



Figure S1. Summary of annotation from public databases (A) and species distribution of the top BLAST hits (B) for assembled high-quality unigenes. NR, NCBI non-redundant protein database; Nt, NCBI nucleotide sequences; KO, KEGG (Kyoto Encyclopedia of Genes and Genome) Ortholog; SwissProt, a manually annotated and reviewed protein sequence database; Pfam, protein family; KOG, euKaryotic Ortholog Groups; GO, Gene Ontology.