

Blood Transcriptome Analysis Reveals Gene Expression Differences between Yangtze Finless Porpoises from Two Habitats: Natural and Ex Situ Protected Waters

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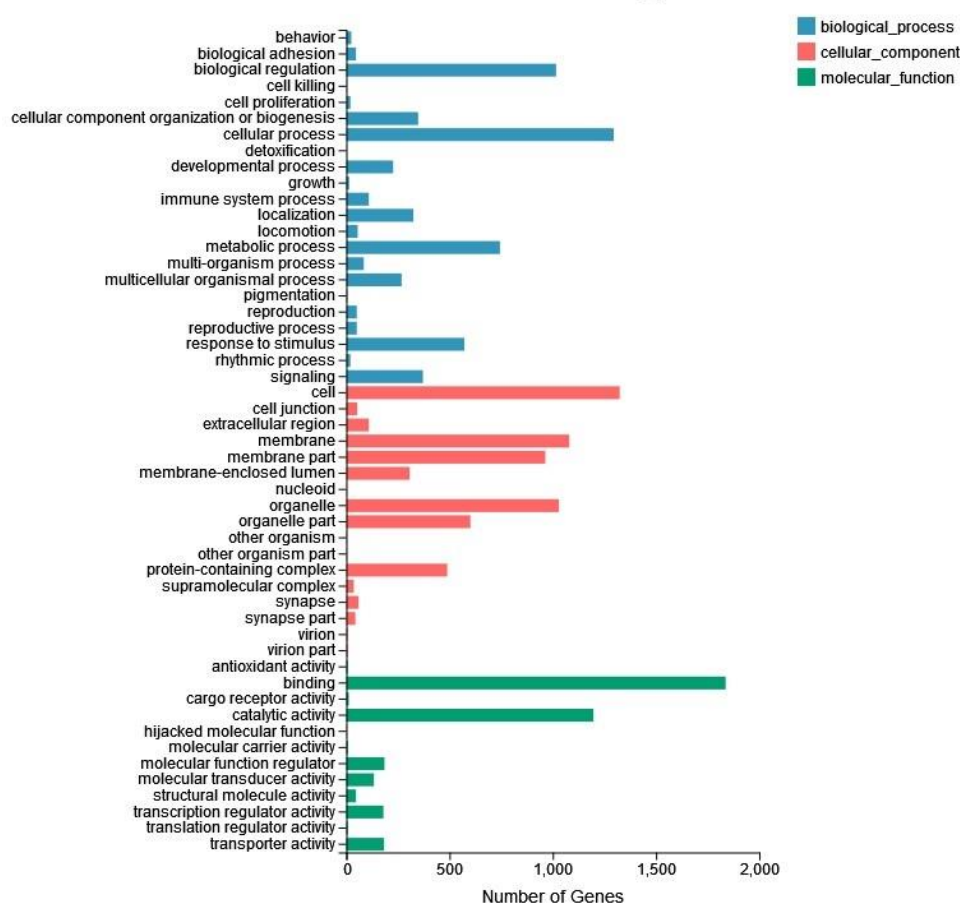


Figure S1. GO classification of differentially expressed genes.

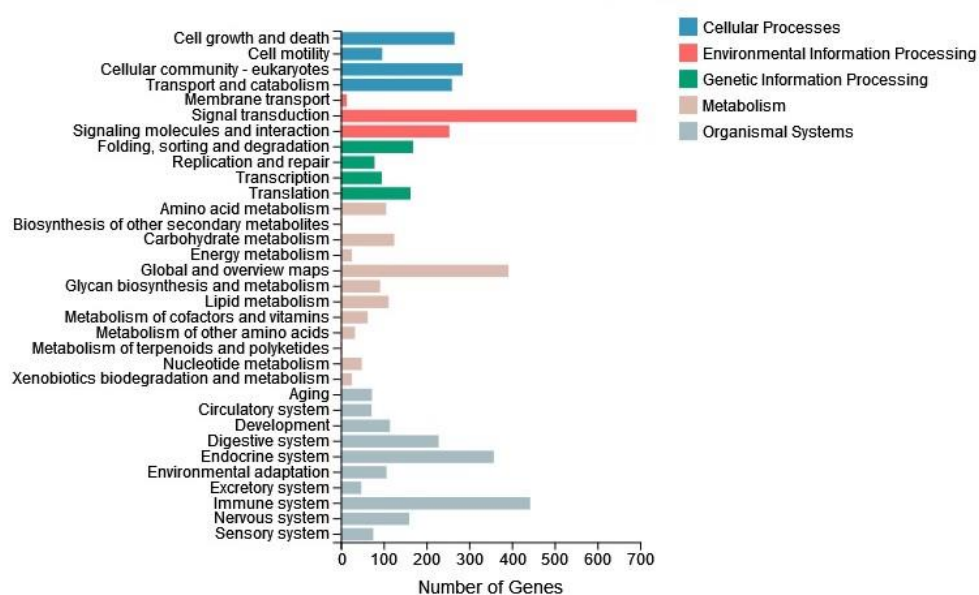


Figure S2. KEGG pathway classification of differentially expressed genes.

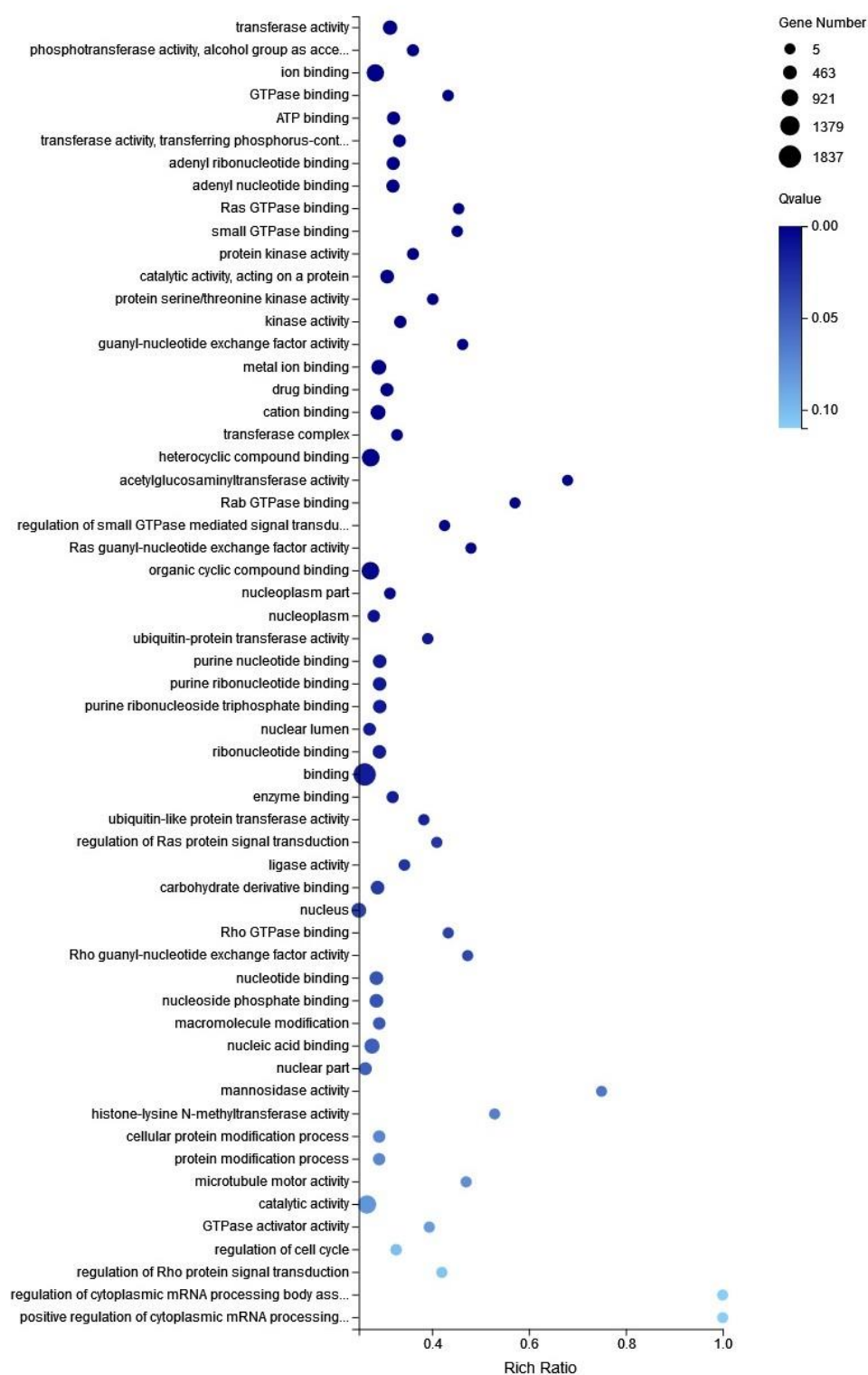


Figure S3. 58 GO terms extremely significantly enriched.

Table S1. Morphological information of Yangtze finless porpoises for transcriptomic analysis.

Code	Group	Sex	Body length(cm)	Body weight(kg)	Estimated age	BMI
CJ_1	CJ	M	150	46.7	5.9	20.76
CJ_2	CJ	M	147	45	5.5	20.82
CJ_3	CJ	M	145.5	44.6	5.4	21.21
XJ_1	XJ	M	146	51.2	5.6	24.02
XJ_2	XJ	M	142	33.7	4.6	16.71
XJ_3	XJ	M	141	40	4.3	20.12

Table S2. Summary of qRT-PCR primer sequences for Yangtze finless porpoise.

Gene ID+A2:E8	Gene name	Full name	Forward primer (5'-3')	Reverse primer (5'-3')
112414847	PRDX2	peroxiredoxin 2	TGGCGTGCTGAAGGAAGAT	GAGAAATATTCCTTGCTGTCGTC
112403388	GPX2	glutathione peroxidase 2	GGACTTCACCCAACCTCAACG	GGTAAAGGTGGGCTGGAATC
112405252	FBXO11	F-box protein 11	GATTACCTCAAATAGTGACCCAAC	ACTTCATTCTCTTCTATTACGCCTT
112411265	PTGS1	prostaglandin-endoperoxide synthase 1	AGTACCGTAACCGAATTGCC	GTCTGTGTTCTACCCCCG
112407459	SMAD4	SMAD family member 4	AGGTGGCTGGTCGGAAG	TGGAGCATTACTCTGCAGTGTTA
112391848	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	AGGTCGGAGTGAACGGATTT	TTCTCAGCCTTGACTGTGCC