Table S2. Primers used in this study.

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| **Primer name** | **Purpose** | **Sequence** (5′–3′)\* |
| PA14-pMAL-*Eco*RI-F | Fusion | CACACAGAATTCGGCGAAAAGGAACCGGAGCT |
| PA14-pMAL-*Pst*I-R | Fusion | CACACACTGCAGTCATCCGCCCTCCGTGTGGAA |
| Δ*traA*-Upstr-*Hind*III-F | Deletion | CACACAAAGCTTGGGTGCTCTTCGAGGTGAT  |
| Δ*traA*-Upstr-*Eco*RI-*Pst*I-R | Deletion | CACACAGAATTCATCCTGCAGTGGTGAAGGAGCTACGGGA |
| Δ*traA*-Dwnstr-*Pst*I-F | Deletion | CACACACTGCAGGCGAAGACGATGGAGTGC |
| Δ*traA*-Dwnstr-*Eco*RI-R | Deletion | CACACAGAATTCAGCTCACGTTGAGCGTCAC |
| Δ*traA*-Verification-F | Deletion | GTGGGCGCTGTACCTCCT |
| Δ*traA*-Verification-R  | Deletion | GCTCATCGGGTTGCTTCTG |
| P*pilA*-*Eco*RI-F | Expression | GACGACGAATTCCGTCATGTTGGACGAGGT |
| P*pilA*-ΔSD-*Xba*I-R | Expression | CAGCAGTCTAGAGCCCGCGGATGGGATTAG |
| TraA-RBS-*Xba*I-F  | Expression | GACGACTCTAGA*GGAAACCAAGAATAGAAATAGAAAGGAGAATTA***GTG**GGAGATATCCCTCATTG |
| TraA-*Hind*III-R | Expression | GACGACAAGCTTGAAGAGCTGCACGTTGAAG |
| TraA-Env-Full-F | Sequencing | CAACATCTTCGTGCGACATC |
| TraA-Env-Full-R | Sequencing | CCAGGTTGATCTTGCTCAGG |
| DK816-SR1 | Sequencing | GACTCCATGAACGCATTGAA |
| DK816-SR2 | Sequencing | TAGCTTGGCTGCTGAATCGT |
| MX6895-SF2 | Sequencing | TCACTGTCTTGTCGGTGTGC |
| MX6895-SR2 | Sequencing | GTTGATGTCGTCTGGGAAGG |
| MX6895-SF1 | Sequencing | GTGGGAGATATCCCTCATTGTT |
| MX6895-SR1 | Sequencing | TGCGTTGCAGTGGTAGAAAG |
| MX6895-SF3 | Sequencing | ACTTCGTGAACTCCGTTGGT |
| MX6895-SR3 | Sequencing | GTTGAGGTTGGCGCAGTG |
| MX6895-SF4 | Sequencing | CTGCGACTCCTCGCTCTT |
| MX6895-SR4 | Sequencing | CCATTGGAGAGGCAGAAGG |
| MX6895-Gap1 | Sequencing | CCATCGTCAAGCTCAACACA |
| DK823-R2 | Sequencing | AATGTTTCGGTGTCACAAGC |
| DK823-FW2 | Sequencing | GATTTCGCGGTTACCTGAAC |
| DK823-FW3 | Sequencing | TCAACGTCATCGAGGACAAC |
| DK823-R3 | Sequencing | CGTTCTTGCACTCGACACAT |

\*Restriction sites are underlined, start codon is in bold and artificial Shine-Dalgarno region is in italics.