

S1 Fig – Maximum likelihood (ML) single protein trees for the 36 genes included in the concatenated alignment of Spang *et al.* 2015.

For all trees, the scale-bar indicates the average number of substitutions per site, and values at nodes represent support calculated by nonparametric bootstrap (out of 100). Bacterial and eukaryotic sequences are indicated in red and blue respectively, while Loki sequences are indicated in green. In each tree, a red arrow indicates the lokiarchaeal sequence corresponding to Lokiarchaeon 1.











