**Table S2. DNA primers used in this work.**

| Code | Description | Sequence | Restriction enzyme[a] |
|---|---|---|---|
| 573 | Complementary to *ct288*; PCR verification of strain *ct288::aadA* | GATCGGATCCCGTTTATTTTAGAGCTCATCAACC | - |
| 599 | Complementary to *ct288*; DNA sequencing. | AGTTCTTGGTTCCAGATACG | - |
| 600 | Complementary to *ct288*; DNA sequencing. | TTCTGAGTCTAGAAGCTGCG | - |
| 627 | Complementary to pEGFP-C1; DNA sequencing | TGGTCCTGCTGGAGTTCGTG | - |
| 628 | Complementary to pEGFP-C1; DNA sequencing | TTATGTTTCAGGTTCAGGG | - |
| 642 | Complementary to pEF6/*myc*-His C; DNA sequencing | TAATACGACTCACTATAGGGC | - |
| 644 | Complementary to pGADT7; DNA sequencing | CTATTCGATGATGAAGATACCCCACCAAACC | - |
| 645 | Complementary to pGADT7; DNA sequencing | AGTGAACTTGCGGGGTTTTTCAGTATCTACGA | - |
| 862 | Construction of pFA147, pFA184, pFA185, pFA139, and pFA197; locus-specific DNA sequencing of strain *ct288::aadA* | GCCAGCCGCACACTATATAAGTATTTGCTCGAACATTCTCC | - |
| 863 | Construction of pFA147, pFA184, pFA185, pFA139, and pFA197 | GGAGAATGTTCGAGCAAATACTTATATAGTGTGCGGCTGGC | - |
| 944 | Construction of pFA147, pFA178, pFA184, pFA185, and pFA139 | GGAATTCCATATGAAAAAGGCTCTGGCTCAACG | NdeI |
| 954 | Construction of pFA147, pFA179, pFA184, pFA185, and pFA139 | CGCGGATCCTTAGTGATTATCTAACAGG | BamHI |
| 977 | Complementary to pGBKT7; DNA sequencing | AAATCATAAGAAATTCGC | - |
| 1350 | Construction of pFA164 | GATCCTCGAGCTGAAGACAGTAGCACAGACAC | XhoI |
| 1351 | Construction of pFA164 and pFA196 | GATCGAATTCTCAGATTTCAACTGGCTTTATAACAGG | EcoRI |
| 1352 | Construction of pFA167 | GATCGAATTCACCATGGAAGACAGTAGCACAGACAC | EcoRI |
| 1354 | Construction of pFA168 | GATCGAATTCACCATGGAAATTTGTGTGACCCAG | EcoRI |

**Table S2.** ***Continued.***

| Code | Description | Sequence | Restriction enzyme[a] |
|---|---|---|---|
| 1355 | Construction of pFA167 and pFA168 | ATAAGAATGCGGCCGCTTAAGCATAATCAGGAACATCATACGGATAGATTTCAACTGGCTTTATAACAGG | NotI |
| 1356 | Complementary to *CCDC146*; DNA sequencing | TAAGAAAGATGGAACTGC | - |
| 1357 | Complementary to *CCDC146*; DNA sequencing | TCTACTAACTTAGACTCC | - |
| 1358 | Complementary to *CCDC146*; DNA sequencing | ATGAAATCCTTCTCCAGC | - |
| 1474 | Construction of pFA178 and PCR verification of strain *ct288::aadA* | CGCGGATCCTTAATATAGTGTGCGGCTGGC | BamHI |
| 1475 | Construction of pFA179 | GGAATTCCATATGAAGTATTTGCTCGAACATTCTCC | NdeI |
| 1476 | Construction of pFA181 and pFA195 | GGAATTCCATATGGAAGACAGTAGCACAGACAC | NdeI |
| 1546 | Construction of pSVP255 | GATCGGTACCAACGGAGCCTTCTAGCTATTTTG | KpnI |
| 1565 | Construction of pSVP255 | ATCTGTCGAAGTGAGGTTTATGGTTTATTTTAGAGCTCATC | - |
| 1566 | Construction of pSVP255 | GATGAGCTCTAAAATAAACCATAAACCTCACTTCGACAGAT | - |
| 1567 | Construction of pSVP255 | GATCGCGGCCGCGGTGATTATCTAACAGGTATTG | NotI |
| 1593 | Construction of pFA181 | CGCGGATCCTTATCTTTGCTTCTCAGCAATCTTC | BamHI |
| 1707 | Construction of pFA195 | GATCGAATTCTCAGATTTCAACTGGCTTTATAACAGG | EcoRI |
| 1730 | Construction of pFA196 | GATCCTCGAGCTCAAATTTGTGTGACCCAG | XhoI |
| 1733 | Construction of pFA197 | GATCGGATCCACCATGGCGAAGGCTCTGGCTCAAGC | BamHI |
| 1734 | Construction of pFA197 | GATCGAATTCTTAAGCATAATCAGGAACATCATACGG | EcoRI |
| 1864 | Complementary to group II intron; PCR verification of strain *ct288::aadA* | ACGGATGCCGAGAATCTG | - |
| 1865 | Complementary to group II intron; PCR verification of strain *ct288::aadA* | TCTCGGAGTATACGGCTCTG | - |
| 1898 | locus-specific DNA sequencing of strain *ct288::aadA* | GATCGAATTCATATAGTGTGCGGCTGGCATG | - |

**Table S2.** ***Continued.***

| Code | Description | Sequence | Restriction enzyme[a] |
|---|---|---|---|
| 1922 | Group II intron retargeting (EBS universal); locus-specific DNA sequencing of strain *ct288::aadA* | CGAAATTAGAAACTTGCGTTCAGTAAAC | - |
| 2186 | Group II intron retargeting (288_114\|115s_IBS1/2); locus-specific DNA sequencing of strain *ct288::aadA* | AAAAAAGCTTATAATTATCCTTAATGTGCATTACGGTGCGCCCAGATAGGGTG | HindIII |
| 2187 | Group II intron retargeting (288_114\|115s_EBS1/d) | CAGATTGTACAAATGTGGTGATAACAGATAAGTCATTACGGGTAACTTACCTTTCTTTGT | BsrG1/ Bsp1407I |
| 2188 | Group II intron retargeting (288_114\|115s_EBS2); locus-specific DNA sequencing of strain *ct288::aadA* | TGAACGCAAGTTTCTAATTTCGGTTCACATCCGATAGAGGAAAGTGTCT | - |
| - | T7 promoter primer; DNA sequencing of pML2 | TAATACGACTCACTATAGGG | |

[a]Restriction sites are underlined.