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|---|--------|--|
| <i>YGL9</i> (J10) | (1) | ATGGAGGCTGTCTACGACACCCATCCCTTCCCGCCTCAACCCCCAATGCTCAGAGAACTCCAGCCCTCTCCATC |
| <i>YGL9</i> (ZH11) | (1) | ATGGAGGCTGTCTACGACACCCATCCCTTCCCGCCTCAACCCCCAATGCTCAGAGAACTCCAGCCCTTTCATC |
| <i>YGL9</i> (J10) | (85) | ACCGTCCCTTC CGGCTTCGCTCTCCC ACCCGGGCTCACCGCCGGCTTCCAGGACAGACCAACCCAGAAAACCA |
| <i>YGL9</i> (ZH11) | (85) | ACCGTCCCTTA CGGCTTCGCTCTCCC ACCCGGGCTCACCGCCGGCTTCCAGGACAGACCAACCCAGAAAACCA |
| <i>YGL9</i> (J10) | (169) | CGCAGCAAGGGAGGGACGACGATGAGGGTAGCGGAGGTACCTCGTCAAGTGAAGGACGGGACAGGCCCTCGTGGATCCCG |
| <i>YGL9</i> (ZH11) | (169) | CGCAGCAAGGGAGGGACGACGATGAGGGTAGCGGAGGTACCTCGTCAAGTGAAGGACGGGACAGGCCCTCGTGGATCCCG |
| <i>YGL9</i> (J10) | (253) | GCGGAGGACGGCTCGGCCACCACGGTACCGGAGTACCTCGTCAAGTGAAGGACGGGACAGGCCCTCGTGGATCCCG |
| <i>YGL9</i> (ZH11) | (253) | GCGGAGGACGGCTCGGCCACCACGGTACCGGAGTACCTCGTCAAGTGAAGGACGGGACAGGCCCTCGTGGATCCCG |
| <i>YGL9</i> (J10) | (337) | GCGGAGGCCATAGCGCGGAGCGTGGTGGCGAGTACGAGACGCCGTGGTGACGCCGCCAACAGGGGAGCGCCGGAGATCCCG |
| <i>YGL9</i> (ZH11) | (337) | GCGGAGGCCATAGCGCGGAGCGTGGTGGCGAGTACGAGACGCCGTGGTGACGCCGCCAACAGGGGAGCGCCGGAGATCCCG |
| <i>YGL9</i> (J10) | (421) | ACTCGCGCTAC TGCGCGACGAGACGCTCGCGCTGACCCGACGCCGAGGATGCGCAGGGCGACGCCGATGCACTTCGCGCG |
| <i>YGL9</i> (ZH11) | (421) | ACTCGCGCTG TGCGCGACGAGACGCTCGCGCTGACCCGACGCCGAGGATGCGCAGGGCGACGCCGATGCACTTCGCGCG |
| <i>YGL9</i> (J10) | (505) | GGGCTTGGATCCGAGGAGTGCCTCGGCCGCTCGCGAGGCCGGCGACGCTGGGGCGACCCGAGGCCGCCGGCGGGCTC |
| <i>YGL9</i> (ZH11) | (505) | GGGCTTGGATCCGAGGAGTGCCTCGGCCGCTCGCGAGGCCGGCGACGCTGGGGCGACCCGAGGCCGCCGGCGGGCTC |
| <i>YGL9</i> (J10) | (589) | ACGCCGCTGCACATCGCGTCGGTACGGGCCGCCGGCGCTCGCGCGCTCGTGGAGCTGGGCCGACCCGAGGCCGGAGCCCC |
| <i>YGL9</i> (ZH11) | (589) | ACGCCGCTGCACATCGCGTCGGTACGGGCCGCCGGCGCTCGCGCGCTCGTGGAGCTGGGCCGACCCGAGGCCGGAGCCCC |
| <i>YGL9</i> (J10) | (673) | GACGGGCAGGCCGGACGCCGCTGGAGCTGGTACGGACGTGCTCGGAAGACGCCAACCCGGGAGCTTCGAGCGG |
| <i>YGL9</i> (ZH11) | (673) | GACGGGCAGGCCGGACGCCGCTGGAGCTGGTACGGACGTGCTCGGAAGACGCCAACCCGGGAGCTTCGAGCGG |
| <i>YGL9</i> (J10) | (757) | CGGCTGGCGCTGGAGGCCGGCAAGGAGCTGGAGAAGGCCGTGACGAGTGGGGGAAGTGGAGAAGGTGGACGCCGC |
| <i>YGL9</i> (ZH11) | (757) | CGGCTGGCGCTGGAGGCCGGCAAGGAGCTGGAGAAGGCCGTGACGAGTGGGGGAAGTGGAGAAGGTGGACGCCGC |
| WT : TGG—Tryptophan <i>ygl9</i> : TGA—Stop codon | | |
| <i>YGL9</i> (J10) | (841) | GGCAGGGCAAGTGGCGGAGTACTTGGGGAGTGGCGCGACGGCGCGACAGGGAGTC TGAGGGCGCTGGGTGGCGAG |
| <i>YGL9</i> (ZH11) | (841) | GGCAGGGCAAGTGGCGGAGTACTTGGGGAGTGGCGCGACAGGGAGTC TGAGGGCGCTGGGTGGCGAG |
| <i>YGL9</i> (J10) | (925) | GACCTGGTGAAGGACTTCGACGCCGGCTGGAGTACGCCGTGGAGGCCGTC AACAAGAGGGAGGCCGGAGGGAG |
| <i>YGL9</i> (ZH11) | (925) | GACCTGGTGAAGGACTTCGACGCCGGCTGGAGTACGCCGTGGAGGCCGTC AACAAGAGGGAGGCCGGAGGGAG |
| <i>YGL9</i> (J10) | (1009) | GGGAAATGGGAGTACCTTGCAACTGGGACATCGAGGAGGGAGCTGGAGGCCGAGACGTCGACGCCGA ACTCC |
| <i>YGL9</i> (ZH11) | (1009) | GGGAAATGGGAGTACCTTGCAACTGGGAGCTGGAGGCCGAGCTGGAGGCCGAGACGTCGACGCCGA ACTCC |
| <i>YGL9</i> (J10) | (1093) | CAGGAGTTCGAGCAGCGCAATCTGGGTGGCTGCTGGCGTGTATGCTCCGCCGCCGCCGCCGGTGC GGGTGA |
| <i>YGL9</i> (ZH11) | (1093) | CAGGAGTTCGAGCAGCGCAATCTGGGTGGCTGCTGGCGTGTATGCTCCGCCGCCGCCGCCGGTGC GGGTGA |

Appendix A Alignment of the 1167 bp coding sequences of *YGL9* between wild-type *Oryza sativa* L.

indica cultivar J10 (Jinhui10) and *Oryza sativa* L. japonica cultivar ZH11 (Zhonghua11). The coding sequences of *YGL9* are consistent between ZH11 and *Oryza sativa* L. japonica cultivar Nipponbare.

The red triangle at the 900th base indicates the mutation site in the *ygl9* mutant.

Appendix B Sequences of primers used in the study

Sequencing primers

| Primers | Forward sequence (5'-3') | Reverse sequence (5'-3') |
|---------|---------------------------|--------------------------|
| S-DNA | CTGCCACTCGCGCCACAAG | AGAATCGAACACCCCTCCGTCG |
| S-cDNA | ATGGAGGCTGTCTACGACACCCATC | GTCGACGGCGACACGCTGTCACC |

Vector construction primers

| Primers | Forward sequence (5'-3') | Reverse sequence (5'-3') |
|----------|--|---------------------------------------|
| YGL9-com | GCCTCTAGAGCGGTAGTCAGACTAACGTGTGA | GCCCCATGGGCCTGGCTGACTCTGCATC |
| YGL9-oe* | <u>TGGTGA</u> TATTCTTGCA GGAA ATTCATGGAGGCT | <u>GCTTGT</u> CGATCGACAGATCAAGCTTACCC |
| YGL9-sub | GTCCTACGACACCCATC | GGCGACCGGGCGGGCG |

Quantitative real-time PCR primers

| Primers | Forward sequence (5'-3') | Reverse sequence (5'-3') |
|---------|--------------------------|--------------------------|
| YGL9 | GGAGGCTGTCTACGACACCCA | TGGTCTGGCCTGGAACACCCG |

| | | |
|--------------------|----------------------------|------------------------------|
| CHLD | GCTTGCAGAAAGCTACACAAGC | AGGCCGTGAGCTAAAGGAGA |
| CHLI | GTTCGAGCCTGGTTGCTTC | CTCTCCACGGTGTCCATCCTG |
| CHLM | CCATCCATTGGCTCCTTATGACA | GTAGCCTACTTACCATCAATGAGTC |
| YGL1 | GATAGAGCTCTGGGCTTCAGTC | GCTTGCCGGAAC TGAAAAGGTAG |
| PORA | TGTACTGGAGCTGGAACAAACAACT | TCAATAGCACATCACTCTCACTCACT |
| CAO1 | GACACCTTCATCTGGGCTCAA | CGAGAGACATCCGGTAGAGC |
| DVR | CAGGTCGAGACCGTCAAGAAC | ATGACCTGGATCGGCACCTTG |
| HEMD | TGGAAGGCTGCTGGAAATCCTAAG | TCCTTGAAGCTCTGAGGCCAA |
| HEMA1 | GAACTCACCAGTCTGAATCATATTGA | CATCCAGTCTACCACTCTCTAATCC |
| PSY1 | GCCTCAAGCAGGCCTATCATC | GTGATGTGCGAGGCATTGGTC |
| PSY2 | GACAAATTCTCGCTGCCAGGTT | GACAGCAGCTCTTGCTTGCCTTGT |
| PDS | GTCCTGATCGAGTGAACGATGAAG | CGAACATGGTCAACAATAGGCATG |
| rbcL | GGAGGGACGTATGTCACCACAAAC | GAGTTACTCGGAATGCTGCCAAG |
| rbcS | GTGGCAACTAACCGTCATCGTC | TGCCTCACCCAAACAACATATAAGTCGT |
| psaA | TGGGGTTGATCCTAACCGAGATACCA | CCTCCGCGAAAAC TAAGAAATTCTG |
| psaL | TCTGAGAACGCAACGTACCAGGTG | AGGTTGGAGAGGTACCAGGCGAC |
| psbA | GCGGTTCCATTCAAGTGTATG | TAACCATGAGCGGCCACAATATT |
| psbO | TCGAGGAGAACGGACGAATCGAC | CTTGGGTCGAGGAAGGACGAAC |
| atpA | TGAATCTCCTGCTCCGGGTATAAT | TGCTGTTTGCCTGGTTGTCT |
| atpG | AGGTGGAGCTCCTACTCCAAGT | TCAGCTTCCCTTCCTTGGTGGT |
| petA | GCAGCAAGGTTATGAAAACCCAC | AACAGCACCCACATTCAACCCT |
| petE | TCCCCTCGAACAAATCGAAATG | CAACTGATCCCCACGTCTGTATT |
| ndhA | CGAGCTGCCGCTCAATCTATTAG | AGGCTGACGCCAAGATTCCATC |
| ndhB | TAACAGCTACTCTAGGGGAATGTT | CTTGGCCCACCCATGAGTAAAT |
| Lhca1 | AGGAGATCAAGAACGGACGATT | GTGCCAAGCTCAAGGGTAGATG |
| Lhca2 | CCTGGTGGTCTGTGGTTGACC | CCTGGAACCAAGCTCCATGACG |
| Lhca3 | GCTCAGGCTCTCTCTGGGAG | CTCAGGGACTGCTGGATGCGA |
| Lhca4 | CCCTCTCCACCTACCTCAACG | TCAACCCGATCTCGTCAGCACC |
| Lhca5 | TCACCTCGACGGCACATTACCT | CTGCTTCAAACCACACTGGCAG |
| Lhca6 | GCGCACCAAGGAGATCAAGAACG | GGACGTGAATGCCGAGAACG |
| Lhcb1.1 | TCAACACAACGCATGGGCTAC | CCTTCATGAAAGCAATGGACCTC |
| cab2R(Lhcb1.2) | TGTACCGGGTGCAGTAGATGTAC | ACCGGTACAGATCTCACCCCTCTC |
| cab1R(Lhcb1.3) | AAGTGAAGTGGGGACCGTAGC | TCTCGTCGCACTAAACCCATCTTC |
| Lhcb2.1 | CACGATCGAGATGGTGCCAAAC | CGGCCTCGGCTTACATTAA |
| Lhcb3 | GACTXCAAGGAGCCCGTGTGG | CCATGAGGACGACCTGGAATCC |
| Lhcb4.1 | TCTTCGCGCGCAATTCAAAC | TGCAAGTCGCCATTAACCACC |
| Lhcb5 | GATGAGCTGCCAACGTGGTACG | CTGAGGCCAAAGGGTCGTAGC |
| Lhcb6 | GCTCATCTCTACTTCGAGGCCG | GCGAAACCCAAC TCTGTGTGTCAG |
| chl _{a/b} | GGTGGTCAAGGTGTCAATTGTCA | ACGCGACTGGATCTTGGAGAG |

* The underlined bases are overlap sequences designed as per the *pEASY*-Uni Seamless Cloning and Assembly Kit user manual.