

Supplementary Table 2: Identified Significant Proteins of Random Forests, ANOVA and t-tests.

Gene	ID	Spot	q	Fold Δ	Fold stage	Season Δ	GI or Ensembl No.	Species	MW (kDa)	Score	Amino Acid Coverage		# Pep.	Human	Function
											%	Ratio			
A2M [†]	α ₂ -Macroglobulin	105	0.002	3.61	E-Ar: SpD	2.60 W	157954061	<i>Ictidomys tridecemlineatus</i>	163	69	4	[65/1463]	5	66932947	Protease inhibitor
ACADVL [‡]	Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial	510	0.025			1.27 W	73955386	<i>Canis familiaris</i>	70	205	31	[199/650]	15	4557235	Fatty acid β-oxidation
ACO2	Aconitase 2, mitochondrial	309	0.010	1.43	LT: FT		27806769	<i>Bos Taurus</i>	85	135	15	[104/700]	10	4501867	TCA cycle
ACO2	Aconitase 2, mitochondrial	310	0.007	1.44	LT: FT		27806769	<i>Bos Taurus</i>	85	198	23	[163/700]	14	4501867	TCA cycle
ACO2	Aconitase 2, mitochondrial	312	0.006	1.47	LT: FT		74268076	<i>Bos Taurus</i>	85	219	25	[198/780]	16	4501867	TCA cycle
ACO2	Aconitase 2, mitochondrial	316	0.007	1.43	LT: FT		74268076	<i>Bos Taurus</i>	85	374	41	[317/780]	26	4501867	TCA cycle
ACO2	Aconitase 2, mitochondrial	319	0.018	1.40	LT: FT		74268076	<i>Bos Taurus</i>	85	396	41	[320/780]	27	4501867	TCA cycle
ACSS1	Acetyl-coenzyme A synthetase 2	359	0.039	1.46	FA: LT		157818027	<i>Rattus norvegicus</i>	75	125	19	[113/602]	9	28416953	Carbohydrate metabolism
ACTC1	Actin, α cardiac muscle 1	870	0.021	1.91	Ent: FT		4885049	<i>Homo sapiens</i>	42	139	41	[121/297]	10		Cardiac muscle contraction
ALB	Albumin	436	0.016	3.24	FT: SpD		30794280	<i>Bos Taurus</i>	69	469	52	[273/527]	27	4502027	Lipid binding
ALB	Albumin	462	0.020	2.49	FT: SpD		E: 11284	<i>Ictidomys tridecemlineatus</i>	69	37	6	[37/606]	3	4502027	Lipid binding
ALB [†]	Albumin	423	0.038	2.47	E-Ar: SpD	1.73 W	E: 11284	<i>Ictidomys tridecemlineatus</i>	69	139	11	[66/606]	7	4502027	Lipid binding
ALDOC	Fructose-bisphosphate aldolase C	1045	0.050	1.57	SpD: Ent		4885063	<i>Homo sapiens</i>	39	30	8	[23/284]	2		Glycolysis and Gluconeogenesis
ANXA5	Annexin A5	1206	0.011	1.49	IBA: SA		149698420	<i>Equus caballus</i>	36	107	27	[88/321]	8	4502107	Regulation of coagulation and apoptosis
APOA1 [†]	Apolipoprotein A-I	1449	0.011	4.01	FT: SpD	1.83 W	E: 02077	<i>Ictidomys tridecemlineatus</i>	31	90	23	[62/267]	6	4557321	Lipid transport
APOA1 [†]	Apolipoprotein A-I	1476	0.003	3.81	E-Ar: SpD	2.05 W	E: 02077	<i>Ictidomys tridecemlineatus</i>	31	58	18	[48/267]	4	4557321	Lipid transport
APOA1 ^{TS}	Apolipoprotein A-I	1486	0.007	4.38	FT: SpD	2.13 W	E: 02077	<i>Ictidomys tridecemlineatus</i>	31	113	30	[80/267]	8	4557321	Lipid transport
ATP5H [‡]	ATP synthase subunit d	1642	0.044			1.21 S	57108097	<i>Canis familiaris</i>	19	86	39	[63/161]	6	5453559	ATP synthesis
BCKDHB [†]	2-Oxoisovalerate dehydrogenase subunit β	1144	0.009	1.37	SpD: LT	1.26 S	4557353	<i>Homo sapiens</i>	43	95	19	[58/312]	6		Branched chain amino acid catabolism
CCT5 [‡]	T-complex protein 1 subunit ε	526	6.E-05			1.16 W	194676636	<i>Bos Taurus</i>	60	104	15	[80/541]	8	24307939	Protein Folding
CCT7	Chaperonin containing TCP1, subunit 7 (eta)	577	0.026	1.36	E-Ar: FA		114051425	<i>Bos Taurus</i>	59	161	31	[142/463]	12	5453607	Protein folding
CCT7 [†]	Chaperonin containing TCP1, subunit 7 (eta)	581	0.011	1.31	IBA: SpD	1.19 W	126344936	<i>Monodelphis domestica</i>	63	103	21	[120/582]	8	5453607	Protein folding
CFL2 ^{TS}	Cofilin-2	1727	2.E-10	7.02	SA: LT	2.76 S	14719392	<i>Homo sapiens</i>	19	151	53	[46/86]	11		Actin regulation
CKM	Muscle creatine kinase	1040	0.023	1.30	SA: IBA		6671762	<i>Mus musculus</i>	43	120	32	[97/301]	8	21536288	Phosphocreatine metabolism
CKM	Muscle creatine kinase	1042	0.003	1.30	FA: IBA		126723370	<i>Oryctolagus cuniculus</i>	43	113	29	[111/381]	8	21536288	Phosphocreatine metabolism
CKM	Muscle creatine kinase	1043	0.008	1.30	FA: IBA		126723370	<i>Oryctolagus cuniculus</i>	43	161	42	[127/301]	11	21536288	Phosphocreatine metabolism
CKM	Muscle creatine kinase	1044	0.021	1.52	FA: Ent		60097925	<i>Bos Taurus</i>	43	117	36	[109/301]	8	21536288	Phosphocreatine metabolism
COQ9	Coenzyme Q9 ubiquinone biosynthesis protein	1225	0.043	1.21	FA: LT		E: 13571	<i>Ictidomys tridecemlineatus</i>	36	36	12	[37/318]	3	40789233	Ubiquinone biosynthesis
CRAT [†]	Carnitine O-acetyltransferase	524	0.018	1.59	IBA: SA	1.41 W	59802828	<i>Mus musculus</i>	71	79	12	[76/626]	6	21618331	Fatty acid β-oxidation
CRAT [‡]	Carnitine O-acetyltransferase	523	0.028			1.28 W	59802828	<i>Mus musculus</i>	71	97	14	[85/626]	7	21618331	Fatty acid β-oxidation
DBT ^{TS}	Dihydroliipoamide branched chain transacylase E2	750	7.E-10	1.59	SA: IBA	1.45 S	197097826	<i>Pongo abelii</i>	58	66	12	[53/444]	5	110671329	Branched chain amino acid catabolism
DLD	Dihydroliipoamide dehydrogenase	629	0.010	1.30	SA: LT		62088986	<i>Homo sapiens</i>	54	177	31	[159/509]	12		Acetyl-CoA biosynthesis from pyruvate
DLST [†]	Dihydroliipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	734	0.032	1.17	SA: LT	1.12 S	E:13084	<i>Ictidomys tridecemlineatus</i>	49	142	19	[87/453]	9	19923748	Lysine metabolism
ECHS1	Mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	1414	0.018	1.31	SpD: FT		90076340	<i>Macaca fascicularis</i>	32	37	4	[12/290]	3	4505369	Fatty acid β-oxidation
EC11 [†]	Dodecenoyl-CoA isomerase	1388	0.023	1.44	IBA: SA	1.23 W	E: 11815	<i>Ictidomys tridecemlineatus</i>	33	59	19	[57/302]	4	62530384	Fatty acid β-oxidation
EEF2 [†]	Eukaryotic translation elongation factor 2	212	0.003	1.71	E-Ar: SpD	1.32 W	55730085	<i>Pongo abelii</i>	95	178	18	[153/858]	16	4503483	Translational elongation
EEF2 [†]	Eukaryotic translation elongation factor 2	223	0.003	1.69	FT: SpD	1.34 W	4503483	<i>Homo sapiens</i>	95	167	16	[125/778]	12		Translational elongation
FABP3 ^{TS}	Fatty acid-binding protein 3, heart	1904	0.033	1.37	E-Ar: SA	1.29 W	20138311	<i>Ictidomys tridecemlineatus</i>	15	41	11	[14/133]	3	4758328	Fatty acid transport
FABP3 [‡]	Fatty acid-binding protein 3, heart	1865	0.009			1.26 W	20138311	<i>Ictidomys tridecemlineatus</i>	15	68	23	[30/133]	5	4758328	Fatty acid transport
FABP3 [‡]	Fatty acid-binding protein 3, heart	1892	0.018			1.24 W	20138311	<i>Ictidomys tridecemlineatus</i>	15	74	18	[24/133]	5	4758328	Fatty acid transport
FABP3 [‡]	Fatty acid-binding protein 3, heart	1903	0.005			1.26 W	20138311	<i>Ictidomys tridecemlineatus</i>	15	81	23	[30/133]	6	4758328	Fatty acid transport
FAM82B [‡]	Regulator of microtubule dynamics protein 1	1436	0.044			1.22 W	194037093	<i>Sus scrofa</i>	36	71	19	[61/314]	6	116875831	Microtubule binding
HADHA	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase, α subunit	380	0.029	2.36	FT: FA		E: 01425	<i>Ictidomys tridecemlineatus</i>	83	308	27	[198/739]	18	161086967	Fatty acid beta-oxidation
HSP90AB1	Heat shock protein 90kDa α (cytosolic), class B member 1	285	0.003	1.38	FT: SA		6807647	<i>Homo sapiens</i>	85	182	20	[146/737]	14		Protein folding

HSPA4 ^{†§}	Heat shock 70kDa protein 4	161	5.E-04	1.45	E-Ar: SA	1.31 W	38327039	<i>Homo sapiens</i>	94	83	7	[53/760]	6		Protein folding
HSPA9	Stress-70 protein, mitochondrial	438	0.026	2.00	FT: SpD		435839	<i>Mus musculus</i>	73	223	32	[214/679]	15	24234688	Protein folding
HSPA9	Stress-70 protein, mitochondrial	446	0.018	2.97	FT: SpD		14917005	<i>Mus musculus</i>	74	77	13	[77/599]	6	24234688	Protein folding
HSPA9	Stress-70 protein, mitochondrial	453	0.023	3.44	FT: SpD		14917005	<i>Mus musculus</i>	74	40	6	[37/599]	3	24234688	Protein folding
HSPB2	Heat shock 27 kDa protein 2	1614	0.011	1.37	SpD: FA		149716491	<i>Equus caballus</i>	20	47	29	[52/182]	3	4504519	Response to heat stress
HSPB6	Heat shock protein, α -crystallin-related, β -6	1709	0.037	1.48	IBA: SA		E: 08172	<i>Ictidomys tridecemlineatus</i>	17	46	24	[38/160]	4	21389433	Cardioprotection from I/R injury
KBTBD10 [†]	Ke1-like protein 23	442	0.021	1.38	LT: SA	1.26 W	57110617	<i>Canis familiaris</i>	68	240	22	[133/606]	14	42741669	Protein catabolic process
LDHB	Lactate dehydrogenase B	1178	0.043	1.36	FA: Ent		109114055	<i>Macaca mulatta</i>	37	199	45	[150/334]	14	291575128	Glucose catabolic process
LONP1	Lon protease-like protein	200	0.011	1.24	FA: LT		429100	<i>Homo sapiens</i>	104	110	12	[105/857]	8		Response to oxidative stress
LONP1	Lon protease-like protein	206	0.017	1.28	FT: Ent		429100	<i>Homo sapiens</i>	104	79	7	[64/857]	6		Response to oxidative stress
MDH1	Cytosolic malate dehydrogenase	1162	0.026	1.22	FA: Ent		387129	<i>Mus musculus</i>	36	81	25	[63/254]	6	5174539	Pyruvate metabolism
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	352	0.039	1.38	FT: LT		67970033	<i>Macaca fascicularis</i>	80	179	20	[144/727]	12	33519475	Oxidative phosphorylation
NDUFS4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4	1685	0.011	1.36	SA: E-Ar		28461229	<i>Bos Taurus</i>	20	112	43	[41/95]	7	4505369	Oxidative phosphorylation
OGDH	Oxoglutarate dehydrogenase (lipoamide)	201	0.045	1.30	FT: LT		149047673	<i>Rattus norvegicus</i>	118	289	22	[223/1034]	20	51873036	Glucose metabolism
OXCT1 [†]	3-Oxoacid CoA transferase 1	691	0.006	1.78	Ent: SA	1.50 W	4557817	<i>Homo sapiens</i>	56	58	8	[35/440]	4		Lipid metabolism
OXCT1 [†]	3-Oxoacid CoA transferase 1	692	0.011	1.57	Ent: SA	1.35 W	4557817	<i>Homo sapiens</i>	56	97	15	[68/440]	7		Lipid metabolism
OXCT1 ^{†§}	3-Oxoacid CoA transferase 1	700	0.002	1.84	Ent: SA	1.54 W	109077088	<i>Macaca mulatta</i>	56	101	20	[86/440]	7	4557817	Lipid metabolism
PARK7	Protein DJ-1	1660	0.048	1.38	FT: IBA		149695427	<i>Equus caballus</i>	20	59	24	[45/189]	5	31543380	Response to oxidative stress
PCBP1 [†]	Poly(rC) binding protein 1	1087	0.002	1.53	SA: IBA	1.25 S	460771	<i>Homo sapiens</i>	38	40	11	[38/356]	3		RNA splicing
PCCA [†]	Propionyl Coenzyme A carboxylase, α polypeptide	425	0.001	1.37	SA: LT	1.18 S	73989252	<i>Canis familiaris</i>	81	243	29	[209/731]	17	189095269	Lipid metabolism
PDHA1 [†]	Pyruvate dehydrogenase E1 component α subunit	976	0.011	1.95	IBA: SA	1.56 W	74006565	<i>Canis familiaris</i>	40	113	23	[82/359]	8	4505685	TCA cycle
PDHB	Pyruvate dehydrogenase (lipoamide) β	1218	0.020	1.51	LT: FA		156564403	<i>Homo sapiens</i>	39	50	6	[16/279]	3		TCA cycle
PDHB	Pyruvate dehydrogenase (lipoamide) β	1221	0.021	1.30	SpD: FT		156564403	<i>Homo sapiens</i>	39	75	14	[38/279]	5		TCA cycle
PDHB [†]	Pyruvate dehydrogenase (lipoamide) β	1343	0.007	2.16	FT: SpD	1.78 W	73985155	<i>Canis familiaris</i>	37	32	9	[32/341]	2	156564403	TCA cycle
PDHX [†]	Pyruvate Dehydrogenase Protein X	748	0.018	1.23	SpD: LT	1.16 S	90075986	<i>Macaca fascicularis</i>	54	50	9	[46/501]	4	203098753	TCA cycle
PDIA3	Protein disulfide isomerase family A, member 3	647	0.018	1.71	LT: FA		217030873	<i>Oryctolagus cuniculus</i>	56	222	39	[195/502]	16	21361657	ER glycoprotein folding
PDP1 [†]	Pyruvate dehydrogenase phosphatase	643	0.046	1.38	E-Ar: SA	1.30 W	73999591	<i>Canis familiaris</i>	82	174	18	[130/738]	11	45439339	Regulation of Pyruvate dehydrogenase
PPP2R1A	α Isoform of regulatory subunit A, protein phosphatase 2	493	0.017	1.27	FT: Ent		21361399	<i>Homo sapiens</i>	65	111	23	[117/509]	9		Regulation of cell growth
SDHA	Succinate dehydrogenase Fp subunit	463	0.036	1.30	FT: IBA		54607098	<i>Mus musculus</i>	73	152	25	[147/584]	11	156416003	Acetyl-CoA metabolic process
STOML2	Stomatin-like protein 2	1028	0.045	1.44	FT: SpD		E: 13653	<i>Ictidomys tridecemlineatus</i>	39	42	14	[50/356]	3	7305503	Mitochondrial sodium/calcium exchange
SUCLG2	Succinate-CoA ligase, GDP-forming β -subunit	877	0.010	1.42	Ent: FT		291393975	<i>Oryctolagus cuniculus</i>	47	86	14	[60/432]	7	157779135	Succinyl-CoA metabolism
TCP1 [†]	T-complex protein 1 subunit α isoform a	609	0.002			1.14 W	186973225	<i>Oryctolagus cuniculus</i>	60	123	19	[107/556]	9	57863257	Protein Folding
TF	Transferrin	333	0.038	2.34	FT: IBA		30909317	<i>Marmota monax</i>	76	144	15	[104/694]	11	4557871	Iron ion transport
TTR ^{†§}	Transthyretin precursor	1878	0.011	2.72	FT: IBA	1.76 S	E: 06729	<i>Ictidomys tridecemlineatus</i>	16	50	35	[51/147]	4	4507725	Thyroid hormone transmembrane transport
YWHAQ ^{†§}	14-3-3 Protein θ isoform 3	1314	6.E-06	1.39	IBA: SA	1.28 W	73979716	<i>Canis familiaris</i>	25	32	11	[25/229]	2	5803227	Inhibition of apoptosis

Spots uniquely identified based on the criteria detailed in methods are listed. Columns are: official symbol (gene), protein identification of match (ID), spot number on master gel (Spot), False Discovery Rate adjusted p-value (q), greatest fold change between mean spot abundances of any two groups (Fold Δ), groups that produced greatest fold change (Fold stage, group in bold has higher mean abundance), fold change between summer homeothermic and winter heterothermic groups for t -test significant spots (Season Δ , W or S indicates abundance is elevated in winter or summer groups, respectively), NCBI GenInfo Identifier or Ensembl protein identifier (GI or Ensembl No.; E: abbreviated for Ensembl protein prefix ENSSTOP000000), species for this GI (Species), molecular mass for this GI (MW, kDa), Spectrum Mill protein score (Score), percent of amino acid coverage (%), ratio of quantity of recovered amino acids over total amino acids (Ratio), number of distinct peptides matched (# pep.), human homolog NCBI GenInfo Identifier (Human), possible function based on NCBI "Gene" information (Function); TCA cycle, tricarboxylic acid cycle; ER, endoplasmic reticulum. Within Gene column: † indicates protein significant by both ANOVA and t -test – q reflects ANOVA adjusted p -value; ‡ indicates protein significant by t -test only – q reflects t -test adjusted p -value; § indicates top Random Forests identifier (Fig. 4); otherwise, spots significant by ANOVA.