

Figure S1. Variation in AGE ORF start- and stop codon predictions for four moderate GC% bacterial genomes.

Represented in bar-graphs are the numbers of total, correct, incorrect, false positive (FP) and false negative (FN) ORF start codon (**Fig. S1A**) and ORF stop codon (**Fig. S1B**) predictions by the BASys, ISGA, RAST and xBASE AGEs (Table 1) in *B. subtilis* 168, *E. coli* K12 MG1655, *L. lactis* KF147 and *L. plantarum* WCFS1 reference genomes (Table 2). FP- and FN predictions were not defined as incorrect predictions, to distinguish between the various types of mis-predictions. In addition, for each reference genome (Ref. Genome), the total number of ORFs present in its genome according to the latest genome information is indicated.

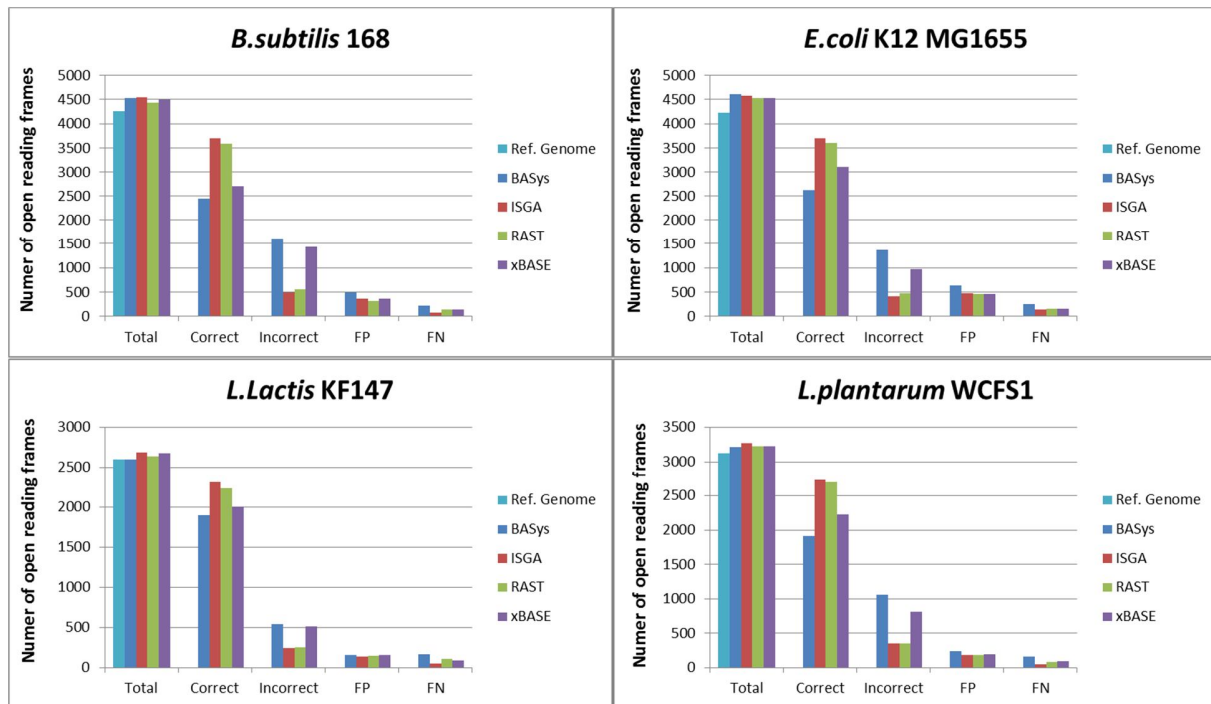


Figure S1A

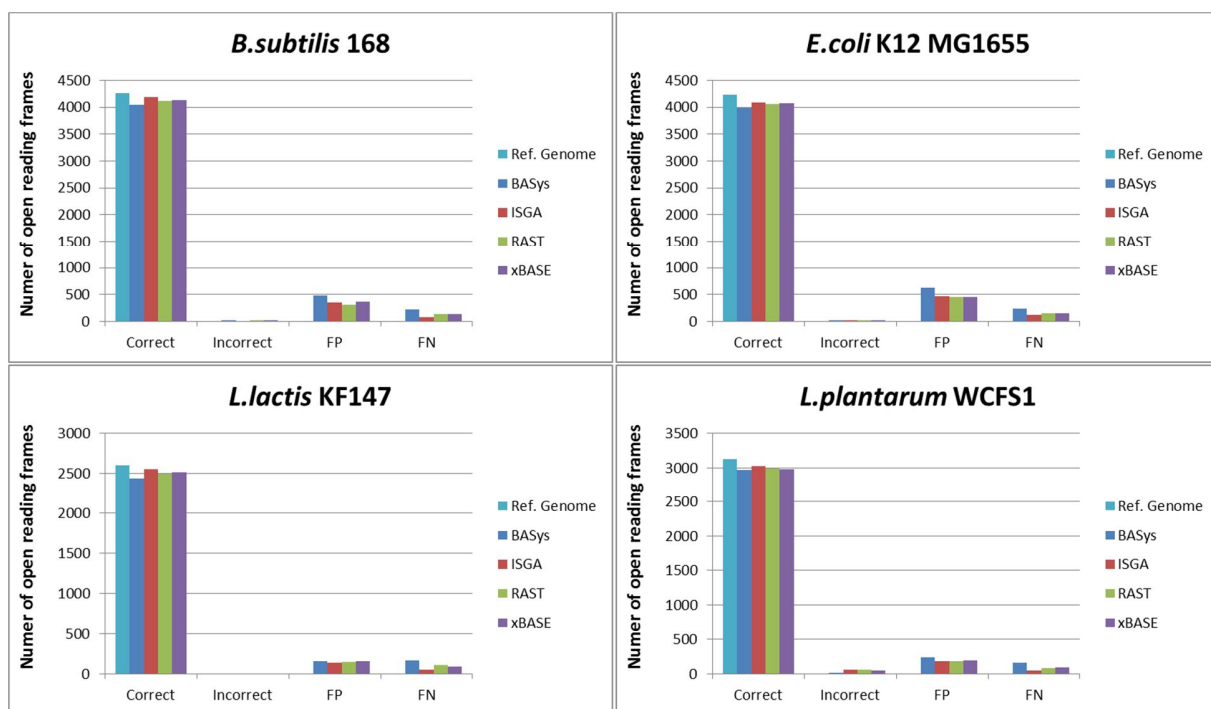


Figure S1B