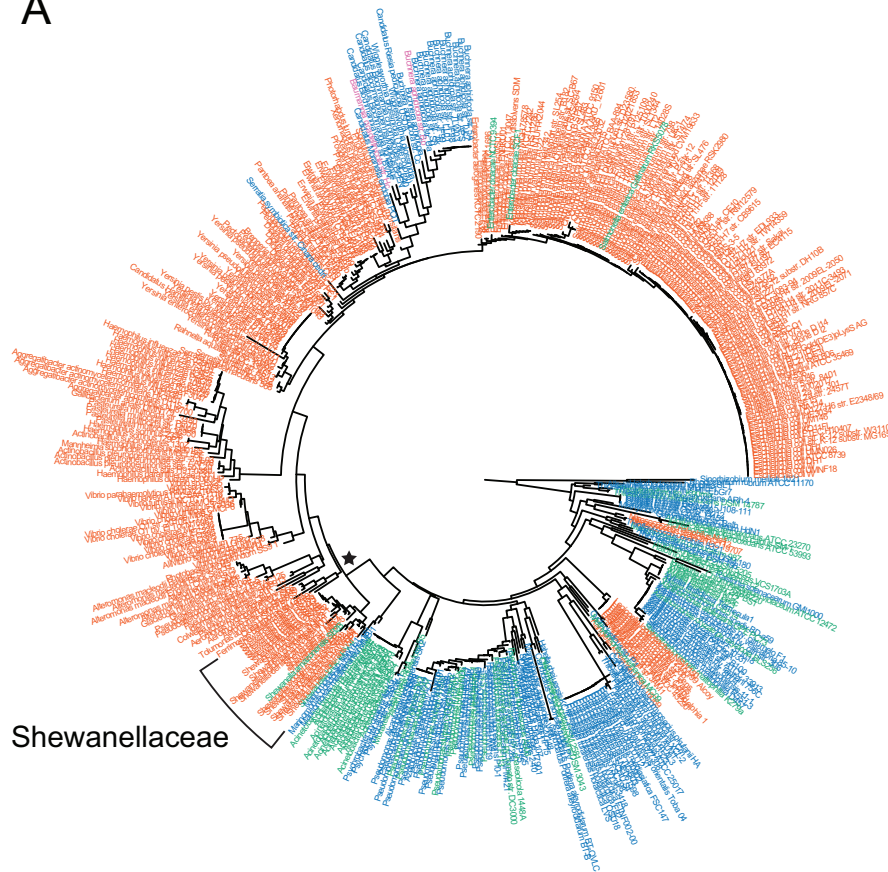
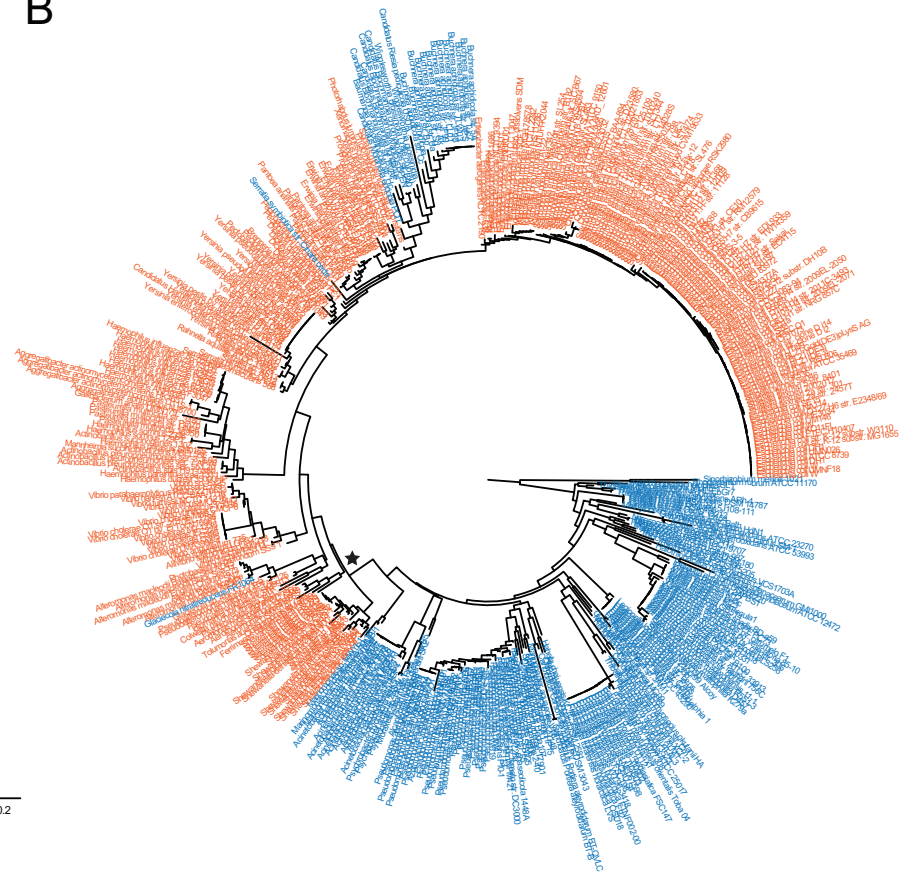


A



- dam + mutH
- dam only
- mutH only
- none

B



- seqA + enrichment
- seqA only
- enrichment only
- none

Supplementary Figure 2. Phylogenetic patterns of DNA methylation usage in *Gammaproteobacteria*. The presence of *dam* and *mutH* genes (A) as well as *seqA* and GATC enrichment at the origin of replication (B) is illustrated on a phylogenetic tree constructed from the 16S sequences of 448 finished genomes. The tree structure is the same for both panels. The scale bar represents the fraction of substitutions per site. The star indicates a node beyond which all but 24 genomes encoded *seqA* and were enriched for GATC motifs in the origin of replication