Table S1 Identified proteins by MS analysis for 110kDa area

ProtScore	% Cov	% Cov (50)	% Cov (95)	Name	Gene name	Accession #
2.03	44.5	2	2	Leukosialin	*SPN*	P16150
1.51	21.3	8.1	4.5	Glutathione hydrolase 6	*GGT6*	Q6P531
1.5	68.2	3.5	3.5	Desert hedgehog protein	*DHH*	O43323
1.48	39.1	6.2	6.2	Kallikrein-10	*KLK10*	O43240
1.35	52.4	10.7	10.7	Small integral membrane protein 32	*SMIM32*	A0A1B0
1.3	34.2	6.3	6.3	DCN1-like protein 5	*DCUN1D5*	Q9BTE7
1.25	60	2.2	0	Heterogeneous nuclear ribonucleoprotein U	*HNRNPU*	Q00839
1.23	69.5	4.1	4.1	Ankyrin repeat domain-containing protein SOWAHD	*SOWAHD*	A6NJG2
1.19	48.9	2.1	0	AT-rich interactive domain-containing protein 4A	*ARID4A*	P29374
1.13	61.7	5.8	0	ZW10 interactor	*ZWINT*	O95229
1.12	41	2.2	0	Inactive phospholipase D5	*PLD5*	Q8N7P1
1.12	38.2	1	0	Serine/threonine-protein kinase LMTK3	*LMTK3*	Q96Q04
1.11	40.9	4.4	0	Squalene monooxygenase	*SQLE*	Q14534
1.07	28	2.4	0	Urocanate hydratase	*UROC1*	Q96N76
1.05	55.1	0.8	0	PHD and RING finger domain-containing protein 1	*PHRF1*	Q9P1Y6
0.99	48.5	2.4	0	WSC domain-containing protein 1	*WSCD1*	Q658N2
0.98	37.3	1.8	0	Phosphoinositide 3-kinase regulatory subunit 5	*PIK3R5*	Q8WYR1
0.97	51.5	1.5	0	OTU domain-containing protein 7A	*OTUD7A*	Q8TE49
0.96	25.8	4.2	0	Transmembrane protease serine 3	*TMPRSS3*	P57727
0.95	20.3	6	6	Tumor necrosis factor ligand superfamily member 15	*TNFSF15*	O95150
0.92	38.5	1.7	0	Otoferlin	*OTOF*	Q9HC10
0.91	26.9	3	0	Matrix metalloproteinase-15	*MMP15*	P51511
0.9	55.2	7.1	0	Ras-related protein Rab-40C	*RAB40C*	Q96S21
0.88	41.3	1.2	0	Oligophrenin-1	*OPHN1*	O60890
0.87	36.8	4.8	0	Ectonucleotide pyrophosphatase/phosphodiesterase family member 6	*ENPP6*	Q6UWR7
0.85	35.6	0.3	0	E3 ubiquitin-protein ligase MYCBP2	*MYCBP2*	O75592
0.85	30.5	6.6	0	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	*DHDH*	Q9UQ10
0.84	43.1	6.4	6.4	Microtubule-associated protein RP/EB family member 3	*MAPRE3*	Q9UPY8
0.83	26.7	2.9	0	Guanylate cyclase soluble subunit beta-1	*GUCY1B1*	Q02153
0.82	51.2	2.3	0	Putative ciliary rootlet coiled-coil protein 2	*CROCC2*	H7BZ55
0.81	43	0.9	0	TBC1 domain family member 9	*TBC1D9*	Q6ZT07
0.79	29	0.7	0	Zinc finger ZZ-type and EF-hand domain-containing protein 1	*ZZEF1*	O43149
0.79	57.6	3	0	Calcium-binding protein 1	*CABP1*	Q9NZU7
0.78	47.7	1.9	0	Heat shock protein 105 kDa	*HSPH1*	Q92598
0.78	27.1	2.3	0	Sodium/hydrogen exchanger 4	*SLC9A4*	Q6AI14
0.78	63.2	7.2	0	Uncharacterized protein C8orf86	*C8orf86*	Q6ZUL3
0.78	41.2	5.1	0	Collectin-10	*COLEC10*	Q9Y6Z7
0.76	40	1.6	0	SLIT-ROBO Rho GTPase-activating protein 2	*SRGAP2*	O75044
0.76	39.4	2.9	0	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	*MGAT4B*	Q9UQ53
0.74	32.2	0.2	0	Transmembrane protein KIAA1109	*KIAA1109*	Q2LD37
0.74	36.8	0.5	0	Pre-mRNA-processing-splicing factor 8	*PRPF8*	Q6P2Q9
0.74	50.2	0.9	0	Partitioning defective 3 homolog B	*PARD3B*	Q8TEW8
0.74	79.6	11.1	0	28 kDa heat- and acid-stable phosphoprotein	*PDAP1*	Q13442
0.72	42.7	0.6	0	Nck-associated protein 5	*NCKAP5*	O14513
0.69	16	1.9	0	Pantetheinase	*VNN1*	O95497
0.68	44.1	0.3	0	A-kinase anchor protein 9	*AKAP9*	Q99996
0.68	37.3	0.8	0	Paternally-expressed gene 3 protein	*PEG*	Q9GZU2
0.67	35.6	1.7	0	Ral guanine nucleotide dissociation stimulator-like 1	*RGL1*	Q9NZL6
0.67	41.8	2.8	0	Myotilin	*MYOT*	Q9UBF9
0.67	43.4	3.8	0	Putative FERM domain-containing protein FRMD8P1	*FRMD8P1*	Q9BZ68
0.67	37.4	5.2	0	Homeobox protein Hox-A5	*HOXA5*	P20719
0.66	51.6	1.8	0	GAS2-like protein 2	*GAS2L2*	Q8NHY3
0.66	23.5	1.9	0	Klotho	*KL*	Q9UEF7
0.65	48.6	1.2	0	Tyrosine-protein kinase BAZ1B	*BAZ1B*	Q9UIG0
0.65	49.5	3.3	0	Coiled-coil domain-containing protein 181	*CCDC181*	Q5TID7
0.65	26.7	1	0	Alpha-2-macroglobulin	*A2M*	P01023
0.65	42	3.2	0	Palmitoyltransferase ZDHHC5	*ZDHHC5*	Q9C0B5
0.65	42.2	2.3	0	Ribosomal protein S6 kinase alpha-1	*RPS6KA1*	Q15418
0.65	36.4	1.9	0	Exocyst complex component 6B	*EXOC6B*	Q9Y2D4
0.61	42.6	1.3	0	Unconventional myosin-If	*MYO1F*	O00160
0.61	36.4	3.2	0	Sorting nexin-20	*SNX20*	Q7Z614
0.6	36.3	1.3	0	PR domain zinc finger protein 2	*PRDM2*	Q13029
0.6	45.6	0.6	0	Chromodomain-helicase-DNA-binding protein 4	*CHD4*	Q14839
0.59	37.2	1.1	0	Putative ATP-dependent RNA helicase DHX57	*DHX57*	Q6P158
0.59	64.3	2	0	Protein FAM47B	*FAM47B*	Q8NA70
0.58	28.8	0.6	0	HEAT repeat-containing protein 5A	*HEATR5A*	Q86XA9
0.56	29.7	4	0	Butyrophilin-like protein 2	*BTNL2*	Q9UIR0
0.55	33.4	1.5	0	Zinc finger protein 40	*HIVEP1*	P15822
0.55	40.5	0.7	0	Ankyrin-2	*ANK2*	Q01484
0.54	45.3	1.7	0	Ubiquitin carboxyl-terminal hydrolase 36	*USP36*	Q9P275
0.54	43.2	1.9	0	Collagen alpha-3(V) chain	*COL5A3*	P25940
0.54	50.5	2.6	0	Spermatogenesis-associated serine-rich protein 2	*SPATS2*	Q86XZ4
0.54	30.9	1.7	0	Oxysterol-binding protein 2	*OSBP2*	Q969R2
0.54	41.3	2.6	0	Serine/threonine-protein kinase PINK1, mitochondrial	*PINK1*	Q9BXM7
0.54	36.1	2	0	Pantothenate kinase 1	*PANK1*	Q8TE04
0.53	40.9	0.9	0	Microtubule-associated protein 2	*MAP2*	P11137
0.53	67.4	3.4	0	IQ domain-containing protein C	*IQCC*	Q4KMZ1
0.53	25.1	0.9	0	Condensin-2 complex subunit G2	*NCAPG2*	Q86XI2
0.53	37.4	1.5	0	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	*PLOD1*	Q02809
0.53	58.3	5.3	0	Dickkopf-related protein 1	*DKK1*	O94907
0.53	44.3	2.5	0	Collagen and calcium-binding EGF domain-containing protein 1	*CCBE1*	Q6UXH8
0.52	50.7	2.3	0	Junctophilin-1	*JPH1*	Q9HDC5
0.52	16	1.6	0	Lipoma-preferred partner	*LPP*	Q93052
0.51	32.5	0.5	0	Zinc finger protein 469	*ZNF469*	Q96JG9
0.51	37	2.1	0	Transmembrane protease serine 11F	*TMPRSS11F*	Q6ZWK6
0.51	43	3.8	0	GH3 domain-containing protein	*GHDC*	Q8N2G8
0.51	33.6	17.8	0	Ninjurin-1	*NINJ1*	Q92982
0.5	43.4	1.6	0	UV radiation resistance-associated gene protein	*UVRAG*	Q9P2Y5
0.5	38.5	4.5	0	Ribonuclease H1	*RNASEH1*	O60930
0.49	37.6	1.1	0	FERM and PDZ domain-containing protein 4	*FRMPD4*	Q14CM0
0.49	23.1	1.2	0	Solute carrier family 12 member 1	*SLC12A1*	Q13621
0.48	45.5	0	0	Histone-lysine N-methyltransferase ASH1L	*ASH1L*	Q9NR48
0.47	94.8	9.4	0	Histone H1.2	*HIST1H1C*	P16403
0.47	33.8	1.1	0	Phosphatidylinositide phosphatase SAC2	*INPP5F*	Q9Y2H2
0.47	28.6	2.6	0	Protein FAM69C	*FAM69C*	Q0P6D2
0.47	23.8	1	0	Neogenin	*NEO1*	Q92859

A representative of the MS results for 110kDa-gp. The ProtScore indicates the reliability of the results, and the higher score is better. % Cov is the coverage of the identified peptide fragment in the amino acid sequence. % Cov (50) and % Cov (90) are the coverages of peptide fragments with a reliability of more than 50% and 90%, respectively. The list includes the proteins ranked at higher than 0.47 of the ProtScore (reliability 66%). Accession # is from the Swiss-Prot database.