

Supporting Information

Microproteomic-Based Analysis of the Goat Milk Protein Synthesis Network and Casein Production Evaluation

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Table S1. Pathway annotation analysis of identified proteins in GMECs

	Pathway	Proteins with pathway annotation (3055)	Pathway ID	Level1	Level2
1	Metabolic pathways	472 (15.45%)	ko01100	Metabolism	Global and overview maps
2	Pathways in cancer	121 (3.96%)	ko05200	Human Diseases	Cancers: Overview
3	Endocytosis	117 (3.83%)	ko04144	Cellular Processes	Transport and catabolism
4	Ribosome	111 (3.63%)	ko03010	Genetic Information Processing	Translation
5	Spliceosome	108 (3.54%)	ko03040	Genetic Information Processing	Transcription
6	Thermogenesis	108 (3.54%)	ko04714	Organismal Systems	Environmental adaptation
7	Human papillomavirus infection	106 (3.47%)	ko05165	Human Diseases	Infectious diseases: Viral
8	Huntington disease	103 (3.37%)	ko05016	Human Diseases	Neurodegenerative diseases
9	RNA transport	102 (3.34%)	ko03013	Genetic Information Processing	Translation
10	Alzheimer disease	100 (3.27%)	ko05010	Human Diseases	Neurodegenerative diseases
11	Regulation of actin cytoskeleton	95 (3.11%)	ko04810	Cellular Processes	Cell motility
12	Protein processing in endoplasmic reticulum	95 (3.11%)	ko04141	Genetic Information Processing	Folding, sorting and degradation
13	Oxidative phosphorylation	89 (2.91%)	ko00190	Metabolism	Energy metabolism
14	Parkinson disease	89 (2.91%)	ko05012	Human Diseases	Neurodegenerative diseases
15	Focal adhesion	89 (2.91%)	ko04510	Cellular Processes	Cellular community - eukaryotes
16	PI3K-Akt signaling pathway	86 (2.82%)	ko04151	Environmental Information Processing	Signal transduction
17	Tight junction	81 (2.65%)	ko04530	Cellular Processes	Cellular community - eukaryotes
18	Carbon metabolism	81 (2.65%)	ko01200	Metabolism	Global and overview maps
19	Human immunodeficiency virus 1 infection	78 (2.55%)	ko05170	Human Diseases	Infectious diseases: Viral
20	Proteoglycans in cancer	75 (2.45%)	ko05205	Human Diseases	Cancers: Overview
21	Viral carcinogenesis	75 (2.45%)	ko05203	Human Diseases	Cancers: Overview
22	Phagosome	74 (2.42%)	ko04145	Cellular Processes	Transport and catabolism
23	Non-alcoholic fatty liver disease (NAFLD)	72 (2.36%)	ko04932	Human Diseases	Endocrine and metabolic diseases
24	Epstein-Barr virus infection	68 (2.23%)	ko05169	Human Diseases	Infectious diseases: Viral
25	Human cytomegalovirus infection	66 (2.16%)	ko05163	Human Diseases	Infectious diseases: Viral
26	MAPK signaling pathway	66 (2.16%)	ko04010	Environmental Information Processing	Signal transduction
27	Influenza A	62 (2.03%)	ko05164	Human Diseases	Infectious diseases: Viral
28	Cellular senescence	56 (1.83%)	ko04218	Cellular Processes	Cell growth and death
29	Necroptosis	56 (1.83%)	ko04217	Cellular Processes	Cell growth and death
30	Herpes simplex infection	55 (1.8%)	ko05168	Human Diseases	Infectious diseases: Viral
31	Apoptosis	54 (1.77%)	ko04210	Cellular Processes	Cell growth and death

32	Lysosome	53 (1.73%)	ko04142	Cellular Processes	Transport and catabolism
33	Human T-cell leukemia virus 1 infection	53 (1.73%)	ko05166	Human Diseases	Infectious diseases: Viral
34	Ras signaling pathway	52 (1.7%)	ko04014	Environmental Information Processing	Signal transduction
35	mRNA surveillance pathway	52 (1.7%)	ko03015	Genetic Information Processing	Translation
36	Hepatitis C	52 (1.7%)	ko05160	Human Diseases	Infectious diseases: Viral
37	Retrograde endocannabinoid signaling	51 (1.67%)	ko04723	Organismal Systems	Nervous system
38	Bacterial invasion of epithelial cells	51 (1.67%)	ko05100	Human Diseases	Infectious diseases: Bacterial
39	Kaposi sarcoma-associated herpesvirus infection	49 (1.6%)	ko05167	Human Diseases	Infectious diseases: Viral
40	Rap1 signaling pathway	49 (1.6%)	ko04015	Environmental Information Processing	Signal transduction
41	MicroRNAs in cancer	49 (1.6%)	ko05206	Human Diseases	Cancers: Overview
42	Biosynthesis of amino acids	49 (1.6%)	ko01230	Metabolism	Global and overview maps
43	Platelet activation	49 (1.6%)	ko04611	Organismal Systems	Immune system
44	Estrogen signaling pathway	48 (1.57%)	ko04915	Organismal Systems	Endocrine system
45	Adrenergic signaling in cardiomyocytes	47 (1.54%)	ko04261	Organismal Systems	Circulatory system
46	Hippo signaling pathway	46 (1.51%)	ko04390	Environmental Information Processing	Signal transduction
47	Ubiquitin mediated proteolysis	46 (1.51%)	ko04120	Genetic Information Processing	Folding, sorting and degradation
48	cGMP-PKG signaling pathway	46 (1.51%)	ko04022	Environmental Information Processing	Signal transduction
49	Tuberculosis	46 (1.51%)	ko05152	Human Diseases	Infectious diseases: Bacterial
50	Leukocyte transendothelial migration	46 (1.51%)	ko04670	Organismal Systems	Immune system
51	Salmonella infection	46 (1.51%)	ko05132	Human Diseases	Infectious diseases: Bacterial
52	Purine metabolism	45 (1.47%)	ko00230	Metabolism	Nucleotide metabolism
53	NOD-like receptor signaling pathway	45 (1.47%)	ko04621	Organismal Systems	Immune system
54	Fluid shear stress and atherosclerosis	44 (1.44%)	ko05418	Human Diseases	Cardiovascular diseases
55	Ribosome biogenesis in eukaryotes	44 (1.44%)	ko03008	Genetic Information Processing	Translation
56	mTOR signaling pathway	44 (1.44%)	ko04150	Environmental Information Processing	Signal transduction
57	Proteasome	44 (1.44%)	ko03050	Genetic Information Processing	Folding, sorting and degradation
58	Hepatocellular carcinoma	43 (1.41%)	ko05225	Human Diseases	Cancers: Specific types
59	Pathogenic Escherichia coli infection	43 (1.41%)	ko05130	Human Diseases	Infectious diseases: Bacterial
60	Axon guidance	43 (1.41%)	ko04360	Organismal Systems	Development
61	cAMP signaling pathway	43 (1.41%)	ko04024	Environmental Information Processing	Signal transduction
62	Oocyte meiosis	43 (1.41%)	ko04114	Cellular Processes	Cell growth and death
63	Chemokine signaling pathway	43 (1.41%)	ko04062	Organismal Systems	Immune system
64	Hepatitis B	42 (1.37%)	ko05161	Human Diseases	Infectious diseases: Viral
65	Insulin signaling pathway	42 (1.37%)	ko04910	Organismal Systems	Endocrine system
66	Oxytocin signaling pathway	41 (1.34%)	ko04921	Organismal Systems	Endocrine system
67	Autophagy - animal	40 (1.31%)	ko04140	Cellular Processes	Transport and catabolism

68	Dilated cardiomyopathy (DCM)	40 (1.31%)	ko05414	Human Diseases	Cardiovascular diseases
69	Sphingolipid signaling pathway	40 (1.31%)	ko04071	Environmental Information Processing	Signal transduction
70	Shigellosis	40 (1.31%)	ko05131	Human Diseases	Infectious diseases: Bacterial
71	Valine, leucine and isoleucine degradation	40 (1.31%)	ko00280	Metabolism	Amino acid metabolism
72	Glycolysis / Gluconeogenesis	38 (1.24%)	ko00010	Metabolism	Carbohydrate metabolism
73	Adherens junction	37 (1.21%)	ko04520	Cellular Processes	Cellular community - eukaryotes
74	RNA degradation	37 (1.21%)	ko03018	Genetic Information Processing	Folding, sorting and degradation
75	Cardiac muscle contraction	37 (1.21%)	ko04260	Organismal Systems	Circulatory system
76	Alcoholism	36 (1.18%)	ko05034	Human Diseases	Substance dependence
77	Complement and coagulation cascades	36 (1.18%)	ko04610	Organismal Systems	Immune system
78	Cell cycle	36 (1.18%)	ko04110	Cellular Processes	Cell growth and death
79	Toxoplasmosis	36 (1.18%)	ko05145	Human Diseases	Infectious diseases: Parasitic
80	Apelin signaling pathway	36 (1.18%)	ko04371	Environmental Information Processing	Signal transduction
81	Hypertrophic cardiomyopathy (HCM)	36 (1.18%)	ko05410	Human Diseases	Cardiovascular diseases
82	HIF-1 signaling pathway	35 (1.15%)	ko04066	Environmental Information Processing	Signal transduction
83	Fc gamma R-mediated phagocytosis	35 (1.15%)	ko04666	Organismal Systems	Immune system
84	Dopaminergic synapse	35 (1.15%)	ko04728	Organismal Systems	Nervous system
85	Neurotrophin signaling pathway	34 (1.11%)	ko04722	Organismal Systems	Nervous system
86	Amoebiasis	34 (1.11%)	ko05146	Human Diseases	Infectious diseases: Parasitic
87	Amino sugar and nucleotide sugar metabolism	33 (1.08%)	ko00520	Metabolism	Carbohydrate metabolism
88	ECM-receptor interaction	33 (1.08%)	ko04512	Environmental Information Processing	Signaling molecules and interaction
89	AGE-RAGE signaling pathway in diabetic complications	33 (1.08%)	ko04933	Human Diseases	Endocrine and metabolic diseases
90	Measles	32 (1.05%)	ko05162	Human Diseases	Infectious diseases: Viral
91	Vibrio cholerae infection	32 (1.05%)	ko05110	Human Diseases	Infectious diseases: Bacterial
92	MAPK signaling pathway - fly	32 (1.05%)	ko04013	Environmental Information Processing	Signal transduction
93	Legionellosis	32 (1.05%)	ko05134	Human Diseases	Infectious diseases: Bacterial
94	AMPK signaling pathway	32 (1.05%)	ko04152	Environmental Information Processing	Signal transduction
95	Fatty acid metabolism	31 (1.01%)	ko01212	Metabolism	Global and overview maps
96	Vascular smooth muscle contraction	31 (1.01%)	ko04270	Organismal Systems	Circulatory system
97	Relaxin signaling pathway	30 (0.98%)	ko04926	Organismal Systems	Endocrine system
98	Cushing syndrome	30 (0.98%)	ko04934	Human Diseases	Endocrine and metabolic diseases
99	Calcium signaling pathway	30 (0.98%)	ko04020	Environmental Information Processing	Signal transduction
100	Wnt signaling pathway	30 (0.98%)	ko04310	Environmental Information Processing	Signal transduction
101	Hippo signaling pathway - fly	30 (0.98%)	ko04391	Environmental Information Processing	Signal transduction
102	Drug metabolism - other enzymes	29 (0.95%)	ko00983	Metabolism	Xenobiotics biodegradation and metabolism

103	Pyruvate metabolism	29 (0.95%)	ko00620	Metabolism	Carbohydrate metabolism
104	Phospholipase D signaling pathway	29 (0.95%)	ko04072	Environmental Information Processing	Signal transduction
105	Aminoacyl-tRNA biosynthesis	29 (0.95%)	ko00970	Genetic Information Processing	Translation
106	Viral myocarditis	29 (0.95%)	ko05416	Human Diseases	Cardiovascular diseases
107	Fatty acid degradation	28 (0.92%)	ko00071	Metabolism	Lipid metabolism
108	Epithelial cell signaling in Helicobacter pylori infection	28 (0.92%)	ko05120	Human Diseases	Infectious diseases: Bacterial
109	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	28 (0.92%)	ko05412	Human Diseases	Cardiovascular diseases
110	Gap junction	28 (0.92%)	ko04540	Cellular Processes	Cellular community - eukaryotes
111	Citrate cycle (TCA cycle)	28 (0.92%)	ko00020	Metabolism	Carbohydrate metabolism
112	Chagas disease (American trypanosomiasis)	28 (0.92%)	ko05142	Human Diseases	Infectious diseases: Parasitic
113	Cysteine and methionine metabolism	27 (0.88%)	ko00270	Metabolism	Amino acid metabolism
114	Renal cell carcinoma	27 (0.88%)	ko05211	Human Diseases	Cancers: Specific types
115	Thyroid hormone signaling pathway	27 (0.88%)	ko04919	Organismal Systems	Endocrine system
116	Synaptic vesicle cycle	27 (0.88%)	ko04721	Organismal Systems	Nervous system
117	IL-17 signaling pathway	27 (0.88%)	ko04657	Organismal Systems	Immune system
118	C-type lectin receptor signaling pathway	27 (0.88%)	ko04625	Organismal Systems	Immune system
119	Antigen processing and presentation	27 (0.88%)	ko04612	Organismal Systems	Immune system
120	Chronic myeloid leukemia	26 (0.85%)	ko05220	Human Diseases	Cancers: Specific types
121	Glucagon signaling pathway	26 (0.85%)	ko04922	Organismal Systems	Endocrine system
122	Glutathione metabolism	26 (0.85%)	ko00480	Metabolism	Metabolism of other amino acids
123	Platinum drug resistance	25 (0.82%)	ko01524	Human Diseases	Drug resistance: Antineoplastic
124	Arginine and proline metabolism	25 (0.82%)	ko00330	Metabolism	Amino acid metabolism
125	Gastric cancer	25 (0.82%)	ko05226	Human Diseases	Cancers: Specific types
126	Pertussis	25 (0.82%)	ko05133	Human Diseases	Infectious diseases: Bacterial
127	Colorectal cancer	25 (0.82%)	ko05210	Human Diseases	Cancers: Specific types
128	GnRH signaling pathway	25 (0.82%)	ko04912	Organismal Systems	Endocrine system
129	TNF signaling pathway	25 (0.82%)	ko04668	Environmental Information Processing	Signal transduction
130	Transcriptional misregulation in cancer	25 (0.82%)	ko05202	Human Diseases	Cancers: Overview
131	Central carbon metabolism in cancer	25 (0.82%)	ko05230	Human Diseases	Cancers: Overview
132	Cell adhesion molecules (CAMs)	25 (0.82%)	ko04514	Environmental Information Processing	Signaling molecules and interaction
133	Pyrimidine metabolism	24 (0.79%)	ko00240	Metabolism	Nucleotide metabolism
134	Small cell lung cancer	24 (0.79%)	ko05222	Human Diseases	Cancers: Specific types
135	Lysine degradation	24 (0.79%)	ko00310	Metabolism	Amino acid metabolism
136	Peroxisome	24 (0.79%)	ko04146	Cellular Processes	Transport and catabolism

137	FoxO signaling pathway	24 (0.79%)	ko04068	Environmental Information Processing	Signal transduction
138	T cell receptor signaling pathway	24 (0.79%)	ko04660	Organismal Systems	Immune system
139	Systemic lupus erythematosus	24 (0.79%)	ko05322	Human Diseases	Immune diseases
140	Toll-like receptor signaling pathway	23 (0.75%)	ko04620	Organismal Systems	Immune system
141	Long-term potentiation	23 (0.75%)	ko04720	Organismal Systems	Nervous system
142	NF-kappa B signaling pathway	23 (0.75%)	ko04064	Environmental Information Processing	Signal transduction
143	Insulin resistance	23 (0.75%)	ko04931	Human Diseases	Endocrine and metabolic diseases
144	Propanoate metabolism	23 (0.75%)	ko00640	Metabolism	Carbohydrate metabolism
145	Pancreatic cancer	23 (0.75%)	ko05212	Human Diseases	Cancers: Specific types
146	Progesterone-mediated oocyte maturation	23 (0.75%)	ko04914	Organismal Systems	Endocrine system
147	Longevity regulating pathway - worm	23 (0.75%)	ko04212	Organismal Systems	Aging
148	Ferroptosis	23 (0.75%)	ko04216	Cellular Processes	Cell growth and death
149	p53 signaling pathway	22 (0.72%)	ko04115	Cellular Processes	Cell growth and death
150	Osteoclast differentiation	22 (0.72%)	ko04380	Organismal Systems	Development
151	Glutamatergic synapse	22 (0.72%)	ko04724	Organismal Systems	Nervous system
152	ErbB signaling pathway	22 (0.72%)	ko04012	Environmental Information Processing	Signal transduction
153	Cholinergic synapse	21 (0.69%)	ko04725	Organismal Systems	Nervous system
154	Serotonergic synapse	21 (0.69%)	ko04726	Organismal Systems	Nervous system
155	Mitophagy - animal	21 (0.69%)	ko04137	Cellular Processes	Transport and catabolism
156	Prostate cancer	21 (0.69%)	ko05215	Human Diseases	Cancers: Specific types
157	PPAR signaling pathway	21 (0.69%)	ko03320	Organismal Systems	Endocrine system
158	Inflammatory mediator regulation of TRP channels	20 (0.65%)	ko04750	Organismal Systems	Sensory system
159	Apoptosis - fly	20 (0.65%)	ko04214	Cellular Processes	Cell growth and death
160	Vasopressin-regulated water reabsorption	20 (0.65%)	ko04962	Organismal Systems	Excretory system
161	Protein export	20 (0.65%)	ko03060	Genetic Information Processing	Folding, sorting and degradation
162	Glioma	20 (0.65%)	ko05214	Human Diseases	Cancers: Specific types
163	DNA replication	20 (0.65%)	ko03030	Genetic Information Processing	Replication and repair
164	EGFR tyrosine kinase inhibitor resistance	20 (0.65%)	ko01521	Human Diseases	Drug resistance: Antineoplastic
165	Acute myeloid leukemia	20 (0.65%)	ko05221	Human Diseases	Cancers: Specific types
166	Parathyroid hormone synthesis, secretion and action	20 (0.65%)	ko04928	Organismal Systems	Endocrine system
167	Pentose phosphate pathway	19 (0.62%)	ko00030	Metabolism	Carbohydrate metabolism
168	Longevity regulating pathway	19 (0.62%)	ko04211	Organismal Systems	Aging
169	Aldosterone synthesis and secretion	19 (0.62%)	ko04925	Organismal Systems	Endocrine system
170	Protein digestion and absorption	19 (0.62%)	ko04974	Organismal Systems	Digestive system

171	Choline metabolism in cancer	19 (0.62%)	ko05231	Human Diseases	Cancers: Overview
172	Cholesterol metabolism	19 (0.62%)	ko04979	Organismal Systems	Digestive system
173	B cell receptor signaling pathway	19 (0.62%)	ko04662	Organismal Systems	Immune system
174	Pancreatic secretion	19 (0.62%)	ko04972	Organismal Systems	Digestive system
175	Salivary secretion	19 (0.62%)	ko04970	Organismal Systems	Digestive system
176	Long-term depression	19 (0.62%)	ko04730	Organismal Systems	Nervous system
177	Natural killer cell mediated cytotoxicity	19 (0.62%)	ko04650	Organismal Systems	Immune system
178	Rheumatoid arthritis	19 (0.62%)	ko05323	Human Diseases	Immune diseases
179	Alanine, aspartate and glutamate metabolism	18 (0.59%)	ko00250	Metabolism	Amino acid metabolism
180	Gastric acid secretion	18 (0.59%)	ko04971	Organismal Systems	Digestive system
181	Breast cancer	18 (0.59%)	ko05224	Human Diseases	Cancers: Specific types
182	Endocrine resistance	18 (0.59%)	ko01522	Human Diseases	Drug resistance: Antineoplastic
183	Longevity regulating pathway - multiple species	18 (0.59%)	ko04213	Organismal Systems	Aging
184	Circadian entrainment	18 (0.59%)	ko04713	Organismal Systems	Environmental adaptation
185	Amyotrophic lateral sclerosis (ALS)	18 (0.59%)	ko05014	Human Diseases	Neurodegenerative diseases
186	Fructose and mannose metabolism	18 (0.59%)	ko00051	Metabolism	Carbohydrate metabolism
187	Phosphatidylinositol signaling system	18 (0.59%)	ko04070	Environmental Information Processing	Signal transduction
188	Glyoxylate and dicarboxylate metabolism	18 (0.59%)	ko00630	Metabolism	Carbohydrate metabolism
189	Melanogenesis	18 (0.59%)	ko04916	Organismal Systems	Endocrine system
190	VEGF signaling pathway	18 (0.59%)	ko04370	Environmental Information Processing	Signal transduction
191	Endometrial cancer	17 (0.56%)	ko05213	Human Diseases	Cancers: Specific types
192	Fc epsilon RI signaling pathway	17 (0.56%)	ko04664	Organismal Systems	Immune system
193	Nucleotide excision repair	17 (0.56%)	ko03420	Genetic Information Processing	Replication and repair
194	Thyroid cancer	17 (0.56%)	ko05216	Human Diseases	Cancers: Specific types
195	Prolactin signaling pathway	17 (0.56%)	ko04917	Organismal Systems	Endocrine system
196	Metabolism of xenobiotics by cytochrome P450	17 (0.56%)	ko00980	Metabolism	Xenobiotics biodegradation and metabolism
197	Tryptophan metabolism	16 (0.52%)	ko00380	Metabolism	Amino acid metabolism
198	Th17 cell differentiation	16 (0.52%)	ko04659	Organismal Systems	Immune system
199	Toll and Imd signaling pathway	16 (0.52%)	ko04624	Organismal Systems	Immune system
200	Signaling pathways regulating pluripotency of stem cells	16 (0.52%)	ko04550	Cellular Processes	Cellular community - eukaryotes
201	TGF-beta signaling pathway	16 (0.52%)	ko04350	Environmental Information Processing	Signal transduction
202	GABAergic synapse	16 (0.52%)	ko04727	Organismal Systems	Nervous system
203	Mismatch repair	16 (0.52%)	ko03430	Genetic Information Processing	Replication and repair

204	Inositol phosphate metabolism	16 (0.52%)	ko00562	Metabolism	Carbohydrate metabolism
205	beta-Alanine metabolism	16 (0.52%)	ko00410	Metabolism	Metabolism of other amino acids
206	Endocrine and other factor-regulated calcium reabsorption	16 (0.52%)	ko04961	Organismal Systems	Excretory system
207	Galactose metabolism	15 (0.49%)	ko00052	Metabolism	Carbohydrate metabolism
208	Leishmaniasis	15 (0.49%)	ko05140	Human Diseases	Infectious diseases: Parasitic
209	Non-small cell lung cancer	15 (0.49%)	ko05223	Human Diseases	Cancers: Specific types
210	Thyroid hormone synthesis	15 (0.49%)	ko04918	Organismal Systems	Endocrine system
211	Jak-STAT signaling pathway	15 (0.49%)	ko04630	Environmental Information Processing	Signal transduction
212	Mineral absorption	15 (0.49%)	ko04978	Organismal Systems	Digestive system
213	Chemical carcinogenesis	15 (0.49%)	ko05204	Human Diseases	Cancers: Overview
214	Glycerophospholipid metabolism	15 (0.49%)	ko00564	Metabolism	Lipid metabolism
215	Adipocytokine signaling pathway	14 (0.46%)	ko04920	Organismal Systems	Endocrine system
216	Phototransduction - fly	14 (0.46%)	ko04745	Organismal Systems	Sensory system
217	Butanoate metabolism	14 (0.46%)	ko00650	Metabolism	Carbohydrate metabolism
218	Melanoma	14 (0.46%)	ko05218	Human Diseases	Cancers: Specific types
219	Renin secretion	14 (0.46%)	ko04924	Organismal Systems	Endocrine system
220	Insulin secretion	13 (0.43%)	ko04911	Organismal Systems	Endocrine system
221	Porphyrin and chlorophyll metabolism	13 (0.43%)	ko00860	Metabolism	Metabolism of cofactors and vitamins
222	Amphetamine addiction	13 (0.43%)	ko05031	Human Diseases	Substance dependence
223	Fatty acid elongation	13 (0.43%)	ko00062	Metabolism	Lipid metabolism
224	SNARE interactions in vesicular transport	13 (0.43%)	ko04130	Genetic Information Processing	Folding, sorting and degradation
225	RIG-I-like receptor signaling pathway	13 (0.43%)	ko04622	Organismal Systems	Immune system
226	Bladder cancer	13 (0.43%)	ko05219	Human Diseases	Cancers: Specific types
227	Glycerolipid metabolism	12 (0.39%)	ko00561	Metabolism	Lipid metabolism
228	African trypanosomiasis	12 (0.39%)	ko05143	Human Diseases	Infectious diseases: Parasitic
229	Hematopoietic cell lineage	12 (0.39%)	ko04640	Organismal Systems	Immune system
230	Drug metabolism - cytochrome P450	12 (0.39%)	ko00982	Metabolism	Xenobiotics biodegradation and metabolism
231	Neuroactive ligand-receptor interaction	12 (0.39%)	ko04080	Environmental Information Processing	Signaling molecules and interaction
232	2-Oxocarboxylic acid metabolism	12 (0.39%)	ko01210	Metabolism	Global and overview maps
233	Tyrosine metabolism	12 (0.39%)	ko00350	Metabolism	Amino acid metabolism
234	Glycine, serine and threonine metabolism	12 (0.39%)	ko00260	Metabolism	Amino acid metabolism
235	Terpenoid backbone biosynthesis	11 (0.36%)	ko00900	Metabolism	Metabolism of terpenoids and polyketides

236	N-Glycan biosynthesis	11 (0.36%)	ko00510	Metabolism	Glycan biosynthesis and metabolism
237	Apoptosis - multiple species	11 (0.36%)	ko04215	Cellular Processes	Cell growth and death
238	Morphine addiction	11 (0.36%)	ko05032	Human Diseases	Substance dependence
239	Base excision repair	11 (0.36%)	ko03410	Genetic Information Processing	Replication and repair
240	Staphylococcus aureus infection	11 (0.36%)	ko05150	Human Diseases	Infectious diseases: Bacterial
241	Prion diseases	11 (0.36%)	ko05020	Human Diseases	Neurodegenerative diseases
242	Autophagy - other	11 (0.36%)	ko04136	Cellular Processes	Transport and catabolism
243	Collecting duct acid secretion	11 (0.36%)	ko04966	Organismal Systems	Excretory system
244	Cytosolic DNA-sensing pathway	11 (0.36%)	ko04623	Organismal Systems	Immune system
245	Olfactory transduction	10 (0.33%)	ko04740	Organismal Systems	Sensory system
246	Arachidonic acid metabolism	10 (0.33%)	ko00590	Metabolism	Lipid metabolism
247	Bile secretion	10 (0.33%)	ko04976	Organismal Systems	Digestive system
248	Ether lipid metabolism	10 (0.33%)	ko00565	Metabolism	Lipid metabolism
249	Biosynthesis of unsaturated fatty acids	10 (0.33%)	ko01040	Metabolism	Lipid metabolism
250	Th1 and Th2 cell differentiation	10 (0.33%)	ko04658	Organismal Systems	Immune system
251	Starch and sucrose metabolism	10 (0.33%)	ko00500	Metabolism	Carbohydrate metabolism
252	Steroid biosynthesis	9 (0.29%)	ko00100	Metabolism	Lipid metabolism
253	Aldosterone-regulated sodium reabsorption	9 (0.29%)	ko04960	Organismal Systems	Excretory system
254	Proximal tubule bicarbonate reclamation	9 (0.29%)	ko04964	Organismal Systems	Excretory system
255	Malaria	9 (0.29%)	ko05144	Human Diseases	Infectious diseases: Parasitic
256	Nicotinate and nicotinamide metabolism	9 (0.29%)	ko00760	Metabolism	Metabolism of cofactors and vitamins
257	Sphingolipid metabolism	9 (0.29%)	ko00600	Metabolism	Lipid metabolism
258	Cocaine addiction	9 (0.29%)	ko05030	Human Diseases	Substance dependence
259	Notch signaling pathway	8 (0.26%)	ko04330	Environmental Information Processing	Signal transduction
260	Type II diabetes mellitus	8 (0.26%)	ko04930	Human Diseases	Endocrine and metabolic diseases
261	One carbon pool by folate	8 (0.26%)	ko00670	Metabolism	Metabolism of cofactors and vitamins
262	Regulation of lipolysis in adipocytes	8 (0.26%)	ko04923	Organismal Systems	Endocrine system
263	Arginine biosynthesis	8 (0.26%)	ko00220	Metabolism	Amino acid metabolism
264	Pentose and glucuronate interconversions	8 (0.26%)	ko00040	Metabolism	Carbohydrate metabolism
265	Cytokine-cytokine receptor interaction	8 (0.26%)	ko04060	Environmental Information Processing	Signaling molecules and interaction
266	Histidine metabolism	8 (0.26%)	ko00340	Metabolism	Amino acid metabolism
267	Folate biosynthesis	8 (0.26%)	ko00790	Metabolism	Metabolism of cofactors and vitamins
268	Antifolate resistance	8 (0.26%)	ko01523	Human Diseases	Drug resistance: Antineoplastic

269	RNA polymerase	8 (0.26%)	ko03020	Genetic Information Processing	Transcription
270	Cortisol synthesis and secretion	7 (0.23%)	ko04927	Organismal Systems	Endocrine system
271	Dorso-ventral axis formation	7 (0.23%)	ko04320	Organismal Systems	Development
272	Inflammatory bowel disease (IBD)	7 (0.23%)	ko05321	Human Diseases	Immune diseases
273	Ascorbate and aldarate metabolism	7 (0.23%)	ko00053	Metabolism	Carbohydrate metabolism
274	Sulfur metabolism	7 (0.23%)	ko00920	Metabolism	Energy metabolism
275	Carbohydrate digestion and absorption	7 (0.23%)	ko04973	Organismal Systems	Digestive system
276	Hedgehog signaling pathway - fly	7 (0.23%)	ko04341	Environmental Information Processing	Signal transduction
277	Other glycan degradation	7 (0.23%)	ko00511	Metabolism	Glycan biosynthesis and metabolism
278	Glycosaminoglycan degradation	6 (0.2%)	ko00531	Metabolism	Glycan biosynthesis and metabolism
279	Other types of O-glycan biosynthesis	6 (0.2%)	ko00514	Metabolism	Glycan biosynthesis and metabolism
280	Synthesis and degradation of ketone bodies	6 (0.2%)	ko00072	Metabolism	Lipid metabolism
281	Phenylalanine metabolism	6 (0.2%)	ko00360	Metabolism	Amino acid metabolism
282	Fatty acid biosynthesis	6 (0.2%)	ko00061	Metabolism	Lipid metabolism
283	Allograft rejection	6 (0.2%)	ko05330	Human Diseases	Immune diseases
284	Hedgehog signaling pathway	6 (0.2%)	ko04340	Environmental Information Processing	Signal transduction
285	Renin-angiotensin system	6 (0.2%)	ko04614	Organismal Systems	Endocrine system
286	Selenocompound metabolism	6 (0.2%)	ko00450	Metabolism	Metabolism of other amino acids
287	Autoimmune thyroid disease	6 (0.2%)	ko05320	Human Diseases	Immune diseases
288	Type I diabetes mellitus	6 (0.2%)	ko04940	Human Diseases	Endocrine and metabolic diseases
289	Glycosphingolipid biosynthesis - globo and isoglobo series	6 (0.2%)	ko00603	Metabolism	Glycan biosynthesis and metabolism
290	Steroid hormone biosynthesis	5 (0.16%)	ko00140	Metabolism	Lipid metabolism
291	Thiamine metabolism	5 (0.16%)	ko00730	Metabolism	Metabolism of cofactors and vitamins
292	Hippo signaling pathway - multiple species	5 (0.16%)	ko04392	Environmental Information Processing	Signal transduction
293	Ovarian steroidogenesis	5 (0.16%)	ko04913	Organismal Systems	Endocrine system
294	Phototransduction	5 (0.16%)	ko04744	Organismal Systems	Sensory system
295	Homologous recombination	5 (0.16%)	ko03440	Genetic Information Processing	Replication and repair
296	Graft-versus-host disease	4 (0.13%)	ko05332	Human Diseases	Immune diseases
297	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	4 (0.13%)	ko00563	Metabolism	Glycan biosynthesis and metabolism
298	Pantothenate and CoA biosynthesis	4 (0.13%)	ko00770	Metabolism	Metabolism of cofactors and vitamins
299	Taste transduction	4 (0.13%)	ko04742	Organismal Systems	Sensory system
300	Basal transcription factors	4 (0.13%)	ko03022	Genetic Information Processing	Transcription
301	Riboflavin metabolism	4 (0.13%)	ko00740	Metabolism	Metabolism of cofactors and

302	Glycosphingolipid biosynthesis - ganglio series	4 (0.13%)	ko00604	Metabolism	vitamins Glycan biosynthesis and metabolism
303	alpha-Linolenic acid metabolism	4 (0.13%)	ko00592	Metabolism	Lipid metabolism
304	Circadian rhythm	3 (0.1%)	ko04710	Organismal Systems	Environmental adaptation
305	Fanconi anemia pathway	3 (0.1%)	ko03460	Genetic Information Processing	Replication and repair
306	Mucin type O-glycan biosynthesis	3 (0.1%)	ko00512	Metabolism	Glycan biosynthesis and metabolism
307	Primary bile acid biosynthesis	3 (0.1%)	ko00120	Metabolism	Lipid metabolism
308	Primary immunodeficiency	3 (0.1%)	ko05340	Human Diseases	Immune diseases
309	Phosphonate and phosphinate metabolism	3 (0.1%)	ko00440	Metabolism	Metabolism of other amino acids
310	Insect hormone biosynthesis	3 (0.1%)	ko00981	Metabolism	Metabolism of terpenoids and polyketides
311	Fat digestion and absorption	3 (0.1%)	ko04975	Organismal Systems	Digestive system
312	Vitamin B6 metabolism	3 (0.1%)	ko00750	Metabolism	Metabolism of cofactors and vitamins
313	Basal cell carcinoma	3 (0.1%)	ko05217	Human Diseases	Cancers: Specific types
314	Retinol metabolism	3 (0.1%)	ko00830	Metabolism	Metabolism of cofactors and vitamins
315	Sulfur relay system	3 (0.1%)	ko04122	Genetic Information Processing	Folding, sorting and degradation
316	Vitamin digestion and absorption	3 (0.1%)	ko04977	Organismal Systems	Digestive system
317	Nitrogen metabolism	3 (0.1%)	ko00910	Metabolism	Energy metabolism
318	Ubiquinone and other terpenoid-quinone biosynthesis	2 (0.07%)	ko00130	Metabolism	Metabolism of cofactors and vitamins
319	D-Glutamine and D-glutamate metabolism	2 (0.07%)	ko00471	Metabolism	Metabolism of other amino acids
320	Phenylalanine, tyrosine and tryptophan biosynthesis	2 (0.07%)	ko00400	Metabolism	Amino acid metabolism
321	Asthma	2 (0.07%)	ko05310	Human Diseases	Immune diseases
322	Neomycin, kanamycin and gentamicin biosynthesis	2 (0.07%)	ko00524	Metabolism	Biosynthesis of other secondary metabolites
323	Mannose type O-glycan biosynthesis	2 (0.07%)	ko00515	Metabolism	Glycan biosynthesis and metabolism
324	Non-homologous end-joining	2 (0.07%)	ko03450	Genetic Information Processing	Replication and repair
325	Biotin metabolism	2 (0.07%)	ko00780	Metabolism	Metabolism of cofactors and vitamins
326	Nicotine addiction	2 (0.07%)	ko05033	Human Diseases	Substance dependence
327	Intestinal immune network for IgA production	2 (0.07%)	ko04672	Organismal Systems	Immune system
328	Cutin, suberine and wax biosynthesis	2 (0.07%)	ko00073	Metabolism	Lipid metabolism

329	Caffeine metabolism	1 (0.03%)	ko00232	Metabolism	Biosynthesis of other secondary metabolites
330	Valine, leucine and isoleucine biosynthesis	1 (0.03%)	ko00290	Metabolism	Amino acid metabolism
331	Linoleic acid metabolism	1 (0.03%)	ko00591	Metabolism	Lipid metabolism
332	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	1 (0.03%)	ko00534	Metabolism	Glycan biosynthesis and metabolism
333	Taurine and hypotaurine metabolism	1 (0.03%)	ko00430	Metabolism	Metabolism of other amino acids
334	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	1 (0.03%)	ko00532	Metabolism	Glycan biosynthesis and metabolism
335	Monobactam biosynthesis	1 (0.03%)	ko00261	Metabolism	Biosynthesis of other secondary metabolites
336	Circadian rhythm - fly	1 (0.03%)	ko04711	Organismal Systems	Environmental adaptation
337	ABC transporters	1 (0.03%)	ko02010	Environmental Information Processing	Membrane transport

Table S2. Identified DEPs in *IRS1* silenced GMECs

Primary_protein_ID	ratio	P value	Class	Description
tr A0A8C2P961 A0A8C2P961_CAPHI	1.679766	0.00638	Up	Uncharacterized protein OS=Capra hircus OX=9925 PE=4 SV=1
tr A0A452GAM5 A0A452GAM5_CAPHI	80.58179	0.007151	Up	Keratin 82 OS=Capra hircus OX=9925 GN=KRT82 PE=3 SV=1
tr A0A452EY08 A0A452EY08_CAPHI	0.651776	0.018808	Down	Protein arginine N-methyltransferase 5 OS=Capra hircus OX=9925 GN=PRMT5 PE=3 SV=1
tr A0A8C2S8I8 A0A8C2S8I8_CAPHI	6.440772	0.019999	Up	MAP7 domain containing 1 OS=Capra hircus OX=9925 PE=4 SV=1
tr A0A452ENI2 A0A452ENI2_CAPHI	1.794928	0.021819	Up	Syntaxin 7 OS=Capra hircus OX=9925 GN=STX7 PE=3 SV=1
tr A0A452FPA3 A0A452FPA3_CAPHI	2.205146	0.025801	Up	KIAA1217 ortholog OS=Capra hircus OX=9925 GN=KIAA1217 PE=4 SV=1
tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	1.598218	0.027044	Up	Phosphodiesterase 12 OS=Capra hircus OX=9925 GN=PDE12 PE=4 SV=1
tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	0.431634	0.030581	Down	Glutaredoxin 5 OS=Capra hircus OX=9925 PE=4 SV=1
tr A0A452EKV1 A0A452EKV1_CAPHI	0.584772	0.033474	Down	Protein MAK16 homolog OS=Capra hircus OX=9925 PE=3 SV=1
tr A0A452FS44 A0A452FS44_CAPHI	2.275074	0.038024	Up	Heme binding protein 2 OS=Capra hircus OX=9925 GN=HEBP2 PE=3 SV=1
tr A0A452E2T3 A0A452E2T3_CAPHI	5.679159	0.043977	Up	Rhophilin Rho GTPase binding protein 2 OS=Capra hircus OX=9925 GN=RHPN2 PE=4 SV=1
tr A0A8C2SL02 A0A8C2SL02_CAPHI	1.63364	0.04659	Up	Myosin XVIIIa OS=Capra hircus OX=9925 PE=4 SV=1

Table S3. GO enriched DEPs

Ontology	GO_term	Protein_ID	log2Foldchange	Up/Down
biological_process	biological regulation	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
biological_process	biological regulation	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	biological regulation	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	biological regulation	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
biological_process	biological regulation	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	biological regulation	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
biological_process	biological regulation	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	cell killing	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	cellular component organization or biogenesis	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
biological_process	cellular component organization or biogenesis	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	cellular component organization or biogenesis	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	cellular component organization or biogenesis	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
biological_process	cellular process	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
biological_process	cellular process	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
biological_process	cellular process	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	cellular process	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	cellular process	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
biological_process	cellular process	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	cellular process	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
biological_process	cellular process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	developmental process	tr A0A452FPA3 A0A452FPA3_CAPHI	1.140874	up
biological_process	developmental process	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	immune system process	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	immune system process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up

biological_process	localization	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	localization	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
biological_process	metabolic process	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
biological_process	metabolic process	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	metabolic process	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	metabolic process	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
biological_process	metabolic process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	multi-organism process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	multicellular organismal process	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	multicellular organismal process	tr A0A452FPA3 A0A452FPA3_CAPHI	1.140874	up
biological_process	negative regulation of biological process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	positive regulation of biological process	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	positive regulation of biological process	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	positive regulation of biological process	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
biological_process	positive regulation of biological process	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	positive regulation of biological process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	regulation of biological process	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
biological_process	regulation of biological process	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	regulation of biological process	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	regulation of biological process	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
biological_process	regulation of biological process	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	regulation of biological process	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
biological_process	regulation of biological process	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	response to stimulus	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
biological_process	response to stimulus	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
biological_process	response to stimulus	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down

biological_process	response to stimulus	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
biological_process	response to stimulus	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
biological_process	rhythmic process	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
biological_process	signaling	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
biological_process	signaling	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	cell	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
cellular_component	cell	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
cellular_component	cell	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	cell	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	cell	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
cellular_component	cell	tr A0A452GAM5 A0A452GAM5_CAPHI	6.332382	up
cellular_component	cell	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
cellular_component	cell	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
cellular_component	cell	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
cellular_component	cell part	tr A0A452E2T3 A0A452E2T3_CAPHI	2.505677	up
cellular_component	cell part	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
cellular_component	cell part	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	cell part	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	cell part	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
cellular_component	cell part	tr A0A452GAM5 A0A452GAM5_CAPHI	6.332382	up
cellular_component	cell part	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
cellular_component	cell part	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
cellular_component	cell part	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
cellular_component	extracellular region	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	extracellular region	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
cellular_component	extracellular region	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up

cellular_component	extracellular region part	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	extracellular region part	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
cellular_component	extracellular region part	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
cellular_component	macromolecular complex	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
cellular_component	macromolecular complex	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	macromolecular complex	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	membrane	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	membrane part	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	membrane-enclosed lumen	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
cellular_component	membrane-enclosed lumen	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	membrane-enclosed lumen	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
cellular_component	membrane-enclosed lumen	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
cellular_component	membrane-enclosed lumen	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
cellular_component	organelle	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
cellular_component	organelle	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	organelle	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	organelle	tr A0A452FS44 A0A452FS44_CAPHI	1.185913	up
cellular_component	organelle	tr A0A452GAM5 A0A452GAM5_CAPHI	6.332382	up
cellular_component	organelle	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up
cellular_component	organelle	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
cellular_component	organelle	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
cellular_component	organelle part	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
cellular_component	organelle part	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
cellular_component	organelle part	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
cellular_component	organelle part	tr A0A452GAM5 A0A452GAM5_CAPHI	6.332382	up
cellular_component	organelle part	tr A0A8C2P961 A0A8C2P961_CAPHI	0.74826	up

cellular_component	organelle part	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
cellular_component	organelle part	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
cellular_component	supramolecular complex	tr A0A452GAM5 A0A452GAM5_CAPHI	6.332382	up
molecular_function	binding	tr A0A452EKV1 A0A452EKV1_CAPHI	-0.77405	down
molecular_function	binding	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
molecular_function	binding	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
molecular_function	binding	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
molecular_function	binding	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
molecular_function	catalytic activity	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down
molecular_function	catalytic activity	tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	-1.21212	down
molecular_function	catalytic activity	tr A0A8C2SJN8 A0A8C2SJN8_CAPHI	0.676464	up
molecular_function	molecular function regulator	tr A0A452ENI2 A0A452ENI2_CAPHI	0.843926	up
molecular_function	structural molecule activity	tr A0A452GAM5 A0A452GAM5_CAPHI	6.332382	up
molecular_function	transcription regulator activity	tr A0A452EY08 A0A452EY08_CAPHI	-0.61755	down

Table S4. Subcellular Localization of DEPs

SeqID	Subcellular_location	Description
tr A0A8C2P961 A0A8C2P961_CAPHI	cyto	Uncharacterized protein OS=Capra hircus OX=9925 PE=4 SV=1
tr A0A452GAM5 A0A452GAM5_CAPHI	mito	Keratin 82 OS=Capra hircus OX=9925 GN=KRT82 PE=3 SV=1
tr A0A452EY08 A0A452EY08_CAPHI	cyto_nucl	Protein arginine N-methyltransferase 5 OS=Capra hircus OX=9925 GN=PRMT5 PE=3 SV=1
tr A0A8C2S8I8 A0A8C2S8I8_CAPHI	E.R.	MAP7 domain containing 1 OS=Capra hircus OX=9925 PE=4 SV=1
tr A0A452ENI2 A0A452ENI2_CAPHI	plas	Syntaxin 7 OS=Capra hircus OX=9925 GN=STX7 PE=3 SV=1
tr A0A452FPA3 A0A452FPA3_CAPHI	nucl	KIAA1217 ortholog OS=Capra hircus OX=9925 GN=KIAA1217 PE=4 SV=1
tr A0A8C2S8I8 A0A8C2S8I8_CAPHI	mito	Phosphodiesterase 12 OS=Capra hircus OX=9925 GN=PDE12 PE=4 SV=1
tr A0A8C2RAM0 A0A8C2RAM0_CAPHI	cyto	Glutaredoxin 5 OS=Capra hircus OX=9925 PE=4 SV=1
tr A0A452EKV1 A0A452EKV1_CAPHI	cyto	Protein MAK16 homolog OS=Capra hircus OX=9925 PE=3 SV=1
tr A0A452FS44 A0A452FS44_CAPHI	cyto	Heme binding protein 2 OS=Capra hircus OX=9925 GN=HEBP2 PE=3 SV=1
tr A0A452E2T3 A0A452E2T3_CAPHI	nucl	Rhophilin Rho GTPase binding protein 2 OS=Capra hircus OX=9925 GN=RHPN2 PE=4 SV=1
tr A0A8C2SL02 A0A8C2SL02_CAPHI	nucl	Myosin XVIIIa OS=Capra hircus OX=9925 PE=4 SV=1