Supplementary Information

FtTA is a CPSF73 homologue that terminates transcription in Archaea

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Supplementary Information Figure 1. Clustal-Omega alignment of diverse archaeal (coral), eukaryotic (green), and bacterial (blue) FttA-homologues.

BLASTp searches of the *T. kodakarensis* FttA protein (WP_011250379.1; TK1428) against all bacterial genomes revealed full-length homologues – containing both KH domains and the metallo-beta-lactamase (MBL) fold – in candidate species of *Rokubacterium*, *Wolfebacterium*, and *Staskawiczibacterium*, as well as *Tenericutes bacterium* and *Desulfuromonadales bacterium* C00003096. It should be noted that all Mollicutes (*e.g.* *Tenericutes* sps.), all Cyanobacteria, and some Firmicutes are devoid of obvious rho homologues. Many eukaryotic CPSF73 proteins contain C-terminal extensions not found in archaeal or bacterial homologues; an exception is the YSH1 protein of *S. cerevisiae*. Conserved (.), well-conserved (:), and invariant (*) residues are noted. An active center histidine (H255 in *T. kodakarensis*) is highlighted in red.
Supplementary Information Figure 2. SDS-PAGE of total cell lysates derived from *T. kodakarensis* strains IR5 and TS559 grown in the absence and presence of NaF. 10 µg of total protein from each strain grown in the absence or presence of 4 mM NaF was resolved via SDS-PAGE prior to transfer and quantification of FttA-levels via Western blots as shown in Figure 4, panel h (n = 3). Lane M contains Magic Mark protein ladders identified by molecular weight in KDa.