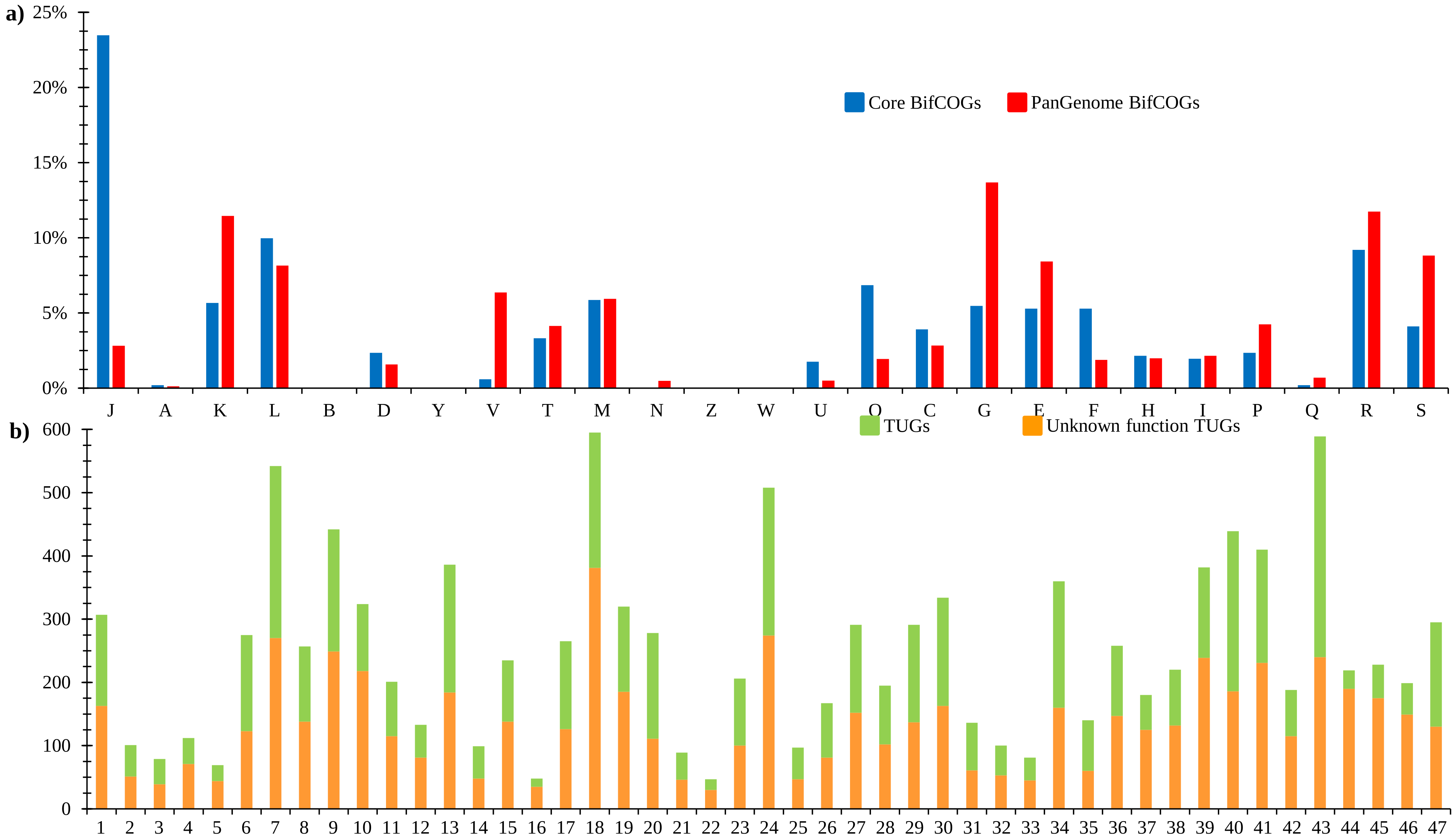

Supplementary Figure 1. COGs functional annotation and Truly Unique Genes (TUGs) of the *Bifidobacterium* genus. Panel a shows the COG functional classification of the core BifCOGs in blue and pangenome BifCOGs in red. Panel b displays in green the number of TUGs in each bifidobacterial genome and in orange the number of TUGs with unknown function, representing 54.1% of the total TUGs pool. COG functional families are abbreviated as follow: [J] Translation, ribosomal structure and biogenesis, [A] RNA processing and modification, [K] Transcription, [L] Replication, recombination and repair, [B] Chromatin structure and dynamics, [D] Cell cycle control, cell division, chromosome partitioning, [Y] Nuclear structure, [V] Defense mechanisms, [T] Signal transduction mechanisms, [M] Cell wall/membrane/envelope biogenesis, [N] Cell motility, [Z] Cytoskeleton, [W] Extracellular structures, [U] Intracellular trafficking, secretion, and vesicular transport, [O] Posttranslational modification, protein turnover, chaperones, [C] Energy production and conversion, [G] Carbohydrate transport and metabolism, [E] Amino acid transport and metabolism, [F] Nucleotide transport and metabolism, [H] Coenzyme transport and metabolism, [I] Lipid transport and metabolism, [P] Inorganic ion transport and metabolism, [Q] Secondary metabolites biosynthesis, transport and catabolism, [R] General function prediction only, [S] Function unknown. Each bifidobacterial genome analysed is number according to the numbering of the species displayed in Table 1.