**Table S1 The primers used in this study**

|  |  |  |  |
| --- | --- | --- | --- |
| Gene ID | Primer | Length (bp) |  |
| Sequence | Tm (°C) |
| **Full-length amplification of CDS** |
| *Px006941* | F：TAAATCTTTGACAAGTCCCCGAR：TTGTTTATAATAAGGTAAGCAC | 5548 | 1494 |  |
| *Px008848* | F：CCTATATCTCTCGTCTCACCR：TGGTATGATTGGTAGGTATG | 4848 | 1746 |
| *Px008849* | F：CCTGTAATAAAGAAGGCTAATCR：ATCAAAAGGAAAGAAAAGCCC | 5157 | 1745 |
| *Px006954* | F：TCGCCAGTTCGTTGTTGATAR：GTCTAAATATCTACAAAACACCGAAC | 5755 | 1657 |
| **Partial-length amplification of CDS** |
| *Px009427**-part* | F：GTTTATGAGAGGGAGTTTAAGGGAR：GCCGTGAACTGGTTGGAAG  | 5558 | 550 |  |
| *Px009428**-part* | F：GTTTATGAGAGGGAGTTTAAGGGAR：GCCGTGAACTGGTTGGAAG | 5558 | 368 |
| *Px000291**-part* | F：CCGCGGACTCGTACCACCGCTR：CCGCGGACTCGTACCACCGCT | 6869 | 789 |
| **qRT-PCR** |  |  |  |  |
| *Px008849* | F: CTACTGGCTTCTCCAACTATAR: TCACTATCGGCTCTATATTATACT | 60.259.8 | 106 |  |
| *Px008848* | F: GATATTGATGCTGAGGCTATACR: TGTAGTAGACTTGGTCATTGTA | 60.160.2 | 142 |
| *Px006941* | F: TGTGTGTCAAGAATGTGCTGATR: GCTTCATACCACATGAAATGATTTG | 61.258.4 | 112 |
| *Px009428* | F: GTTTATGAGAGGGAGTTTAAGGGAR: GGCTACTTCCAAATCCTTCTC | 61.862.0 | 107 |
| *Px006054* | F: TCGCCAGTTCGTTGTTGATAGCCR: TGGCAACTCCGAAAGTGAACCCT | 66.266.9 | 140 |
| *Px002081* | F: ATGAAGGTTACGGCTCCACCR: GTAGTTCTCGTCATACAAATGGTACAC | 64.061.8 | 235 |
| *Px000291* | F: GCACGGGGCTCAGACGCTTAR: GCCTCCTTCATTCCAAGCACCT | 65.764.4 | 123 |
| *Px001933* | F: CTTGGTAGTGCCATACTGCTGTR: ACCTCCTTCATTCCAAGCACCT | 57.361.7 | 168 |
| *Px003089* | F: ATGCTAGAAATTTGCTTGAACGATAR: TGACGCAAATATACTCAGCTATCC | 63.860.8 | 121 |
| *Px006942* | F: TTTTGGCAGTTGGTTGTGTTCAR: TTGTTGATTTATCACTCTGGTTCC | 61.458.4 | 151 |
| *Px001969* | F: GCATACCAAGTGGAGGGCGR: TGTGGTACGAGTCTGCCGAA | 61.159.6 | 130 |
| *Px009427* | F: CCAAGCATATGGGACAAGGTGR: AGTCAAGGCCCAATTCCTTGG | 59.059.6 | 162 |
| *Px013730* | F: CGGTGTTTCTACATCGGCTTTCR: GTTGGTGTGGTCGAATACGC | 61.558.5 | 118 |
| PCR production was confirmed by Sanger sequencing |
| **Prokaryotic expression of *Px008848*** |
| *Px008848*-expression-F | **#**F：AAGCTTCCTATATCTCTCGTCTCACC |  |  |  |
| *Px008848*-expression-R | **#** R：CTCGAGTGGTATGATTGGTAGGTATG |  |  |
| **#**: Sequences of restriction enzyme site of *BamH*I and *Xho*I were underlined. |
| **Mutant strain of *Px008848*** |
| CRISPR-F | **\****TAATACGACTCACTATAGG***N20**GTTTTAGAGCTAG |  |  |  |
| CRISPR-R | AAAAGCACCGACTCGGTGCC |  |  |
| sgRNA-1 | TTACTCCCGAGTTGCCTACG |  |  |
| sgRNA-5 | GTGCGCTAAGAATCTGCTTC |  |  |
| **\***: A T7 polymerase-binding site sequence was in italic, N20 (marked in bold) can be replaced by corresponding sequence of sgRNA-1 or sgRNA-5. Partial sequence of sgRNA scaffold plasmid was underlined. The whole sgRNA scaffold sequence was artificially synthetized and cloned to plasmid as a scaffold plasmid (sequence is same to GenBank ID: MG917725). |
| **Mutant detection in *Px008848*** |
| *Px008848*-test-F | GTAAAGGCGAAAACATTTGG |  |  |  |
| *Px008848*-test-R | GTAGCCTGGTTATACAATTCACAAG |  |  |
| **Transgenic *A. thaliana* over-expressing *Px008848*** |
| *KnpI*-8848-F | ¶ *GG*GGTACCCCTATATCTCTCGTCTCACC |  |  |  |
| *PstI*-8848-R | ¶ *AA*CTGCAGTGGTATGATTGGTAGGTATG |  |  |  |
| ¶: The oligo sequences were marked in italic. Sequences of restriction enzyme site were underlined. |