



Fig. S1. A phylogenetic tree of ribokinase family proteins from the Archaea and Bacteria. Ribokinase family proteins that have been experimentally characterized were used to retrieve homologs from 18 selected archaeal species. Proteins that displayed at least 30% identity are included in the analysis. Proteins that displayed at least 30% identity from the Bacteria are also included. Proteins from Crenarchaeota are indicated in red, those from Euryarchaeota in black, and those from Bacteria in blue. Archaeal species are abbreviated as described in Fig. 7. Bacterial species are abbreviated as follows: *vso*, *Virgibacillus soli*; *bga*, *Bacillus galactosidilyticus*; *cma*, *Catellibacillus marimammalium* M35/04/3; *pba*, *Pasteurellaceae bacterium* 15-036681; *fbl*, *Ferrimonas balearica*; *Pmz*, *Prevotella multisaccharivorax*; *crh*, *Clostridia bacterium* BRH_c25; *cla*, *Caldanaerobacter subterraneus*; *thc*, *Thermus* sp. CCB_US3_UF1; *thi*, *Thermus islandicus* DSM 21543; *svi*, *Streptomyces viridosporus*; *spr*, *Streptomyces prasinopilosus*; *tda*, *Thermanaerotherix daxensis*; *lar*, *Longilinea arvoryzae*; *dae*, *Desulfotomaculum aeronauticum* DSM 10349; *pha*, *Paludifilum halophilum* DSM 102817; *pfl*, *Planomicrobium flavidum*; *pya*, *Pontibacillus yanchengensis* Y32; *bsp*, *Bacillus* sp. OK048; *gtn*, *Geobacillus thermodenitrificans* NG80-2; *aob*, *Alistipes obesi*; *pbor*, *Paludisphaera borealis*; *plb*, *Planctomycetales bacterium* 71-10; *plh*, *Planctomyces* sp. SH-PL62; *ttr*, *Thermobaculum terrenum* ATCC BAA-798; *tal*, *Tranquillimonas alkanivorans* DSM 19547; *mpe*, *Maribius pelagius*; *aua*, *Aureimonas* sp. AU22; *sae*, *Skermanella aerolata* KACC 11604; *rxv*, *Rubrobacter xylanophilus* DSM 9941; *mia*, *Mesoaciditoga lauensis* DSM 25116; *oap*, *Ornatilinea apprima* P3M-1; *has*, *Halanaerobium saccharolyticum* DSM 6643; *hco*, *Halanaerobium congolense* and *lba*, *Lentisphaerae bacterium* GWF2_45_14. The tree was constructed with Phyml at Phylogeny.fr after aligning the sequences with MUSCLE. Group numbers are designated in Fig. 7. Asterisks indicate groups that divided with the addition of the bacterial sequences.