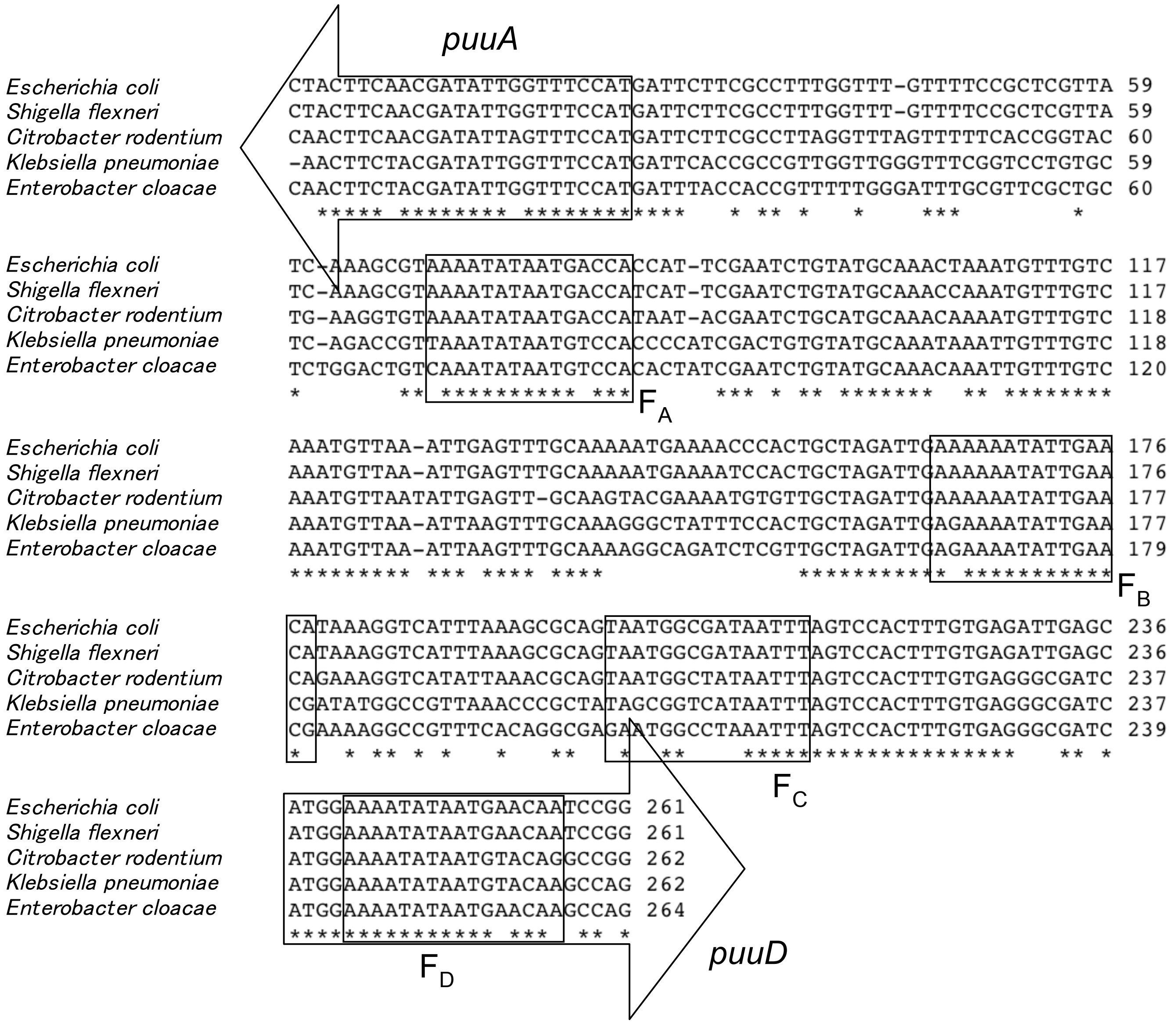

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Escherichia coli       CTACTTCAACGATATTGGTTTCCATGATTCTTCGCCTTTGGTTT-GTTTTCCGCTCGTTA 59
Shigella flexneri      CTACTTCAACGATATTGGTTTCCATGATTCTTCGCCTTTGGTTT-GTTTTCCGCTCGTTA 59
Citrobacter rodentium  CAACTTCAACGATATTAGTTTCCATGATTCTTCGCCTTAGGTTTAGTTTTTCACCGGTAC 60
Klebsiella pneumoniae  -AACTTCTACGATATTGGTTTCCATGATTCACCGCCGTTGGTTGGGTTTCGGTCCTGTGC 59
Enterobacter cloacae   CAACTTCTACGATATTGGTTTCCATGATTTACCACCGTTTTTGGGATTTGCGTTCGCTGC 60
                         ***** ******** ************   * ** *   *    ***        *

Escherichia coli       TC-AAAGCGTAAAATATAATGACCACCAT-TCGAATCTGTATGCAAACTAAATGTTTGTC 117
Shigella flexneri      TC-AAAGCGTAAAATATAATGACCATCAT-TCGAATCTGTATGCAAACCAAATGTTTGTC 117
Citrobacter rodentium  TG-AAGGTGTAAAATATAATGACCATAAT-ACGAATCTGCATGCAAACAAAATGTTTGTC 118
Klebsiella pneumoniae  TC-AGACCGTTAAATATAATGTCCACCCCATCGACTGTGTATGCAAATAAATTGTTTGTC 118
Enterobacter cloacae   TCTGGACTGTCAAATATAATGTCCACACTATCGAATCTGTATGCAAACAAATTGTTTGTC 120
                       *       ** ********** ***      *** * ** *******  ** ********

Escherichia coli       AAATGTTAA-ATTGAGTTTGCAAAAATGAAAACCCACTGCTAGATTGAAAAAATATTGAA 176
Shigella flexneri      AAATGTTAA-ATTGAGTTTGCAAAAATGAAAATCCACTGCTAGATTGAAAAAATATTGAA 176
Citrobacter rodentium  AAATGTTAATATTGAGTT-GCAAGTACGAAAATGTGTTGCTAGATTGAAAAAATATTGAA 177
Klebsiella pneumoniae  AAATGTTAA-ATTAAGTTTGCAAAGGGCTATTTCCACTGCTAGATTGAGAAAATATTGAA 177
Enterobacter cloacae   AAATGTTAA-ATTAAGTTTGCAAAAGGCAGATCTCGTTGCTAGATTGAGAAAATATTGAA 179
                       ********* *** **** ****              *********** ***********

Escherichia coli       CATAAAGGTCATTTAAAGCGCAGTAATGGCGATAATTTAGTCCACTTTGTGAGATTGAGC 236
Shigella flexneri      CATAAAGGTCATTTAAAGCGCAGTAATGGCGATAATTTAGTCCACTTTGTGAGATTGAGC 236
Citrobacter rodentium  CAGAAAGGTCATATTAAACGCAGTAATGGCTATAATTTAGTCCACTTTGTGAGGGCGATC 237
Klebsiella pneumoniae  CGATATGGCCGTTAAACCCGCTATAGCGGTCATAATTTAGTCCACTTTGTGAGGGCGATC 237
Enterobacter cloacae   CGAAAAGGCCGTTTCACAGGCGAGAATGGCCTAAATTTAGTCCACTTTGTGAGGGCGATC 239
                       *   * ** * *   *   **   *  **    ********************   ** *

Escherichia coli       ATGGAAAATATAATGAACAATCCGG 261
Shigella flexneri      ATGGAAAATATAATGAACAATCCGG 261
Citrobacter rodentium  ATGGAAAATATAATGTACAGGCCGG 262
Klebsiella pneumoniae  ATGGAAAATATAATGTACAAGCCAG 262
Enterobacter cloacae   ATGGAAAATATAATGAACAAGCCAG 264
                       *************** ***  ** *
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Figure S1. Alignment of the intergenic region between *puuA* and *puuD*. Alignment of the intergenic region between *puuA* and *puuD* in *Escherichia coli* str. K-12 substr. MG1655 (accession No. NC_000913), *Shigella flexneri* 5 str. 8401 (accession No. CP000266), *Citrobacter rodentium* ICC168 (accession No. FN543502), *Klebsiella pneumoniae* 342 (accession No. CP000964), *Enterobacter cloacae* subsp. cloacae ATCC13047 (accession No. CP001918). ORFs of *puuA* and *puuD* are surrounded by clear arrows. Boxes mark the 15-bp PuuR-binding motifs in F_A, F_B, F_C, and F_D, as determined by DNase I footprint assays.