

Species (kingdom, phylum)	Genomic location (strand)	Frameshifting signal sequence	Length	Efficiency
Methanocaldococcus fervens AG86 (Archaea, Euryarchaeota)	NC_013156.1:1122916-1122992(+)	AAA_AAG_GAA_AAT_AAT_GAC_GTA_AAA_AAA_AAA_ACA_AGA_ATA_AAT_ TAA_ATA_ATG_AAT_CAA_ATA_ATA_ATG_AGA_ATA_ATA_AT	77 bp	63%
Methanocaldococcus sp. FS406-22 (Archaea, Euryarchaeota)	NC_013887.1:1224237-1224313(+)	GAG_CAA_AAA_AAT_GAT_GAC_GTA_AAA_AAA_AAC_ATG_ATG_AAA_TAA_ GAA_ATG_AGT_TTG_AAG_AAG_AAA_ATG_AGG_ATT_CAA_AT	77 bp	40%
Delftia acidovorans SPH-1 (Bacteria; Betaproteobacteria)	NC_010002.1:6395640-6395711(-)	AAG_GTG_GGA_GCG_CCC_GCC_ACA_AAA_AAA_GCC_TGA_GCC_CCC_GCG_ GCC_CCG_CGC_CAC_AGG_CAA_GGG_CTG_CGG_GGG	72 bp	10%