Supporting information

Fig S1. Phylogenetic comparison of four upregulated genes from the contiguous genomic region. Phylogenetic arrangement of species containing the contiguous genomic region (with the region removed) and select upregulated genes from all species that had the contiguous region. Trees include the whole genome phylogeny (A), amino acid ABC transporter substrate-binding protein (B), formylmethanofuran dehydrogenase subunit A (C), coenzyme PQQ synthesis protein E (D), and sigma-54-dependent Fis family transcriptional regulator (E). Trees were rooted with species A33_M4_a for consistency as no outgroup was available for the contiguous region. Species names in the phylogenies were color coded based on the order listed in the whole genome phylogeny to improve visualizing incongruencies. The black asterisks indicate potential horizontal transfer events. Node support values were calculated using rapid bootstrapping and those with less than 50% support have been collapsed. Scale bar indicates substitutions per site.
