Supplementary figures

*Escherichia coli*

![Graph showing orthologs and paralogs for *Escherichia coli*](image1)

*Bacillus subtilis*

![Graph showing orthologs and paralogs for *Bacillus subtilis*](image2)

*Natrialba magadii*

![Graph showing orthologs and paralogs for *Natrialba magadii*](image3)

Figure S1: Full $dN/dS$ results obtained with InParanoid as a working definition of orthology.
Figure S2: Full $dN/dS$ results obtained with the Orthologous Matrix (OMA) working definition of orthology.
**Escherichia coli**

Figure S3: Full \(dN/dS\) results obtained with the OrthoFinder working definition of orthology.
Figure S4: Full \( dN/dS \) results obtained with the ProteinOrtho working definition of orthology.
Figure S5: Full $dN/dS$ results obtained with alignments covering at least 80% of both proteins.
**Escherichia coli**

![Graph showing dN/dS results for Escherichia coli genome identifiers.]

**Bacillus subtilis**

![Graph showing dN/dS results for Bacillus subtilis genome identifiers.]

**Natrialba magadii**

![Graph showing dN/dS results for Natrialba magadii genome identifiers.]

Figure S6: Full $dN/dS$ results obtained with proteins no more that 70% identical.
Figure S7: Full $dN/dS$ results obtained with proteins within usual codon usage.
**Escherichia coli**

Figure S8: Full $dN/dS$ results using Muse and Gaut's estimate of background codon frequencies.