**Descriptions of Supplementary files**

**Figure S1: The WGCNA gene expression modules underlying the molecular pathways of settlement and metamorphosis in *C. gigas* and *R. venosa* respectively.** *n* indicates the number of genes in the module and the average expression (z-score) of all the genes under the module was calculated for each developmental stage.

**Table S1: The information of *C. gigas* and *R. venosa* samples used in this study.**

**Table S2: The raw expression counts of 5,427 orthologous genes across different developmental stages in C. gigas and R. venosa, respectively.**

**Table S3: The enriched GO terms and KEGG pathways of the upregulated genes and the downregulated genes shared by both *C. gigas* and *R. venosa* during larval settlement and metamorphosis.**

**Table S4: The lists of differentially expressed genes that are unique to *C. gigas* and *R. venosa*, respectively.**