Supplemental Table 1. Summary of all unequivocally identified proteins

Gene Symbol	ID	Spot	State	Max Fold	*q*	Accession #	Species	Size kDa	Score	AA Coverage		Peps	Human	Function
										%	Ratio			
AARS	Alanyl-tRNA synthetase	274	SD > LAr	1.6	6.8E-03	73957020	*Canis familiaris*	94	81	4.7	[40/852]	5	109148542	Protein synthesis
ACADL	Acyl-CoA dehydrogenase (long chain)	1144	LT > SD	1.6	1.6E-02	47522692	*Sus scrofa*	48	187	28.3	[99/350]	12	189069248	Fatty acid and AA metabolism, β-oxidation
ACADL	Acyl-CoA dehydrogenase (long chain)	1152	ET > SD	1.6	1.3E-02	47522692	*Sus scrofa*	48	148	22.6	[79/350]	10	4501857	Fatty acid and AA metabolism, β-oxidation
ACO2	Aconitase 2	565	SD > LT	1.6	8.2E-03	74268076	*Bos taurus*	85	161	15.9	[124/780]	11	4501867	TCA cycle
ACTN3	α-Actinin 3	344	SA > ET	1.9	2.1E-02	7304855	*Mus musculus*	103	254	26.3	[216/820]	19	4557241	Actin anchoring
ALB	Albumin	656	Ent > SD	1.9	4.1E-03	30794280	*Bos taurus*	69	132	19.7	[104/527]	9	28592	Steroid, fatty acid and TH transport
ALB	Albumin	669	Ent > SA	2.2	5.5E-03	E:00000011284	*Ictidomys tridecemlineatus*	70	115	10.7	[66/616]	8	28592	Steroid, fatty acid and TH transport
ALB	Albumin	691	Ent > SA	2.2	5.4E-03	E:00000011284	*Ictidomys tridecemlineatus*	70	141	13.5	[83/616]	10	28592	Steroid, fatty acid and TH transport
ALB	Albumin	701	Ent > SA	2.3	3.2E-03	E:00000011284	*Ictidomys tridecemlineatus*	70	126	13.5	[83/616]	9	28592	Steroid, fatty acid and TH transport
ALB	Albumin	710	Ent > SA	2.0	7.5E-03	E:00000011284	*Ictidomys tridecemlineatus*	70	54	4.1	[25/616]	4	28592	Steroid, fatty acid and TH transport
ALDH2	Aldehyde dehydrogenase 2, mitochondrial precursor	1011	SD > IBA	1.4	4.2E-02	6753036	*Mus musculus*	57	256	32.4	[142/439]	19	25777732	Alcohol oxidation
ALDH9A1	4-Trimethylamino-butyraldehyde dehydrogenase	1069	LT > SD	1.5	1.1E-02	281348862	*Ailuropoda melanoleuca*	56	98	11.5	[59/513]	7	62511242	GABA synthesis
ALDOA	Fructose-bisphosphate aldolase A	1365	SD > LT	1.5	7.7E-03	73958481	*Canis familiaris*	40	93	12.0	[34/284]	6	4557305	Glycolysis
ALDOA	Fructose-bisphosphate aldolase A	1376	SA > IBA	1.7	2.5E-02	156120479	*Bos taurus*	39	173	29.6	[84/284]	12	49456715	Glycolysis
ALDOA	Fructose-bisphosphate aldolase A	1384	SD > Ent	1.5	8.0E-04	73958481	*Canis familiaris*	40	184	28.2	[80/284]	11	4557305	Glycolysis
ALDOA	Fructose-bisphosphate aldolase A	1391	SA > LT	1.5	1.7E-02	156120479	*Bos taurus*	39	314	58.1	[165/284]	19	4557305	Glycolysis
ALDOA	Fructose-bisphosphate aldolase A	1396	SD > LT	1.7	1.3E-04	156120479	*Bos taurus*	39	280	43.0	[122/284]	18	4557305	Glycolysis
ALDOA	Fructose-bisphosphate aldolase A	1401	SA > LT	1.6	3.4E-02	4557976	*Homo sapiens*	39	205	27.9	[79/283]	14	4557305	Glycolysis
ANKRD2	Ankyrin repeat domain-containing protein 2	1337	IBA > SD	1.7	5.9E-03	E:00000006002	*Ictidomys tridecemlineatus*	39	77	17.7	[62/351]	5	11967781	Response to stress, injury, hypertrophy
ANKRD2	Ankyrin repeat domain-containing protein 2	1339	Ent > SD	1.6	4.1E-03	73998490	*Canis familiaris*	37	60	12.5	[41/329]	4	11967781	Response to stress, injury, hypertrophy
ANKRD2	Ankyrin repeat domain-containing protein 2	1374	LAr > SD	3.2	2.9E-03	E:00000006002	*Ictidomys tridecemlineatus*	39	137	26.8	[94/351]	9	119570301	Response to stress, injury, hypertrophy
APOA1	Apolipoprotein A-1	1840	Ent > SA	2.5	1.0E-02	E:00000002077	*Ictidomys tridecemlineatus*	24	79	35.0	[71/203]	6	4557321	Cholesterol transport
APOA1	Apolipoprotein A-1	1846	LAr > SA	3.4	1.9E-04	E:00000002077	*Ictidomys tridecemlineatus*	24	207	59.1	[120/203]	14	4557321	Cholesterol transport
ARHGDIA	Rho GDP-dissociation inhibitor 1	1891	IBA > SA	1.4	7.8E-03	31982030	*Mus musculus*	23	100	0.0	[0/124]	7	4757768	small guanine nucleotide exchange
ATP2A1	SR/ER Ca^{2+}-ATPase 1	282	SA >	2.5	2.7E-	36031132	*Mus musculus*	109	119	10.2	[93/914]	8	27886529	Excitation-contraction

			ET		04									coupling
ATP2A1	SR/ER Ca^{2+}-ATPase 1	283	SD > ET	2.6	3.6E-04	36031132	*Mus musculus*	109	50	6.0	[55/914]	4	27886529	Excitation-contraction coupling
ATP2A1	SR/ER Ca^{2+}-ATPase 1	288	SD > LT	2.1	3.7E-02	36031132	*Mus musculus*	109	72	7.7	[70/914]	5	27886529	Excitation-contraction coupling
ATP2A1	SR/ER Ca^{2+}-ATPase 1	291	SD > IBA	2.2	5.1E-03	36031132	*Mus musculus*	109	40	4.8	[44/914]	3	27886529	Excitation-contraction coupling
ATP2A1	SR/ER Ca^{2+}-ATPase 1	294	SD > ET	4.6	2.7E-04	36031132	*Mus musculus*	109	138	11.1	[101/914]	10	27886529	Excitation-contraction coupling
ATP2A1	SR/ER Ca^{2+}-ATPase 1	300	SD > ET	3.8	2.7E-04	36031132	*Mus musculus*	109	85	7.7	[70/914]	6	27886529	Excitation-contraction coupling
ATP2A1	SR/ER Ca^{2+}-ATPase 1	309	SD > LAr	2.9	5.7E-03	36031132	*Mus musculus*	109	70	6.2	[57/914]	5	27886529	Excitation-contraction coupling
BTF3L4	Basic transcription factor 3-like 4	2064	LT > SA	1.4	4.8E-03	126305710	*Monodelphis domestica*	31	55	11.9	[34/287]	4	46255705	Transcription factor
CAT	Catalase	771	IBA > SA	1.8	1.5E-03	E:00000007701	*Ictidomys tridecemlineatus*	60	216	34.0	[179/527]	15	13562132	H_2O_2 catabolism
CFL2	Cofilin-2	2127	ET > SA	1.6	5.6E-03	14719392	*Homo sapiens*	19	110	65.1	[56/86]	7		regulation of actin filament dynamics
CKM	Creatine kinase, muscle	1370	IBA > Ar	2.6	5.6E-03	281337438	*Ailuropoda melanoleuca*	43	67	15.5	[59/381]	5	21536288	Energy homeostasis
CKM	Creatine kinase, muscle	1388	SA > LT	1.4	4.1E-02	281337438	*Ailuropoda melanoleuca*	43	302	43.6	[166/381]	19	119577741	Energy homeostasis
CMPK1	Cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	1968	IBA > SD	1.4	3.6E-02	194207483	*Equus caballos*	20	101	33.3	[58/174]	8	12644008	Nucleic acid synthesis
CRAT	Carnitine O-acetyltransferase	776	LT > SD	1.5	2.6E-02	E:00000001334	*Ictidomys tridecemlineatus*	70	154	19.5	[120/617]	12	13111705	AcylCoA/CoA regulation
CRYAB	AlphaB-crystallin	2054	LT > SD	2.3	5.6E-03	13162243	*Nannospalax ehrenbergi*	20	75	27.7	[47/170]	6	4503057	Chaperone
DLST	Dihydrolipoamide S-succinyltransferase	1018	ET > SA	1.5	2.7E-02	21313536	*Mus musculus*	49	153	18.5	[69/374]	11	643589	TCA cycle
DLST	Dihydrolipoamide S-succinyltransferase	1196	ET > SA	1.4	4.1E-02	62512126	*Rattus norvegicus*	49	96	8.6	[32/374]	7	643589	TCA cycle
DPYSL3	Dihydropyrimidinase-like 3	832	IBA > ET	1.5	1.0E-02	50417352	*Homo sapiens*	74	208	13.7	[83/604]	13		Cytoskeletal remodeling
DPYSL3	Dihydropyrimidinase-like 3	834	Ent > SD	1.4	3.8E-02	4503379	*Homo sapiens*	62	130	16.1	[79/490]	9		Cytoskeletal remodeling
DUSP3	Dual specificity protein phosphatase 3	2051	LT > SA	2.8	2.7E-04	E:00000012358	*Ictidomys tridecemlineatus*	21	42	22.7	[42/185]	3	4758208	Protein phosphatase
ECH1	Enoyl CoA hydratase 1, peroxisomal	1667	IBA > SD	2.0	8.8E-04	999015860	*Urocitellus parryi*	27	172	24.1	[79/328]	11	70995211	β-oxidation
ETFA	Electron-transfer-flavoprotein, α polypeptide	1640	LT > SD	1.5	1.7E-02	74000809	*Canis familiaris*	35	212	48.7	[162/333]	12	4503607	β-oxidation
ETFDH	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	791	IBA > SA	1.6	1.4E-02	281354353	*Ailuropoda melanoleuca*	68	278	36.5	[222/608]	19	260170	ETC
FABP3	Fatty acid-binding protein, heart	2247	LT > SA	1.5	3.9E-03	20138311	*Ictidomys tridecemlineatus*	15	61	18.9	[10/53]	4	4758328	Fatty acid transport
FABP3	Fatty acid-binding protein, heart	2257	LT > SD	2.6	2.0E-03	20138311	*Ictidomys tridecemlineatus*	15	74	45.3	[24/53]	5	4758328	Fatty acid transport
FABP3	Fatty acid-binding protein, heart	2288	LT > SD	2.5	1.5E-03	20138311	*Ictidomys tridecemlineatus*	15	73	45.3	[24/53]	5	4758328	Fatty acid transport
FABP3	Fatty acid-binding protein, heart	2293	LT > SD	2.4	2.0E-03	20138311	*Ictidomys tridecemlineatus*	15	122	56.6	[30/53]	9	4758328	Fatty acid transport

FABP4	Fatty acid-binding protein, adipocyte	2280	LT > SD	2.4	3.3E-02	20138310	*Ictidomys tridecemlineatus*	15	126	0.0	[0/52]	8	4557579	Fatty acid transport
GARS	Glycyl-tRNA synthetase	601	Ar > SA	1.3	1.6E-02	293346809	*Rattus norvegicus*	82	184	17.8	[115/648]	12	600727	aminoacyl-tRNA synthetase
GFM1	G elongation factor, mitochondrial 1 isoform 3	519	SD > IBA	1.4	1.3E-02	76660421	*Bos taurus*	84	53	5.7	[43/753]	4	14285174	Mitochondrial protein synthesis
GPD1	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	1575	SD > LT	1.8	5.7E-04	E:00000004439	*Ictidomys tridecemlineatus*	38	349	47.1	[163/346]	23	33695088	Aerobic respiration, E-donor, glycerol-3-phosphate shuttle
GPD1	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	1609	SA > IBA	1.3	4.3E-02	33695088	*Homo sapiens*	38	74	7.1	[19/269]	5		Aerobic respiration, E-donor, glycerol-3-phosphate shuttle
HADHA	Trifunctional enzyme subunit α	587	Ent > SA	1.4	2.6E-02	E:00000001425	*Ictidomys tridecemlineatus*	81	36	1.4	[10/739]	3	862457	β-oxidation
HADHA	Trifunctional enzyme subunit α	600	Ent > SA	1.7	5.7E-03	E:00000001425	*Ictidomys tridecemlineatus*	81	221	16.2	[120/739]	16	862457	β-oxidation
HADHA	Trifunctional enzyme subunit α	604	Ent > SA	1.7	4.8E-04	E:00000001425	*Ictidomys tridecemlineatus*	81	94	4.1	[30/739]	7	862457	β-oxidation
HADHA	Trifunctional enzyme subunit α	607	SA > Ent	1.4	1.9E-02	E:00000001425	*Ictidomys tridecemlineatus*	81	214	11.8	[87/739]	15	595267	β-oxidation
HADHA	Trifunctional enzyme subunit α	608	LT > SA	1.6	5.7E-03	E:00000001425	*Ictidomys tridecemlineatus*	81	76	3.5	[26/739]	6	862457	β-oxidation
HADHA	Trifunctional enzyme subunit α	609	ET > SA	1.7	3.9E-02	E:00000001425	*Ictidomys tridecemlineatus*	81	135	8.9	[66/739]	10	862457	β-oxidation
HADHA	Trifunctional enzyme subunit α	615	LT > SA	1.5	2.7E-04	E:00000001425	*Ictidomys tridecemlineatus*	81	145	8.9	[66/739]	11	862457	β-oxidation
HBB	β-hemoglobin	2310	LAr > SA	3.6	1.2E-04	999016132	*Urocitellus parryi*	14	136	68.7	[101/147]	9	4504351	O_2 transport
HBB	β-hemoglobin	2316	Ar > SA	3.3	1.2E-04	122689	*Spermophilus townsendii*	16	104	61.6	[90/146]	7	4504351	O_2 transport
HBB	β-hemoglobin	2318	Ar > SA	3.2	2.7E-04	122637	*Marmota marmot marmota*	16	87	44.5	[65/146]	6	4504351	O_2 transport
HIBADH	3-Hydroxyisobutyrate dehydrogenase, mitochondrial	1681	LT > SA	1.4	5.3E-03	E:00000003688	*Ictidomys tridecemlineatus*	32	143	31.8	[95/299]	9	23308751	Valine catabolism
HSPA4	Heat shock 70kDa protein 4	246	SA > Ar	2.1	2.1E-02	4579909	*Homo sapiens*	94	53	4.9	[41/840]	4		Chaperone
HSPB1	Heat shock protein β1	1863	IBA > LAr	3.2	3.0E-05	291390901	*Oryctolagus cuniculus*	23	63	18.1	[37/204]	4	4504517	Stress resistance/actin organization
HSPB1	Heat shock protein β1	1878	Ent >LAr	1.8	1.4E-03	291390901	*Oryctolagus cuniculus*	23	59	18.1	[37/204]	4	4504517	Stress resistance/actin organization
HSPB6	Heat shock protein β6	2073	IBA > LT	3.2	8.2E-03	291412016	*Oryctolagus cuniculus*	17	40	29.6	[48/162]	3	21389433	Response to heat shock, ischemia/reperfusion
HSPB6	Heat shock protein β6	2084	LT > SA	1.6	1.7E-02	E:00000008172	*Ictidomys tridecemlineatus*	17	52	29.4	[47/160]	4	21389433	Response to heat shock, ischemia/reperfusion
HSPD1	60 kDa Heat shock protein, mitochondrial	806	Ar > SD	1.6	4.3E-02	90077962	*Macaca fascicularis*	61	444	39.4	[226/573]	28	31542947	Mitochondrial protein folding
HSPD1	60 kDa Heat shock protein, mitochondrial	812	Ar > SA	1.5	1.3E-02	90077962	*Macaca fascicularis*	61	426	44.7	[256/573]	26	31542947	Mitochondrial protein folding
IDH3A	Isocitrate dehydrogenase [NAD], α subunit	1327	IBA > SA	1.5	1.5E-02	68565568	*Pongo pygmaeus abelii*	40	115	22.7	[65/286]	8	5031777	TCA cycle, redox
IDH3A	Isocitrate dehydrogenase [NAD], α subunit	1350	IBA > SD	1.7	2.3E-02	68565568	*Pongo pygmaeus abelii*	40	153	28.0	[80/286]	11	5031777	TCA cycle, redox
IMMT	Mitofilin	657	Ent > SD	3.6	3.0E-05	E:00000011319	*Ictidomys tridecemlineatus*	83	53	5.3	[39/738]	4	154354964	Mitochondrial crisate morphology

IMMT	Mitofilin	673	Ent > SD	1.4	8.7E-03	E:00000011319	*Ictidomys tridecemlineatus*	83	126	12.5	[92/738]	9	154354964	Mitochondrial crisate morphology
MCCC1	Methylcrotonoyl-CoA carboxylase subunit α, mitochondrial	590	LAr > SA	1.5	3.0E-02	E:00000009303	*Ictidomys tridecemlineatus*	75	54	5.3	[36/678]	4	12276066	Mitochondrial AA degradation
MDH1	Malate dehydrogenase, cytoplasmic	1472	LT > SD	1.6	4.2E-02	E:00000012741	*Ictidomys tridecemlineatus*	36	198	38.1	[127/333]	13	5174539	Malate-aspartate shuttle
MDH1	Malate dehydrogenase, cytoplasmic	1523	LT > SD	1.7	2.6E-02	E:00000012741	*Ictidomys tridecemlineatus*	36	207	47.2	[157/333]	14	5174539	Malate-aspartate shuttle
MDH2	Malate dehydrogenase, mitochondrial	1552	IBA > SA	1.5	2.1E-02	999617	*Sus scrofa*	33	276	60.3	[141/234]	18	2906146	TCA cycle, malate-aspartate shuttle
MRPL12	mitochondrial ribosomal protein L12	2089	LT > LAr	2.2	1.5E-02	E:00000006153	*Ictidomys tridecemlineatus*	19	65	21.3	[37/174]	5	27436901	Mitochondrial protein synthesis
MVP	Major vault protein	269	SD > ET	1.8	4.1E-03	E:00000001327	*Ictidomys tridecemlineatus*	99	279	26.3	[234/889]	20	194378554	Protein signal transduction
MYH4	Myosin heavy chain 4	25	SA > ET	1.8	5.1E-03	67189167	*Mus musculus*	223	100	5.3	[98/1859]	8	153791586	Contraction
NDRG2	N-myc downstream regulated protein family 2	1159	Ent > SD	2.1	9.6E-03	73977281	*Canis familiaris*	41	104	19.7	[73/371]	7	42544211	Sodium absorption, cell proliferation, differentiation
NME2	Nucleoside diphosphate kinase B	2141	SA > ET	3.0	8.2E-03	4505409	*Homo sapiens*	17	94	48.6	[35/72]	7		Nucleoside triphosphate synthesis (non-ATP)
OGDH	2-Oxoglutarate dehydrogenase	275	SD > ET	2.3	1.7E-02	29145087	*Mus musculus*	116	49	5.0	[51/1019]	4	2160381	TCA cycle
OGDH	2-Oxoglutarate dehydrogenase	298	SD > ET	1.5	1.8E-02	85861164	*Mus musculus*	116	87	6.6	[62/943]	6	51873036	TCA cycle
PDHA1	Pyruvate dehydrogenase E1 component, α subunit	1232	IBA > SA	1.8	4.0E-05	74006561	*Canis familiaris*	43	61	6.2	[24/390]	4	4505685	Glycolysis – TCA cycle link
PDHA1	Pyruvate dehydrogenase E1 component, α subunit	1237	ET > SA	1.7	2.7E-04	74006561	*Canis familiaris*	43	119	10.8	[42/390]	8	4505685	Glycolysis – TCA cycle link
PDHA1	Pyruvate dehydrogenase E1 component, α subunit	1238	ET > SA	2.1	9.2E-05	74006561	*Canis familiaris*	43	59	6.2	[24/390]	4	4505685	Glycolysis – TCA cycle link
PDK4	Pyruvate dehydrogenase kinase, isozyme 4	1244	IBA > SD	2.1	1.2E-04	12585306	*Ictidomys tridecemlineatus*	47	173	22.9	[76/332]	11	4505693	Glucose metabolism
PGM1	Glucose phosphomutase 1	737	LAr > Ent	5.3	1.3E-02	E:00000006771	*Ictidomys tridecemlineatus*	62	327	37.3	[212/568]	22	60551975	1-6 phosphate transfer
PGM1	Glucose phosphomutase 1	741	SA > Ent	3.3	2.2E-02	227330633	*Mus musculus*	61	281	37.8	[182/482]	20	60551975	1-6 phosphate transfer
PGM1	Glucose phosphomutase 1	742	SA > Ent	2.0	3.6E-02	73621393	*Macaca fascicularis*	61	161	22.2	[107/482]	11	21361621	1-6 phosphate transfer
PGM1	Glucose phosphomutase 1	749	SD > Ent	1.8	3.0E-02	73621393	*Macaca fascicularis*	61	139	18.9	[91/482]	10	21361621	1-6 phosphate transfer
PGM1	Glucose phosphomutase 1	751	SD > Ent	4.2	7.5E-03	73621393	*Macaca fascicularis*	61	368	52.7	[254/482]	25	21361621	1-6 phosphate transfer
PGM1	Glucose phosphomutase 1	752	Ent > LAr	1.4	3.8E-02	227330633	*Mus musculus*	61	210	24.7	[119/482]	14	189926	1-6 phosphate transfer
PGM1	Glucose phosphomutase 1	757	Ent > LAr	1.8	1.3E-02	E:00000006771	*Ictidomys tridecemlineatus*	62	382	45.1	[256/568]	26	60551975	1-6 phosphate transfer
PKM2	Pyruvate kinase	865	SA > LT	1.7	3.3E-03	3659945	*Oryctolagus cuniculus*	58	292	29.8	[134/450]	19	33286418	Glycolysis
PKM2	Pyruvate kinase	868	SA > LT	1.6	1.6E-02	73916936	*Felis catus*	58	219	24.5	[130/531]	14	33286418	Glycolysis
PKM2	Pyruvate kinase	869	SA > LT	1.7	1.6E-02	67464392	*Homo sapiens*	60	353	31.2	[171/548]	22	189998	Glycolysis
PKM2	Pyruvate kinase	870	SA > Ent	1.7	7.7E-03	74000677	*Canis familiaris*	58	369	39.6	[210/531]	24	33286418	Glycolysis

PKM2	Pyruvate kinase	875	SA > LT	1.6	7.7E-03	157833510	*Felis catus*	58	394	41.9	[222/530]	25	33286418	Glycolysis
PRDX1	Peroxiredoxin 1	1888	LT > SA	1.5	1.3E-03	73977959	*Canis familiaris*	22	132	53.8	[64/119]	10	4505591	Antioxidant function
PRDX3	Peroxiredoxin 3	1866	LT > SD	1.5	1.1E-02	E:00000002268	*Ictidomys tridecemlineatus*	28	144	43.2	[111/257]	9	5802974	Antioxidant function
PSMD14	Proteasome 26S subunit, non-ATPase, 14	1614	SD > LT	1.5	3.2E-03	74004396	*Canis familiaris*	33	60	6.9	[15/219]	4	5031981	Protein degradation via ubiquitin pathway
PYGM	Glycogen phosphorylase	379	SA > LT	1.6	2.3E-02	231257	*Oryctolagus cuniculus*	97	207	17.5	[133/762]	15	5032009	Glycogenolysis
PYGM	Glycogen phosphorylase	388	SA > ET	1.6	2.5E-02	126723305	*Oryctolagus cuniculus*	97	326	25.4	[194/763]	23	5032009	Glycogenolysis
PYGM	Glycogen phosphorylase	412	SA > LT	2.2	7.7E-03	126723305	*Oryctolagus cuniculus*	97	147	11.0	[84/763]	11	5032009	Glycogenolysis
PYGM	Glycogen phosphorylase	414	SA > LT	1.6	2.8E-02	126723305	*Oryctolagus cuniculus*	97	144	11.0	[84/763]	10	5032009	Glycogenolysis
PYGM	Glycogen phosphorylase	423	SA > LT	1.8	4.4E-02	126723305	*Oryctolagus cuniculus*	97	313	24.3	[185/763]	22	5032009	Glycogenolysis
PYGM	Glycogen phosphorylase	520	SD > LT	1.8	1.3E-03	126723305	*Oryctolagus cuniculus*	97	287	21.0	[160/763]	21	5032009	Glycogenolysis
ST13	Heat shock 70kD protein binding protein isoform 4	1002	SD > ET	1.4	2.6E-02	73969009	*Canis familiaris*	25	41	10.7	[23/216]	3	19923193	HSP70-HSP90 association
SUCLA2	Succinate-CoA ligase, β subunit	1182	ET > SD	1.4	5.0E-02	194221896	*Equus caballos*	50	223	23.5	[109/463]	15	11321583	TCA cycle
TBCA	Tubulin folding cofactor A	2194	LT > SA	1.4	3.9E-05	999015971	*Ictidomys tridecemlineatus*	13	128	44.4	[48/108]	8	4759212	β-tubulin folding
TF	Transferrin	525	LAr > SA	1.6	3.8E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	157	19.2	[124/646]	11	4557871	Iron transport
TF	Transferrin	538	LAr > SA	1.6	4.1E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	119	16.6	[107/646]	10	4557871	Iron transport
TF	Transferrin	541	LAr > SA	1.7	3.9E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	225	25.2	[163/646]	16	4557871	Iron transport
TF	Transferrin	542	LAr > SA	1.7	2.5E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	220	26.0	[168/646]	16	4557871	Iron transport
TF	Transferrin	543	LAr > SA	1.6	4.7E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	338	33.8	[218/646]	22	4557871	Iron transport
TF	Transferrin	544	Ent > SA	1.7	1.7E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	133	18.1	[117/646]	10	4557871	Iron transport
TF	Transferrin	548	LAr > SA	1.7	2.5E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	201	26.8	[173/646]	15	4557871	Iron transport
TF	Transferrin	829	Ent > SA	1.6	2.1E-02	E:00000012640	*Ictidomys tridecemlineatus*	72	151	20.9	[135/646]	11	4557871	Iron transport
TPI1	Triosephosphate isomerase 1	1786	SD > Ent	1.6	8.0E-04	17389815	*Homo sapiens*	27	263	79.5	[198/249]	15		Glycolysis and gluconeogenesis
TPT1	Translationally controlled tumor protein	1940	SD > IBA	1.9	4.0E-05	999018489	*Ictidomys tridecemlineatus*	6	32	25.5	[13/51]	2	4507669	Calcium binding and microtubule stabilization
TRAP1	TNF receptor-associated protein 1	625	LT > SA	1.4	6.4E-03	E:00000004451	*Ictidomys tridecemlineatus*	79	64	6.5	[45/695]	4	1082886	Chaperone
TRAP1	TNF receptor-associated protein 1	628	IBA > SA	1.4	2.6E-02	84781723	*Rattus norvegicus*	80	153	18.5	[116/626]	11	1082886	Chaperone
TUBA3D	α-Tubulin	900	Ent > SA	1.3	3.6E-02	67463741	*Bos taurus*	50	300	44.3	[163/368]	19	34784746	Movement, polymerization
TUBB2C	Tubulin β-2C chain	956	Ent > SA	1.4	7.6E-03	5174735	*Homo sapiens*	50	358	38.4	[140/365]	24		Movement, polymerization

UBA1	Ubiquitin-activating enzyme E1	267	SD > ET	1.6	1.3E-04	74007348	*Canis familiaris*	113	38	4.0	[41/1015]	3	23510338	Protein degradation, DNA repair
UBA1	Ubiquitin-activating enzyme E1	276	SD > LAr	1.4	2.6E-02	23510338	*Homo sapiens*	118	36	1.4	[14/978]	3		Protein degradation, DNA repair
UBA1	Ubiquitin-activating enzyme E1	310	SD > LAr	1.5	2.6E-02	126722847	*Oryctolagus cuniculus*	118	195	14.5	[142/978]	14	23510338	Protein degradation, DNA repair
UBA52	Polyubiquitin – ubiquitin moiety fusion product	2386	LT > Ent	1.8	1.3E-02	940395	*Cricetulus sp.*	74	41	5.8	[38/658]	3	4507761	Protein degradation
VCL	Vinculin	241	LT > SD	1.3	4.1E-02	194206025	*Equus caballos*	124	359	17.2	[195/1134]	23	4507877	Cytoskeleton, cell-cell and cell-matrix junctions, F-actin anchoring
WARS	Tryptophanyl-tRNA synthetase, cytoplasmic isoform 2	957	Ar >s SA	1.3	4.2E-02	256818746	*Mus musculus*	54	44	7.3	[29/395]	3	47419914	Translation
YWHAG	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, γ polypeptide	1687	Ent > SA	1.2	4.1E-03	82407948	*Homo sapiens*	28	166	30.1	[50/166]	11	193785841	Signal transduction

Official gene symbols and names are listed for each unequivocally identified protein which differed significantly among sampled states by ANOVA after multiple test correction (*q* value). Supporting protein identification information such as recovered peptides and score are included. Maximum pairwise fold change between sampled states are reported (states which produced this fold change are also noted). Ensembl accession numbers all begin with ENSSTOP, and are denoted by ‘E:’.