**Additional file 4**

**Tracing key genes associated with *Pinctada margaritifera* albino phenotype from juvenile to cultured pearl harvest stages by multiple whole transcriptome sequencing**

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Figure S1.

Figure S1 Summarized REVIGO treemaps plot for gene ontology enrichment analysis between the P. margaritifera albino *versus* black wild-type phenotype

A. Juvenile dataset, UP-regulated genes in Albino phenotype

B. Juvenile dataset, DOWN-regulated genes in Albino phenotype

C. Mantle dataset, UP-regulated genes in Albino phenotype

D. Mantle dataset, DOWN-regulated genes in Albino phenotype

E. Pearl Sac dataset, UP-regulated genes in Albino phenotype

F. Pearl Sac dataset, DOWN-regulated genes in Albino phenotype

G. Common Mantle – Juvenile DOWN-regulated genes in Albino phenotype

H. Common Mantle – Pearl Sac DOWN-regulated genes in Albino phenotype

A.



B.



C.



D.



E.



F.



G.



H.

Figure S2.

Figure S2. Signaling pathways (sp) potentially impacted by deregulated genes in albino pearl oyster *P. margaritifera* versus black-wild type

The pathways plots are obtained from KAAS server using DEGs nucleotide sequences. Green boxes show deregulated genes in albino phenotype versus black wild-type in :

A, B, D, E : Mantle dataset

C, F : Juvenile dataset



A.



B.



C.



D.



E.



F.

Figure S3.

Figure S3. Composition plots of albino and black wild-type populations of pearl oyster P. margaritifera based on filtered SNPs called with Freebayes in both Juvenile and Mantle datasets

