



Figure S2. Homology analysis of assembled transcripts. E value distribution (a, b) and identity distribution (c, d) of the matches in the Swiss-Prot (a, c) and RefSeq (b, d) databases. (a,b) The number inside the pie chart indicates the number of transcripts recorded using that E value. Alignment by BLASTx with an E value threshold of  $1 \times 10^{-5}$ .