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 S1B

- **B. subtilis 168**
  - Graph showing the number of open reading frames for different tools.
  - Tools compare: Ref. Genome, BASeq, RAST, and xBASE.

- **E. coli K12 MG1655**
  - Graph showing the number of open reading frames for different tools.
  - Tools compare: Ref. Genome, BASeq, RAST, and xBASE.

- **L. lactis KF147**
  - Graph showing the number of open reading frames for different tools.
  - Tools compare: Ref. Genome, BASeq, RAST, and xBASE.

- **L. plantarum WCFS1**
  - Graph showing the number of open reading frames for different tools.
  - Tools compare: Ref. Genome, BASeq, RAST, and xBASE.