**Table S1.** Primers used in this study.

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| **Primers** | **Sequence\*** | **Application** |
| 5’ efa Arm 1 | 5’ – CAAGCATACACTTCTAGAGCACCA – 3’ | *efaCBA* deletion |
| 3’ efa Arm 1 | 5’ - GAACGGTGAATTCTTGAACAGCTAAGTTAAA – 3’ | *efaCBA* deletion |
| 5’ efa Arm 2 | 5’ – GAACTGGAATTCAACAAAAATCCA – 3’ | *efaCBA* deletion |
| 3’ efa Arm 2 | 5’ – TTCTATTAGTCTCCCGGGATTATCA – 3' | *efaCBA* deletion |
| 5’ mntH1 Arm 1 | 5’ – CAAGACCCCTGCAGCACA – 3’ | *mntH1* deletion |
| 3’ mntH1 Arm 1 | 5’ - CATAATTAAGCATGCTTTCCGTTTTC – 3’ | *mntH1* deletion |
| 5’ mntH1 Arm 2 | 5’ – TTATGGCATGCTAACTGGTTTAACG – 3’ | *mntH1* deletion |
| 3’ mntH1 Arm 2 | 5’ – CATCGTGCGAATTCGTTCATCATAG – 3’ | *mntH1* deletion |
| 5’ mntH2 Arm 1 | 5’ – GTAATCTAGAACATAAATTAAACAAC – 3’ | *mntH2* deletion |
| 3’ mntH2 Arm 1 | 5’ – ATGTTCTTCTGAATTCTGCAAT – 3’ | *mntH2* deletion |
| 5’ mntH2 Arm 2 | 5’ – CGTTAGCCGAGAATTCTGCCTATG – 3’ | *mntH2* deletion |
| 3’ mntH2 Arm 2 | 5’ – GAAAATCCCGGGCAAGAGAAAG – 3’ | *mntH2* deletion |
| efaCBA Fwd | 5’ – CTGATGGATCC*TTAGTTAGTTAG***AGGAGG** AATTTCATGAGAAAAAGCTTTAACTTAGCTG – 3’ | *efaCBA* complement |
| efaCBA Rev | 5’ – GAGGAAATTGTGGCTCGAGTAAT – 3’ | *efaCBA* complement |
| mntH1 Fwd | 5’ – GAACACTGCAG*TTAGTTAGTTAG***AGGAGG**  GATGTTGGATGAAAGAAAAGA – 3’ | *mntH1* complement |
| mntH1 Rev | 5’ - GTATTTCATCTTTCCTATTCTAGAATTTCTTACG – 3’ | *mntH1* complement |
| mntH2 Fwd | 5’ – TTTTACTGCAG*TTAGTTAGTTAG***AGGAGG**  AATTGAATTGCAGAATTCAGAAC – 3’ | *mntH2* complement |
| mntH2 Rev | 5’ - GAAATGCTTTTAACGCATGCGGCG – 3’ | *mntH2* complement |
| efaA L | 5’ – TGCCGCTTATATTTGGGAAA – 3’ | qRT-PCR |
| efaA R | 5’ – CGCCTTCTGTTCCTTCTTTG – 3’ | qRT-PCR |
| mntH1 L | 5’ – GAGAAAGCCAAAGCAATTCG – 3’ | qRT-PCR |
| mntH1 R | 5’ – TTGACCCGAAGCCAGTAAAG – 3’ | qRT-PCR |
| mntH2 L | 5’ – CCGTGTTGAAATGGGTGAAC – 3’ | qRT-PCR |
| mntH2 R | 5’ – AATTCCACAACCGTCCAAAC – 3’ | qRT-PCR |
| sodA L | 5’ – CAGCGATTGAAAAACATCCA – 3’ | qRT-PCR |
| sodA R | 5’ – TTCATCAAAGCTGCCAAATG – 3’ | qRT-PCR |
| Efa 500 F | 5’ – CATTTACAGGAGCATTCGTTG – 3’ | IE strain screening |
| Efa 1300 R | 5’ – TAAGTGGTGGTGAGCAAAC – 3’ | IE strain screening |
| MntH1 Conf F | 5’ – GAAATGTGTGAACAAGATAGATTG – 3’ | IE strain screening |
| MntH1 Conf R | 5’ – CAACTTTTCCAGTCAGCC – 3’ | IE strain screening |
| MntH2 Conf F | 5’ – GCAAAACGAAAGAAGGAATTG – 3’ | IE strain screening |
| MntH2 Conf R | 5’ – CGACTCTTCAACACCAACC – 3’ | IE strain screening |

**\***Underlined bases correspond to restriction sites included to aid in the cloning of PCR products.

\*Italicized bases correspond to the termination site (in 3 frames) included for cloning into the pTG001 vector.   
\*Bold bases correspond to the perfect ribosomal binding site included to ensure gene expression from pTG001 constructs.