Supplementary Figure S1.

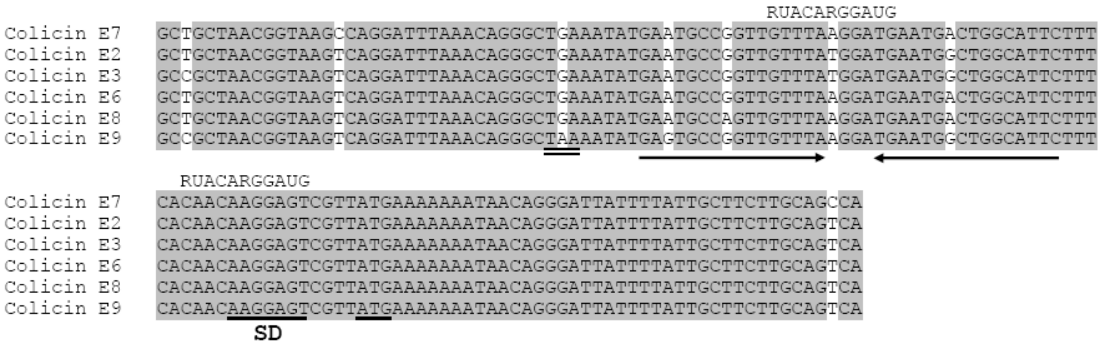

Figure Legends

Figure S1. Sequence alignment of the *cei*-*cel* intercistronic region and the *cel* leader region from several E group Col plasmids. Identical nucleotides are indicated by gray shading The overall sequence identity is 99%. Accession numbers are provided in the text. The *cei* stop codon is double underlined. The two horizontal inverted arrows indicate the T1 transcriptional terminator. The Shine-Dalgarno (SD) sequence and the ATG start codon for the *cel* coding region are underlined. The CsrA binding consensus sequence is shown above the potential binding region in *cel* mRNA (R = A or G). The T1 hairpin sequence and the *cel* SD sequence between these E group Col plasmids displayed high similarity to the consensus sequence, as they match the SELEX-derived consensus binding sequence in 8 and 7 out of 11 positions, respectively.