

# Supplemental Table S6

Gene	Peptide sequence	m/z	charge state	retention time
Aldh2	GYFIQPTVFGDVK	735,88	2+	8464,1
Aldh2	YGLAAAVFTK	520,79	2+	6045,2
Apoa1	VAPLGAEQLQESAR	670,86	2+	4884,8
Apoa1	SNPTLNEYHTR	444,55	3+	1328,1
Apoe	LGPLVEQGR	485,27	2+	2303,2
Apoe	TANLGAGAAQPLRDR	504,27	3+	3095,3
App	THTHIVIPYR	412,90	3+	2845,6
App	VESLEQEAANER	687,83	2+	3678,6
Atp2b2	GIIDSTHTEQR	419,55	3+	2145,4
Atp2b2	NVFDGIFR	484,25	2+	7882,2
Atp5b	IGLFGGAGVGK	488,29	2+	6290,2
Atp5b	VVDLLAPYAK	544,82	2+	7307,6
Atp5o	LGNTQGISAFSTIMSVHR	683,36	3+	8294,1
Atp5o	LVRPPVQVYGIEGR	528,31	3+	5435,7
Cadm2	DGAELPDPDR	542,75	2+	3507,4
Cadm2	GKPLPEPVLWTK	455,60	3+	5175,3
Cap2	SALFAQLNQGEAITK	795,93	2+	6710,7
Cap2	VEYQEDRNDLVISETLK	727,36	3+	5763,9
Cntn1	DGEYVVEVR	533,27	2+	3556,5
Cntn1	GPPGPPGGLR	452,75	2+	2980,0
Glul	ATSASSHLNK	529,27	2+	1830,1
Glul	LTGFHETSINIDFSAGVANR	717,35	3+	5769,9
Got2	ASAELALGENNEVLK	779,41	2+	5847,2
Got2	VGASFLQR	439,25	2+	4295,1
Ndufb10	PDSWDKDVYPEPPSR	596,61	3+	3499,7
Ndufb10	TPAPSPQTSLPNPITYLTK	1013,55	2+	9237,9
Ndufs2	AVTNMTLNFGPQHAAHGVLR	562,54	4+	4192,5
Ndufs2	LLNIQPPPR	524,32	2+	5219,7
phtf2	QVLVTVMK	459,28	2+	5875,9
Prkcb	IYIQAHIDR	376,88	3+	2989,5
Prkcb	LTDFNFLMVLGK	699,38	2+	11666,8
Prrt2	NSLQQGDVDGAQR	694,33	2+	1519,3
Prrt2	QEPASKPDVNR	612,30	2+	1324,4
Psm11	TGQAAELGGLLK	579,33	2+	5633,3
Psm11	YVRPFLNSISK	441,92	3+	4118,2
Rap1gds1	DLASAQLVQILHR	488,62	3+	6796,0
Rap1gds1	DQEVLLQTGR	579,81	2+	3447,4
Scai	HILELASILDVR	460,27	3+	8878,7
Tomm70a	AAAFEQLQK	503,27	2+	3516,8
Tomm70a	FALAAQAK	438,75	2+	1955,3
Vim	KVESLQEEIAFLK	511,96	3+	6998,8
Vim	QDVNDASLAR	536,26	2+	4081,6