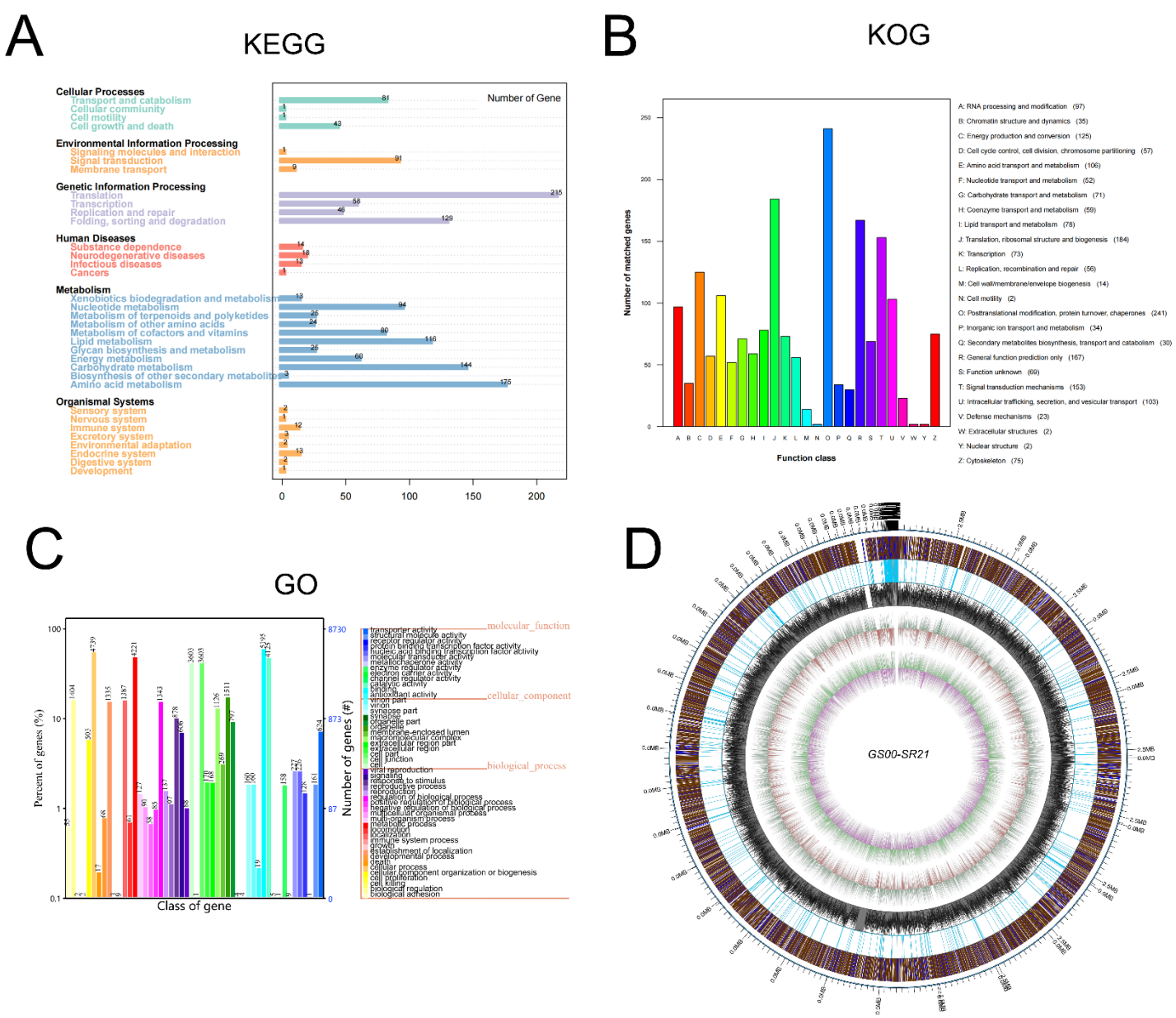


Figure S1. A. Bar chart showing the number of annotated genes in the KEGG database; B. Statistical classification of Gene Ontology (GO) categories; C. Statistical annotation of Eukaryotic Orthologous Groups (KOG) classification；D. Variant map of GS00 and SR21 genomes. The outermost circle represents the positional coordinates of the reference sequence. Moving inward, the subsequent circles depict InDel distribution (blue: deletions; ochre: insertions); SNP density distribution; read coverage depth; GC content; GC skew distribution.