



Supplementary Figure S3. Analysis of codon usage bias (CUB) for the 13 strains. (A) The RSCU analysis of preferred codons for each of 20 amino acids. (B) The ENc-plot. The standard curve (red color) $ENc = 2 + GC_{3s} + 29/[GC_{3s}^2 + (1 - GC_{3s})^2]$ represents the expected ENc to GC_{3s} . ENc represents the effective number of codons, and GC_{3s} for the third synonymous codon position GC content. If genes follow the standard curve, CUB is determined primarily by the nucleotide composition of genes.