

## Appendix A DEPs in M group compared with S+M group

Nu m	Accession	GN	Full Name	Scor e	% Cov	Fold Change
1	tr W5P8W6 W5P8W6_S HEEP	COL12A1	collagen type XII alpha 1 chain	152. 2	50.3	3.538
2	tr W5QCP9 W5QCP9_S HEEP	COL6A3	collagen type VI alpha 3 chain	134. 58	48.5	2.014444 444
3	tr W5QDG8 W5QDG8_S HEEP	FN1	fibronectin 1	76.7 1	32.9	1.694711 111
4	tr W5P7G4 W5P7G4_SH EEP	TNC	tenascin C	60.7 2	32.4	2.148388 889
5	tr W5QIN8 W5QIN8_SH EEP	FBN1	fibrillin 1	50.3 6	24.1	1.831877 778
6	tr W5PK03 W5PK03_SH EEP	POSTN	periostin	41.9	51	2.5662
7	tr W5NTT7 W5NTT7_S HEEP	LOC443512	collagen type I alpha 2 chain	36.2 5	33.3	2.984011 111
8	tr W5PGT5 W5PGT5_SH EEP	MYH11	myosin heavy chain 11	32.3 3	33.4	1.524911 111
9	tr W5PTE9 W5PTE9_SH EEP	COL6A1	collagen type VI alpha 1 chain	30.4 7	46.3	2.106266 667
10	tr W5PWT4 W5PWT4_S HEEP	TNN	tenascin N	30.1 5	35.9	1.6309
11	tr W5PZM9 W5PZM9_S HEEP	ANXA5	annexin A5	25.5	59	1.5739
12	tr W5QCY8 W5QCY8_S HEEP	LOC101106 199	hemoglobin fetal subunit beta	25.2 8	95.2	0.473755 556
13	tr W5PCP8 W5PCP8_SH EEP	BGN	biglycan	24.7 1	62.9	2.863077 778
14	tr W5PNK3 W5PNK3_S HEEP	ACAN	aggrecan	23.4 8	17	2.130333 333
15	tr W5PQA8 W5PQA8_S HEEP	PRDX6	peroxiredoxin 6	22.5 3	70	0.648544 444
16	tr W5QFP0 W5QFP0_SH EEP	THBS1	thrombospondin 1	20.3 9	24.3	1.771111 111
17	tr W5PTN6 W5PTN6_SH EEP	COL6A2	collagen type VI alpha 2 chain	18.6 9	34.5	2.363044 444
18	tr W5NTW3 W5NTW3_S HEEP	ITIH1	inter-alpha-trypsin inhibitor heavy chain 1	16.1 6	25.9	1.546111 111
19	tr W5Q0F3 W5Q0F3_SH EEP	TGFBI	transforming growth factor beta induced	15.9	43.6	1.715688 889
20	tr W5NU63 W5NU63_S HEEP	MYH10	myosin heavy chain 10	15.5 7	36.8	1.720022 222

21	tr W5PTU7 W5PTU7_SH_EEP	CA2	carbonic anhydrase 2	15.28	57.4	0.656222222
22	tr W5QI03 W5QI03_SHEEP	TPM1	tropomyosin 1	14.09	56.8	1.749766667
23	tr W5Q8B4 W5Q8B4_SH_EEP	FKBP10	FK506 binding protein 10	11.25	25.8	1.7217
24	tr W5PWZ2 W5PWZ2_SHHEEP	GAL-1	galectin 1	10.41	93.5	2.075466667
25	tr W5PZK7 W5PZK7_SH_EEP	ACTA2	actin, alpha 2, smooth muscle, aorta	10.36	59.2	1.790177778
26	tr W5Q3W1 W5Q3W1_SHHEEP	AEBP1	AE binding protein 1	9.72	19.3	1.613377778
27	tr W5NRA2 W5NRA2_SHHEEP	S100A2	S100 calcium binding protein A2	9.03	32.7	0.613744444
28	tr W5PD82 W5PD82_SH_EEP	CALD1	caldesmon 1	8.44	43.2	1.734288889
29	tr W5NU76 W5NU76_SHHEEP	FMOD	fibromodulin	7.88	27.5	2.658611111
30	tr C5IWT0 C5IWT0_SH_EEP	ARF4	ADP ribosylation factor 4	7.79	62.2	1.542144444
31	tr W5NQH6 W5NQH6_SHHEEP	S100A9	S100 calcium binding protein A9	7.59	59.4	0.537177778
32	tr W5Q0R4 W5Q0R4_SH_EEP	CRYAB	crystallin alpha B	6.94	54.9	0.588655556
33	tr W5Q233 W5Q233_SH_EEP	VCAN	versican	6.21	11.6	1.654466667
34	tr W5Q5Z3 W5Q5Z3_SH_EEP	KRT77	keratin 77	6.04	28.5	0.630633333
35	tr W5NQK9 W5NQK9_SHHEEP	S100A8	S100 calcium binding protein A8	5.53	37.1	0.531144444
36	tr W5P6X4 W5P6X4_SH_EEP	EIF3K	eukaryotic translation initiation factor 3 subunit K	5.22	28.4	0.658333333
37	tr W5NRH4 W5NRH4_SHHEEP	LOC101113302	family with sequence similarity 25 member A	5	69.5	0.5088
38	tr W5P5Q2 W5P5Q2_SH_EEP	MVP	major vault protein	4.76	20.6	1.664911111
39	tr W5PF11 W5PF11_SH_EEP	SEC23A	Sec23 homolog A, coat complex II component	4.66	15.4	2.144877778
40	tr W5PHI8 W5PHI8_SH_EEP	DPT	dermatopontin	4.49	33.8	1.836255556

41	tr W5NUU3 W5NUU3_S HEEP	TPM3	tropomyosin 3	4.34	46	1.528044 444
42	tr W5P9G2 W5P9G2_SH EEP	FKBP9	FK506 binding protein 9	4.29	19.1	1.673833 333
43	tr W5NPI9 W5NPI9_SHE EP	LOC101112 657	keratin, high-sulfur matrix protein, IIIA3	4.28	47	0.617488 889
44	tr W5Q4M3 W5Q4M3_S HEEP	COL5A2	collagen type V alpha 2 chain	4.2	18.2	2.088311 111
45	tr W5PLB7 W5PLB7_SH EEP	PGLYRP1	peptidoglycan recognition protein 1	4.13	28.8	0.595011 111
46	tr W5NTB3 W5NTB3_S HEEP	CST6	cystatin E/M	4.1	45.6	0.633144 444
47	tr W5P742 W5P742_SHE EP	LGALS7	galectin-7	4	71.9	0.622722 222
48	tr W5NQJ0 W5NQJ0_SH EEP	S100A12	S100 calcium binding protein A12	3.92	56.5	0.498288 889
49	tr W5PQL4 W5PQL4_SH EEP	TPM2	tropomyosin 2	3.79	57.8	1.862333 333
50	tr W5QGQ2 W5QGQ2_S HEEP	LOC101102 969	lysozyme C, tracheal isozyme	3.73	48	0.4557
51	tr W5PFB9 W5PFB9_SH EEP	ALPL	alkaline phosphatase, liver/bone/kidney	3.69	26.4	2.083533 333
52	tr W5QHS2 W5QHS2_S HEEP	MGP	matrix Gla protein	3.52	41.8	1.763644 444
53	tr W5NV75 W5NV75_S HEEP	BAC5	5 kDa bactinecin precursor	3.17	32.3	0.637377 778
54	tr W5QIT6 W5QIT6_SH EEP	FERMT2	fermitin family member 2	3.05	25.8	1.783055 556
55	tr W5Q2C8 W5Q2C8_SH EEP	KERA	keratocan	2.72	25.1	1.591755 556
56	tr W5PB94 W5PB94_SH EEP	RAD23B	RAD23 homolog B, nucleotide excision repair protein	2.7	16.3	3.3842
57	tr W5NYL0 W5NYL0_S HEEP	MAOA	monoamine oxidase A	2.7	24.3	1.863466 667
58	tr W5QI78 W5QI78_SHE EP	CTSK	cathepsin K	2.67	19.4	2.108788 889
59	sp P11839 CASB_SHEEP	CSN2	casein beta	2.62	22.1	6.580755 556
60	tr W5Q6G1 W5Q6G1_S HEEP	ALDH1L2	aldehyde dehydrogenase 1 family member L2	2.5	22.1	2.238222 222
61	tr W5PE54 W5PE54_SH EEP	GGCT	gamma-glutamylcyclotra nsferas	2.28	32.6	0.563466 667
62	tr W5NXE1 W5NXE1_S	CBFB	core-binding factor beta	2.19	41.3	1.566633

	HEEP		subunit			333
63	tr W5P240 W5P240_SHE EP	LOC101110 777	WAP four-disulfide core domain protein 18-like	2.16	82.1	0.488855 556
64	sp P54230 CTHL1_SHEE P	CATHL1A	procyclic dodecapeptide	2.14	50.3	0.652177 778
65	tr W5Q1W7 W5Q1W7_S HEEP	PALLD	palladin	2.13	15.2	1.892677 778
66	tr W5Q3J3 W5Q3J3_SHE EP	COLGALT1	procollagen galactosyltransferase 1	2.11	18.5	0.515133 333
67	tr W5NUW9 W5NUW9_ SHEEP	HSPB8	heat shock protein family B (small) member 8	2.08	17.3	0.541233 333
68	tr W5Q9F1 W5Q9F1_SH EEP	SSR1	transforming growth factor beta 1	2.06	20.7	1.709466 667
69	tr W5NXI9 W5NXI9_SH EEP	TRADD	TNFRSF1A associated via death domain	2.06	26.4	0.666066 667
70	tr W5NXM6 W5NXM6_ SHEEP	PTX3	pentraxin 3	2.06	17.6	3.643077 778
71	tr W5Q108 W5Q108_SH EEP	PDLIM4	PDZ and LIM domain 4	2.06	24.2	1.9324
72	tr W5Q5R9 W5Q5R9_SH EEP	TXNRD1	thioredoxin reductase 1	2.04	20.6	1.509966 667
73	tr W5NR14 W5NR14_SH EEP	IDH3A	isocitrate dehydrogenase 3 (NAD(+)) alpha	2.04	16.7	2.416388 889
74	tr W5PI50 W5PI50_SHE EP	GLRX	glutaredoxin (thioltransferase)	2.04	46.2	0.584811 111
75	tr W5NQH5 W5NQH5_S HEEP	HYI	PDZ and LIM domain 4	2.02	29.1	2.643966 667
76	tr W5P530 W5P530_SHE EP	LOC101104 705	plasminogen activator inhibitor 2-like	2.02	10.1	1.760344 444
77	tr W5NQ36 W5NQ36_S HEEP	ECI2	enoyl-CoA delta isomerase 2	2.01	14	1.745666 667
78	tr W5NYA8 W5NYA8_S HEEP	SCAMP2	secretory carrier membrane protein 2	2.01	12.5	1.547855 556
79	tr W5PJL0 W5PJL0_SHE EP	PPP1R13L	protein phosphatase 1 regulatory subunit 13 like	2	14.1	1.5325
80	tr W5PEP0 W5PEP0_SH EEP	PARVA	parvin alpha	2	16.1	1.909266 667
81	tr W5NXM5 W5NXM5_ SHEEP	NOL3	nucleolar protein 3	2	31.6	0.619044 444
82	tr W5PIM8 W5PIM8_SH EEP	GALK1	galactokinase 1	2	27.2	5.361788 889
83	tr W5PIF9 W5PIF9_SHE EP	TGFB1I1	transforming growth factor beta 1 induced	2	27.4	3.128255 556

			transcript 1			
84	tr W5PMA0 W5PMA0_S HEEP	AP2S1	adaptor related protein complex 2 sigma 1 subunit	2	16.9	1.624677 778
85	tr W5QCT3 W5QCT3_S HEEP	CGREF1	prolactin regulatory element binding	2	12.8	1.526988 889
86	tr W5Q501 W5Q501_SH EEP	GNAS	guanine nucleotide-binding protein G(s) subunit alpha isoforms short	1.91	15.6	1.627777 778
87	tr W5PPP4 W5PPP4_SH EEP	BDH2	3-hydroxybutyrate dehydrogenase 2	1.82	25.3	1.582477 778
88	tr W5P0V6 W5P0V6_SH EEP	SCCPDH	saccharopine dehydrogenase (putative)	1.62	11.9	0.559633 333
89	tr W5P6C1 W5P6C1_SH EEP	ADSS	adenylosuccinate synthase	1.26	12.9	26.84505 556
90	tr W5Q553 W5Q553_SH EEP	ITGAV	integrin subunit alpha V	1.19	17.5	2.020988 889
91	tr W5P5C5 W5P5C5_SH EEP	GYG1	glycogenin 1	1.19	13	2.067766 667
92	tr W5PFI3 W5PFI3_SHE EP	NNT	nicotinamide nucleotide transhydrogenase	1.17	12.7	2.748955 556
93	tr W5Q6T6 W5Q6T6_SH EEP	TTC37	tetratricopeptide repeat domain 37	1.07	14.1	0.371111 111
94	tr W5NVD7 W5NVD7_S HEEP	COPS4	COP9 signalosome subunit 4	0.97	15.5	1.620255 556
95	tr W5Q337 W5Q337_SH EEP	GLRX5	glutaredoxin 5	0.96	43.7	0.563222 222
96	tr W5Q1I8 W5Q1I8_SHE EP	PPM1F	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent 1F	0.96	18.6	2.434011 111
97	tr W5Q245 W5Q245_SH EEP	ZNF326	zinc finger protein 326	0.95	12.6	1.5449
98	tr W5Q860 W5Q860_SH EEP	UFD1L	ubiquitin recognition factor in ER associated degradation 1	0.84	13.4	0.587044 444

**Table S2 DEPs in H group compared with S+M group**

Num	Accession	GN	Full Name	Score	% Cov	Fold Change
1	tr W5P8W6 W5P8W6_SHEEP	COL12A1	collagen type XII alpha 1 chain	152.2	50.3	1.79755
2	tr W5QCP9 W5QCP9_SHEEP	COL6A3	collagen type VI alpha 3 chain	134.58	48.5	2.52185
3	tr W5Q6J4 W5Q6J4_SHEEP	KRT84	keratin 84	76.38	88.5	0.617316667
4	tr W5Q5X4 W5Q5X4_SHEEP	KRT36	keratin 36	65.27	74.6	0.6365
5	tr W5P7G4 W5P7G4_SHEEP	TNC	tenascin C	60.72	32.4	1.6635
6	tr W5QIN8 W5QIN8_SHEEP	FBN1	fibrillin 1	50.36	24.1	1.582333333
7	tr W5Q5H8 W5Q5H8_SHEEP	FGA	Fibrinogen alpha chain	49.78	50.9	0.661133333
8	tr W5Q6D3 W5Q6D3_SHEEP	LOC10111178	keratin, type II cytoskeletal 6A-like	47.68	66.1	0.533783333
9	tr W5PK03 W5PK03_SHEEP	POSTN	periostin	41.9	51	1.8903
10	tr W5Q611 W5Q611_SHEEP	KRT1	keratin 1	39.21	52.7	0.662583333
11	tr W5Q160 W5Q160_SHEEP	KRT10	keratin 10	35.5	53	0.572366667
12	tr W5PGT5 W5PGT5_SHEEP	MYH11	myosin heavy chain 11	32.33	33.4	1.78545
13	tr C5ISA2 C5ISA2_SHEEP	TUBA4A	tubulin alpha 4a	31.1	60.3	0.627916667
14	tr W5PTE9 W5PTE9_SHEEP	COL6A1	collagen type VI alpha 1 chain	30.47	46.3	2.890433333
15	tr W5PWT4 W5PWT4_SHEEP	TNN	tenascin N	30.15	35.9	1.50035
16	tr W5P8T8 W5P8T8_SHEEP	SERPINB5	serpin family B member 5	29.63	79.1	0.65305
17	tr W5PDG3 W5PDG3_SHEEP	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	27.69	66.8	0.61015
18	tr W5PQE5 W5PQE5_SHEEP	SERPINH1	serpin family H member 1	25.69	59.8	1.562216667
19	tr W5PZM9 W5PZM9_SHEEP	ANXA5	annexin A5	25.5	59	1.525483333
20	tr W5QCY8 W5QCY8_SHEEP	LOC101106199	hemoglobin fetal subunit beta	25.28	95.2	0.22005
21	tr W5PCP8 W5PCP8_SHEEP	BGN	biglycan	24.71	62.9	3.607283333
22	tr W5PNK3 W5PNK3_SHEEP	ACAN	aggrecan	23.48	17	2.087416667
23	tr W5PXU6 W5PXU6_SHEEP	SERPINF1	serpin family F member 1	21.45	49	1.758233333
24	tr W5PJ54 W5PJ54_SHEEP	DPYSL2	dihydropyrimidinase-related protein 2	19.55	42.7	1.68525
25	tr W5PTN6 W5PTN6_SHEEP	COL6A2	collagen type VI alpha 2 chain	18.69	34.5	3.150833333
26	tr W5P9M9 W5P9M9_SHEEP	LOC101103862	serpin B4-like	17.74	49.4	0.644283333
27	tr W5QHQ7 W5QHQ7_SHEEP	NCL	nucleolin	17.39	43.9	0.616216667
28	tr W5QFB2 W5QFB2_SHEEP	OLFML3	olfactomedin like 3	17.32	42.9	1.558216667

29	tr W5PYU4 W5PYU4_SHEEP	LAMB2	laminin subunit beta 2	16.52	24.8	1.65725
30	tr W5QBD7 W5QBD7_SHEEP	YWHAZ	tyrosine 3-monoxygenase/triptophan 5-monoxygenase activation protein zeta	16.5	74.5	0.636983333
31	tr W5Q0F3 W5Q0F3_SHEEP	TGFBI	transforming growth factor beta induced	15.9	43.6	1.7678
32	tr W5NU63 W5NU63_SHEEP	MYH10	myosin heavy chain 10	15.57	36.8	1.566666667
33	tr W5P748 W5P748_SHEEP	LGALS7B	galectin-7	15.38	84.9	0.607966667
34	tr W5P430 W5P430_SHEEP	SBSN	suprabasin	14.12	64.4	0.49365
35	tr W5NZX9 W5NZX9_SHEEP	SPTBN1	spectrin beta, non-erythrocytic 1	12.55	22.1	1.6139
36	tr W5NRS4 W5NRS4_SHEEP	LOC101115597	keratin-associated protein 13-1-like	12.1	70.1	0.556683333
37	tr W5P3C8 W5P3C8_SHEEP	CALML5	calmodulin	10.93	68.5	0.61055
38	tr W5P214 W5P214_SHEEP	TAGLN	transgelin	10.59	68.4	1.72595
39	tr W5PZK7 W5PZK7_SHEEP	ACTA2	actin, alpha 2, smooth muscle, aorta	10.36	59.2	1.950883333
40	tr W5Q3W1 W5Q3W1_SHEEP	AEBP1	AE binding protein 1	9.72	19.3	1.805516667
41	tr W5NRA2 W5NRA2_SHEEP	S100A2	S100 calcium binding protein A2	9.03	32.7	0.662116667
42	tr W5PD82 W5PD82_SHEEP	CALD1	caldesmon 1	8.44	43.2	1.677266667
43	tr W5QCI3 W5QCI3_SHEEP	CYB5R3	estrogen receptor 1	7.76	41.5	1.6671
44	tr W5Q9D5 W5Q9D5_SHEEP	VTN	vitronectin	7.6	24.4	1.593766667
45	tr W5NQH6 W5NQH6_SHEEP	S100A9	S100 calcium binding protein A9	7.59	59.4	0.350166667
46	tr W5QAR2 W5QAR2_SHEEP	F13A1	coagulation factor XIII A chain	7.3	29.4	1.721083333
47	tr W5QGS8 W5QGS8_SHEEP	LOC101102969	lysozyme C, tracheal isozyme	6.8	56	0.408466667
48	tr W5PFL8 W5PFL8_SHEEP	CD9	CD9 molecule	6.31	31.5	1.576416667
49	tr W5Q233 W5Q233_SHEEP	VCAN	versican	6.21	11.6	1.516583333
50	tr W5PT40 W5PT40_SHEEP	PTGIS	prostaglandin I2 synthase	6.06	20.8	2.640966667
51	tr W5PK26 W5PK26_SHEEP	LASP1	LIM and SH3 protein 1	5.68	35.4	1.553716667
52	tr W5P2Q0 W5P2Q0_SHEEP	CHAD	chondroadherin	5.63	44.7	2.880683333
53	tr W5PIJ5 W5PIJ5_SHEEP	CDH13	cadherin 13	5.54	20.6	1.648433333
54	tr W5NQK9 W5NQK9_SHEEP	S100A8	S100 calcium binding protein A8	5.53	37.1	0.355933333
55	tr W5NRH4 W5NRH4_SHEEP	LOC101113302	family with sequence similarity 25 member A	5	69.5	0.462783333
56	tr W5Q438 W5Q438_SHEEP	GNB2	G protein subunit beta 2	4.63	36.6	1.682566667
57	tr W5Q3G8 W5Q3G8_SHEEP	OLFML1	olfactomedin like 1	4.53	35.6	1.8363
58	tr W5PHI8 W5PHI8_SHEEP	DPT	dermatopontin	4.49	33.8	2.51785

59	tr W5NR21 W5NR21_SHEEP	S100A7	S100 calcium binding protein A7	4.41	42.1	0.380666667
60	tr W5NRP7 W5NRP7_SHEEP	LOC101106046	keratin-associated protein 13-1-like	4.2	30.5	0.608616667
61	tr W5PLB7 W5PLB7_SHEEP	PGLYRP1	peptidoglycan recognition protein 1	4.13	28.8	0.546366667
62	tr W5QCY7 W5QCY7_SHEEP	SPP2	secreted phosphoprotein 2	4.1	25.6	1.7576
63	tr W5P742 W5P742_SHEEP	LGALS7	galectin-7	4	71.9	0.55875
64	tr W5NQJ0 W5NQJ0_SHEEP	S100A12	S100 calcium binding protein A12	3.92	56.5	0.208866667
65	tr W5PQL4 W5PQL4_SHEEP	TPM2	tropomyosin 2	3.79	57.8	2.3991
66	tr W5PFB9 W5PFB9_SHEEP	ALPL	alkaline phosphatase, liver/bone/kidney	3.69	26.4	1.7548
67	tr W5NWX6 W5NWX6_SHEEP	APOC3	apolipoprotein C3	3.63	35.5	1.52055
68	tr W5PNP1 W5PNP1_SHEEP	MFGE8	milk fat globule-EGF factor 8 protein	3.58	17.8	1.90855
69	tr W5QBE7 W5QBE7_SHEEP	RPLP1	ribosomal protein lateral stalk subunit P1	3.33	41.2	0.649216667
70	tr W5Q9H0 W5Q9H0_SHEEP	MMP2	matrix metallopeptidase 2	3.27	17.2	1.541316667
71	tr W5P4S2 W5P4S2_SHEEP	TXNL1	thioredoxin like 1	3.2	25.4	1.6515
72	tr W5NV75 W5NV75_SHEEP	BAC5	5 kDa bactinecin precursor	3.17	32.3	0.661566667
73	tr W5QIT6 W5QIT6_SHEEP	FERMT2	fermitin family member 2	3.05	25.8	1.813433333
74	tr W5PLD4 W5PLD4_SHEEP	PSORS1C2	psoriasis susceptibility 1 candidate 2	3.02	45.2	0.59795
75	tr W5P5S7 W5P5S7_SHEEP	PDLIM7	PDZ and LIM domain 7	2.99	16.8	1.55575
76	tr W5NYR7 W5NYR7_SHEEP	AKAP12	A-kinase anchoring protein 12	2.93	17.8	0.6428
77	sp O77727 K1C15_SHEEP	KRT15	keratin 15	2.7	33.1	0.57955
78	tr W5NYL0 W5NYL0_SHEEP	MAOA	monoamine oxidase A	2.7	24.3	2.0866
79	tr W5P0K8 W5P0K8_SHEEP	CLIC2	chloride intracellular channel 2	2.67	32.8	1.76125
80	tr W5QI78 W5QI78_SHEEP	CTSK	cathepsin K	2.67	19.4	1.6495
81	tr W5QJ36 W5QJ36_SHEEP	SPTB	spectrin beta, erythrocytic	2.63	16.9	0.510266667
82	tr W5PEJ5 W5PEJ5_SHEEP	OMD	osteomodulin	2.59	13.8	1.566216667
83	tr W5PGW8 W5PGW8_SHEEP	XPNPEP1	X-prolyl aminopeptidase 1	2.46	21.3	1.521916667
84	tr W5PET7 W5PET7_SHEEP	TACSTD2	tumor associated calcium signal transducer 2	2.27	22.6	0.631683333
85	tr W5P5Y5 W5P5Y5_SHEEP	CSNK1A1	casein kinase 1 alpha 1	2.25	30.6	0.592966667
86	tr W5NRL8 W5NRL8_SHEEP	EIF3A	eukaryotic translation initiation factor 3 subunit A	2.24	26.4	0.637633333
87	tr W5NXE1 W5NXE1_SHEEP	CBFB	core-binding factor beta subunit	2.19	41.3	1.55825
88	tr W5QH58 W5QH58_SHEEP	DNAJB11	DnaJ heat shock protein	2.16	22.6	2.22975

			family (Hsp40) member B11			
89	tr W5P422 W5P422_SHEEP	DMKN	dermokine	2.16	18.5	0.619533333
90	tr W5P240 W5P240_SHEEP	LOC101110777	WAP four-disulfide core domain protein 18-like	2.16	82.1	0.582866667
91	sp P54230 CTHL1_SHEEP	CATHL1A	procyclic dodecapeptide	2.14	50.3	0.54045
92	tr W5Q1W7 W5Q1W7_SHEEP	PALLD	palladin	2.13	15.2	1.693966667
93	tr W5Q3J3 W5Q3J3_SHEEP	COLGALT1	procollagen galactosyltransferase 1	2.11	18.5	0.34525
94	tr W5NZC4 W5NZC4_SHEEP	STX12	syntaxin 12	2.11	27.5	1.6238
95	tr W5QG43 W5QG43_SHEEP	MYLK	myosin light chain kinase	2.1	14.3	2.006716667
96	tr W5NQP5 W5NQP5_SHEEP	SOD3	superoxide dismutase 3	2.08	23.8	1.91545
97	tr W5NUW9 W5NUW9_SHEEP	HSPB8	heat shock protein family B (small) member 8	2.08	17.3	0.5977
98	tr W5PQJ1 W5PQJ1_SHEEP	EIF4H	eukaryotic translation initiation factor 4H	2.07	30.7	1.9049
99	tr W5QC63 W5QC63_SHEEP	ARMC10	armadillo repeat containing 10	2.06	20.3	1.64895
100	tr W5NXM6 W5NXM6_SHEEP	PTX3	pentraxin 3	2.06	17.6	2.207983333
101	tr W5PGD6 W5PGD6_SHEEP	BZW2	basic leucine zipper and W2 domains 2	2.05	23.3	0.55945
102	tr W5NYQ9 W5NYQ9_SHEEP	TIMM44	translocase of inner mitochondrial membrane 44	2.05	23.3	2.799116667
103	tr W5Q5R9 W5Q5R9_SHEEP	TXNRD1	thioredoxin reductase 1	2.04	20.6	1.582883333
104	tr W5NR14 W5NR14_SHEEP	IDH3A	isocitrate dehydrogenase 3 (NAD(+)) alpha	2.04	16.7	1.932533333
105	tr W5Q9H1 W5Q9H1_SHEEP	ZYX	zyxin	2.04	11.2	1.589416667
106	tr W5P9U7 W5P9U7_SHEEP	LOC101104114	serpin B4-like	2.03	33.9	0.350866667
107	tr W5P2P0 W5P2P0_SHEEP	SPINK6	serine protease inhibitor Kazal-type 6	2.03	41.3	0.58865
108	tr W5QH84 W5QH84_SHEEP	TRA2B	transformer 2 beta homolog	2.02	37	0.5209
109	tr W5NQH5 W5NQH5_SHEEP	HYI	hydroxypyruvate isomerase (putative)	2.02	29.1	2.1133
110	tr W5PEM1 W5PEM1_SHEEP	PTGES3	prostaglandin E synthase 3	2.02	13.1	0.6316
111	tr W5P648 W5P648_SHEEP	RAB14	member RAS oncogene family	2.01	23.9	1.695566667
112	tr W5Q1M0 W5Q1M0_SHEEP	GLB1	galactosidase beta 1	2.01	14.8	1.556516667
113	tr W5NQ36 W5NQ36_SHEEP	ECI2	enoyl-CoA delta isomerase 2	2.01	14	1.720033333
114	tr W5QB48 W5QB48_SHEEP	LOC101109584	pentatricopeptide repeat domain 1	2.01	26.9	1.549316667
115	tr W5NVF2 W5NVF2_SHEEP	LOC101119195	reticulocalbin-3-like	2	31.9	2.402983333

116	tr W5P8W4 W5P8W4_SHEEP	LOC101109939	major allergen Equ c 1-like	2	23.6	1.7457
117	tr W5Q2P3 W5Q2P3_SHEEP	LETM1	leucine zipper and EF-hand containing transmembrane protein 1	2	19.9	1.579416667
118	tr W5PXM3 W5PXM3_SHEEP	PSPC1	paraspeckle component 1	2	25.6	0.565666667
119	tr W5PQD7 W5PQD7_SHEEP	GID8	GID complex subunit 8 homolog	2	17.9	0.636566667
120	tr W5PYG7 W5PYG7_SHEEP	EIF3L	eukaryotic translation initiation factor 3 subunit L	2	10.7	1.5344
121	tr W5Q5T7 W5Q5T7_SHEEP	ATP6V1C1	ATPase H+ transporting V1 subunit C1	2	20.7	1.548766667
122	tr W5Q8Q6 W5Q8Q6_SHEEP	KANK2	KN motif and ankyrin repeat domains 2	2	13.1	1.680616667
123	tr W5PEP0 W5PEP0_SHEEP	PARVA	parvin alpha	2	16.1	2.0847
124	tr W5Q6B3 W5Q6B3_SHEEP	LOC101112255	prefoldin subunit 4	2	32.1	0.642033333
125	tr W5NZH7 W5NZH7_SHEEP	PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta [ <i>Ovis aries</i> ]	2	12.5	0.652233333
126	tr W5P623 W5P623_SHEEP	GIPC1	GIPC PDZ domain containing family member 1	2	12.9	0.636083333
127	tr W5NYZ6 W5NYZ6_SHEEP	CD81	CD81 molecule	2	18.6	1.97655
128	tr W5PK38 W5PK38_SHEEP	VASP	vasodilator stimulated phosphoprotein	2	24.6	1.584616667
129	tr W5PIM8 W5PIM8_SHEEP	GALK1	galactokinase 1	2	27.2	4.373383333
130	tr W5PIF9 W5PIF9_SHEEP	TGFB1I1	transforming growth factor beta 1 induced transcript 1	2	27.4	3.351733333
131	tr W5P0I2 W5P0I2_SHEEP	NDUFA7	NADH:ubiquinone oxidoreductase subunit A7	2	33.3	1.524333333
132	tr W5NS40 W5NS40_SHEEP	KRTAP27-1		2	12.4	0.521066667
133	tr W5Q501 W5Q501_SHEEP	GNAS	guanine nucleotide-binding protein G(s) subunit alpha isoforms short	1.91	15.6	1.61605
134	tr W5PPP4 W5PPP4_SHEEP	BDH2	3-hydroxybutyrate dehydrogenase 2	1.82	25.3	1.535466667
135	tr W5P396 W5P396_SHEEP	LSM2	LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated	1.77	28.7	1.640666667
136	tr W5NRY1 W5NRY1_SHEEP	NDUFV2	NADH:ubiquinone oxidoreductase core subunit V2	1.7	19.9	0.6532
137	tr W5PW51 W5PW51_SHEEP	NAA15	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	1.68	14.6	1.572916667

138	sp Q2TCH3 ACLY_SHEEP	ACLY	ATP citrate lyase	1.66	13.7	1.561116667
139	tr W5Q9C4 W5Q9C4_SHEEP	NIT2	nitrilase family member 2	1.39	19.8	0.62955
140	tr W5QDF2 W5QDF2_SHEEP	ATG3	autophagy related 3	1.38	5.4	1.87125
141	tr W5P682 W5P682_SHEEP	UBQLN2	ubiquilin 2	1.34	7.2	1.671433333
142	tr W5PDE3 W5PDE3_SHEEP	SPTLC1	serine palmitoyltransferase long chain base subunit 1	1.34	10.1	1.857233333
143	tr W5P6C1 W5P6C1_SHEEP	ADSS	adenylosuccinate synthase	1.26	12.9	29.94138333
144	tr W5PKQ1 W5PKQ1_SHEEP	SORBS3	sorbin and SH3 domain containing 3	1.18	17.5	1.69475
145	tr W5PFI3 W5PFI3_SHEEP	NNT	nicotinamide nucleotide transhydrogenase	1.17	12.7	2.483616667
146	tr W5Q3M9 W5Q3M9_SHEEP	SEPT6	septin 6	1.07	17.2	1.59775
147	tr W5Q245 W5Q245_SHEEP	ZNF326	zinc finger protein 326	0.95	12.6	1.896283333
148	tr W5QAL0 W5QAL0_SHEEP	PRKCSH	protein kinase C substrate 80K-H	0.91	14.7	1.607166667
149	tr W5PEU0 W5PEU0_SHEEP	CAMK2G	calcium/calmodulin dependent protein kinase II gamma	0.9	20.2	2.92405
150	tr W5P9G3 W5P9G3_SHEEP	DSCAML1	DS cell adhesion molecule like 1	0.88	16.3	1.524833333
151	tr W5Q860 W5Q860_SHEEP	UFD1L	ubiquitin recognition factor in ER associated degradation 1	0.84	13.4	0.4541