**S2 Table. Primers used in this study**

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| **Target gene** |  | **Primer sequence (5'-3')** |
| ***Primers for construction of mutants and 3×FLAG-tagged strain \**** | | |
| SPI-14 | F | ATGCAAACGTTAGAACGGTTTTTTCTTTTCGTTACGGG GTGTAGGCTGGAGCTGCTTCG |
| R | ATGCACTTTGATATAAAAGATTTAAAATTATTCCTTGCT CATATGAATATCCTCCTTAG |
| *STM14\_1001- STM14\_1004* | F | ATGCAAACGTTAGAACGGTTTTTTCTTTTCGTTACGGG GTGTAGGCTGGAGCTGCTTCG |
| R | TCATAATTTTTTCCTCAATAAACCAGCGCCAACAGGGG CATATGAATATCCTCCTTAG |
| *STM14\_1005- STM14\_1008* | F | ATGAAAAGTATTGAAAAGGATAAATATCAGGATATTCG GTGTAGGCTGGAGCTGCTTCG |
| R | ATGCACTTTGATATAAAAGATTTAAAATTATTCCTTGC CATATGAATATCCTCCTTAG |
| *STM14\_1005* | F | ATGAAAAGTATTGAAAAGGATAAATATCAGGATATTCG GTGTAGGCTGGAGCTGCTTCG |
| R | TCAGAATGAACGTGGCATCTCCAGCACATGCTCAGCGA CATATGAATATCCTCCTTAG |
| *STM14\_1006* | F | GTGCCTATAAGACTATATAGCCAGTTATCAACTATTAA GTGTAGGCTGGAGCTGCTTCG |
| R | TTATGATGAACGGCTTAAAAATGATTTGTGTATATTCT CATATGAATATCCTCCTTAG |
| *STM14\_1007* | F | ATGAACGATACACTTTCTAATACCCAGCAATCACGTGA GTGTAGGCTGGAGCTGCTTCG |
| R | TTACATCCCTGTATAATTTGGTCCGTTGCCACCTTCAGGC CATATGAATATCCTCCTTAG |
| *loiA* (*STM14\_1008*) | F | ATGCACTTTGATATAAAAGATTTAAAATTATTCCTTGC GTGTAGGCTGGAGCTGCTTCG |
| R | TCACTCAGTCTGAGCTGTGAGCATAGTAACCAGTTTTTG CATATGAATATCCTCCTTAG |
| *hilD* | F | ATGGAAAATGTAACCTTTGTAAGTAATAGTCATCAGCGT GTGTAGGCTGGAGCTGCTTCG |
| R | TTAATGGTTCGCCATTTTTATGAATGTCGATGGCGTAG CATATGAATATCCTCCTTAG |
| SPI-1 | F | ACAGGCGTAATGAAATCGTACCAGAGGCGCAAGGTTAA GTGTAGGCTGGAGCTGCTTCG |
| R | AGTAAAAAGACAGGAAGACAGCTATAAAATTTTTTCAT CATATGAATATCCTCCTTAG |
| *fnr* | F | ATGATCCCGGAAAAGCGAATTATACGGCGCATTCAGTC GTGTAGGCTGGAGCTGCTTCG |
| R | TTAAGCGACGTTGCGGGTATGACCGGCGAGGGCCGCCAG CATATGAATATCCTCCTTAG |
| *arcB* | F | ATGAAGCAAATTCGTATGCTGGCGCAATACTATGTCGA GTGTAGGCTGGAGCTGCTTCG |
| R | TCATTTTTTTTCCGCGTTTGCCACCCAGGCTTTCAGCAC CATATGAATATCCTCCTTAG |
| *arcA* | F | ATGCAGACCCCGCACATTCTTATCGTTGAAGACGAGTT GTGTAGGCTGGAGCTGCTTCG |
| R | TTAATCCTGCAGGTCGCCGCAGAAGCGATAACCTTCGCC CATATGAATATCCTCCTTAG |
| *loiA -3×FLAG* | F | CACAAAAACTGGTTACTATGCTCACAGCTCAGACTGAG GACTACAAAGACCATGACGGTG |
| R | AGGTGGCAACGGACCAAATTATACAGGGATGTAACGCTA TTACGCCCCGCCCTGCCACTCA |
| *hilA-3×FLAG* | F | AAAGATGGAAACAGGATCCCCGCTTGATTAAATTACGG GACTACAAAGACCATGACGGTG |
| R | CGATGATAAAAAAATAATGCATATCTCCTCTCTCAGATT TTACGCCCCGCCCTGCCACTCA |
| ***Primers for identification of the mutants and 3×FLAG-tagged strain*** | | |
| SPI-14 | F | TTTTCCGCCAAAGGTGACT |
| R | TCACCAGCGTCCTACCAGAT |
| *STM14\_1001- STM14\_1004* | F | TTTTCCGCCAAAGGTGACT |
| R | ACGAACCGCATCACGAAT |
| *STM14\_1005- STM14\_1008* | F | TGTTGGCGCTGGTTTATT |
| R | TCACCAGCGTCCTACCAGAT |
| *STM14\_1005* | F | TGTTGGCGCTGGTTTATT |
| R | GCGAGAAATAATCAGCCAACT |
| *STM14\_1006* | F | TGCTCCCATATCTACCAACC |
| R | CGTGATTGCTGGGTATTAGA |
| *STM14\_1007* | F | GTTGGCTGATTATTTCTCGC |
| R | GGTATAATGCCTCACTCTGC |
| *loiA* (*STM14\_1008*) | F | TCCGTCTATCTCAGTAACACC |
| R | TCACCAGCGTCCTACCAGAT |
| *hilD* | F | AGCAGCAGATTACCGCACAG |
| R | CCCATCCTGATAGAGCGTGT |
| SPI-1 | F | TTCTGTCAATCTCACTGCTTAT |
| R | CCAACCGTAAAAGTGACCAT |
| *fnr* | F | GGGATAGCTCAGACTTACGC |
| R | CATAGCCATACAGGGTCTCC |
| *arcB* | F | ACGATTTCCCTGGTGTTGG |
| R | GCTAACGGCAGGTGAGATG |
| *arcA* | F | GACATAAGAAACAGCCAGTAA |
| R | GGTTAGGATGACAGCCGTTT |
| *loiA -3×FLAG* | F | TCCGTCTATCTCAGTAACACC |
| R | GAAGGGACAGGAATGTTTGA |
| *hilA-3×FLAG* | F | TTCTGGAAAGTGAACAGCGT |
| R | TGGGCGATAGCGTAAAGTAG |
| ***Primers for construction of clone and complemented strain*** | | |
| *loiA* | F | GCTCTAGAACGGGTTAACCTGATGACC |
| R | CGGGATCCTCACTCAGTCTGAGCTGTG |
| *hilD* | F | GCTCTAGATACCGCACAGGACACAGG |
| R | CGGGATCCTTAATGGTTCGCCATTTT |
| *arcB* | F | CGGGATCCCGTGATGAGGGGCGCTA |
| R | GGAATTCTCATTTTTTTTCCGCGTT |
| *arcA* | F | CGGGATCCTTTTGACACTGTCGGGTC |
| R | GGAATTCTTAATCCTGCAGGTCGCC |
| *loiA-His6* | F | CGCGGATCCAGCCACAACGATGCACTTTG |
| R | CCCAAGCTTTCACTCAGTCTGAGCTGTGAGCA |
| *arcA-His6* | F | CGCGGATCCATGCAGACCCCGCACATT |
| R | CCCAAGCTTTTAATCCTGCAGGTCGCC |
| ***qRT-PCR primers*** | |  |
| *16S rRNA* | F | GAAAGCGTGGGGAGCAAAC |
| R | ACATGCTCCACCGCTTGTG |
| *hilA* | F | CGCTGGCAGAATGCTACCTC |
| R | TGTTTGAATAGCAAACTCCCGA |
| *hilC* | F | TTTTCATGCGGACTTGTTGC |
| R | CTCAGCCTGTGACCATTTGC |
| *hilD* | F | GCTTTCGGAGCGGTAAACTG |
| R | CCAAGTCGTTGCGTCGGTAT |
| *hilE* | F | GCTTACAACCACAACCCGAC |
| R | CAGCACGCCTTCTTTCACC |
| *rtsA* | F | TATTACGGCATCAGGGCCA |
| R | ACTCTTGCTACGCCTGTTTCTA |
| *sipB* | F | AAGCGACAGAGGCGAAAGAG |
| R | AGATTATCCTGCTCACCCTGG |
| *spaO* | F | ACAGAGCGACCGTTTGAGTTG |
| R | ATGTGCAACAATTTCCCTTCC |
| *prgK* | F | GCTGAGCCTGATTTTACCGC |
| R | AGCCTGCTGACATCACGGA |
| *invF* | F | TGTGCAGCAGAGCGTTGG |
| R | TGGGTGATGTTCTCGTGGC |
| *loiA* | F | AAACACCACGCCAGCCTTAT |
| R | CGGACTTGGATACTCCCTGAG |
| *invH* | F | TCGGCTGTGCTCAGGTGC |
| R | TCTTCGCAAGGTCTGACGG |
| ***Primers for EMSAs and CHIP-qPCR*** | | |
| P*hilC* | F | CAATAAGCAGTTTGCGACAT |
| R | AGCAAATAATGCAGAAAATGC |
| P*hilD* | F | ACTCACAGCCGTTCAGTGAG |
| R | CTTCAAGCGTCACGTTAACT |
| P*loiA* | F | CTGTTCAAGATTACGTATACG |
| R | GGCGTATCATTGTTTGTGG |
| P*cydA* | F | ATTACTCTTTGCAAAAACAA |
| R | GAACTTGGTCATATCTTTAT |

\* Primers were designed carry extensions homologous to 38–40 bp (underlined) of the target gene; F, forward; R, reverse.