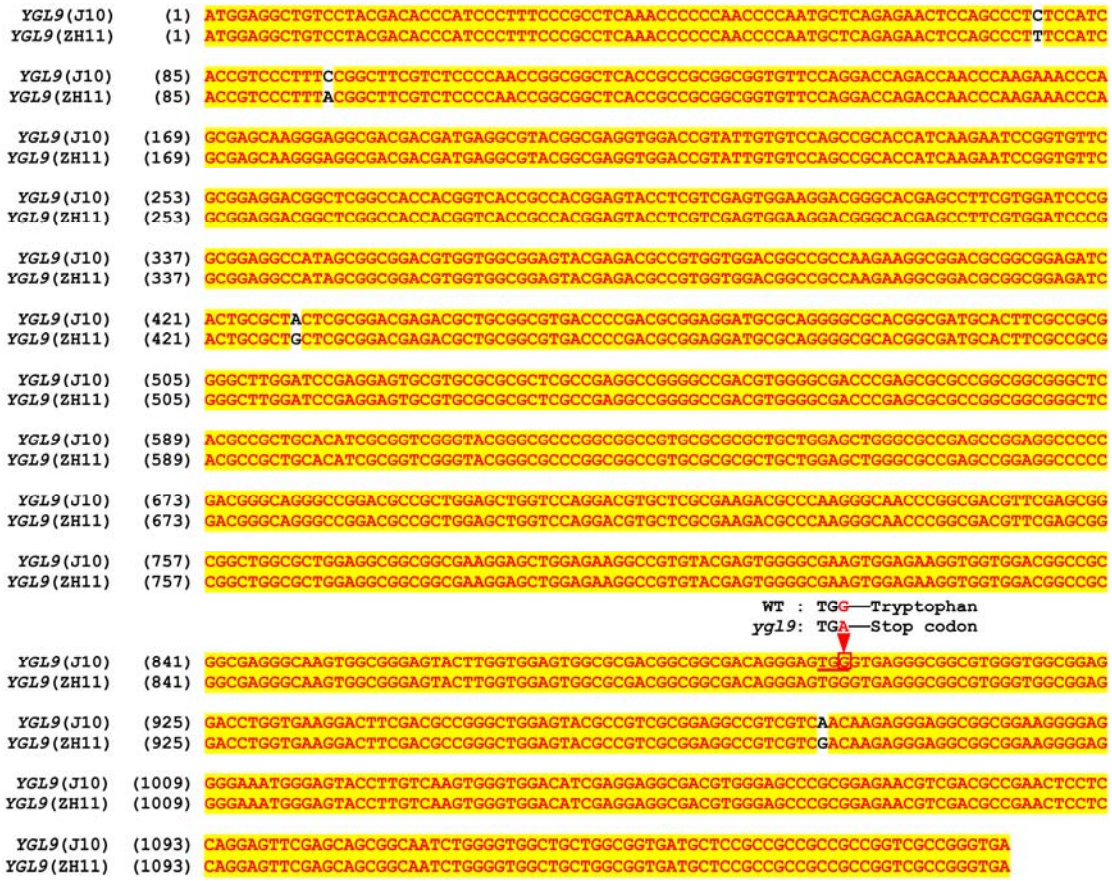

Appendix A Alignment of the 1167 bp coding sequences of *YGL9* between wild-type *Oryza sativa* L. indica cultivar J10 (Jinhui10) and *Oryza sativa* L. japonica cultivar ZH11 (Zhonghua11). The coding sequences of *YGL9* are consistent between ZH11 and *Oryza sativa* L. japonica cultivar Nipponbare. The 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	AGAATCGAACACCCTCCGTCG
S-cDNA	ATGGAGGCTGTCCTACGACACCCATC	GTCGACGGCGACACGCTGTCACC
Vector construction primers		
Primers	Forward sequence (5′-3′)	Reverse sequence (5′-3′)
YGL9-com	GCCTCTAGAGCGGTCAGTCAGACTAACGTGTGA	GCCCCATGGGCCTGGGCTGACTCTGCATC
YGL9-oe*	TGGTGATTATTTCTTGCAGGAATTCATGGAGGCT GTCCTACGACACCCATC	GCTTGTCGATCGACAGATCAAGCTTCACCC GGCGACCGGCGGCGGC
YGL9-sub	GCCCTCGAGATGGAGGCTGTCCTACGACACCCA	GCCACTAGTCCCCCGGCGACCGGCGGCGGC
Quantitative real-time PCR primers		
Primers	Forward sequence (5′-3′)	Reverse sequence (5′-3′)
YGL9	GGAGGCTGTCCTACGACACCCA	TGGTCTGGTCCTGGAACACCG

CHLD	GCTTGCAGAAAGCTACACAAGC	AGGCCGTGAGCTAAAGGAGA
CHLI	GTTCGAGCCTGGTTTGCTTGC	CTCTCCACGGTGTTCCATCCTG
CHLM	CCATCCATTGGTCTCCTTATGACA	GTAGCCTACTTACCATCAATGAGTC
YGL1	GATAGAGCTCTGGGGCTTCAGTC	GCTTGCCGGAACTGAAAAGGTAG
PORA	TGTACTGGAGCTGGAACAACAACT	TCAATAGCACATCACTCTCACTCACT
CAO1	GACACCTTCATCTGGGCTTCAA	CGAGAGACATCCGGTAGAGC
DVR	CAGGTCGAGACCGTCAAGAAC	ATGACCTGGATCGGCACCTTG
HEMD	TGGAAGGCTGCTGGAAATCCTAAG	TCCTTGGAAGCTCTGAGGCCAA
HEMA1	GAACTCACCAGTCTGAATCATATTGA	CATCCAGTCTACCACTTCTCTAATCC
PSY1	GCCTCAAGCAGGCCTATCATC	GTGATGTGCGAGGCATTTGGTC
PSY2	GACAAATTCTGCGTGCCAGGTT	GACAGCAGCTTCTTTGCCTTGTT
PDS	GTTCCTGATCGAGTGAACGATGAAG	CGAACATGGTCAACAATAGGCATG
rbcL	GGAGGGACGTATGTCACCACAAAC	GAGTTACTCGGAATGCTGCCAAG
rbcS	GTGGCAACTAAGCCGTCATCGTC	TGCCTCACCCAACAACATATAGTCGT
psaA	TGGGGTTGATCCTAAGGAGATACCA	CCTCCGCGAAAACTAAGAAATTCTG
psaL	TCTGAGAAGCCAACGTACCAGGTG	AGGTTGGAGAGGTACCAGGCGAC
psbA	GCGGTTCCCTATTCAGTGCTATG	TAACCATGAGCGGCCACAATATT
psbO	TCGAGGAGAAGGACGGAATCGAC	CTTTGGGTCGAGGAAGGACGAAC
atpA	TGAATCTCCTGCTCCGGGTATAAT	TGCTGTTTTGCCGGTTTGTCT
atpG	AGGTGGAGCTCCTCTACTCCAAGT	TCAGCTTCCCTTCCTTGGTGGT
petA	GCAGCAAGGTTATGAAAACCCAC	AACAGCACCCACATTCAACCCT
petE	TCCCCTCGAACAAATCGAAATG	CAACTGATCCCCACGTCTGTATT
ndhA	CGAGCTGCCGCTCAATCTATTAG	AGGCTGACGCCAAAGATTCCATC
ndhB	TAACAGCTACTCTAGGGGGAATGTT	CTTGCCCCACCCATGAGTAAAT
Lhca1	AGGAGATCAAGAACGGACGATT	GTGCCAAGCTCAAGGGTAGATG
Lhca2	CCTGGTGGTCTGTGGTTTGACC	CCTGGAACCAAGCTCCCATGACG
Lhca3	GCTCAGGCTCTTCTCTCTGGGAG	CTCAGGGACTGCTTGGATGCGA
Lhca4	CCCTTCTCCCACCTACCTCAACG	TCAACCCGATCTTCGTCAGCACC
Lhca5	TCACCTCGACGGCACATTACCT	CTGCTTCAAACCACACTGGCAG
Lhca6	GCGCACCAAGGAGATCAAGAACG	GGACGTGAATGCCGAGAAGACG
Lhcb1.1	TCAACAACAACGCATGGGCCTAC	CCTTCATGAAAGCAATGGACCTC
cab2R(Lhcb1.2)	TGTACGCGGTGCAGTAGATGTAC	ACCGGTACAGATCTCACCCTCTC
cab1R(Lhcb1.3)	AAGTGAAGTGGGGGACCGTAGC	TCTCGTCGCACTAAACCCATCTTC
Lhcb2.1	CACGATCGAGATGGTGCCAAC	CGGCCTGCGGCTTACATTAA
Lhcb3	GACTTCAAGGAGCCCGTGTGG	CCATGAGGACGACCTGGAATCC
Lhcb4.1	TCTTTCGCGCGCAATTCAAAC	TGCAAGTCGCCATTAACCACC
Lhcb5	GATGAGCTCGCCAAGTGGTACG	CTGAGGCCAAAAGGGTCGTAGC
Lhcb6	GCTCATCTTCTACTTCGAGGCCG	GCGAAACCCAACTCTGTGTGTCAG
chla/b	GGTGGTCAAGGTGTCATTGTCAT	ACGCGACTGGATCTTTGGAGAG

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