Supplemental Materials for
De novo assembly and comparative transcriptome characterization of Poecilobdella javanica provide insight into blood feeding of medicinal leech

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Running title: De Novo Assembly of Leech Transcriptome
Supplement Figure S1. Clean reads in leech RNA-seq. (A) Reads counts in all the RNA-seq libraries. (B) An example of per base sequence quality of clean reads in 20-day RNA-seq library. Clean reads were generated by filtering out low-quality reads (containing Ns and with more than 30% of bases with Phred quality score of $\leq 30$) and adaptor sequences.
Supplement Figure S2. The abundance histogram of K-mer in leech RNA-seq. The KmerGenie was used to estimate the best k-mer length for the de novo assembly [1]. The best k-mer lengths range from 19 to 31.
Supplement Figure S3. The gene expression correlations among time points. The gene expression levels were estimated using RSEM (v1.3.0) [2].
Supplement Figure S4. Heatmap of differentially expressed BUSCO single-copy orthologs in assembled transcriptomes.
References