

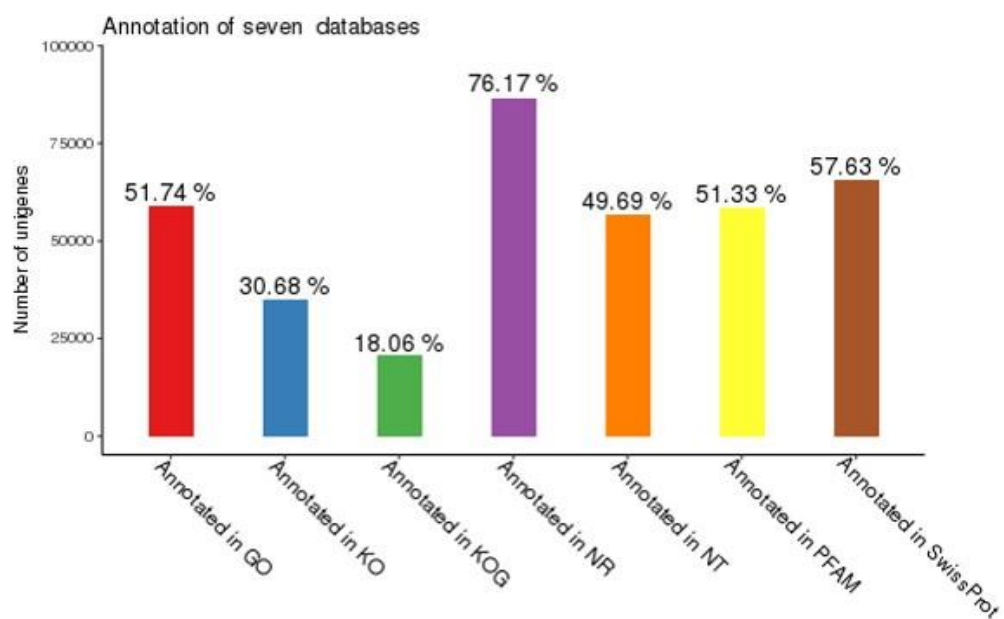


Fig. S1. The number of genes annoated in seven databases of transcriptome. NR, NCBI Non-redundant Protein; NT, NCBI Nucleotide Sequences; GO, Gene Ontology; KO, KEGG Orthology; KOG, Eukaryotic Orthologous Groups; Pfam, Protein Family Database; Swissprot, A manually annotated and reviewed protein sequence database.