	Isoform H14 of myeloperoxidase	3.54	3	2	2	2	2.32	650	73.8	9.11	Lysosome	Response to reactive oxygen species	Chromatin binding	Yes
IP100246058	Q8WUM4	PACAP	Programmed cell death 6-interacting protein	1.84	2	1	1	1	2.98	868	96.0	6.52	Centrosome	Apoptosis	Calcium-dependent protein binding	No
IP100255554	Q86SQ6		Similar to G protein-coupled receptor 123	2.89	1	1	1	1	2.96	1280	137.3	8.85	Plasma membrane	Cell surface receptor linked signal transduction		No
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		Yes
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

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Supplementary Table 2: Contd...

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
IPi00290856	Q9Y5Y7	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
IPi00291136	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	
IPi00291737	Q8WWA0	DKFZp686N0152	Intelectin-1	6.07	1	1	1	1	2.70	313	34.9	6.01	Extracellular region	Regulation of protein amino acid phosphorylation	Sugar binding	Yes	
IPi00291866	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	
IPi00292946	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	
IPi00293088	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	
IPi00293275	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
IPi00293539	P55287	CDH6	Isoform 2 of cadherin-11	8.51	4	4	4	9	13.00	693	76.4	5.35	Extracellular region	Skeletal system development	Calcium ion binding	Yes	1
IPi00294398	Q16836	HADHSC	Isoform 1 of hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	9.55	3	1	1	1	3.48	314	34.3	8.85	Mitochondrion	Fatty acid metabolic process	3-hydroxyacyl-CoA dehydrogenase activity	Yes	
IPi00295414	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	
IPi00296141	Q9UHL4	DPP7	Dipeptidyl peptidase 2	6.50	2	2	2	6	11.04	492	54.3	6.32	Lysosome	Proteolysis	Aminopeptidase activity	Yes	
IPi00296654	Q8N4F0	KRTHB6	Bactericidal/permeability-increasing protein-like 1	12.66	2	3	3	11	16.27	458	49.1	8.72	Extracellular region	Lipid binding	Lipid binding	Yes	1
IPi00296777	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	
IPi00297056	Q9UBG3	CRNN	Cornulin	24.44	2	5	5	8	12.64	495	53.5	6.10	Cell fraction	Cell adhesion	Calcium ion binding	No	
IPi00298690			43 kDa protein	13.73	6	2	3	5	5.56	386	43.3	7.02		Cell adhesion	Antigen binding	No	
IPi00298994	Q9Y490	XB	Talin-1	0.43	1	1	1	1	2.29	2541	269.6	6.07	Ruffle	Cell motion	Actin binding	No	

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**Supplementary Table 2: 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
IP 00299547	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
IP 00300786	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
IP 00300865	Q8WW52	MT1X	Isoform 1 of protein FAM151A	3.59	1	1	1	5	6.35	585	64.0	6.67	Integral to membrane			No
IP 00301395	Q9H3G5		Probable serine carboxypeptidase CPVL	6.51	4	2	2	4	5.03	476	54.1	5.62		Proteolysis	Carboxypeptidase activity	Yes
IP 00303335	Q9Y5Z1		Nebulin	0.24	3	1	1	1	2.28	6669	772.4	9.07	Cytoskeleton	Muscle organ development	Actin binding	No
IP 00304273	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
IP 00304639	P11532	DMD	Dystrophin Dp427c isoform	0.46	3	1	1	1	2.15	3677	425.3	5.91	Cell	Cell morphogenesis	Actin binding	No
IP 00306339	B2RDA1	SPP1	Osteopontin isoform b precursor	39.33	4	1	9	40	25.70	300	33.8	4.61	Extracellular region	Skeletal system development	Cytokine activity	Yes
IP 00306378	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
IP 00306543	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
IP 00307214	O75952	GP1BA	Isoform 4 of calcium-binding tyrosine phosphorylation-regulated protein	20.36	1	1	1	1	3.43	221	23.9	7.91	Cytoskeleton		Calcium ion binding	No
IP 00307325	O43829	ZFP161	Zinc finger protein 161 homolog	4.45	1	1	1	1	2.73	449	50.9	6.04	Nucleus	Negative regulation of transcription from RNA polymerase II promoter	DNA binding	No
IP 00307446	Q9BYE9	PCDH24	Cadherin-related family member 2	3.21	1	3	3	5	10.39	1310	141.5	4.50	Plasma membrane	Regulation of cell growth	Calcium ion binding	Yes
IP 00329538	Q16651	PRSS8	Prostasin	4.08	1	1	1	7	5.19	343	36.4	5.85	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP 00333276	Q81VL0	FLII	Isoform 3 of neuron navigator 3	0.55	3	1	1	1	2.16	2186	235.1	8.56	Nuclear envelope		Nucleotide binding	No
IP 00334282	Q92520	FAM3C	Protein FAM3C	28.63	3	4	4	21	75.86	227	24.7	8.29	Extracellular	Cytokine activity	Cytokine activity	Yes

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Supplementary Table 2: 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
IP100335448	Q8IUW3	CLEC10A	Isoform 2 of spermatogenesis-associated protein 2-like protein	11.84	1	1	1	1	2.57	152	17.0	7.85				No
IP100335581	Q6ZT12	UBR3	Isoform 1 of E3 ubiquitin-protein ligase UBR3	1.06	2	1	1	1	2.67	1888	212.3	6.10	Integral to membrane	Suckling behavior	Ubiquitin-protein ligase activity	No
IP100374563	Q5XG79	MANBA	Agrin	4.11	2	6	6	16	22.37	2045	214.7	6.40	Extracellular region	Regulation of transcription, DNA-dependent Proteolysis	Structural molecule activity Endopeptidase activity	Yes Yes
IP100375426	Q6LAF8	HBA2	Cathepsin H	8.05	2	2	2	4	10.32	323	36.2	8.10	Lysosome	Cell surface receptor linked signal transduction		Yes 1
IP100375705	Q5TFQ8	SIRPB1	Signal-regulatory protein beta-1 isoform 3	9.55	8	2	3	4	4.64	398	43.3	7.83	Plasma membrane			Yes 1
IP100376170			18 kDa protein	12.88	1	1	1	1	2.66	163	17.8	6.77				Yes 1
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 1
IP100383975	Q86T07		Full-length cDNA clone CSQDN001YP04 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
IP100384401	Q9UL85		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
IP100385252	P04206	HRG	Ig kappa chain V-III region G0L	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

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Supplementary Table 2: 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
IP100385555	P04430		Ig kappa chain V-I region BAN	16.67	1	1	1	6	8.55	108	11.8	8.44	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100385830	Q6P0N0	MIS18BP1	Isoform 2 of kinetochore-associated protein KNL-2 homolog	3.02	2	1	1	2	2.43	496	56.4	9.38	Chromosome	M phase of mitotic cell cycle	DNA binding	No
IP100385896	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
IP100386131	P06311		Ig kappa chain V-III region IARC/BL41	12.50	1	1	1	3	5.12	128	14.1	6.61	Extracellular region	Complement activation, classical pathway	Antigen binding	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
IP100387024	P01596		Ig kappa chain V-I region CAR	16.82	3	1	1	12	20.48	107	11.7	9.41	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100387098	P01606		Ig kappa chain V-I region OU	16.67	1	1	1	42	44.58	108	11.8	9.91	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100387101	P01609		Ig kappa chain V-I region Scw	27.78	11	2	2	29	35.40	108	11.8	6.00	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100387105	P01612		Ig kappa chain V-I region Mev	16.51	1	1	1	1	2.79	109	11.9	6.57	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100387106	P01613		Ig kappa chain V-I region Ni	30.36	2	2	2	19	21.11	112	12.2	5.36	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100387113	P01619		Ig kappa chain V-III region B6	14.81	1	1	1	7	9.59	108	11.6	9.25	Extracellular region	Complement activation, classical pathway	Antigen binding	Yes
IP100387119	P01624		Ig kappa chain V-III region POM	16.51	1	1	1	1	2.53	109	11.9	8.94	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100387120	P01625		Ig kappa chain V-IV region Len	28.95	4	2	2	15	16.42	114	12.6	7.93	Extracellular region	Complement activation, classical pathway	Antigen binding	No
IP100395488	Q6EMK4	VASN	Vasorin	20.21	1	7	7	75	127.25	673	71.7	7.39	Extracellular region	Complement activation, classical pathway	Antigen binding	Yes
IP100396004	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	Intermediate filament	Structural molecule activity	No

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Supplementary Table 2: 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
IP100396056	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	GTPase activity	No	No
IP100397361	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	Nucleotide binding	Yes	1
IP100397801	Q5D862	FLG2	Flaggrin-2	6.32	1	6	6	19	14.63	2391	247.9	8.31	Extracellular region	Structural molecule activity	Structural	No	No
IP100398442	Q96J92	WNK4	Isoform 2 of serine/threonine-protein kinase WNK4	5.43	4	1	1	1	0.00	663	73.3	6.81	Plasma membrane	Protein amino acid phosphorylation	Nucleotide binding	No	No
IP100398625	Q86YZ3	HRNR	Hornerin	17.93	1	15	15	82	32.61	2850	282.2	10.04	Cornified envelope	Ectoderm development	Calcium ion binding	No	No
IP100401870	Q9H8M5	CNNM2	Isoform 3 of metal transporter CNNM2	4.01	3	1	1	1	2.82	574	62.8	7.06	Integral to membrane	Ion transport		Yes	4
IP100410467	Q6ZS94	C1orf229	Putative uncharacterized protein C1orf229	14.77	1	1	1	1	2.66	237	24.3	11.59				No	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	No
IP100412407	Q9BYF7	SOC2A2	Serpine peptidase inhibitor, clade B (ovalbumin), member 4, isoform CRA_a	29.00	6	2	8	53	29.52	369	42.3	6.05			Enzyme inhibitor activity	No	No
IP100413787	Q9NXR8	ING3	Isoform 2 of inhibitor of growth protein 3	17.39	5	1	1	2	2.20	92	11.3	4.61	Histone acetyltransferase complex	Chromatin organization	Histone acetyltransferase activity	No	No
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	No
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	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	Yes
IP100418163	Q6U2E9	ACTB	complement component 4B preproprotein	35.26	6	1	37	279	281.76	1744	192.6	7.27	Extracellular space	Complement activation	Endopeptidase inhibitor activity	Yes	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	Yes

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Supplementary Table 2: 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
IP100419215	D3DUV3	A2ML1	Alpha-2-macroglobulin-like protein 1	4.47	2	5	5	6	13.93	1454	161.0	5.73	Extracellular region	Regulation of hydrolase activity	Enzyme inhibitor	Yes
IP100419516	Q96G25		Isoform 1 of mediator of RNA polymerase II transcription subunit 8	7.09	2	1	1	2	5.08	268	29.1	7.44	Nucleoplasm	Transcription	RNA polymerase II transcription factor activity	No
IP100440727	Q96HN0	BRD4	Isoform 1 of bromodomain-containing protein 4	1.17	1	1	1	1	2.16	1362	152.1	9.19	Nucleolus	Protein amino acid phosphorylation	DNA binding	No
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
IP100448781	Q6PIP6	LRRRC8B	Inositol monophosphatase 2 variant 2	27.06	3	1	1	1	2.91	85	9.4	5.80	Extracellular region	Phosphorus metabolic process	Magnesium ion binding	No
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	Cell fraction	Skeletal system development	Enzyme inhibitor	No
IP100455315	P07355	ANXA2	Isoform 1 of annexin A2	31.27	7	7	7	28	28.83	339	38.6	7.75	Cell fraction	Protein folding	Oxidoreductase activity	Yes 1
IP100465016	O00391	QSOX1	Isoform 2 of sulfhydryl oxidase 1	7.62	4	3	3	10	18.63	604	66.8	8.56	Golgi membrane	Response to reactive oxygen species	Nucleotide binding	No
IP100465436	Q8TAK2		Catalase	2.85	1	1	1	2	3.31	527	59.7	7.39	Lysosome	Muscle system process	Actin binding	No
IP100465439	P04075		Fructose-bisphosphate aldolase A	7.42	2	2	2	2	2.30	364	39.4	8.09	Extracellular region	Excretion		Yes 1
IP100470360	Q96J84	KIRREL	Isoform 1 of kin of IRRE-like protein 1	2.11	2	1	1	1	2.48	757	83.5	5.73	Plasma membrane	Release of cytochrome c from mitochondria	Death receptor binding	No
IP100472003	P55957	C4A	Isoform 4 of BH3-interacting domain death agonist	15.15	3	1	1	3	2.37	99	11.3	9.69	Extracellular region	Regulation of complement activation, lectin pathway	Enzyme inhibitor	Yes
IP100478003	P01023	AGT	Alpha-2-macroglobulin	40.71	7	38	38	232	361.38	1474	163.2	6.46	Extracellular region	Intracellular signaling cascade	Nucleotide binding	No
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	Posttranscriptional regulation of gene expression		Yes
IP100479116	P22792	CPN2	Carboxypeptidase N subunit 2	7.89	1	2	2	10	10.00	545	60.6	5.99	Extracellular region	Cell morphogenesis	Pattern binding	No
IP100479723	P02751	FN1	Isoform 10 of fibronectin	9.42	18	11	11	35	26.04	2176	239.5	5.88	ER-Golgi intermediate compartment			

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Supplementary Table 2: 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
IP 00480192	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	No
IP 00514248	Q5T0S4	PPT1	cDNA FLJ53673, highly similar to Palmitoyl-protein thioesterase 1	5.60	3	1	1	1	2.56	232	26.0	6.54	Cell fraction	DNA catabolic process, endonucleolytic	Palmitoyl-(protein) hydrolase activity	No	No
IP 00514271	Q5TEK7	PDE4B	Phosphodiesterase 4B, cAMP-specific	17.48	3	1	1	2	4.85	103	11.2	8.57	Cell fraction		Cyclic-nucleotide phosphodiesterase activity	Yes	1
IP 00514669	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	No
IP 00514908	Q5T749	KPRP	Keratinocyte proline-rich protein	1.55	1	1	1	1	2.34	579	64.1	8.27	Extracellular region			No	No
IP 00515016	Q5TD07	TTK	NAD(P)H dehydrogenase, quinone 2	9.33	2	1	1	1	2.49	193	21.5	6.52	Cytoplasm	Oxidation reduction	Dihyronicotin amide riboside quinone reductase activity	No	No
IP 00550936	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	No
IP 00552147	Q5JT61	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	6.94	7	1	1	1	2.18	173	19.6	9.10	Plasma membrane	Intracellular signaling cascade	Guanyl-nucleotide exchange factor activity	Yes	Yes
IP 00552768	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	No
IP 00552937	Q5JS37		NHL repeat-containing protein 3	19.02	3	3	3	5	10.25	347	38.3	6.43	Extracellular region			Yes	1
IP 00553215	Q5NV65	TRY8	V1-5 protein	10.83	1	1	1	1	2.31	120	12.7	5.91	Extracellular region			No	No
IP 00554618	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	No
IP 00554711	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
IP 00555565	Q58FF6	HSP90AB4P	Putative heat shock protein HSP 90-beta 4	4.75	1	1	1	1	2.60	505	58.2	4.73	Cytoplasm	Protein folding	Nucleotide binding	No	No
IP 00555577	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

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Supplementary Table 2: 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
IP10055640	Q13164	MAPK7	Isoform 4 of mitogen-activated protein kinase 7	3.10	7	1	1	1	2.27	451	50.1	7.12	MAPKKK cascade	MAPKKK cascade	Nucleotide binding	No
IP10055609	Q59F40		Zinc finger, MYND domain-containing 10 variant (fragment)	5.91	1	1	1	1	2.32	254	26.9	8.88				No
IP100556368	Q9UMR2	hCG_1998531	ATP-dependent RNA helicase DDX19B isoform 3	4.59	4	1	1	1	2.33	370	41.8	7.88	Nuclear envelope	RNA localization	Nucleotide binding	No
IP100556658	Q59HE4		Putative uncharacterized protein (fragment)	11.65	3	1	1	3	5.33	103	11.7	7.84		Transport	Lipid binding	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
IP100607725	Q4VA16	CDH5	CDH5 protein	1.94	3	1	1	1	2.67	669	74.4	5.36	Cell fraction	Blood vessel development	Calcium ion binding	Yes 2
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
IP100607878	Q15375		Isoform 3 of ephrin type-A receptor 7	6.45	6	1	1	2	2.42	279	31.8	5.20	Membrane	Cell morphogenesis	Nucleotide binding	Yes 1
IP100619939	Q9BYF1	HBA1	Isoform 2 of angiotensin-converting enzyme 2	7.21	2	1	1	1	3.17	555	63.9	5.08	Extracellular region	Regulation of cytokine production	Viral receptor activity	Yes 1
IP100640131	Q5T6T5	PAEP	Progesterone-associated endometrial protein	34.13	7	3	3	14	15.40	126	14.9	5.29	Cell fraction			No
IP100640731	B7ZBH1	EIF6	Eukaryotic translation initiation factor 6	16.67	2	1	1	6	9.92	108	11.8	6.27		Mature ribosome assembly	Ribosome binding	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
IP100641749	Q5VZ66	ECM29	Isoform 1 of Janus kinase and microtubule-interacting protein 3	3.79	1	1	1	1	3.00	844	98.5	5.66	Golgi apparatus			No
IP100642248	F2Z3J9		Prostaglandin reductase 1 isoform 2	6.31	2	1	1	1	2.40	301	32.9	7.20	Extracellular region	Fatty acid metabolic process	Alcohol dehydrogenase (NAD) activity	No
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

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Supplementary Table 2: 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
IP100643492			28 kDa protein	8.61	1	1	1	1	2.88	244	27.8	8.12				
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
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 1
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
IP100645888	Q96I49		GALNS protein	7.80	3	1	1	1	2.71	205	22.9	6.99	Lysosome		N-acetylgalactosamine-4-sulfatase activity	Yes 7
IP100646291	Q86V85	C2	Integral membrane protein GPR180	3.41	1	1	1	2	2.39	440	49.4	7.39	Integral to membrane			Yes 1
IP100646304	P23284	FBLN1	Peptidyl-prolyl cis-trans isomerase B	6.02	1	1	1	2	2.64	216	23.7	9.41	ER	Protein folding	Peptidyl-prolyl cis-trans isomerase activity	Yes 1
IP100646605	Q5T4S7	UBR4	Isoform 3 of E3 ubiquitin-protein ligase UBR4	0.41	4	1	1	1	2.33	5159	571.5	6.04	Cytoskeleton	Proteolysis	Ubiquitin-protein ligase activity	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
IP100654807	Q17R18	KIF6	Uncharacterized protein	2.11	3	1	1	1	2.14	758	86.2	6.42	Male germ cell nucleus	Microtubule-based process	Nucleotide 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 1
IP100740198	Q54ER1		RNA recognition motif, RNP-1 domain containing protein	9.59	3	1	1	1	2.67	292	33.8	6.58	Spliceosome	RNA processing	Nucleotide binding	
IP100741892	Q6UXG3	CD300LG	Isoform 3 of CMRF35-like molecule 9	7.21	5	1	1	5	8.22	222	24.9	5.69	Endosome	Immune response		Yes 1
IP100743194	A2NUV5	IGKV	Kappa light chain variable region (fragment)	22.31	13	3	3	10	12.17	121	13.2	7.28	Extracellular region	Complement activation, classical pathway		Yes
IP100743628	Q8WVG9		Isoform 2 of G-protein coupled receptor 98	1.68	4	1	1	1	2.86	1967	217.0	4.86	Stereocilia coupling link	Cell adhesion	Calcium ion binding	Yes 7
IP100746718			Profilaggrin	1.82	3	2	2	4	2.45	1212	132.0	9.63		Ectoderm development	Structural molecule activity	

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Supplementary Table 2: 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
IP100746753	Q04592		Protein convertase subtilisin/kexin type 5	0.88	1	1	1	1	2.35	1590	176.9	5.97	Extracellular region	Skeletal system development	Endopeptidase activity	
IP100747970	C9K0F9	MYST3	Uncharacterized protein	2.06	2	1	1	1	2.23	728	84.1	6.55	Histone acetyltransferase complex	Immune system development	DNA binding	No
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
IP100749196	Q6P531	APOC2	Isoform 2 of gamma-glutamyltransferase 6	4.56	3	1	1	1	4.73	461	47.5	6.04	Integral to membrane	Peptide metabolic process	Gamma-glutamyl transferase activity	No
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
IP100759806	Q9BT62	ENO1	Isoform MBP-1 of alpha-enolase	7.62	2	2	2	2	5.01	341	36.9	6.28	Phospho pyruvate hydratase complex	Negative regulation of transcription from RNA polymerase II promoter	Magnesium ion binding	No
IP100759832	P31946	CASP14	Isoform short of 14-3-3 protein beta/alpha	7.79	2	1	1	2	3.78	244	27.8	4.83	Nucleoplasm	P protein complex assembly	Transcription cofactor activity	No
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	Biliverdin 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				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	
IP100788848	A8MW49	FABP1	Uncharacterized protein	11.29	2	1	1	1	2.86	124	13.8	5.26	Cell fraction	Lipid transport	Chromatin binding	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	

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Supplementary Table 2: 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
IP100789078	P00441		Superoxide dismutase	51.11	2	3	3	3	4.15	135	13.9	6.11	Cytoplasm	MAPKKK cascade	Superoxide dismutase activity	
IP100789173	C9J7H8	LDHB	Uncharacterized protein	10.95	3	1	1	1	3.21	137	14.8	5.54	Cell fraction	Monosaccharide metabolic process	Nucleotide binding	No
IP100789337	B0AZS6	YWHAZ	cDNA FLJ51775, highly similar to 14-3-3 protein zeta/delta	11.18	2	1	1	1	3.71	170	19.3	4.86				No
IP100789477	B7Z4X2		cDNA FLJ58679, highly similar to Lactotransferrin	18.77	8	9	9	71	110.13	666	73.1	7.85	Extracellular region	Transition metal ion transport	Endopeptidase activity	
IP100789511			25 kDa protein	6.17	3	1	1	2	5.23	227	25.3	5.36		Retinoid metabolic process	Carboxypeptidase 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	
IP100791674			12 kDa protein	14.15	9	1	1	1	2.75	106	11.9	5.19		Response to radiation	Enzyme inhibitor activity	
IP100792087			Uncharacterized protein	5.13	3	1	1	1	3.14	234	26.3	4.54	Protein complex assembly			
IP100792115	Q68DS3	SERPINA5	Putative uncharacterized protein	29.38	2	1	3	3	12.31	160	17.8	5.05	Extracellular region	Skeletal system development	Sugar binding	No
IP100793097			DKFZp686H17246 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	
IP100793341	B4DXK4	KRT72	11 kDa protein	15.09	1	1	1	1	2.23	106	11.3	10.95	Cytoskeleton		Structural molecule activity	No
IP100794247			18 kDa protein	8.13	4	1	1	1	2.33	160	17.9	6.68	Cytosol	Arginine metabolic process	Magnesium ion binding	
IP100794777	A6NIW5	PRDX2	Uncharacterized protein	12.50	3	1	1	4	5.45	136	15.1	6.13		MAPKKK cascade	Peroxidase activity	No
IP100795118	Q02388		Isoform 2 of collagen alpha-1 (VII) chain	0.79	2	1	1	1	0.00	2912	292.1	6.23	Extracellular region	Cell adhesion	Enzyme inhibitor activity	Yes
IP100795307	Q9ULI3	HEG1	Isoform 2 of protein HEG homolog 1	1.98	2	1	1	2	3.18	1012	106.4	6.11	Extracellular region		Calcium ion binding	Yes 1
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		

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IP100796137			38 kDa protein	6.55	11	2	2	27	16.06	336	37.8	5.48					
IP100796189	A8MUZ1	ICOSLG	cDNA FLJ33173 fis, clone ADRGL2002191, highly similar to ICOS ligand	5.41	4	1	1	2	2.25	185	20.1	5.83	Integral to membrane	Cell activation			Yes 1
IP100796316	Q5T0H8		cDNA FLJ53327, highly similar to gelsolin	22.70	6	8	8	157	137.16	705	77.7	5.69			Actin binding		No
IP100796552	Q3KRI5	ACE	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 1, isoform CRA_1	2.11	6	1	1	1	2.64	616	70.6	6.90	Cell fraction	Blood vessel development	Actin binding		Yes
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	Ecoterm development	Structural molecule activity		No
IP100797014			8 kDa protein	17.39	1	1	1	1	2.58	69	8.0	5.33					
IP100797221	P04406		Glyceraldehyde-3-phosphate dehydrogenase	8.99	5	1	1	7	9.12	267	28.6	9.09					
IP100797270	P60174	TPI1	Isoform 1 of triosephosphate isomerase	27.71	4	4	4	6	7.59	249	26.7	6.90	Cell fraction				
IP100815875	Q1HG43	DUOXA1	Isoform 1 of dual oxidase maturation factor 1	8.16	3	1	1	1	3.35	343	37.8	6.79	ER	Protein localization			No 5
IP100827643	A2IP16		HRV Fab 027-VL (fragment)	14.16	1	1	1	1	2.16	113	12.4	9.41					No
IP100827657			40 kDa protein	5.06	9	1	1	1	2.49	356	39.9	7.61	Cell fraction	Regulation of DNA recombination	Nucleotide binding		No
IP100827906	A2JA16		Anti-mucin1 light chain variable region (fragment)	16.82	1	1	1	5	7.34	107	11.6	8.46					No
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 by plasma membrane fusion	Pattern binding		Yes 1
IP100829834	P04434		Ig kappa chain V-III region VH (fragment)	15.52	1	1	1	2	2.72	116	12.7	5.94	Extracellular region	Complement activation, classical pathway	Antigen binding		Yes
IP100829912	P01602	IGKV1-5	Ig kappa chain V-I region HK102 (fragment)	13.68	2	1	1	1	2.47	117	12.8	6.51	Extracellular region	Complement activation, classical pathway	Antigen binding		Yes

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Supplementary Table 2: 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
IPi00830092	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	Skeletal system development		Yes
IPi00843910	P04066	FUCA1	Tissue alpha-L-fucosidase	6.44	2	2	2	2	3.11	466	53.7	6.84	Cell fraction	Polysaccharide catabolic process	Alpha-L-fucosidase activity	Yes
IPi00844132			43 kDa protein	8.56	6	2	3	11	14.03	397	43.0	6.39	regulation of type IIa hypersensitivity	Cell surface receptor linked signal transduction		
IPi00845506	Q6UXB8	LYPD2	Isoform 2 of peptidase inhibitor 16	22.22	2	5	5	24	24.57	270	29.7	5.71	Membrane	Putative serine protease inhibitor	Peptidase inhibitor	Yes 1
IPi00847635	P01011	SERPINA3	Isoform 1 of alpha-1-antichymotrypsin	57.68	3	17	17	2197	2756.94	423	47.6	5.52	Extracellular region	Tissue homeostasis	DNA binding	Yes
IPi00847847			Protein of unknown function DUF1725 domain containing protein	8.00	1	1	1	1	2.45	200	23.7	9.25				
IPi00852577	Q6DHW4	LTBP2	HCG2040025	65.09	4	1	4	79	58.66	106	11.4	7.87				Yes
IPi00853468	Q32KK2		Arylsulfatase A isoform b	23.17	4	6	6	43	53.59	423	44.9	5.87	Cell fraction	Autophagy	Arylsulfatase activity	
IPi00855927	A6ZIE2	MUC1	MUC1 isoform M8	15.81	24	2	2	3	6.63	215	22.9	7.46	Extracellular region	Female pregnancy		Yes 2
IPi00869004	P01009		Isoform 3 of alpha-1-antitrypsin	15.03	3	3	3	11	8.42	306	34.7	5.19	Extracellular region	Response to hypoxia	Protease binding	Yes
IPi00871227	Q96RW7	AGRN	Isoform 1 of hemicentin-1	0.59	2	2	2	8	5.45	5635	613.0	6.49	Extracellular region	Blood coagulation	Calcium ion binding	Yes
IPi00871326	Q9NSM6		cDNA FLJ57256, highly similar to plexin-A1	1.01	2	1	1	1	2.29	1873	208.4	6.87	Cell fraction			No
IPi00872814			68 kDa protein	3.82	8	2	2	2	5.23	576	67.6	6.40	Uropod	Cell motion	Actin binding	
IPi00873341			155 kDa protein	3.90	3	3	3	10	5.45	1383	154.7	6.21	Plasma membrane	Protein amino acid dephosphorylation activity	Phosphoprotein phosphatase	
IPi00873761	Q2I377		Small proline rich protein	23.29	2	1	1	4	6.13	73	8.1	8.72	Cytoplasm	Ectoderm development	Structural molecule activity	No
IPi00873924	Q9UNH2	IL18BP	Isoform A of Interleukin-18-binding protein	6.19	1	1	1	5	7.58	194	21.1	7.39	Extracellular region	Adaptive immune response	Cytokine binding	Yes
IPi00874274	Q6AWA4	DKFZp686O0870	Uncharacterized protein	1.13	3	1	1	1	2.53	1685	191.7	8.66	Transcription factor TFIIC complex	Transcription	DNA binding	No
IPi00877625	C9JPQ9	FGG	Uncharacterized protein	10.92	6	1	1	3	2.90	119	13.5	7.20	Extracellular region	Cell activation	Calcium ion binding	No

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IP100877967	C9JUV37	F2	Uncharacterized protein	17.90	2	3	3	20	22.76	324	35.9	4.82	Cell fraction	Protein import into nucleus, translocation	Endopeptidase activity	Yes
IP100878073	Q9BRT3	GPATCH1	Protein C17orf37	20.00	2	1	1	1	4.26	115	12.4	4.37	Cytoplasm	Cellular homeostasis	Selenium binding	No
IP100878488			21 kDa protein	6.57	15	1	1	2	2.75	198	21.1	5.45	Integral to membrane	Peptide metabolic process	Gamma-glutamyl transferase activity	
IP100879328			30 kDa protein	28.62	5	5	5	44	25.00	276	30.0	7.42		Autophagic vacuole formation	Endopeptidase activity	
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
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	
IP100884926	P02763		Alpha-1-acid glycoprotein 1 precursor	67.66	2	10	15	565	889.87	201	23.5	5.11	Extracellular region			
IP100887765	P78559	MAP1A	Isoform 1 of microtubule-associated protein 1A	0.82	3	1	1	1	2.99	2803	305.3	4.92	Cytosol	Negative regulation of microtubule depolymerization	Actin binding	No
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		Hemicentin 2	0.37	4	1	1	1	2.31	3783	405.3	5.67				
IP100890703	B1N7B8	ASAH1	Cryocystaiglobulin 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	
IP100892952	C9JIE7	LRRIQ1	Uncharacterized protein	11.49	3	1	1	9	8.75	148	15.4	9.22	Extracellular region	Cell adhesion		Yes 1
IP100893223	C9JMK5	PIK3IP1	Uncharacterized protein	17.93	5	2	2	7	10.52	145	16.0	7.90	Integral to membrane			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
IP100893588			Protein	9.29	8	1	1	4	5.44	183	20.1	4.64	Cornified envelope		Structural molecule activity	

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IP100893864	D2KT85	CFB	Complement factor B	12.90	10	5	5	7.02	589	65.7	6.39	Extracellular region	Immune effector process	Complement binding	Yes
IP100894365	E7EVS6		cDNA FLJ52842, highly similar to actin, cytoplasmic 1	13.39	28	3	3	8.93	351	39.2	5.59	Extracellular region	Cell morphogenesis	Nucleotide binding	No
IP100895848	O95498	HBB	Isoform 4 of vascular non-inflammatory molecule 2	7.18	1	1	1	2.34	195	21.9	5.53	Plasma membrane	Cellular amino acid derivative metabolic process	Hydrolase activity	Yes 1
IP100895917	FCGR3A	FCGR3A	Low affinity immunoglobulin gamma Fc region receptor III-A isoform d precursor	4.74	4	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	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	207.36	900	99.8	6.47		Acute inflammatory response	Enzyme inhibitor activity	Yes
IP100902923	Q2L696		Nucb2 splice variant	2.82	3	1	1	2.22	390	46.6	5.22	Extracellular region	Autophagy	DNA binding	Yes 2
IP100908532	B4DWL3	LAMP1	cDNA FLJ57633, highly similar to Lysosome-associated membrane glycoprotein 1	4.40	2	1	1	2.90	364	39.0	8.87	Autophagy			
IP100908562	B4DLI3		cDNA FLJ51237, moderately similar to carcinoembryonic antigen-related cell adhesion molecule 8	13.28	2	2	2	11.96	256	27.8	8.44				Yes
IP100908582	E7EPM0		cDNA FLJ50164, highly similar to protein flightless-1 homolog	1.18	2	1	1	2.22	1183	135.1	6.13	Nucleolus	Muscle system process	Actin binding	No
IP100908730	B4DPJ4		cDNA FLJ55126, highly similar to procollagen C-endopeptidase enhancer 1	19.34	2	2	2	5.57	181	19.5	7.02	Extracellular region			Yes
IP100908732	B4DJW4		cDNA FLJ58003, highly similar to 1-O-acylceramide synthase	7.63	2	1	1	2.14	236	25.8	7.87		Lipid metabolic process	Phosphatidylcholine-sterol O-acyltransferase activity	Yes

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IP100908746	B4DRT4	PEBP1	cDNA FLJ51535, highly similar to Phosphatidy lethanolamine-binding protein 1	60.65	4	5	5	16	21.33	155	17.3	6.00		Regulation of neurotransmitter levels	Nucleotide binding	No
IP100908754	B4DW94	RAP1B	cDNA FLJ50714, moderately similar to Ras-related protein Rap-1b	8.76	6	1	1	3	5.78	137	15.3	8.13	Cytosol	Intracellular signaling cascade	Nucleotide binding	No
IP100908762	B4DJ70	LGALS3BP	cDNA FLJ53509, highly similar to Galectin-3-binding protein	10.14	3	3	3	20	19.83	414	46.5	5.26	Membrane	Defense response	Scavenger receptor activity	Yes
IP100908926	E7ESD8		cDNA FLJ52974, highly similar to neural cell adhesion molecule 1, 140 kDa isoform	4.15	5	1	1	1	2.25	313	33.3	5.44	Extracellular region	Cell adhesion		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
IP100908979	E7ER24		Primary amine oxidase	5.53	6	2	2	2	5.20	597	67.3	6.83	Extracellular region	Oxidation reduction	Pattern binding	Yes
IP100909039	E7ESS4		cDNA FLJ53671, highly similar to Intercellular adhesion molecule 1	4.52	4	1	1	1	2.32	310	33.7	8.35		Cell activation	Integrin binding	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
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
IP100909399	E9PCE8		Xaa-Pro dipeptidase isoform 3	2.33	3	1	1	1	2.18	429	47.2	6.07		Proteolysis	Aminopeptidase activity	No
IP100909516	E7EV34		cDNA FLJ58558, highly similar to Tripeptidyl-peptidase 1	15.73	6	4	4	25	15.10	496	53.8	6.38		Tissue homeostasis	Endopeptidase activity	Yes
IP100909841	E9PS23		cDNA FLJ51435, moderately similar to Cofilin-1	17.86	2	1	1	1	2.78	112	12.5	6.60	Intracellular	Actin binding		No

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IPi00909914	E9PGL4		cDNA FLJ50884, highly similar to Beta-hexosaminidase alpha chain	9.83	4	2	2	3	8.07	356	40.9	4.96	ER	Skeletal system development	Beta-N-acetylhexosaminidase activity	No
IPi00910374	B4DHP1	OVGP1	cDNA FLJ57304, highly similar to oviduct-specific glycoprotein	8.11	1	1	1	1	2.28	185	21.1	10.36		Polysaccharide catabolic process	Chitinase activity	No
IPi00910380	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
IPi00910625	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
IPi00910706	B4DNR3	ABHD14B	cDNA FLJ52710, highly similar to abhydrolase domain-containing protein 14B	17.30	6	2	2	4	8.82	185	19.8	6.40			Hydrolase activity	No
IPi00910738	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
IPi00910803	B4DNW9		cDNA FLJ57491, moderately similar to T-cell antigen CD7	13.25	2	1	1	4	5.57	166	17.7	8.21				Yes
IPi00910870	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
IPi00910922	B4DE34	MXRA8	cDNA FLJ54995, highly similar to hom sapiens matrix-remodelling associated 8 (MXRA8), mRNA	3.81	5	1	1	1	3.09	341	38.0	7.06	Integral to membrane			Yes 1
IPi00911039	B4E3B6		cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1	2.39	3	1	1	1	2.37	586	63.9	5.55	RNA catabolic process	RNA catabolic process	Nucleotide binding	No
IPi00915959			shock 70 kDa protein 1 7 kDa protein	26.15	6	1	1	1	2.52	65	7.4	4.01	Spindle pole	Cell cycle	Calcium ion binding	No
IPi00917198	B8ZZ35	NAGA	N-acetylglactosaminidase, alpha-	13.21	3	2	2	5	5.94	212	23.7	5.54	Lysosome		Alpha-N-acetylglactosaminidase activity	No

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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
IP100917285	B4DFW2	TIMP2	cDNA FLJ57920, highly similar to metalloproteinase inhibitor 2	7.91	3	1	1	2	177	20.0	7.17	Extracellular region	Regulation of nucleotide metabolic process	Enzyme inhibitor activity	No
IP100917736	E9PHH2		Uncharacterized protein	2.97	4	1	1	2.11	505	57.1	7.14		Membrane fusion process	Pattern binding	Yes
IP100922121	F2YBS6		cDNA FLJ52524, moderately similar to matrix metalloproteinase-9	5.43	2	1	1	2.50	276	31.1	7.14	Extracellular matrix	Proteolysis	Metalloendo peptidase activity	No
IP100922190	B7Z2X6		cDNA FLJ52145, highly similar to G-protein coupled receptor family C group 5 member B	6.32	4	1	1	2.63	190	20.7	6.67			Receptor activity	Yes 1
IP100922193	B4DJZ2		cDNA FLJ59705, highly similar to transcription factor 7-like 2	5.01	1	1	1	7.01	339	38.0	9.31			DNA binding	No
IP100924548	C9JNR0	IL1R2	Uncharacterized protein	8.30	3	1	1	2.58	229	26.3	7.40	Integral to membrane	Immune response	Cytokine receptor activity	Yes
IP100924593	Q75MP7		cDNA FLJ52880, highly similar to malate dehydrogenase, mitochondrial	6.42	2	1	1	3.10	296	30.9	8.43	Mitochondrion	Monosaccharide metabolic process	Malate dehydrogenase activity	No
IP100925377	E9PHY0		cDNA FLJ52440, highly similar to lysosomal acid phosphatase	10.83	3	3	3	8.65	360	40.9	8.05			Acid phosphatase activity	Yes 1
IP100926171	O43490		Isoform 5 of prominin-1	1.94	8	1	1	2.28	825	92.7	7.36	Extracellular region	Sensory perception		Yes 5
IP100926770	C9JMT3	GRM7	Uncharacterized protein	9.19	1	1	1	2.35	185	21.2	6.76	Plasma membrane	Conditioned taste aversion	Adenylate cyclase inhibiting metabotropic glutamate receptor activity	No
IP100927191	P16278		Isoform 3 of beta-galactosidase	15.30	8	7	7	27.17	647	72.7	6.25	Cytosol		Beta-galactosidase	Yes
IP100927883	E9PCV0		cDNA FLJ53268, highly similar to beta-glucuronidase	6.53	4	2	2	11.98	505	58.3	6.99	Lysosome	Polysaccharide catabolic process	Beta-glucuronidase activity	Yes 1

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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
IP 00930404	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
IP 00935818	Q1RMG2	HADH	adenosylhomo cysteinase isoform 2	3.22	2	1	1	1	2.63	404	44.6	6.47	Cytoplasmic membrane-bounded vesicle	One-carbon metabolic process	Adenosylhomo cysteinase activity	No
IP 00939169	O75882	CREG1	Isoform 3 of attractin	1.67	5	2	2	2	3.16	1198	133.6	6.98	Extracellular region	Defense response	Sugar binding	Yes 1
IP 00939281	Q7Z4R8	PVRL2	UPF0669 protein C6orf120	10.99	1	1	1	5	5.85	191	20.8	4.84	Extracellular region			Yes
IP 00939624	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
IP 00939673	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	
IP 00940517	C9J1L3	VSIG4	Uncharacterized protein	16.74	7	2	2	9	16.40	227	25.4	7.14		Regulation of cytokine production		Yes 1
IP 00940960	P61916	NPC2	Epididymal secretory protein E1	25.83	2	2	2	3	4.30	151	16.6	7.65	Lysosome	Lipid transport	Steroid binding	Yes
IP 00941125	Q6W4X9	DMD	Mucin-6	0.46	2	1	1	11	11.87	2393	252.2	7.36	Extracellular region	Tissue homeostasis	Structural molecule activity	Yes
IP 00941565	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
IP 00941929	Q9Y464	TNXB	Tenascin XB	0.48	11	1	1	1	2.46	2280	245.0	5.26	Extracellular region	Cytoskeleton organization	Pattern binding	Yes
IP 00942625	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			
IP 00943326	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		
IP 00943343	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
IP 00944942	C9J9N0	DNASE1L3	Uncharacterized protein	8.67	4	1	1	1	2.34	173	20.2	8.25	Extracellular region	DNA catabolic process, endonucleolytic	DNA binding	Yes
IP 00945229	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 1

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Supplementary Table 2: 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
IP100945650	Q5F8Y0	ACPP	cDNA FLJ54158, highly similar to Prostatic acid phosphatase collagen alpha-3(VI) chain isoform 4 precursor	12.75	3	3	3	33	18.24	353	40.4	6.01	Lysosome		Acid phosphatase activity	Yes 1
IP100946286	COL6A3	COL6A3	collagen alpha-3(VI) chain isoform 4 precursor	4.20	9	7	7	8	13.33	2570	278.0	8.15	Extracellular region	Cell adhesion	Enzyme inhibitor activity	Yes
IP100946705	Q6UX73		Isoform 2 of UPF0764 protein C16orf89	3.60	6	1	1	5	7.44	361	40.6	5.87	Extracellular region			No
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
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
IP100947292	FZZZ29	PLS3	5 kDa protein	47.62	1	1	1	1	2.56	42	4.8	4.35		Cytoskeleton organization	Actin binding	No
IP100952944			Uncharacterized protein	10.65	4	4	4	13	20.31	676	70.8	5.07	Extracellular region	Fatty acid metabolic process	Pattern binding	No
IP100953396	A9NIU4	OBSCN	Uncharacterized protein	0.62	5	1	1	1	3.30	5602	610.6	5.60	Cytosol		Nucleotide binding	No
IP100953536	C9J4E6	CDHR5	Uncharacterized protein	3.70	4	1	1	2	5.73	487	53.3	5.25	Plasma membrane	phosphorylation	Calcium ion binding	Yes
IP100953631	C8YZ26	MCL1	Myeloid cell leukemia ES variant	9.64	1	1	1	1	2.33	197	21.2	9.92		Regulation of apoptosis		Yes 1
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				
IP100956313			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
IP100964365	E9PHT9		cDNA FLJ52002, highly similar to annexin A5	9.82	4	1	1	1	2.69	163	18.2	5.06			Calcium ion binding	No

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Supplementary Table 2: 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
IP100965211	E7EM93			50 kDa protein	4.05	2	1	1	3	3.47	444	50.0	6.79		Hydrolase activity		No	
IP100965393	Q59EG5			cDNA FLJ50201, highly similar to Beta-mannosidase	3.41	2	2	2	2	5.62	822	94.4	5.31		Carbohydrate metabolic process	Cation binding	Yes	
IP100965913				Protein	15.42	11	6	6	80	58.24	454	51.5	6.95					
IP100966865				17 kDa protein	7.74	3	1	1	1	2.25	155	17.0	6.27					
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	
IP100967527	Q5URX0	SERPING1		ENC-1AS	4.83	2	1	1	1	2.37	331	38.2	6.44			Cation binding	No	
IP100968042	D6RBJ2			Uncharacterized protein	27.33	6	2	2	3	10.11	150	16.3	4.77	Membrane	Homophilic cell adhesion	Calcium ion binding	Yes	
IP100968182	D6RBJ7	GC		Uncharacterized protein	20.11	5	4	4	57	33.06	348	38.8	5.50	Extracellular space		Vitamin D binding	Yes	
IP100969060				Uncharacterized protein	8.07	4	1	1	3	4.59	161	18.3	8.32					
IP100969122	P04229			MHC class I antigen (fragment)	16.02	11	1	1	1	3.02	181	21.0	7.39					
IP100969595	D6W5J8	hCG_1639753		HCG1639753, isoform CRA_a	29.87	1	1	1	9	26.45	77	8.3	6.24				No	
IP100973131				MHC class I antigen (fragment)	5.86	30	1	1	1	2.73	273	31.6	5.67			Binding		No
IP100973362	B7Z6J1			cDNA FLJ55035, highly similar to Dihydrolyipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	8.43	3	1	1	5	7.92	166	17.9	8.06					
IP100973378	Q8NAU3			cDNA FLJ34780 fis, clone NT2NE2003705, weakly similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 2	11.54	3	1	1	1	2.15	130	16.2	9.36	Ribonucleoprotein complex		Nucleic acid binding	No	

LC-MS/MS: Liquid chromatography-tandem mass spectrometry, MW: Molecular weight, COMPA: Cartilage oligomeric matrix protein, ER: Endoplasmic reticulum, NA: Normoalbuminuria, GPI: Glycosylphosphatidylinositol, ATP: Adenosine triphosphate, PSMs: Peptide spectrum match, AA: Amino acids?, TM: Transmembrane domain

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