Supplementary Table 7: List of unique proteins identified in MA group compared to control, NA and MiA groups

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00002147	P36222	CHI3L1	Chitinase-3-like protein 1	13.05	2	3	3	4	7.26	383	42.6	8.46	Extracellular region	Polysaccharide catabolic process	Chitinase activity	Yes	
IPI00003351	Q16610	ECM1	Isoform 1 of extracellular matrix protein 1	19.07	4	6	6	14	27.31	540	60.6	6.71	Extracellular region	Positive regulation of signal transduction	Laminin binding	Yes	
IPI00004500	O15049	N4BP3	NEDD4-binding protein 3	3.49	1	1	1	1	2.98	544	60.4	8.10	Extrinsic to membrane			No	
IPI00005721	P59665	DEFA1	Neutrophil defensin 1	32.98	2	1	1	5	12.60	94	10.2	6.99	Extracellular region	Cell killing		Yes	
IPI00007199	Q9UK55	SERPINA10	Protein Z-dependent protease inhibitor	7.23	1	2	2	4	11.31	484	55.1	7.64	Extracellular region	Response to wounding	Enzyme inhibitor activity	Yes	
IPI00007240	P05160	F13B	Coagulation factor XIII B chain	2.27	1	1	1	1	3.18	661	75.5	6.39	Extracellular region	Blood coagulation		Yes	
IPI00008753	P80297	MT1X	Metallothionein-1X	19.67	6	1	1	1	3.20	61	6.1	7.96	Nucleus	Response to inorganic substance	Copper ion binding	No	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00011252	P07357	C8A	Complement component C8 alpha chain	14.21	1	5	5	9	17.85	584	65.1	6.47	Extracellular region	Adaptive immune response		Yes	
IPI00012587	P60484	PTEN	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	9.43	1	1	1	2	3.36	403	47.1	6.37	Mitochondrion	Regulation of cyclin-dependent protein kinase activity	Magnesium ion binding	No	
IPI00012760	Q6NT58	LEP	Leptin	7.78	1	1	1	1	3.80	167	18.6	6.37	Extracellular region	Ovulation from ovarian follicle	Hormone activity	Yes	
IPI00013682	Q5J1K8	ART3	Isoform 3 of Ecto-ADP-ribosyltransferase 3	6.94	6	2	2	3	6.38	389	43.9	6.06	Plasma membrane	Protein amino acid ADP-ribosylation	NAD + ADP-ribosyltransferase activity	Yes	
IPI00015309	Q99456	KRT12	Keratin, type I cytoskeletal 12	1.82	1	1	1	1	3.10	494	53.5	4.78	Cytoskeleton	Sensory perception	Structural molecule activity	No	
IPI00017704	Q14019	COTL1	Coactosin-like protein	11.27	1	1	1	1	4.77	142	15.9	5.67	Cytoskeleton	Defense response	Actin binding	No	
IPI00019399	P35542	SAA4	Serum amyloid A-4 protein	8.46	1	1	1	4	9.23	130	14.7	9.07	Extracellular region	Acute inflammatory response		Yes	
IPI00019568	P00734	F2	Prothrombin (fragment)	32.48	2	13	13	53	104.29	622	70.0	5.90	Extracellular region	Protein import into nucleus, translocation	Endopeptidase activity	No	
IPI00019576	P00742	F10	Coagulation factor X	6.15	1	2	2	3	7.09	488	54.7	5.94	Cell fraction	Proteolysis	Endopeptidase activity	Yes	1
IPI00019580	P00747	PLG	Plasminogen	9.14	5	5	5	18	20.79	810	90.5	7.24	Cell fraction	Proteolysis	Endopeptidase activity	Yes	
IPI00019581	P00748	F12	Coagulation factor XII	2.93	1	1	1	5	8.73	615	67.8	7.74	Extracellular region	Kinin cascade	Endopeptidase activity	Yes	
IPI00019591	Q53F89	CFB	cDNA FLJ55673, highly similar to complement factor B	24.25	18	14	23	191	181.91	1266	140.9	7.18	Extracellular region	Complement activation	Serine-type endopeptidase activity	Yes	
IPI00020996	P35858	IGFALS	Insulin-like growth factor-binding protein complex acid labile subunit	7.60	2	3	3	11	20.47	605	66.0	6.79	Cell fraction	Cell aadhesion	Insulin-like growth factor binding	Yes	
IPI00021856	P02655	APOC2	Apolipoprotein C-II	20.79	1	1	1	6	19.30	101	11.3	4.72	Extracellular region	Cholesterol efflux	Lipase inhibitor activity	Yes	
IPI00022389	P02741	CRP	Isoform 1 of C-reactive protein	5.36	1	2	2	5	17.55	224	25.0	5.63	Extracellular region	Adaptive immune response	Calcium ion binding	Yes	
IPI00022394	P02747	C1QC	Complement C1q subcomponent subunit C	7.35	1	1	1	2	7.75	245	25.8	8.41	Extracellular region	Adaptive immune response		Yes	
IPI00023019	P04278	SHBG	Isoform 1 of sex hormone-binding globulin	22.14	8	5	5	18	34.90	402	43.8	6.71	Lysosome	Reproductive developmental process	Steroid binding	Yes	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00026256	P14384	CPM	Filaggrin	2.51	6	3	3	4	6.38	4061	434.9	9.25	Plasma membrane	Proteolysis	Carboxypeptidase activity	Yes	
IPI00028911	Q14118	DAG1	Dystroglycan	3.02	4	2	2	9	14.32	895	97.4	8.56	Plasma membrane	Morphogenesis of an epithelium	Calcium ion binding	Yes	1
IPI00029039	Q53S56	PAP	Regenerating islet-derived protein 3-alpha	13.14	1	1	1	4	16.13	175	19.4	7.64	Cell fraction	Acute inflammatory response	Sugar binding	Yes	
IPI00029193	Q04756	HGFAC	Hepatocyte growth factor activator	1.83	2	1	1	1	3.10	655	70.6	7.24	Extracellular region	Proteolysis	Endopeptidase activity	Yes	1
IPI00029235	P24592	IGFBP6	Insulin-like growth factor-binding protein 6	6.25	1	1	1	8	8.57	240	25.3	7.81	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes	
IPI00029739	Q14006	HF	Isoform 1 of complement factor H	13.24	4	10	11	31	51.54	1231	139.0	6.61	Cell fraction	Immune effector process		Yes	
IPI00032195	Q16082	HSPB2	Heat shock protein beta-2	6.19	1	1	1	1	3.20	307	33.1	6.64	Cell fraction	Response to unfolded protein	Enzyme activator activity	No	
IPI00032288	Q9H8J5	MANSC1	MANSC domain-containing protein 1	3.48	1	1	1	1	3.44	431	46.8	6.54	Integral to membrane		Chitinase activity	Yes	1
IPI00032291	P01031	C5	Complement C5	7.34	2	7	7	15	16.92	1676	188.2	6.52	Extracellular region	MAPKKK cascade	Enzyme inhibitor activity	Yes	
IPI00032328	P01042	KNG1	Isoform HMW of kininogen-1	21.89	4	1	12	61	54.73	644	71.9	6.81	Extracellular region	Muscle system process	Pattern binding	Yes	
IPI00033583	Q96P63	SERPINB12	Serpin B12	4.20	2	1	1	2	3.48	405	46.2	5.53	Cytoplasm	Regulation of catabolic process	Enzyme inhibitor activity	No	
IPI00069985	Q9Y5B2		Junction adhesion molecule	4.25	4	1	1	1	3.06	259	28.1	8.29	Plasma membrane	Defense response		Yes	1
IPI00150200	P07307	ASGR2	Isoform 3 of asialoglycoprotein receptor 2	3.83	7	1	1	1	3.53	287	32.5	5.80	Integral to membrane	Endocytosis	Asialoglycoprotein receptor activity	No	1
IPI00176710	Q5VSP4	LCN1P1	Putative lipocalin 1-like protein 1	6.79	2	1	1	2	3.17	162	17.9	5.00	Extracellular region	Proteolysis	Enzyme inhibitor activity	Yes	
IPI00218732	Q96P91	PON1	Serum paraoxonase/ arylesterase 1	14.65	2	4	4	6	12.30	355	39.7	5.22	Cell fraction	Cellular amino acid derivative metabolic process	Aryldialkyl phosphatase activity	No	
IPI00218875	Q567T5		Isoform C of osteopontin	25.44	7	5	5	9	29.23	287	32.3	4.55	Extracellular region	Skeletal system development	Cytokine activity	Yes	
IPI00219648	O75379	VAMP4	Isoform 2 of vesicle-associated membrane protein 4	15.00	2	1	1	1	3.00	140	16.2	6.60	Golgi membrane	Vesicle-mediated transport		No	1
IPI00221362	Q9ULZ3	PYCARD	Isoform 3 of apoptosis-associated speck-like protein containing a CARD	11.85	3	1	1	3	5.02	135	15.0	7.44	Cytosol	Regulation of cytokine production	Endopeptidase activity	No	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00232492	Q14134	TRIM29	Isoform beta of tripartite motif-containing protein 29	3.51	2	1	1	1	3.05	570	63.8	6.98	Cytoplasm	Transcription	DNA binding	No	
IPI00290315	P10645	CHGA	Chromogranin-A	22.54	2	5	5	11	15.81	457	50.7	4.60	Extracellular region	Circulatory system process	Calcium ion binding	Yes	
IPI00291175	P18206	VCL	Isoform 1 of vinculin	4.41	3	3	3	6	9.74	1066	116.6	6.09	Extracellular region	Cell motion	Actin binding	No	
IPI00292530	P19827	ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1	18.44	6	11	11	40	53.82	911	101.3	6.79	Extracellular region	Cell activation	Enzyme inhibitor activity	Yes	1
IPI00293350	Q99598	TSNAX	Translin-associated protein X	14.14	1	1	1	1	3.33	290	33.1	6.55	Perinuclear region of cytoplasm	Gamete generation	DNA binding	No	
IPI00294004	P07225	PROS1	Vitamin K-dependent protein S	3.55	5	2	2	5	10.79	676	75.1	5.67	Golgi lumen	Blood coagulation	Enzyme inhibitor activity	Yes	
IPI00294395	Q05CV3	C8B	Complement component C8 beta chain	14.38	1	5	5	16	31.63	591	67.0	8.13	Extracellular region	Adaptive immune response	Protein complex binding	Yes	1
IPI00297284	P18065	IGFBP2	Insulin-like growth factor-binding protein 2 precursor	8.54	3	2	2	4	10.67	328	35.1	7.50	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes	
IPI00298497	P02675	FGB	Fibrinogen beta chain	42.97	3	14	14	112	102.53	491	55.9	8.27	Extracellular region	Cell activation	Protein binding	Yes	
IPI00298547	Q99497	PARK7	Protein DJ-1	7.94	1	1	1	1	3.00	189	19.9	6.79	Mitochondrion	Response to reactive oxygen species	Peroxiredoxin activity	No	
IPI00298971	P04004	VTN	Vitronectin	21.13	2	8	8	53	33.25	478	54.3	5.80	Extracellular region	Immune response	Pattern binding	Yes	
IPI00299435	Q13790	APOF	Apolipoprotein F precursor	3.99	1	1	1	1	2.99	326	35.4	5.64	Extracellular region	Lipid transport	Lipid transporter activity	Yes	
IPI00299503	P80108	GPLD1	Isoform 1 of phosphatidylinositol-glycan-specific phospholipase D	1.79	1	1	1	1	3.14	840	92.3	6.37	Extracellular region	GPI anchor metabolic process	Phospholipase activity	Yes	
IPI00305380	P22692	IGFBP4	Insulin-like growth factor-binding protein 4	12.02	1	3	3	7	15.42	258	27.9	7.15	Extracellular region	Skeletal system development	Insulin-like growth factor binding	Yes	
IPI00305469			Adapter molecule crk isoform b	8.33	3	1	1	1	3.75	204	22.9	5.48	Endosome	Regulation of transcription	SH3/SH2 adaptor activity		
IPI00306483	Q5T0F9	CC2D1B	Isoform 3 of coiled-coil and C2 domain-containing protein 1B	3.38	4	1	1	1	3.03	532	59.3	9.07				No	
IPI00328550	P35443	THBS4	Thrombospondin-4	5.31	5	3	3	3	6.79	961	105.8	4.68	Extracellular region	Cell motion	Pattern binding	Yes	
IPI00328609	P29622	SERPINA4	Kallistatin	24.59	1	7	7	15	28.37	427	48.5	7.75	Extracellular region		Enzyme inhibitor activity	Yes	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00329775	Q96IY4	CPB2	Isoform 1 of carboxypeptidase B2	10.17	3	3	3	3	10.66	423	48.4	7.71	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes	
IPI00384697	P02768	ALB	Isoform 2 of serum albumin	10.55	10	4	4	40	26.02	417	47.3	6.35	Extracellular region	Cytolysis by symbiont of host cells	DNA binding	Yes	
IPI00413587	P55957	BID	Isoform 1 of BH3-interacting domain death agonist	14.36	3	2	2	2	3.28	195	22.0	5.44	h_ deathPathway: Induction of apoptosis through DR and DR/Death Receptors	Release of cytochrome c from mitochondria	Death receptor binding	No	
IPI00414467	Q5KU26	COLEC12	Isoform 1 of collectin-12	1.35	1	1	1	1	2.98	742	81.5	5.69	Integral to membrane	Protein complex assembly	Scavenger receptor activity	No	1
IPI00465431	Q9Y2P4	SLC27A6	Galectin-3	4.40	1	1	1	1	3.09	250	26.1	8.56	Plasma membrane	Very-long-chain fatty acid metabolic process	Nucleotide binding	Yes	
IPI00477227	Q8N1N4	KRT78	Isoform 1 of keratin, type II cytoskeletal 78	13.27	2	4	6	16	17.10	520	56.8	6.02	Cytoskeleton		Structural molecule activity	No	
IPI00514229	Q5T093	RER1	RER1 retention in ER 1 homolog	19.66	2	1	1	1	3.27	117	13.4	10.40	Retrograde vesicle-mediated transport	Retrograde vesicle-mediated transport, Golgi to ER		N	1
IPI00515092	Q5TBF5	OGN	Osteoglycin	12.69	2	2	2	9	15.48	268	30.4	8.34	Extracellular region		Growth factor activity	No	
IPI00552123	Q5J876		Isoform 2 of V-set and immunoglobulin domain-containing protein 4	19.31	7	4	4	6	11.33	321	35.5	8.15	Extracellular region		Enzyme inhibitor activity	Yes	
IPI00556324	Q59F63		Transforming growth factor, beta-induced, 68kDa variant (fragment)	5.79	5	1	1	2	6.60	242	25.8	5.55				No	
IPI00556415	Q59FA5		Transgelin variant	15.34	2	2	2	3	9.88	163	18.3	6.58	Plasma membrane	Muscle organ development	Actin binding	No	
IPI00639831	Q9H948		Isoform 2 of selenocysteine insertion sequence-binding protein 2	2.56	2	1	1	4	6.67	781	87.3	8.76	Nucleus	Translation	RNA binding	No	
IPI00643525	Q5JNX2		Uncharacterized protein	35.26	5	1	37	277	281.76	1744	192.6	7.08	Extracellular region	Adaptive immune response	Enzyme inhibitor activity	Yes	
IPI00643888	Q8N1K5	THEMIS	Isoform 3 of protein THEMIS	3.49	4	1	1	4	6.27	544	62.5	6.27	Cytoplasm, nucleus	Cell activation	Developmental protein	No	
IPI00644184	Q8IWX7	UNC45B	Isoform 2 of protein unc-45 homolog B	2.12	3	1	1	1	3.21	850	94.8	7.85	Muscle organ development	Muscle organ development		No	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00644989	Q53RC7	DAF	Isoform 1 of protein disulfide-isomerase A6	3.18	2	1	1	2	3.19	440	48.1	5.08	Protein folding	Protein folding	Protein disulfide isomerase activity	Yes	
IPI00645500	E9PFN7		cDNA FLJ55526, highly similar to complement C2	17.57	13	1	10	34	67.82	723	80.1	7.46	Extracellular region	Adaptive immune response	Endopeptidase activity	Yes	
IPI00646773	P06396	GSN	Isoform 2 of gelsolin	35.16	7	15	15	155	147.00	731	80.6	5.85	Cytoplasm, cytoskeleton	Response to acid	Actin binding	Yes	
IPI00746033			47 kDa protein	5.49	3	1	1	1	3.53	419	47.1	7.46	Lysosome		Alpha-N-acetyl glucosaminidase activity		
IPI00749381	Q9NS71	GKN1	Gastrokine-1	7.04	1	1	1	2	6.83	199	22.0	6.32	Extracellular region	Digestion	Growth factor activity	Yes	1
IPI00790784	Q3I0J7		Isoform 2 of alpha-1-antitrypsin	13.37	4	3	3	8	10.46	359	40.2	5.47	Extracellular region	Response to hypoxia	Protease binding	No	1
IPI00792354			10 kDa protein	11.76	1	1	1	1	3.28	85	9.6	7.90					
IPI00795257	Q6YHK3	CD109	32 kDa protein	9.90	7	2	2	4	3.29	293	31.5	7.61	Extracellular region		Enzyme inhibitor activity	Yes	
IPI00796012	Q15020	SART3	Squamous cell carcinoma antigen 1	8.23	3	1	1	1	3.15	158	18.2	7.55	Cytoplasm	Immune response	Enzyme inhibitor activity		
IPI00796636	Q9UP81	HBB	Hemoglobin (fragment)	45.71	9	3	3	4	16.42	105	11.5	6.37	Hemoglobin complex	Oxygen transport	Heme binding	No	
IPI00797778			91 kDa protein	4.97	3	1	1	1	3.38	825	90.7	9.09	MAPKKK cascade	Spliceosome assembly	RNA binding		
IPI00807475	P16383	GCFC2	Isoform 2 of GC-rich sequence DNA-binding factor	2.56	2	1	1	3	9.13	743	84.8	6.20	Nucleus	Transcription	DNA binding	No	
IPI00815665	Q6PK75	PRSS2	Trypsin-2	14.17	8	2	2	4	11.33	247	26.5	4.92	Extracellular region	Proteolysis	Endopeptidase activity	Yes	
IPI00828004	Q8NG19		MFP	26.82	6	4	4	11	15.23	261	26.7	9.32	Extracellular matrix	Cell adhesion	Binding	No	
IPI00844090	Q9UML4	COL5A1	Collagen alpha-1 (V) chain	2.94	1	3	3	3	7.38	1838	183.4	5.06	Extracellular region	Blood vessel development	Pattern binding	Yes	
IPI00847442	Q1JUQ5	FKBP12-Exip2	FK506 binding protein12	15.22	3	1	1	1	3.83	92	10.1	5.90	Cell fraction	Cell activation	Peptidyl-prolyl cis-trans isomerase activity		
IPI00847557	Q92835	INPP5D	Isoform 3 of phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1	1.95	3	1	1	3	6.25	976	109.2	8.68	Cytosol	Regulation of cytokine production	Inositol or phosphati dylinositol phosphatase activity	No	
IPI00871427	A8MSY9		Uncharacterized protein	2.59	5	1	1	2	6.20	926	106.8	5.38	Extracellular region		Calcium ion binding	No	
IPI00873598			Uncharacterized protein	9.23	14	1	6	35	23.45	455	49.1	4.79	Cytoskeleton	Ectoderm development	Structural molecule activity		

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00878623	B0QYF8	MB	Myoglobin	54.55	6	6	6	27	55.81	143	16.0	7.69	Stress fiber	Response to reactive oxygen species	Oxygen transporter activity	No	
IPI00878987	Q86Y46	KRT73	Isoform 2 of keratin, type II cytoskeletal 73	9.45	9	3	4	50	38.59	381	42.0	8.25	Cytoskeleton		Structural molecule activity	Yes	
IPI00879231	P08697	SERPINF2	Alpha-2-antiplasmin	23.63	5	7	7	48	66.87	491	54.5	6.29	Extracellular space	Acute inflammatory response	Protease binding	Yes	
IPI00879357	A8W476		Cadherin 13 soluble isoform 2	15.43	3	2	2	10	36.02	175	19.6	8.47	Extracellular region	Angiogenesis	Calcium ion binding	Yes	
IPI00879573	P05546	SERPIND1	Heparin cofactor 2	14.03	2	5	5	14	29.25	499	57.0	6.90	Extracellular region	Chemotaxis	Pattern binding	Yes	
IPI00879984	C9JCT1	KLKB1	cDNA FLJ51250, highly similar to plasma kallikrein	2.53	4	1	1	1	3.79	514	57.6	8.34	Extracellular region	Kinin cascade	Endopeptidase activity	No	
IPI00883722	Q6LBM9	CFHL1P	Complement factor H-related 1	17.71	6	3	4	19	20.14	271	30.8	7.81				Yes	
IPI00890724	Q6E0U4	DMKN	Isoform 7 of dermokine	4.61	8	1	1	1	4.22	369	35.3	6.43	Extracellular region			Yes	
IPI00893264			30 kDa protein	7.64	3	1	1	1	3.39	275	29.9	6.10	Integral to membrane				
IPI00893729	B1Q3B4	FTL	Ferritin (fragment)	14.85	2	1	1	2	6.63	101	11.2	8.78		Cellular iron ion homeostasis	Ferric iron binding	No	
IPI00893884			Uncharacterized protein	14.94	10	1	1	1	3.00	87	9.8	4.61		Sensory perception	Calcium ion binding		
IPI00895858	E9PE45		72 kDa type IV collagenase isoform b	3.11	2	1	1	1	3.73	610	68.8	5.34	Extracellular region	Skeletal system development	Endopeptidase activity	No	
IPI00902680			cDNA FLJ39696 fis, clone SMINT2011033, highly similar to Sorting and assembly machinery component 50 homolog	10.95	3	1	1	1	3.13	274	30.2	8.62	Protein complex assembly	Protein complex assembly			
IPI00903238	E7EU55		cDNA FLJ11717 fis, clone HEMBA1005241	14.96	2	1	1	2	3.15	127	14.5	6.54	Cytosol	Release of cytochrome c from mitochondria	Gamma-glutamylcyclotransferase activity	No	
IPI00909207	B4DF70		cDNA FLJ60461, highly similar to Peroxiredoxin-2	15.85	6	3	3	4	6.68	183	20.1	8.78	Cell fraction	MAPKKK cascade	Peroxidase activity	No	
IPI00909308	B4DTK3		cDNA FLJ57891, highly similar to Tropomyosin beta chain	8.23	16	1	1	1	3.28	158	17.8	4.81				No	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00909509	B4DNH8		cDNA FLJ59138, highly similar to Annexin A2	19.07	6	3	3	13	7.19	194	21.7	6.35			Calcium ion binding	No	
IPI00909594	Q8TCS7	C7	cDNA FLJ58413, highly similar to complement component C7	13.17	1	1	4	7	11.07	486	53.7	5.40	Extracellular region	Adaptive immune response		Yes	
IPI00910358	B4DVT0		cDNA FLJ53460, highly similar to Y + L amino acid transporter 1	6.20	2	1	1	1	3.29	484	53.3	5.30	Plasma membrane	Protein complex assembly	Amine transmembrane transporter activity	No	13
IPI00910755	E7EUG1		cDNA FLJ51707, highly similar to heat-shock protein 105 kDa	4.54	1	1	1	14	22.09	639	71.2	8.46		Response to unfolded protein	Nucleotide binding	No	
IPI00911004	E7EPA8		cDNA FLJ59939, highly similar to protein disulfide-isomerase	7.17	3	1	1	2	8.57	223	24.5	9.57	Cell fraction	Cellular amino acid derivative metabolic process	Protein disulfide isomerase activity	Yes	
IPI00915302	Q8TDA8	GSS	Glutathione synthetase	5.51	2	1	1	4	3.39	363	40.3	5.11	Cell fraction	Peptide metabolic process	Nucleotide binding	No	
IPI00916240			16 kDa protein	19.46	2	1	2	3	10.14	149	16.4	6.30	Extracellular region	Cell proliferation	Sugar binding		
IPI00922577	B7Z3P3		cDNA FLJ53768, highly similar to hepatocyte growth factor-like protein	6.10	6	1	1	1	3.25	164	17.8	9.11				Yes	
IPI00922737	B7ZAK5		ADAM DEC1 isoform 2	3.84	2	1	1	1	3.94	391	43.5	7.01	Extracellular region	Proteolysis	Endopeptidase activity	No	
IPI00923515	B9EJG1	AMY2A	Amylase, alpha 2A	4.15	3	1	1	2	3.61	265	30.3	7.05		Carbohydrate metabolic process	Catalytic activity	Yes	
IPI00924537	C9JXX4	IGFBP5	Uncharacterized protein	6.01	2	1	1	2	3.49	233	25.5	7.31	Extracellular region	Skeletal system development	Insulin-like growth factor binding	Yes	
IPI00925214	D6RJG1	CASP12	Uncharacterized protein	7.58	1	1	1	23	12.71	277	31.0	5.74	Intracellular	Apoptosis	Cysteine-type endopeptidase activity	No	
IPI00939926	Q95460	MR1	MHC class I antigen (fragment)	15.73	100	1	1	1	3.38	89	10.4	8.50					
IPI00940046	E7ERV9	ASAH1	cDNA FLJ40980 fis, clone UTERU2014464, highly similar to acid ceramidase	9.51	4	2	2	11	21.74	305	34.6	7.77		Membrane lipid metabolic process	Hydrolase activity	No	
IPI00945490	C9J8S2	RARRES2	Uncharacterized protein	17.61	2	1	1	1	3.54	159	17.8	10.21		Retinoid metabolic process		Yes	
IPI00946055	CPB1		Uncharacterized protein	22.03	6	1	1	2	3.88	59	6.6	5.22	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes	

Contd...

Supplementary Table 7: Contd...

Accession	Accession ID	Gene name	Description	Σ coverage	Σ number of proteins	Σ number of unique peptides	Σ number of peptides	Σ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal	TM
IPI00953573	C9JX84		Uncharacterized protein	15.71	5	8	8	36	47.08	885	99.2	5.80		Polysaccharide metabolic process	Enzyme inhibitor activity	No	
IPI00965297	D6RJF7	NEK11	Uncharacterized protein	11.79	6	1	1	1	3.13	212	24.2	9.22			ATP binding	No	
IPI00967340	Q6P1X2	LRBA	LRBA protein	1.83	3	1	1	1	3.35	2575	286.8	5.52			Binding	No	
IPI00967366	D6REX5	SEPP1	Uncharacterized protein	11.29	4	2	2	5	11.14	310	35.1	7.66			Selenium binding	Yes	
IPI00972938	P00740	F9	Coagulation factor IX	6.62	2	2	2	7	9.62	423	47.6	6.11	Golgi lumen				
IPI00973279	O95613	PCNT	Isoform 2 of pericentrin	1.05	2	1	1	1	3.10	3139	355.7	5.47	Cytoplasm	G2/M transition of mitotic cell cycle	Calmodulin binding	No	

MFP: Multi-functional protein, ER: Endoplasmic reticulum, GPI: Glycosylphosphatidylinositol, MW: Molecular weight, MA: Macroalbuminuria, MiA: Microalbuminuria, NA: Normoalbuminuria, PSM: Peptide spectrum match, AA: Amino acids, TM; Transmembrane domain