## Supplementary File 6. Putative SD and start codon sites in *rcsD* in Enterobacteriaceae.

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| --- | --- | --- | --- |
| Species | Predicted SDa | Spacer length between SD and start site | Predicted start site (fragment length of predicted *rcsD-hpt*) |
| *Yersinia pestis* | AAAAGG | 8 bp | ATT (312bp) |
| *Yersinia pseudotuberculosis* | AAAAGG | 8 bp | ATT (312bp) |
| *Escherichia coli* | AGGAAG | 14 bp | ATT (327 bp) |
| *Shigella boydii* | AGGAAG | 14 bp | ATT (327 bp) |
| *Shigella boydii* | GAGCAA | 4 bp | ATG (351 bp) |
| *Serratia fonticola* | AGAACA | 4 bp | ATG (357 bp) |
| *Proteus mirabilis* | GAGGC | 10 bp | TTG (372 bp) |
| *Yersinia frederiksenii* | AGGAAG | 7 bp | ATT (381 bp) |
| *Erwinia amylovora* | AGGACG | 8 bp | ATC (576 bp) |
| *Klebsiella quasipneumoniae* | AGGAGG | 14 bp | ATT (327 bp) |
| *Klebsiella quasipneumoniae* | AGCACG | 3 bp | ATG (351 bp) |

SDa, Shine–Dalgarno sequence.