

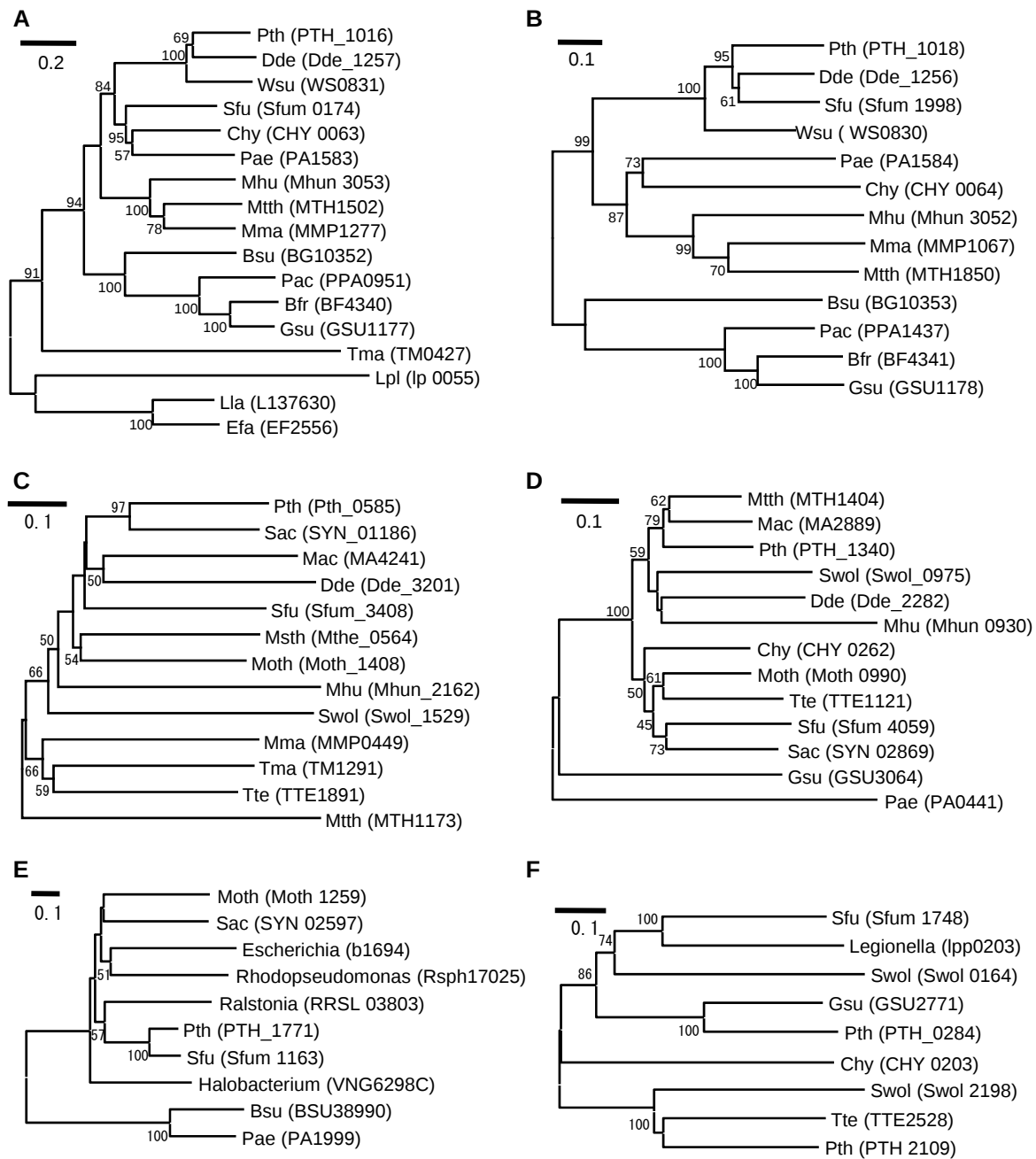


Fig. S4. Neighbor-joining trees showing phylogenetic relationships of CDSs in *P. thermopropionicum* showing atypical codon usages with corresponding genes in other organisms. (A) COG2009, succinate dehydrogenase cytochrome subunit; (B) COG0479, succinate dehydrogenase FeS subunit; (C) COG1149, ATPase containing a ferredoxin domain; (D) COG0145 acetone carboxylase, beta subunit; (E) COG4670 acyl CoA:acetate/3-ketoacid CoA transferase; (F) COG1943 transposase. CDSs are shown with organism names (see Table S1) and locus tags in parentheses. The numbers at the branch nodes are bootstrap values (per 100 trials); only values greater than 50 are shown. A scale bar indicates substitution per site.