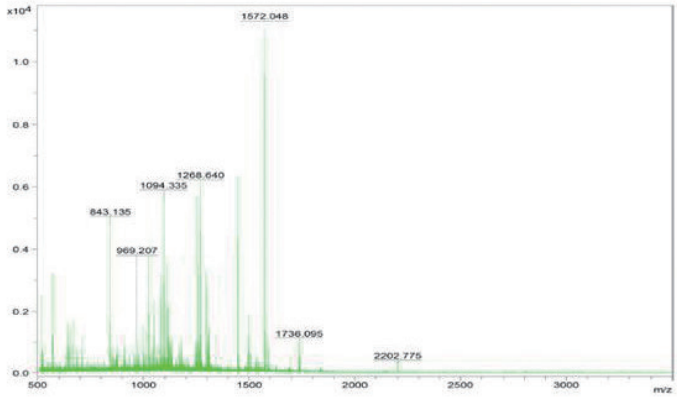

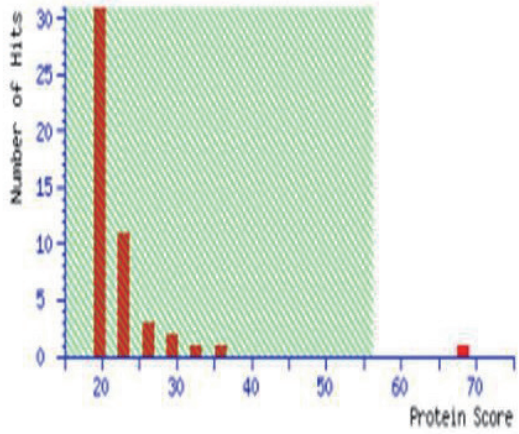

Protein sequence coverage: 44%

Matched peptides shown in ***bold red***.

1 MSTR**SVSSSS YR**RMFGGPGT ASRPSSSRSY VTTSTRTYSL GSALRPSTSR
51 SLYASSPGGV YATRSSAVR**L RSSVPGVR**LL QDSVDFSLAD AINTEFKNTR
101 TNEK**VELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLK**G QGK**SRLGDLY**
151 **EEEMR**ELRRQ VDQLTNDKAR VEVER**DNLAE DIMR**LR**EKLQ EEMLQR**EEAE
201 NTLQSFRQDV DNASLARLDL ERK**VESLQEE IAFLKK**LHEE EIQELQAQIQ
251 EQHVQIDVDV SKPDLTAALR DVR**QQYESVA AKNLQEAEEW YK**SK**FADLSE**
301 **AANRNNDALR QAK**QESTEYR RQVQSLTCEV DALKGTNESL ERQMR**EMEEN**
351 **FAVEAANYQD TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY**
401 **RKLLEGEESR** ISLPLPNFSS LNLRETNLDS LPLVDTHSKR **TLLIKTVETR**
451 DGQVINETSQ HHDDLE

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	M	Peptide
5	-	12	871.6740	870.6667	871.4035	0.7368	0	R.SVSSSSYR.R
5	-	12	873.0610	872.0537	871.4035	0.6502	0	R.SVSSSSYR.R
70	-	78	969.2070	968.1997	969.5720	1.3722	1	R.LRSSVPGVR.L
105	-	113	1116.3970	1115.3897	1114.5618	0.8279	0	K.VELQELNDR.F
114	-	122	1126.4330	1125.4257	1124.5978	0.8279	1	R.FANYIDKVR.F
123	-	129	906.1020	905.0947	905.4607	0.3659	0	R.FLEQQNK.I
123	-	129	907.1370	906.1297	905.4607	0.6691	0	R.FLEQQNK.I
130	-	139	1170.4120	1169.4047	1168.7067	0.6980	0	K.ILLAELEQLK.G
130	-	139	1170.5790	1169.5717	1168.7067	0.8650	0	K.ILLAELEQLK.G
144	-	155	1496.8910	1495.8837	1496.6929	0.8092	1	K.SRLGDLYEEEMR.E
146	-	155	1253.5110	1252.5037	1253.5598	1.0560	0	R.LGDLYEEEMR.E
146	-	155	1255.4950	1254.4877	1253.5598	0.9280	0	R.LGDLYEEEMR.E
176	-	184	1077.3000	1076.2927	1075.4968	0.7959	0	R.DNLAEDIMR.L
187	-	196	1304.6300	1303.6227	1302.6601	0.9626	1	R.EKLQEEMLQR.E
189	-	196	1046.3340	1045.3267	1045.5226	0.1959	0	K.LQEEMLQR.E
189	-	196	1047.3070	1046.2997	1045.5226	0.7771	0	K.LQEEMLQR.E
224	-	236	1534.9810	1533.9737	1532.8450	1.1288	1	K.VEELQEEIAFLKK.L
274	-	282	1024.2240	1023.2167	1022.5032	0.7135	0	R.QQYESVAAK.N
283	-	292	1310.5750	1309.5677	1308.5986	0.9691	0	K.NLQEAEEWYK.S
295	-	304	1094.3350	1093.3277	1092.5200	0.8078	0	K.FADLSEAANR.N
305	-	313	1029.2540	1028.2467	1028.5363	0.2895	1	R.NNDALRQAK.Q
346 - 364			2202.5870	2201.5797	2201.8535	0.3738	0	R.EMEENFAVEAANYQDTIGR.L + Oxidation (M)
346 - 364			2202.7750	2201.7677	2201.8535	0.1858	0	R.EMEENFAVEAANYQDTIGR.L + Oxidation (M)
365	-	378	1736.0950	1735.0877	1733.8076	1.2801	1	R.LQDEIQNMKEEMAR.H
365	-	378	1736.2310	1735.2237	1733.8076	1.4161	1	R.LQDEIQNMKEEMAR.H
374	-	381	1040.2270	1039.2197	1040.5185	1.2988	1	K.EEMARHLR.E
379 - 390			1527.7340	1526.7267	1526.8205	0.0938	1	R.HLREYQDLLNVK.M

Supplementary Figure 1. Peptide mass fingerprinting (PMF) analysis of differentially expressed proteins and vimentin MS-MS analysis.