

Supplementary materials

Table S1. Statistical table of comparison results

Sample	Clean Reads	Clean Data	Clean Reads %	Clean Data %
A1	40319378	6023459384	98.52%	98.13%
A2	40875518	6104016406	98.54%	98.1%
A3	45376654	6781707862	98.42%	98.06%
B1	45606250	6813867670	98.33%	97.94%
B2	46106970	6859749842	98.78%	97.98%
B3	46785220	6951291616	98.69%	97.75%
D1	44758046	6659266898	98.83%	98.03%
D2	44404336	6604330928	98.73%	97.9%
D3	44668798	6636755076	98.83%	97.89%

Table S2. Summary of annotated genes in different databases

	Number of genes	Percentage (%)
NR	46123	24.88
GO	19384	10.46
KEGG	7172	3.87
eggNOG	38720	20.89
Swissprot	36036	19.44
In all database	4151	2.24



Figure S1. GO categorization of the genes in the hemolymph transcriptome of *S. broughtonii*. Each annotated sequence is assigned at least one GO term.

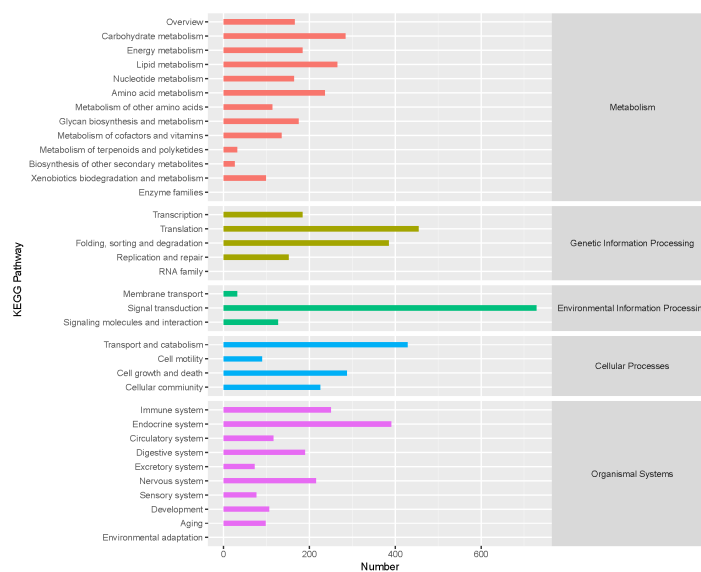


Figure S2 KEGG assignment of the genes in the hemolymph transcriptome of *S. broughtonii*.

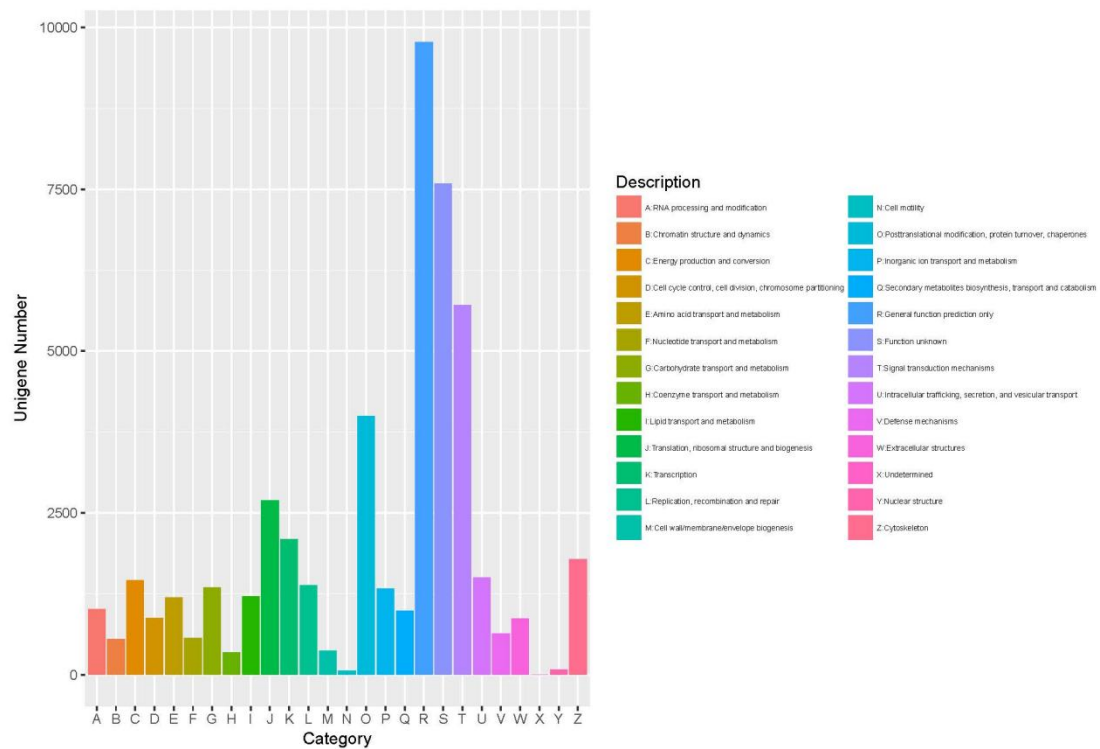


Figure S3. eggNOG (evolutionary genealogy of genes: Non-supervised Orthologous Groups) classification of the genes in the hemolymph transcriptome of *S. broughtonii*.