



Figure S2. Functional classification of the *de novo* transcriptome assembly of *Mallotus japonicus*. (a) Homology based annotation summary for the assembled transcripts of *M. japonicus*; (b) Sequence-similarity distribution plot for the annotated transcripts using top blastx hits; (c) Gene ontology (GO) distribution plot for *M. japonicus* transcriptome assembly. GO terms for the annotated transcripts are summarized in three functional categories: biological processes (BP), molecular function (MF), and cellular component (CC); (d) Top 15 KEGG pathways represented by the assembled transcripts of *M. japonicus* based on the number of assigned transcripts.