1	Transcriptome analysis on the exoskeleton formation in early developmetal
2	stages and reconstruction scenario in growth-moulting in Litopenaeus vannamei
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Fig. S1 Summary of the homology search for all unigenes against the NR database. (a) E-value
distribution of the best blast hits; (b) Similarity distribution of the best blast hits; (c) Species

18 distribution of the best blast hits.

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Fig. S2. Real-time quantitative PCR (qRT-PCR) validation. Eight differentially expressed genes
were selected for validation in nine early development stages (A) and eight moulting stages (B).
Expression results of qRT-PCR are shown on the left and expression profiles of RNA-sequencing
on the right. The data are expressed as the mean +SD after normalization.