Supplementary Table 2: The peptide sequences identified in tandem mass spectrometry (MS/MS) analysis for the differentially expressed proteins

Spot ID[a]	Gene name	Identity /Accession No.[b]	Peptide sequences[c]
272	KRT10	Keratin, type I cytoskeletal 10/ P13645	K.HGNSHQGEPR.D R.LENEIQTYR.S R.SQYEQLAEQNR.K
400	KRT19	Keratin, type I cytoskeletal 19/ P08727	R.QNQEYQR.L K.FETEQALR.M R.APSIHGGSGGR.G R.VLDELTLAR.T R.IVLQIDNAR.L K.DAEAWFTSR.T R.LEQEIATYR.S K.NHEEEISTLR.G K.AALEDTLAETEAR.F R.DYSHYYTTIQDLR.D
84	KRT1	Keratin, type II cytoskeletal 1/ P04264	K.YEDEINKR.T K.YEELQITAGR.H K.LALDLEIATYR.T K.WELLQQVDTSTR.T K.QISNLQQSISDAEQR.G R.THNLEPYFESFINNLR.R R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G
420	KRT8	Keratin, type II cytoskeletal 8/ P05787	K.LLEGEESR.L R.QLYEEEIR.E K.LSELEAALQR.A K.YEELQSLAGK.H K.LALDIEIATYR.K R.ASLEAAIADAEQR.G R.TEMENEFVLIK.K R.LEGLTDEINFLR.Q R.SNMDNMFESYINNLR.R
446	KRT8	Keratin, type II cytoskeletal 8/ P05787	K.LLEGEESR.L R.QLYEEEIR.E K.LSELEAALQR.A K.LALDIEIATYR.K R.TEMENEFVLIK.K R.LEGLTDEINFLR.Q R.SNMDNMFESYINNLR.R R.SNMDNMFESYINNLR.R + Oxidation (M) R.ELQSQISDTSVVLSMDNSR.S
492	CAPZA2	F-actin-capping protein subunit alpha-2/ P47755	R.TSVETALR.A R.LLLNNDNLLR.E K.FIIHAPPGEFNEVFNDVR.L K.IEGYEDQVLITEHGDLGNGK.F
78	MYL6	Myosin light polypeptide 6/ P60660	K.ILYSQCGDVMR.A K.DQGTYEDYVEGLR.V
95	TPM1	Tropomyosin alpha-1 chain/ P09493	R.KYEEVAR.K K.HIAEDADR.K K.LVIIESDLER.A R.IQLVEEELDR.A K.ATDAEADVASLNR.R
219	TPM1	Tropomyosin alpha-1 chain/ P09493	R.QLEEQLR.I K.HIAEDADR.K R.AELSEGQVR.Q K.LVIIESDLER.A R.IQLVEEELDR.A R.KLVIIESDLER.A K.ATDAEADVASLNR.R
319	TPM1	Tropomyosin alpha-1 chain/ P09493	R.KYEEVAR.K R.QLEEQLR.I K.HIAEDADR.K R.AELSEGQVR.Q

			K.LVIIESDLER.A R.IQLVEEELDR.A
769	TPM4	Tropomyosin alpha-4 chain/ P67936	K.HIAEEADR.K K.LVILEGELER.A R.IQLVEEELDR.A K.IQALQQQADEAEDR.A
770	TPM4	Tropomyosin alpha-4 chain/ P67936	K.HIAEEADR.K K.AEGDVAALNR.R K.LVILEGELER.A K.AEGDVAALNRR.I R.IQLVEEELDR.A K.IQALQQQADEAEDR.A
291	TBCB	Tubulin-folding cofactor B/ Q99426	R.LGEYEDVSR.V R.IHVIDHSGAR.L K.YTISQEAYDQR.Q
826	LDHB	Lactate dehydrogenase B/ P07195	K.IVVVTAGVR.Q K.FIIPQIVK.Y R.IHPVSTMVK.G K.LKDDEVAQLK.K K.SADTLWDIQK.D R.VIGSGCNLDSAR.F K.SLADELALVDVLEDK.L K.LIAPVAEEEATVPNNK.I K.GEMMDLQHGSLFLQTPK.I + Oxidation (M)
532	GLRX3	Glutaredoxin-3/ O76003	ELPQVSFVK ENGELLPILR ELKENGELLPILR ELKENGELLPILR IDRLDGAHAPELTK YEISSVPTFLFFK AYSNWPTYPQLYVK AYSNWPTYPQLYVK HNIQFSSFDIFSDEEVR HNIQFSSFDIFSDEEVR HASSGSFLPSANEHLKEDLNLR HASSGSFLPSANEHLKEDLNLR HNIQFSSFDIFSDEEVRQGLK AKSLLVVHFWAPWAPQCAQMNEVMAELAK
236	CYB5A	Cytochrome b5/ P00167	K.FLEEHPGGEEVLR.E K.TFIIGELHPDDRPK.L R.EQAGGDATENFEDVGHSTDAR.E
470	GSTP1	Glutathione S-transferase P/ P09211	M.PPYTVVYFPVR.G K.YISLIYTNYEAGK.D K.EEVVTVETWQEGSLK.A K.FQDGDLTLYQSNTILR.H K.DQQEAALVDMVNDGVEDLR.C K.ALPGQLKPFETLLSQNQGGK.T K.DQQEAALVDMVNDGVEDLR.C + Oxidation (M)
466	APOA1	Apolipoprotein A-I/ P02647[§]	K.VAPLGEEFR.E K.AKPVLEDLR.Q K.WHEEVEIYR.Q R.QQLAPYSDDLR.Q
489	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1/ O94760[§]	K.GHVLLHR.T K.DENATLDGGDVLFTGR.E
170	NAA10	N-alpha-acetyltransferase 10, NatA catalytic subunit / P41227	K.GNSPPSSGEACR.E
508	SMS	Spermine synthase/ P52788	K.RLPPIVR.G K.NGSFANLR.I R.YWPTADGR.L R.HSTLDFMLGAKADGETILK.G + Oxidation (M)
436	TPI1	Triosephosphate isomerase/ P60174[§]	FFVGGNWK HVFGESDELIGQK DCGATWVVLGHSER VVLAYEPVWAIGTGK VVLAYEPVWAIGTGK RHVFGESDELIGQK

			VTNGAFTGEISPGMIK Oxidation (M) VAHALAEGLGVIACIGEK VPADTEVVCAPPTAYIDFAR VPADTEVVCAPPTAYIDFAR VPADTEVVCAPPTAYIDFARQK ELASQPDVDGFLVGGASLKPEFVDIINAK ELASQPDVDGFLVGGASLKPEFVDIINAK
215	EIF4E	Eukaryotic translation initiation factor 4E/ Q32Q75	K.IAIWTTECENR.E K.TESNQEVANPEHYIK.H
35	EIF6	Eukaryotic translation initiation factor 6/ P56537	NSLPDTVQIR NSLPDTVQIR ETEEILADVLK LNEAQPSTIATSMR LNEAQPSTIATSMR Oxidation (M) LNEAQPSTIATSMR Oxidation (M) ASFENNCEIGCFAK ASFENNCEIGCFAK HGLLVPNNTTDQELQHIR HGLLVPNNTTDQELQHIR Oxidation (M) LSALGNVTTCNDYVALVHPDLDR LSALGNVTTCNDYVALVHPDLDR TSIEDQDELSSLLQVPLVAGTVNR TSIEDQDELSSLLQVPLVAGTVNR Oxidation (M) QTVADQVLVGSYCVFSNQGGLVHPK QTVADQVLVGSYCVFSNQGGLVHPK
375	RPSA	40S ribosomal protein SA/ P08865	R.LLVVTDPR.A K.FAAATGATPIAGR.F R.YVDIAIPCNNK.G R.FTPGTFTNQIQAAFR.E R.AIVAIENPADVSVISSR.N R.EHPWEVMPDLYFYR.D R.EHPWEVMPDLYFYR.D + Oxidation (M) R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y
605	RPSA	40S ribosomal protein SA/ P08865	R.LLVVTDPR.A K.FAAATGATPIAGR.F R.YVDIAIPCNNK.G R.FTPGTFTNQIQAAFR.E R.AIVAIENPADVSVISSR.N R.EHPWEVMPDLYFYR.D R.EHPWEVMPDLYFYR.D + Oxidation (M)
383	CCT2	T-complex protein 1 subunit beta/ P78371	K.RVPDHHPC.- K.HGINCFINR.Q K.IHPQTIIAGWR.E R.GATQQILDEAER.S R.AAHSEGNTTAGLDMR.E R.QVLLSAAEAAEVILR.V K.LIHFSGVALGEACTIVLR.G R.VQDDEVGDGTTSVTVLAAELLR.E
473	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1/ P09936	K.LGFEDGSVLK.Q K.NEAIQAAHDAVAQEGQCR.V
849	UBE2A	Ubiquitin-conjugating enzyme E2 A/ P49459	VSAIVEQSWR VSAIVEQSWR RVSAIVEQSWR LTIEFTEEYPNKPPTVR LTIEFTEEYPNKPPTVR MFHPNVYADGSICLDILQNR MFHPNVYADGSICLDILQNR Oxidation (M) MFHPNVYADGSICLDILQNR 2 Oxidation (M)
110	YWHAB	14-3-3 protein beta/alpha/ P31946	K.EMQPTHPIR.L K.EMQPTHPIR.L + Oxidation (M) K.DSTLIMQLLR.D K.DSTLIMQLLR.D + Oxidation (M) K.KEMQPTHPIR.L + Oxidation (M) K.AVTEQGHELSNEER.N K.TAFDEAIAELDTLNEESYK.D
771	YWHAE	14-3-3 protein epsilon/ P62258	K.DSTLIMQLLR.D

			R.YLAEFATGNDR.K K.VAGMDVELTVEER.N K.AASDIAMTELPPTHPIR.L K.AASDIAMTELPPTHPIR.L + Oxidation (M)
38	YWHAG	14-3-3 protein gamma / P61981	K.DSTLIMQLLR.D K.DSTLIMQLLR.D + Oxidation (M) K.EHMQPTHPIR.L K.EHMQPTHPIR.L + Oxidation (M) K.NVTELNEPLSNEER.N
205	YWHAQ	14-3-3 protein theta/ P27348	K.EMQPTHPIR.L K.EMQPTHPIR.L + Oxidation (M) K.DSTLIMQLLR.D K.DSTLIMQLLR.D + Oxidation (M) K.KEMQPTHPIR.L + Oxidation (M) R.YLAEVACGDDR.K K.AVTEQGAELSNEER.N
165	YWHAZ	14-3-3 protein zeta/delta/ P63104	K.EMQPTHPIR.L K.EMQPTHPIR.L + Oxidation (M) R.YLAEVAAGDDK.K K.DSTLIMQLLR.D K.DSTLIMQLLR.D + Oxidation (M) K.KEMQPTHPIR.L + Oxidation (M) R.DICNDVLSLLEK.F K.SVTEQGAELSNEER.N K.GIVDQSQQAYQEAFEISK.K
764	YWHAZ	14-3-3 protein zeta/delta/ P63104	K.EMQPTHPIR.L K.EMQPTHPIR.L + Oxidation (M) K.DSTLIMQLLR.D K.DSTLIMQLLR.D + Oxidation (M) K.KEMQPTHPIR.L K.KEMQPTHPIR.L + Oxidation (M) K.FLIPNASQAESK.V K.SVTEQGAELSNEER.N
257	FTH1	Ferritin heavy chain/ P02794	K.ELGDHVTNLR.K K.YFLHQSHEER.E R.QNYHQDSEAAINR.Q
748	SLC9A3R1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1/ O14745§	R.AQEAPGQAEPPAAAEVQGAGNENEPR.E
583	SERPINB2	Plasminogen activator inhibitor 2/ P05120	K.LNGLYPFR.V R.ANFSGMSER.N K.MAEDEVEVYIPQFK.L
243	PHB	Prohibitin / P35232	K.QVAQQEAER.A R.FDAGELITQR.E K.DLQNVNITLR.I R.IFTSIGEDYDER.V K.LEAAEDIAYQLSR.S K.FGLALAVAGGVVNSALYNVDAGHR.A
536	POLR1C	DNA-directed RNA polymerases I and III subunit RPAC1/ O15160	R.VVLGEFGVR.N K.FSPVATASYR.L R.LGLIPIHADPR.L R.NQGDEEGTEIDTLQFR.L
857	SRSF1	Serine/arginine-rich splicing factor 1/ Q07955	R.DAEDAVYGR.D R.DGTGVVEFVR.K R.DGYDYDGYR.L R.SHEGETAYIR.V R.IYVGNLPPDIR.T R.EAGDVCYADVYR.D R.GGPPFAFVEFEDPR.D
264	LSM3	U6 snRNA-associated Sm-like protein LSm3/ P62310	R.GDGVVLVAPPLR.V
302	CHMP4B	Charged multivesicular body protein 4b/ Q9H444	K.RAALQALK.R K.GGPTPQEAIQR.L K.QLAQIDGTLSTIEFQR.E
44	COPE	Coatomer subunit epsilon/ O14579	K.FGVVLDEIKPSSAPELQAVR.M
92	TTR	Transthyretin/ P02766§	K.SLGISPFHEFAEVVFTANDSGPR.H
761	ANXA5	Annexin A5/ P08758	K.FITIFGTR.S

			R.SEIDLFNIR.K K.GAGTDDHTLIR.V R.GTVTDFPGFDER.A K.GLGTDEESILTLLTSR.S K.QVYEEEYGSSLEDDVVGDTSGYYQR.M
296	CAPNS1	Calpain small subunit 1/ P04632	R.THYSNIEANESEEVR.Q R.ILGGVISAISEAAAQYNPEPPPPR.T
852	C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial / Q07021	K.AFVDFLSDEIK.E R.EVSFQSTGESEWK.D K.ALVLDCHYPEDEVGQEDEAESDIFSIR.E

a. Numbering correspond to the match IDs in 2D gels
b. Protein name and accession number in Uni-Prot
c. Peptide sequences identified using MS/MS analysis