

Supplementary Table S1 KEGG pathways for *Pelodiscus sinensis*

No.	Pathway description	Members	Count (%)	Pathway ID
1	Metabolic pathways	2674	10.09	ko01100
2	Focal adhesion	1627	6.14	ko04510
3	Regulation of actin cytoskeleton	1348	5.09	ko04810
4	Amoebiasis	1256	4.74	ko05146
5	ECM-receptor interaction	1076	4.06	ko04512
6	Pathways in cancer	1060	4.00	ko05200
7	Protein digestion and absorption	867	3.27	ko04974
8	MAPK signaling pathway	784	2.96	ko04010
9	Endocytosis	778	2.94	ko04144
10	RNA transport	775	2.92	ko03013
11	Dilated cardiomyopathy	737	2.78	ko05414
12	Huntington's disease	732	2.76	ko05016
13	Vascular smooth muscle contraction	713	2.69	ko04270
14	Hypertrophic cardiomyopathy (HCM)	700	2.64	ko05410
15	Tight junction	687	2.59	ko04530
16	Chemokine signaling pathway	667	2.52	ko04062
17	Fc gamma R-mediated phagocytosis	652	2.46	ko04666
18	Adherens junction	633	2.39	ko04520
19	Spliceosome	587	2.22	ko03040
20	Bacterial invasion of epithelial cells	578	2.18	ko05100
21	Ubiquitin mediated proteolysis	572	2.16	ko04120
22	Calcium signaling pathway	561	2.12	ko04020
23	Phagosome	557	2.10	ko04145
24	Protein processing in endoplasmic reticulum	549	2.07	ko04141
25	Viral myocarditis	540	2.04	ko05416
26	Axon guidance	533	2.01	ko04360
27	Influenza A	532	2.01	ko05164
28	mRNA surveillance pathway	527	1.99	ko03015
29	Tuberculosis	519	1.96	ko05152
30	Salivary secretion	517	1.95	ko04970
31	Shigellosis	506	1.91	ko05131
32	Insulin signaling pathway	503	1.90	ko04910
33	Pathogenic <i>Escherichia coli</i> infection	499	1.88	ko05130
34	Purine metabolism	493	1.86	ko00230
35	Alzheimer's disease	493	1.86	ko05010
36	Wnt signaling pathway	473	1.79	ko04310
37	Leukocyte transendothelial migration	454	1.71	ko04670
38	<i>Vibrio cholerae</i> infection	426	1.61	ko05110
39	Neurotrophin signaling pathway	423	1.60	ko04722

No.	Pathway description	Members	Count (%)	Pathway ID
40	Glutamatergic synapse	391	1.48	ko04724
41	Measles	386	1.46	ko05162
42	Toxoplasmosis	385	1.45	ko05145
43	Cardiac muscle contraction	381	1.44	ko04260
44	Neuroactive ligand-receptor interaction	376	1.42	ko04080
45	Lysine degradation	363	1.37	ko00310
46	Small cell lung cancer	361	1.36	ko05222
47	Hepatitis C	360	1.36	ko05160
48	Gastric acid secretion	350	1.32	ko04971
49	Complement and coagulation cascades	343	1.29	ko04610
50	Basal transcription factors	341	1.29	ko03022
51	Phosphatidylinositol signaling system	339	1.28	ko04070
52	GnRH signaling pathway	336	1.27	ko04912
53	Cell cycle	329	1.24	ko04110
54	Natural killer cell mediated cytotoxicity	326	1.23	ko04650
55	Lysosome	317	1.20	ko04142
56	Osteoclast differentiation	316	1.19	ko04380
57	T cell receptor signaling pathway	314	1.19	ko04660
58	Pyrimidine metabolism	311	1.17	ko00240
59	Oocyte meiosis	310	1.17	ko04114
60	Cytokine-cytokine receptor interaction	306	1.15	ko04060
61	ErbB signaling pathway	305	1.15	ko04012
62	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	304	1.15	ko05412
63	Pancreatic secretion	300	1.13	ko04972
64	B cell receptor signaling pathway	288	1.09	ko04662
65	TGF-beta signaling pathway	286	1.08	ko04350
66	Jak-STAT signaling pathway	283	1.07	ko04630
67	Cholinergic synapse	282	1.06	ko04725
68	Cell adhesion molecules (CAMs)	282	1.06	ko04514
69	Prostate cancer	277	1.05	ko05215
70	Fc epsilon RI signaling pathway	271	1.02	ko04664
71	Ribosome biogenesis in eukaryotes	269	1.02	ko03008
72	VEGF signaling pathway	261	0.99	ko04370
73	Long-term potentiation	258	0.97	ko04720
74	Gap junction	254	0.96	ko04540
75	Amyotrophic lateral sclerosis (ALS)	253	0.95	ko05014
76	Inositol phosphate metabolism	247	0.93	ko00562
77	Progesterone-mediated oocyte maturation	247	0.93	ko04914
78	Chagas disease (American	244	0.92	ko05142

No.	Pathway description	Members	Count (%)	Pathway ID
	trypanosomiasis)			
79	Chronic myeloid leukemia	241	0.91	ko05220
80	Melanogenesis	238	0.90	ko04916
81	Systemic lupus erythematosus	234	0.88	ko05322
82	Glioma	229	0.86	ko05214
83	Parkinson's disease	223	0.84	ko05012
84	Peroxisome	221	0.83	ko04146
85	Long-term depression	221	0.83	ko04730
86	Dorso-ventral axis formation	219	0.83	ko04320
87	PPAR signaling pathway	216	0.82	ko03320
88	Adipocytokine signaling pathway	216	0.82	ko04920
89	Pertussis	215	0.81	ko05133
90	Renal cell carcinoma	207	0.78	ko05211
91	RNA degradation	206	0.78	ko03018
92	Bile secretion	204	0.77	ko04976
93	Glycerophospholipid metabolism	204	0.77	ko00564
94	p53 signaling pathway	202	0.76	ko04115
95	Apoptosis	201	0.76	ko04210
96	Notch signaling pathway	196	0.74	ko04330
97	Staphylococcus aureus infection	193	0.73	ko05150
98	NOD-like receptor signaling pathway	186	0.70	ko04621
99	Leishmaniasis	184	0.69	ko05140
100	Hematopoietic cell lineage	184	0.69	ko04640
101	Pancreatic cancer	184	0.69	ko05212
102	Toll-like receptor signaling pathway	182	0.69	ko04620
103	Non-small cell lung cancer	181	0.68	ko05223
104	Endometrial cancer	180	0.68	ko05213
105	Colorectal cancer	179	0.68	ko05210
106	Oxidative phosphorylation	176	0.66	ko00190
107	Epithelial cell signaling in Helicobacter pylori infection	171	0.65	ko05120
108	mTOR signaling pathway	170	0.64	ko04150
109	Acute myeloid leukemia	160	0.60	ko05221
110	ABC transporters	156	0.59	ko02010
111	Prion diseases	152	0.57	ko05020
112	Rheumatoid arthritis	152	0.57	ko05323
113	Melanoma	151	0.57	ko05218
114	Vasopressin-regulated water reabsorption	148	0.56	ko04962
115	Arginine and proline metabolism	144	0.54	ko00330
116	Antigen processing and presentation	144	0.54	ko04612
117	RNA polymerase	142	0.54	ko03020

No.	Pathway description	Members	Count (%)	Pathway ID
118	Bladder cancer	140	0.53	ko05219
119	N-Glycan biosynthesis	139	0.52	ko00510
120	RIG-I-like receptor signaling pathway	139	0.52	ko04622
121	Aldosterone-regulated sodium reabsorption	139	0.52	ko04960
122	Arachidonic acid metabolism	139	0.52	ko00590
123	Type II diabetes mellitus	139	0.52	ko04930
124	Fat digestion and absorption	138	0.52	ko04975
125	Carbohydrate digestion and absorption	136	0.51	ko04973
126	Drug metabolism-cytochrome P450	135	0.51	ko00982
127	Glycolysis / Gluconeogenesis	133	0.50	ko00010
128	Ribosome	132	0.50	ko03010
129	Basal cell carcinoma	132	0.50	ko05217
130	Endocrine and other factor-regulated calcium reabsorption	128	0.48	ko04961
131	Hedgehog signaling pathway	127	0.48	ko04340
132	Valine, leucine and isoleucine degradation	123	0.46	ko00280
133	Phototransduction-fly	120	0.45	ko04745
134	Pyruvate metabolism	118	0.45	ko00620
135	Metabolism of xenobiotics by cytochrome P450	115	0.43	ko00980
136	Malaria	114	0.43	ko05144
137	Cytosolic DNA-sensing pathway	113	0.43	ko04623
138	Tyrosine metabolism	113	0.43	ko00350
139	Glycerolipid metabolism	111	0.42	ko00561
140	Linoleic acid metabolism	108	0.41	ko00591
141	Olfactory transduction	108	0.41	ko04740
142	Retinol metabolism	105	0.40	ko00830
143	Starch and sucrose metabolism	105	0.40	ko00500
144	Fructose and mannose metabolism	103	0.39	ko00051
145	Drug metabolism-other enzymes	102	0.38	ko00983
146	Tryptophan metabolism	102	0.38	ko00380
147	Thyroid cancer	102	0.38	ko05216
148	Ether lipid metabolism	101	0.38	ko00565
149	Aminoacyl-tRNA biosynthesis	101	0.38	ko00970
150	Mineral absorption	100	0.38	ko04978
151	African trypanosomiasis	100	0.38	ko05143
152	Amino sugar and nucleotide sugar metabolism	98	0.37	ko00520
153	Nucleotide excision repair	98	0.37	ko03420
154	Other types of O-glycan biosynthesis	98	0.37	ko00514

No.	Pathway description	Members	Count (%)	Pathway ID
155	Glycine, serine and threonine metabolism	97	0.37	ko00260
156	Vitamin digestion and absorption	96	0.36	ko04977
157	Autoimmune thyroid disease	94	0.35	ko05320
158	Citrate cycle (TCA cycle)	94	0.35	ko00020
159	Nicotinate and nicotinamide metabolism	93	0.35	ko00760
160	beta-Alanine metabolism	92	0.35	ko00410
161	Steroid hormone biosynthesis	91	0.34	ko00140
162	Fatty acid metabolism	89	0.34	ko00071
163	Primary immunodeficiency	87	0.33	ko05340
164	Sphingolipid metabolism	86	0.32	ko00600
165	Allograft rejection	86	0.32	ko05330
166	Butanoate metabolism	85	0.32	ko00650
167	Cysteine and methionine metabolism	84	0.32	ko00270
168	Propanoate metabolism	84	0.32	ko00640
169	Glutathione metabolism	84	0.32	ko00480
170	Base excision repair	84	0.32	ko03410
171	Galactose metabolism	83	0.31	ko00052
172	Type I diabetes mellitus	80	0.30	ko04940
173	Taste transduction	78	0.29	ko04742
174	DNA replication	74	0.28	ko03030
175	Glycosaminoglycan biosynthesis-heparan sulfate	73	0.28	ko00534
176	Histidine metabolism	70	0.26	ko00340
177	MAPK signaling pathway-fly	67	0.25	ko04013
178	Alanine, aspartate and glutamate metabolism	66	0.25	ko00250
179	Intestinal immune network for IgA production	66	0.25	ko04672
180	Circadian rhythm-mammal	65	0.25	ko04710
181	alpha-Linolenic acid metabolism	65	0.25	ko00592
182	Graft-versus-host disease	65	0.25	ko05332
183	Biosynthesis of unsaturated fatty acids	64	0.24	ko01040
184	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	64	0.24	ko00563
185	Pantothenate and CoA biosynthesis	63	0.24	ko00770
186	Proteasome	61	0.23	ko03050
187	Renin-angiotensin system	61	0.23	ko04614
188	Glycosphingolipid biosynthesis-lacto and neolacto series	60	0.23	ko00601
189	Proximal tubule bicarbonate	60	0.23	ko04964

No.	Pathway description	Members	Count (%)	Pathway ID
	reclamation			
190	Pentose and glucuronate interconversions	59	0.22	ko00040
191	Homologous recombination	59	0.22	ko03440
192	Phototransduction	57	0.22	ko04744
193	Pentose phosphate pathway	55	0.21	ko00030
194	Collecting duct acid secretion	53	0.20	ko04966
195	Steroid biosynthesis	52	0.20	ko00100
196	Mismatch repair	50	0.19	ko03430
197	Selenocompound metabolism	47	0.18	ko00450
198	Mucin type O-Glycan biosynthesis	47	0.18	ko00512
199	Porphyrin and chlorophyll metabolism	46	0.17	ko00860
200	Nitrogen metabolism	46	0.17	ko00910
201	Maturity onset diabetes of the young	45	0.17	ko04950
202	Primary bile acid biosynthesis	43	0.16	ko00120
203	Phenylalanine metabolism	41	0.15	ko00360
204	One carbon pool by folate	41	0.15	ko00670
205	SNARE interactions in vesicular transport	41	0.15	ko04130
206	Asthma	40	0.15	ko05310
207	Glycosaminoglycan biosynthesis-chondroitin sulfate	39	0.15	ko00532
208	Fatty acid biosynthesis	38	0.14	ko00061
209	Regulation of autophagy	38	0.14	ko04140
210	Circadian rhythm-fly	38	0.14	ko04711
211	Protein export	37	0.14	ko03060
212	Other glycan degradation	37	0.14	ko00511
213	Valine, leucine and isoleucine biosynthesis	36	0.14	ko00290
214	Glycosaminoglycan biosynthesis-keratan sulfate	35	0.13	ko00533
215	Non-homologous end-joining	34	0.13	ko03450
216	Glyoxylate and dicarboxylate metabolism	33	0.12	ko00630
217	Glycosaminoglycan degradation	31	0.12	ko00531
218	Sulfur metabolism	30	0.11	ko00920
219	Taurine and hypotaurine metabolism	28	0.11	ko00430
220	Ascorbate and aldarate metabolism	25	0.09	ko00053
221	Terpenoid backbone biosynthesis	24	0.09	ko00900
222	Folate biosynthesis	24	0.09	ko00790
223	Glycosphingolipid biosynthesis-ganglio series	23	0.09	ko00604

No.	Pathway description	Members	Count (%)	Pathway ID
224	Riboflavin metabolism	23	0.09	ko00740
225	Sulfur relay system	20	0.08	ko04122
226	Caffeine metabolism	19	0.07	ko00232
227	Vitamin B6 metabolism	17	0.06	ko00750
228	Glycosphingolipid biosynthesis - globo series	16	0.06	ko00603
229	Fatty acid elongation	16	0.06	ko00062
230	Synthesis and degradation of ketone bodies	16	0.06	ko00072
231	D-Arginine and D-ornithine metabolism	15	0.06	ko00472
232	Phenylalanine, tyrosine and tryptophan biosynthesis	15	0.06	ko00400
233	Thiamine metabolism	13	0.05	ko00730
234	Cyanoamino acid metabolism	13	0.05	ko00460
235	Ubiquinone and other terpenoid-quinone biosynthesis	11	0.04	ko00130
236	Biotin metabolism	8	0.03	ko00780
237	Butirosin and neomycin biosynthesis	8	0.03	ko00524
238	D-Glutamine and D-glutamate metabolism	5	0.02	ko00471
239	Polyketide sugar unit biosynthesis	4	0.02	ko00523
240	Lysine biosynthesis	4	0.02	ko00300
241	Insect hormone biosynthesis	3	0.01	ko00981
242	Lipoic acid metabolism	3	0.01	ko00785