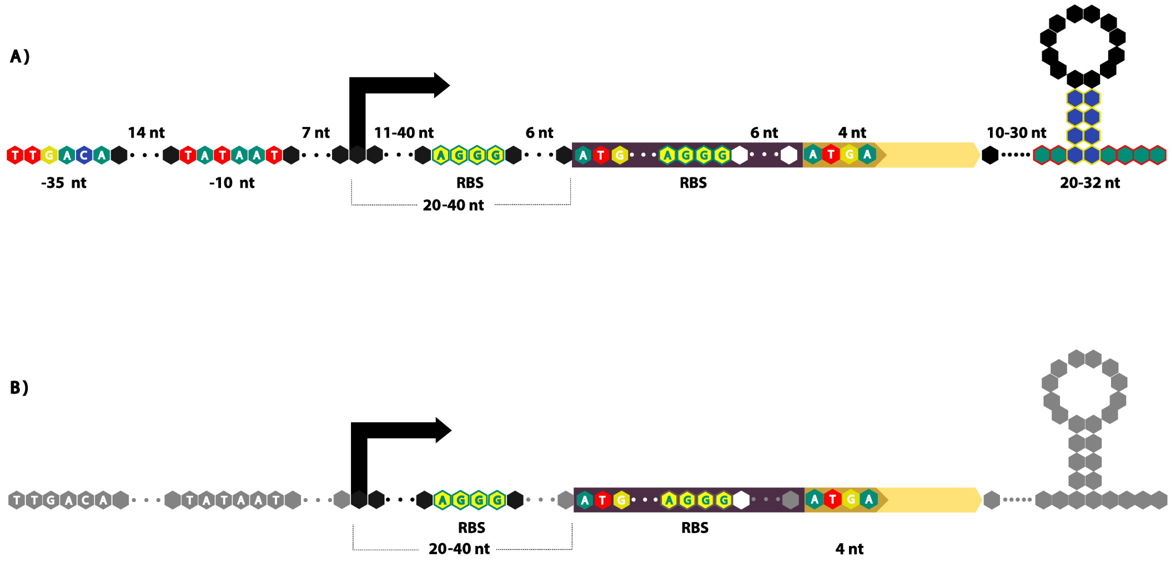

Figure S1. Architecture of genetic elements in bacteria different of K-12 MG1655

We performed the same analysis as for *E. coli* strain K-12 MG1655 in *E. coli* strains K-12 W3110 and BL21 (DE3), in *Salmonella typhimurium* SL1344, and in *Pseudomonas aeruginosa* strains PA14 and PAO1 (see, Table S2 and S3). A) Consensus architecture of *E. coli* K12 MG1655, B) Summary of the consensus architecture of all the other bacteria, where genetic elements in colors are those conserved as in K-12 MG1655 and those in gray have limited information to get consensus. We identified that the genetic elements conserved in all bacteria are: transcription start site, translation start codon, translation stop codon, ribosomal binding sites, genes overlap in 4 bp and the average distance between the TSS and the RBS range from 20 to 40 bp.