

Integrated metabolomic and transcriptomic analyses identify critical genes in eicosapentaenoic acid biosynthesis and metabolism in the sea urchin *Strongylocentrotus intermedius*

Heng Wang ^{1,†}, Jun Ding ^{1,†,*}, Siyu Ding ¹, Yaqing Chang ^{1,*}

¹ Key Laboratory of Mariculture& Stock Enhancement in North China's Sea, Ministry of Agriculture and Rural Affairs, Dalian Ocean University, Dalian, 116023, China; hengwang@dlou.edu.cn (H. Wang); siyu19860608@163.com (S. Ding)

Equal contributors

* Correspondence: dingjun19731119@hotmail.com (J. Ding);
changlab@hotmail.com (Y. Chang)

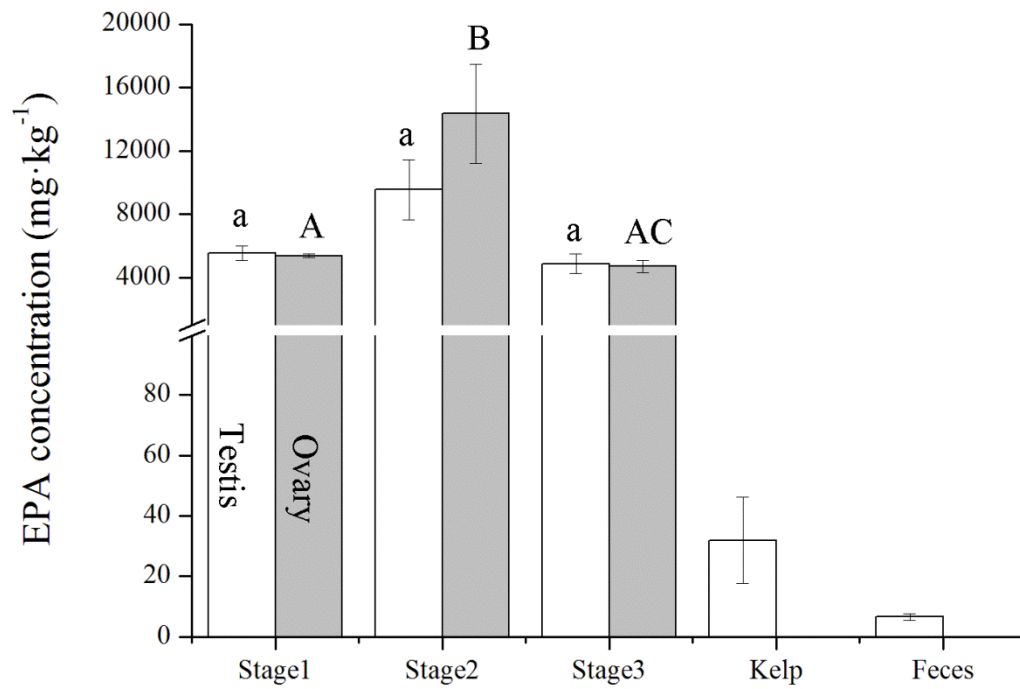
Tel.: +86-411-84762871

Supplementary Table S1 Biometrics of the sea urchin *Strongylocentrotus intermedius* sampled for RNA and metabolite extraction.

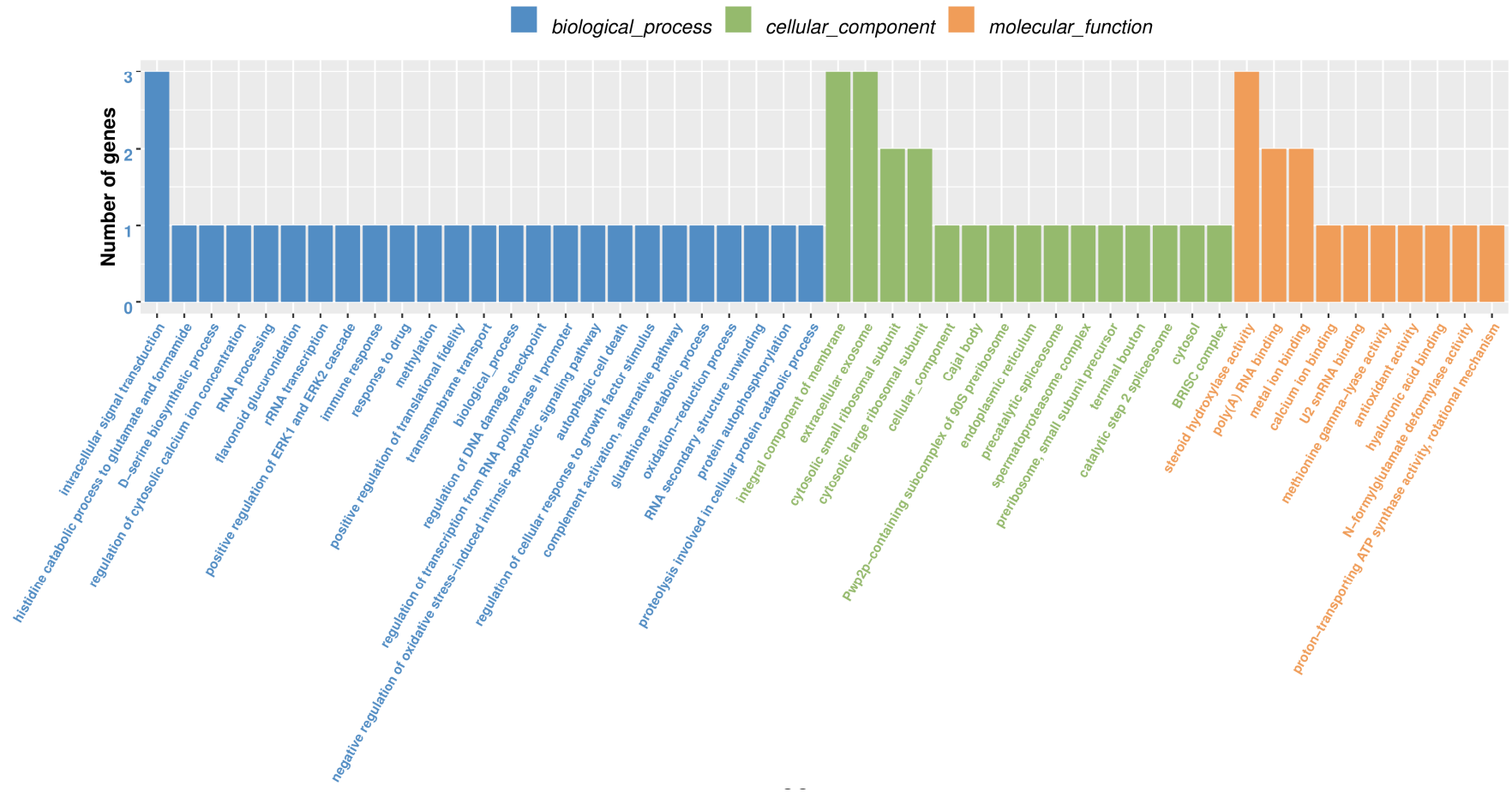
Stage	Shell diameter (cm)	Shell height (cm)	Wet body weight (g)	Wet gonad weight (g)	Gonado-somatic index (%)
1	3.85 ± 0.69	2.19 ± 0.48	17.68 ± 0.97	0.70 ± 0.05	3.98 ± 0.25
2	4.14 ± 0.94	2.22 ± 0.79	29.28 ± 1.56	3.67 ± 0.27	12.52 ± 0.50
3	5.50 ± 1.59	3.31 ± 0.88	48.79 ± 2.72	8.37 ± 0.80	17.16 ± 0.81

Supplemental Table S2 The primers used in this study

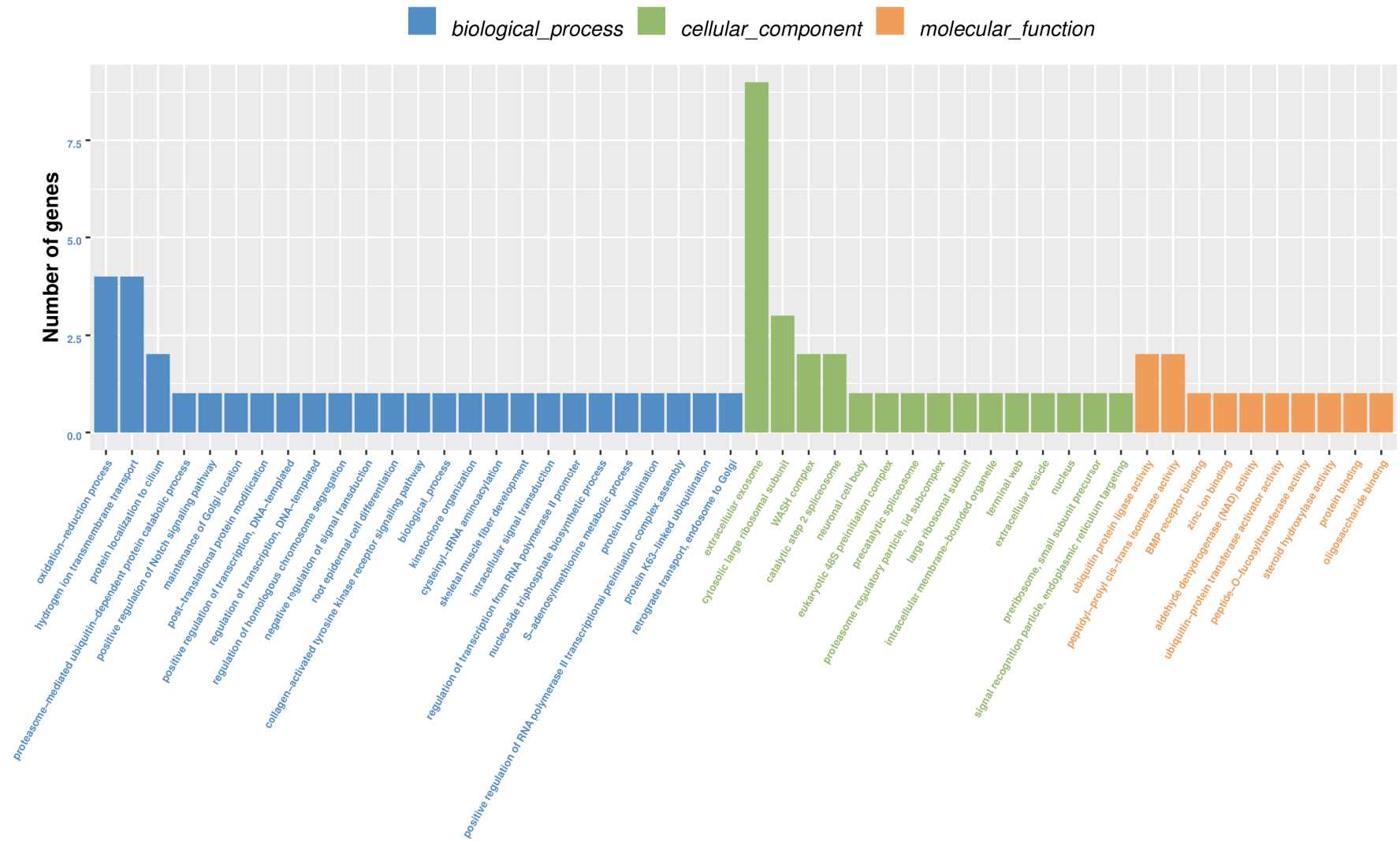
Gene	Forward primer (5'→3')	Reverse primer (5'→3')
Adh5	AGTGAATACACCGTCGTTGCTGAG	CACAGCCAGACCTACACATCCAAC
Aldh7a1	AGCCATAGCCAGAGTCAGACAGG	ATCTGCCTCACGACCTCACCTC
Acat2	TGGTTCCGGCCTGAGGACAATAG	AGGACAGACCGCTACGAAGATGG
Cyp2j2	AGATGGATCAGGTGGTCGGAAGAG	CGTCAGCATCAGCCATGTGAGG
Cyp2r1	CCTTCAAGAAGCCAGACCACTCAC	TGGAATAGCGCAGGTGAGGTAGG
Cyp2u1	GCCTCCGTCGCCTCCTAGTC	TTCGCTCATCACCAACAATCCTCTG
Cyp3a14	CTCCGCTTGCCAATCGTCCTATG	ACCATGCTTCTCTTGCTCTTGTCC
Ecm3	TAACGGAATCGCCTTCAACGCTAC	GCCGATGCCAGATGTCTCAGATG
Fads2	ACTCGCACACGACTTCGATAACG	GCCAGGAGGAAGGAGAAGATGTTG
Gpx1	TTGCTACGATGACGCCGAATCC	GCAGAATGACGCCGTATTGACAAC
Hsd17b12	AGCTGACCGGACTGGACATCG	ACGACAGACAGGCAGTTGATGTTG
Tecr	CGCCACCATGCCTATCACCAAC	GGTCACGCAGGACAATGTGGATAC



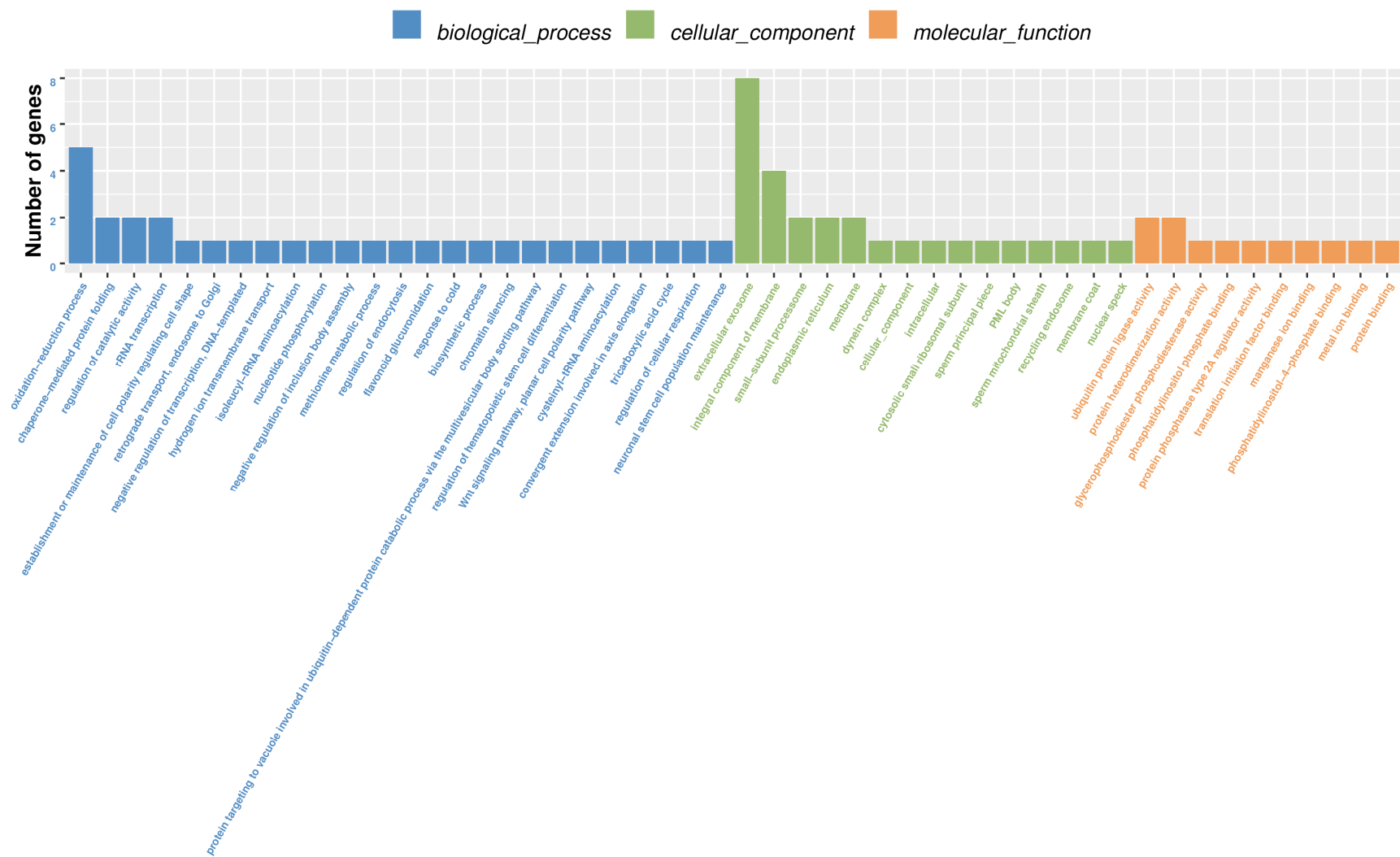
Supplemental Figure S1. Eicosapentaenoic acid (EPA) concentration in each developmental gonad of sea urchin, kelp, and feces. a, b, c (testis) and A, B, C (ovary) indicate significant differences among stages within each sex ($p < 0.05$).



(A)



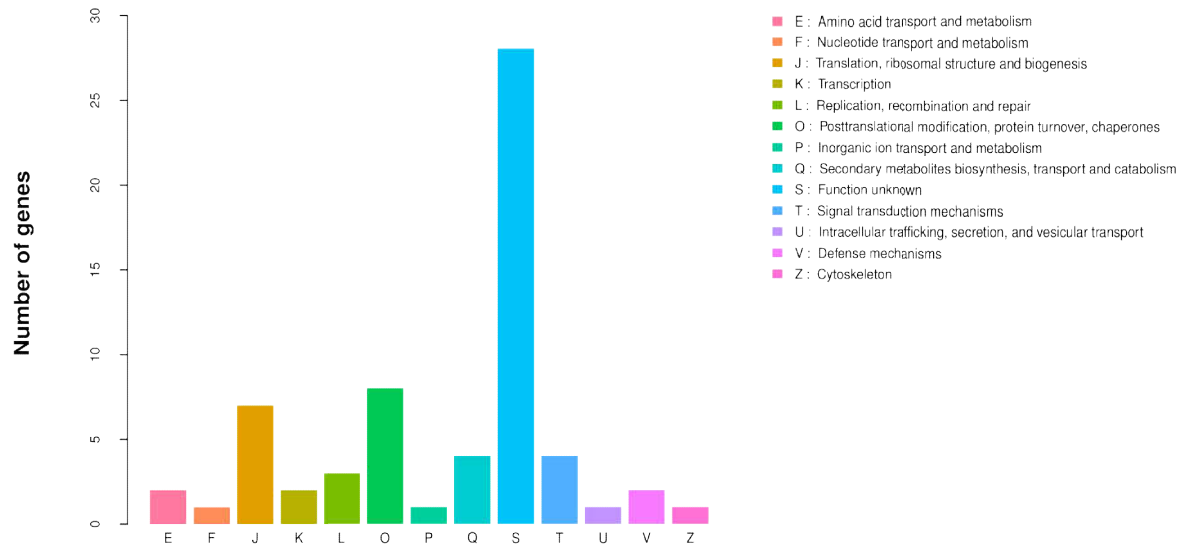
(B)



(C)

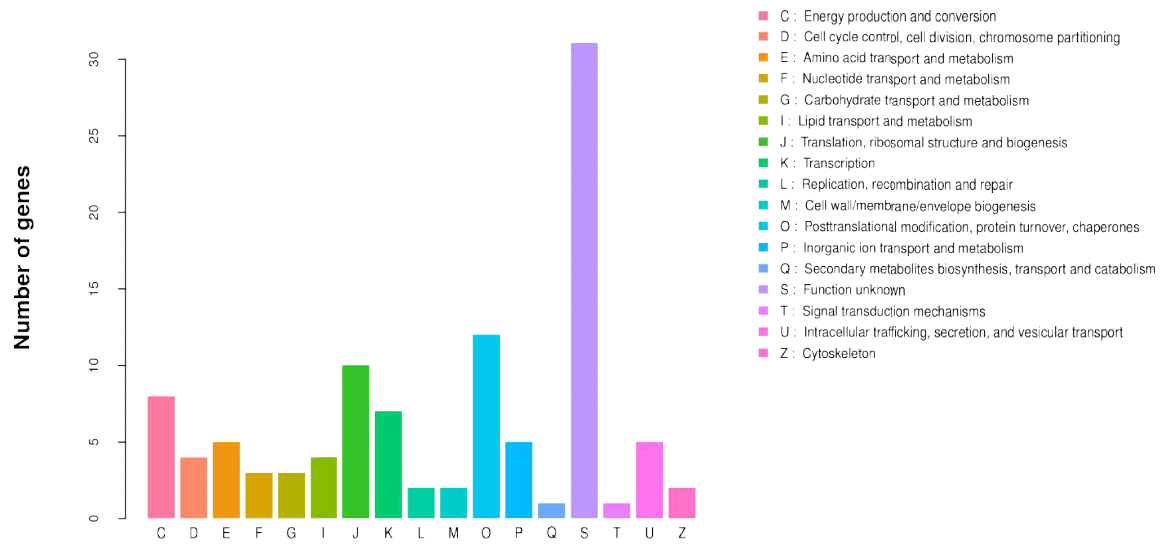
Supplemental Figure S2. Gene Ontology (GO) annotation of *Strongylocentrotus intermedius* genes

eggNOG functional categories



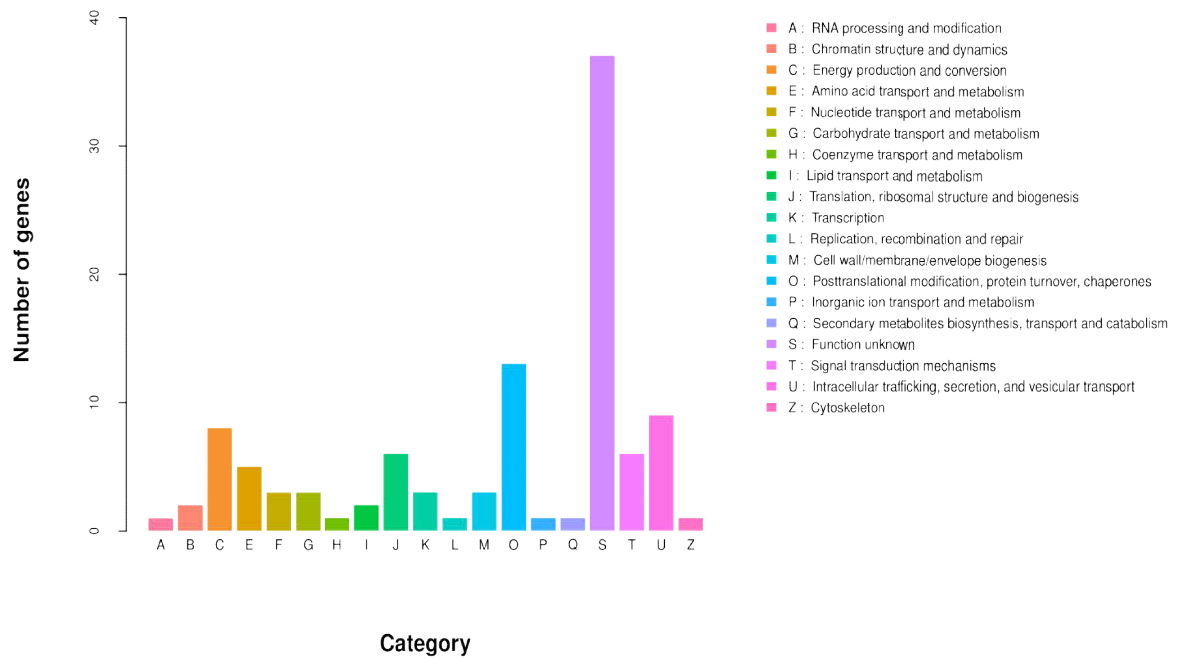
(A)

Category



(B)

Category



(C)

Supplemental Figure S3. Evolutionary genealogy of genes: Non-supervised Orthologous Group functional classifications of *Strongylocentrotus intermedius*.