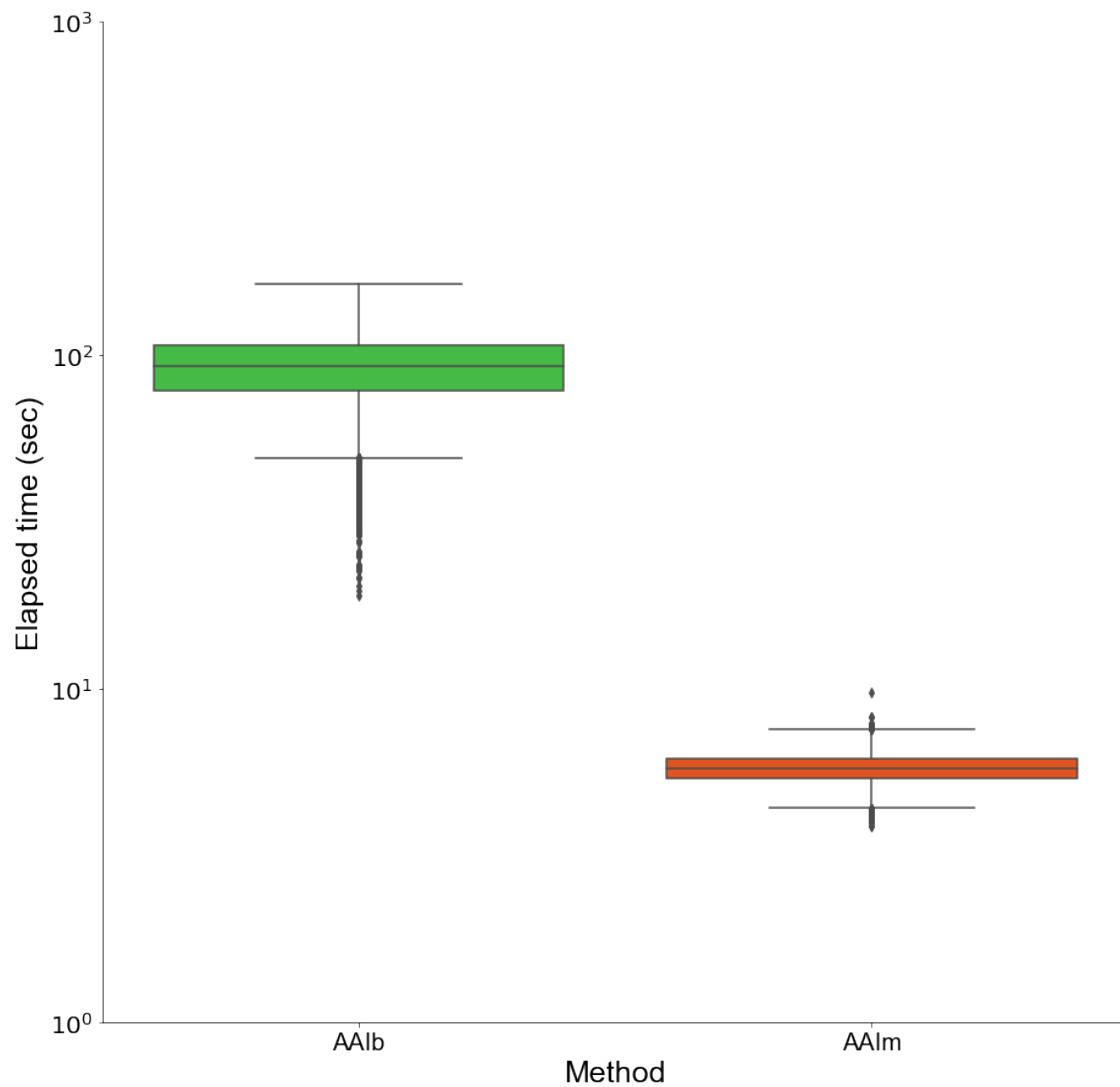
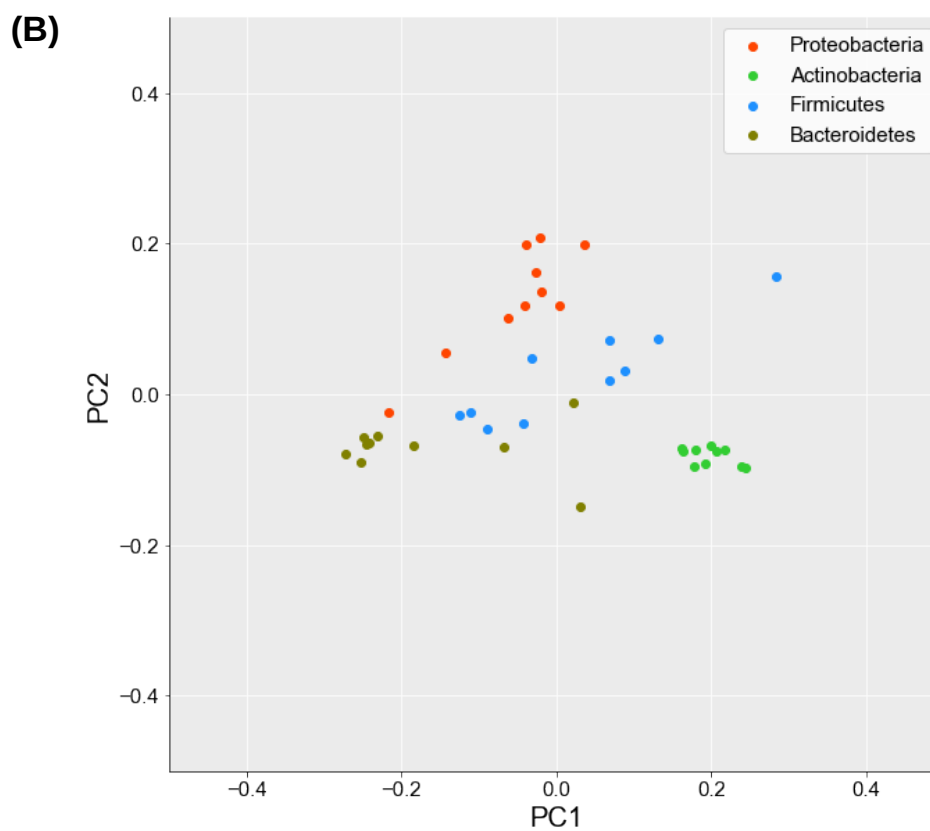
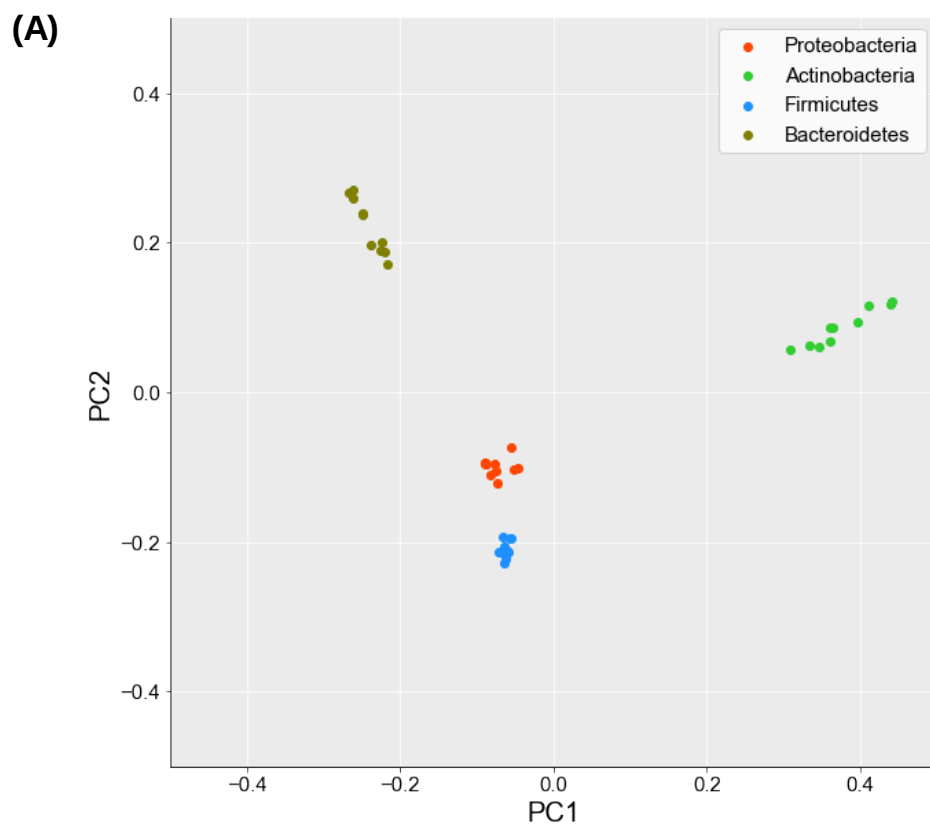
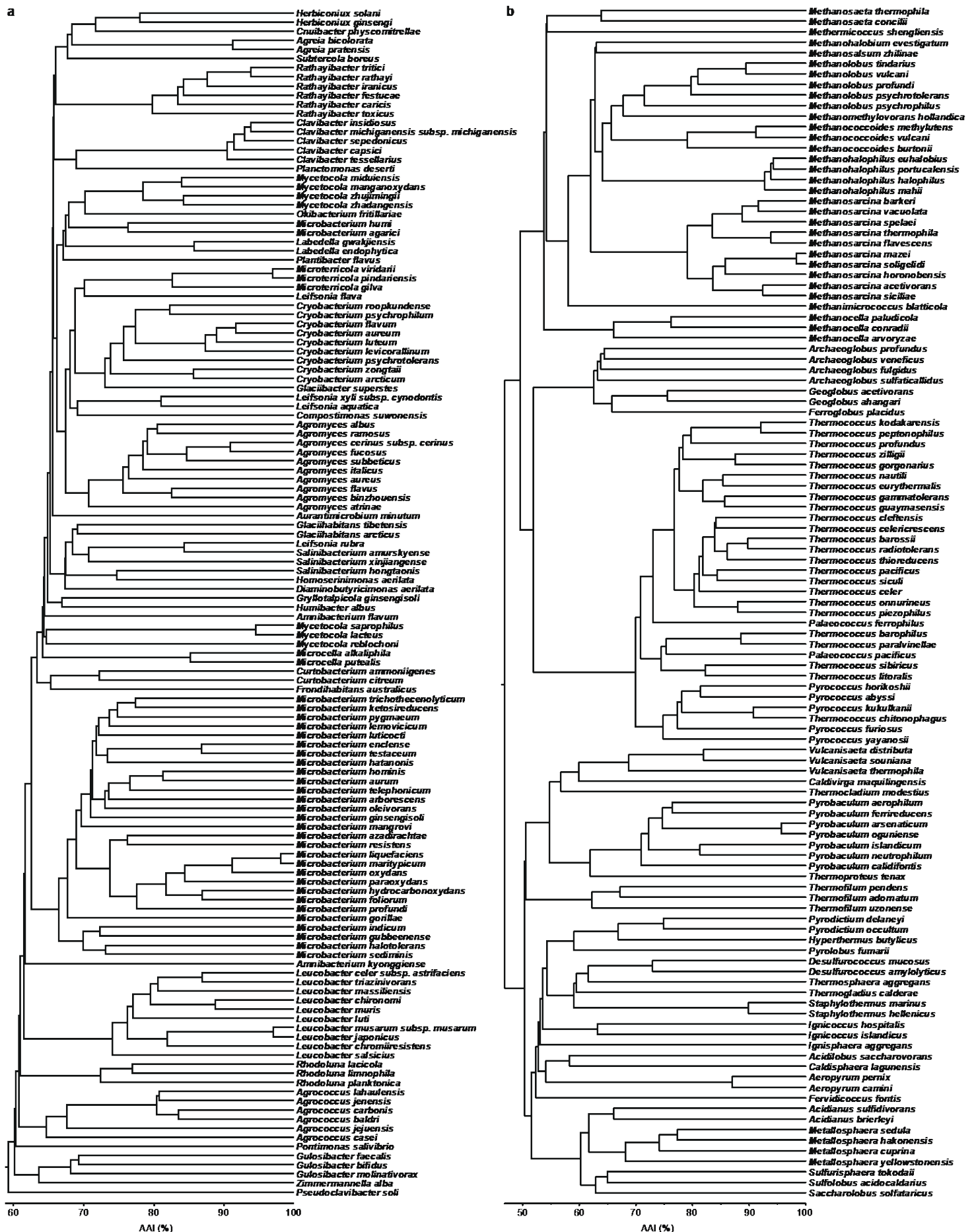




Supplementary data Fig. S1. Performance of BLASTp+ (AAIb) and MMSeqs2 (AAIIm) on AAI calculation tasks using 30 CPU cores on the set of 7,210 bacterial pairs.



Supplementary data Fig. S2. Principal coordinate analysis on 40 bacterial genomes from 4 different phyla. (A) PCoA plot drawn with AAI matrix. (B) PCoA plot drawn with ANI (OrthoANIu) matrix.



Supplementary data Fig. S3. UPGMA dendrogram from the extended set of prokaryotic species, constructed with AAI values and the EzAAI clustering module. (A) Dendrogram constructed with 130 type strain genomes under family *Microbacteriaceae*. (B) Dendrogram constructed with 113 archaeal type strain genomes.