

Figure S1. Graphical genotypes of the parental lines (A) Hwaseong, (B) TR20, and (C) four genotype groups from the F₂ plants. White and black bars indicate the Hwaseong and *O. rufipogon* chromosome segments, respectively.

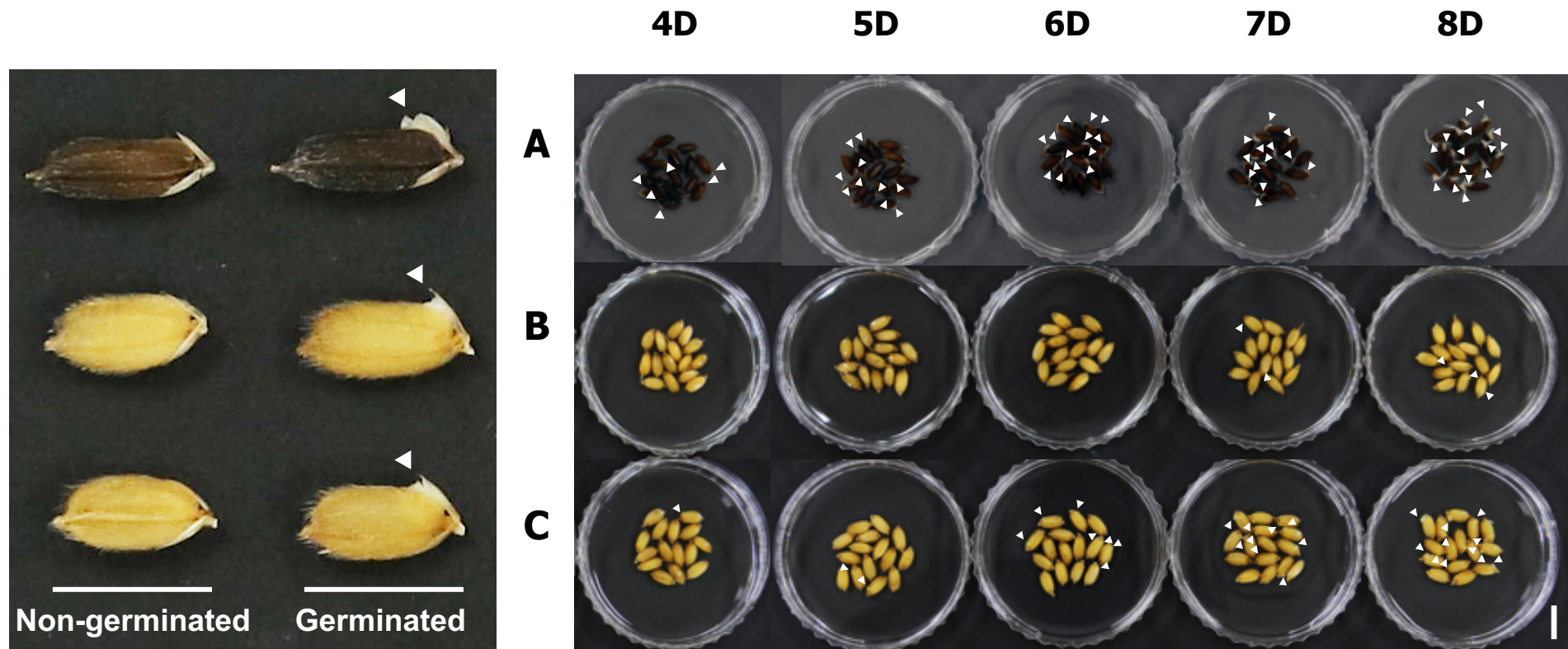


Figure S2. Determination of seed germination of (A) *O. rufipogon*, (B) Hwaseong, and (C) TR20 on filter papers (60 mm) in the petri dishes (60 mm) at 13 °C for 4 - 8 days after incubation. Arrowheads indicate the germinated embryo.

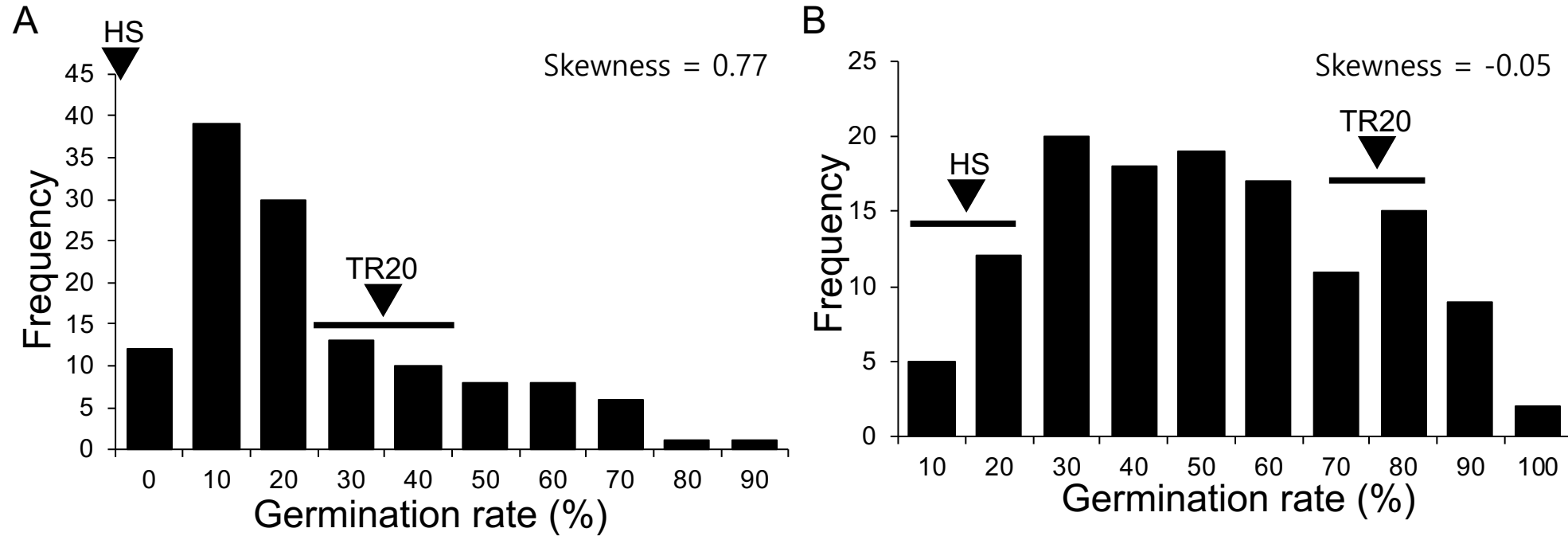


Figure S3. Frequency distribution of LTG at 6 days (A) and 7 days (B) after incubation of the 224 F_2 plants, respectively. Triangles and horizontal lines denote mean germination rates and standard error of the parental lines, respectively.

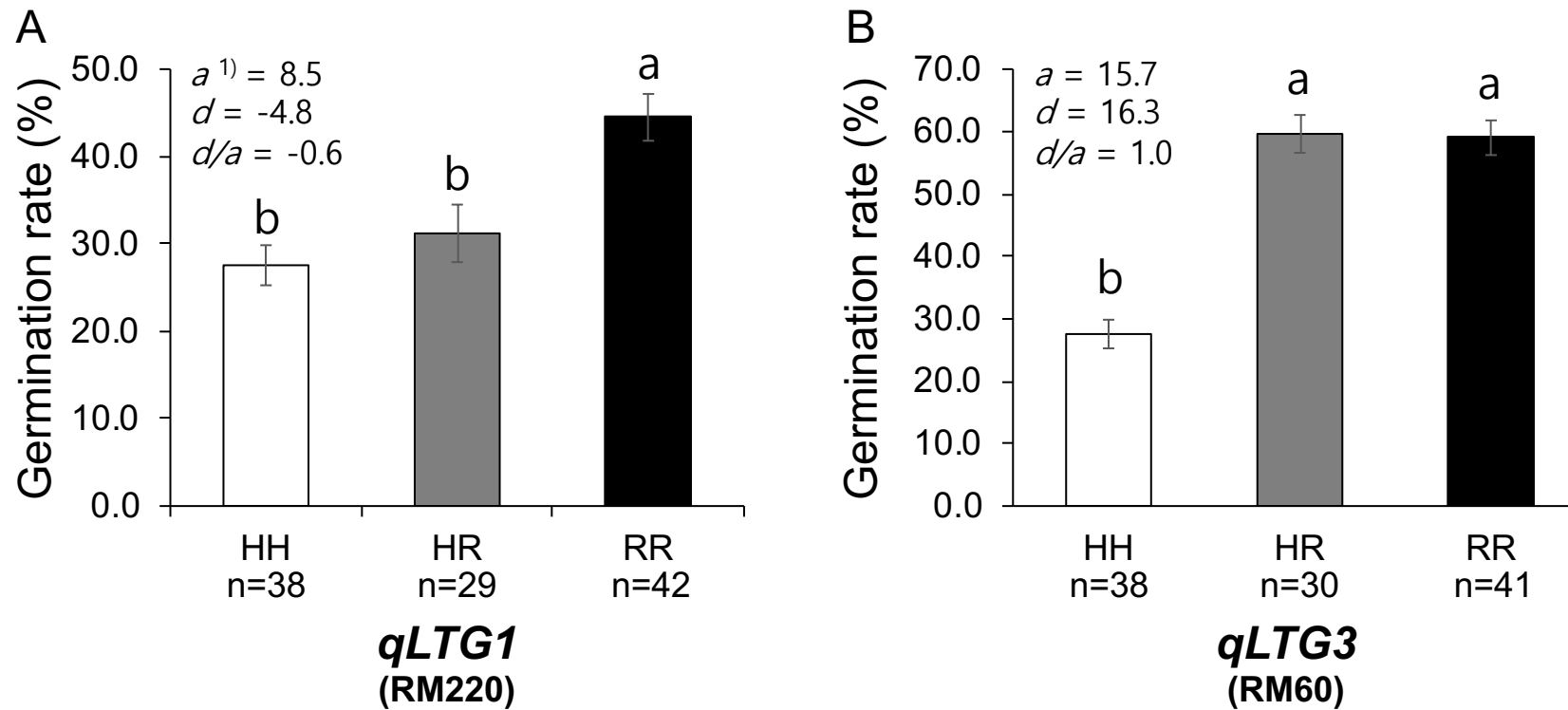


Figure S4. Comparison of the germination rates in plants that are segregating at (A) *qLTG1* and (B) *qLTG3* regions without other LTG QTL. RR, RH, and HH, mean *O. rufipogon* homozygous, heterozygous, and Hwaseong homozygous with the number of F₂ individuals, respectively. Additive effect (*a*) of the *O. rufipogon* allele, dominance effect of the *O. rufipogon* allele (*d*), and degree of dominance (*d/a*) were indicated in each figure. The same letter above box is not significantly different between the genotypes at $P = 0.05$ based on Tukey's test.

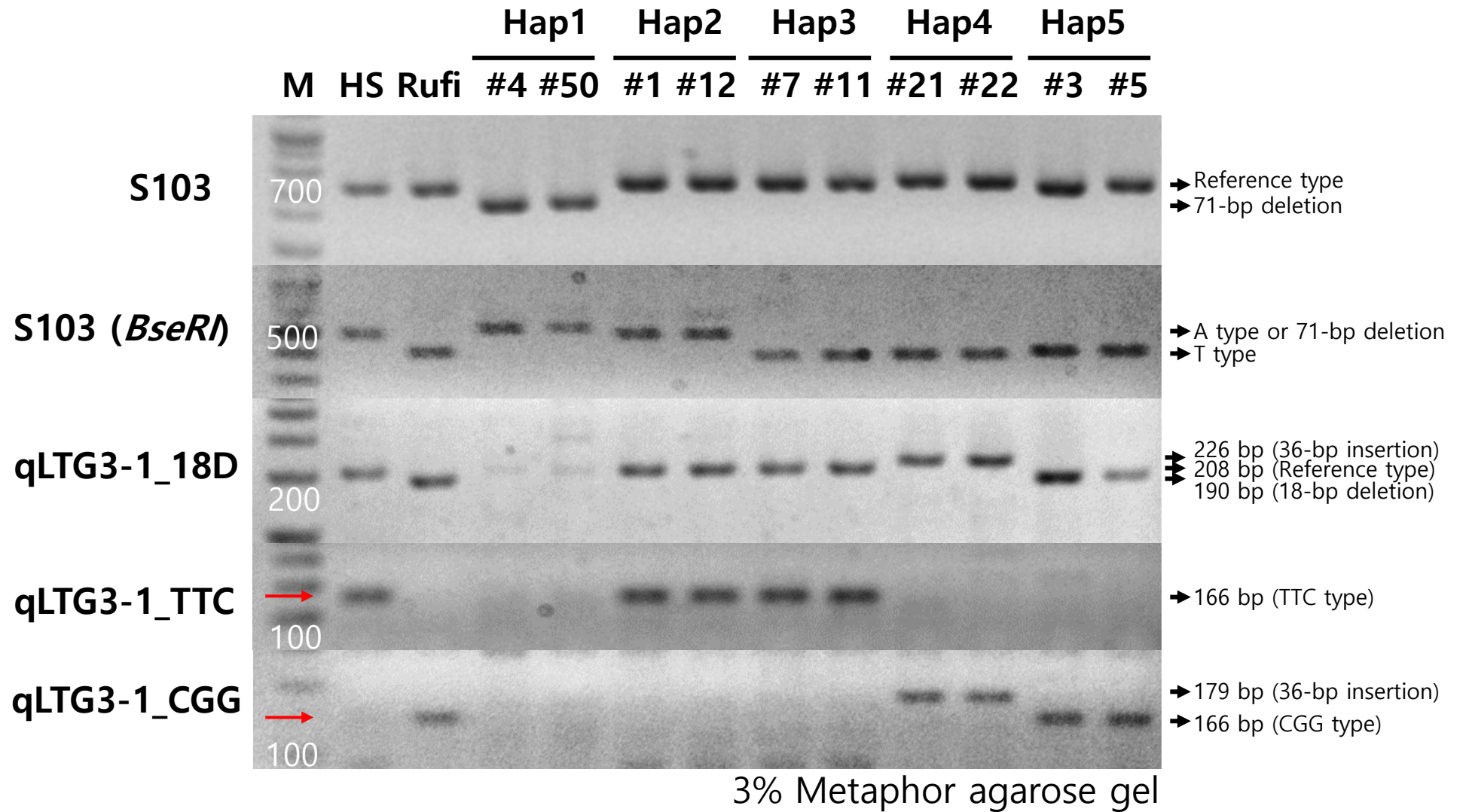


Figure S5. PCR amplicons of the markers used for genotyping parental lines and rice accessions for haplotype analysis. HS: Hwaseong, Rufi: *O. rufipogon*, #: RWG accession number, and M: 100-bp size marker.

A

qLTG3-1_(18D, TTC, CGG) forward

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Ref  GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
HS   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
Rufi GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
4    GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
50   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
79   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
87   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
92   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
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A/T**18-bp deletion**

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Ref  CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
HS   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
Rufi CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
4    -----
50   -----
79   -----
87   -----
92   -----

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71-bp deletion**qLTG3-1_(TTC, CGG) reverse**

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Ref  CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
HS   CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
Rufi -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
4    CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
50   CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
79   CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
87   CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
92   CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
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TTC/CGG

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Ref  TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
HS   TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
Rufi TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
4    TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
50   TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
79   TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
87   TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
92   TTCAGGTGGAGGAGGAAGCGGCGCGGAGAGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGG
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qLTG3-1_18D reverse**B****qLTG3-1_(18D, TTC, CGG) forward**

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Ref  GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
HS   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
Rufi GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
21   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
22   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
47   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
54   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
70   GATCGCCACGCTCCTGGCCCTGAACCTCCACTTCTTACACCTTCTCCGACGCGTGCGGGCTG
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A/T**18-bp deletion**

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Ref  CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
HS   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
Rufi CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
21   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
22   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
47   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
54   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
70   CCAGTGCGGCTCATGCCCTAGTCCCAGCGGAGGAGGCGGTGGCGGTGGCGGTGGCGGTGG
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qLTG3-1_(TTC, CGG) reverse

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Ref  CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
HS   CGGTGTTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
Rufi -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
21   -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
22   -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
47   -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
54   -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
70   -----GTGAGGAGGCGTGGAGGTGGTGGCGGGAGCGCGGAGTTTCAGGTGGAGGCGGCGG
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TTC/CGG

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Ref  -----AGGCGGCGGTTTCAGGTGGAGGAGGAAGCGGCGG
HS   -----AGGCGGCGGTTTCAGGTGGAGGAGGAAGCGGCGG
Rufi -----AGGCGGCGGTTTCAGGTGGAGGAGGAAGCGGCGG
21   TGGTGGAGGAAGCGGAGGCGGAGGTTTCAGGTGGAGGAGGAAGCGGCGG
22   TGGTGGAGGAAGCGGAGGCGGAGGTTTCAGGTGGAGGAGGAAGCGGCGG
47   TGGTGGAGGAAGCGGAGGCGGAGGTTTCAGGTGGAGGAGGAAGCGGCGG
54   TGGTGGAGGAAGCGGAGGCGGAGGTTTCAGGTGGAGGAGGAAGCGGCGG
70   TGGTGGAGGAAGCGGAGGCGGAGGTTTCAGGTGGAGGAGGAAGCGGCGG
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36-bp insertion**qLTG3-1 CGG reverse**

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Ref  CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
HS   CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
Rufi CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
21   CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
22   CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
47   CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
54   CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
70   CGGAGGTTTCAGGCGGTGGAGGAAGCGGAGGCGGCGGAGGAGGAAGCGGCGGCGGCGG
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qLTG3-1_18D reverse

Figure S6. Sequence comparisons of the Ref (Nipponbare), HS (Hwas eong), Rufi (*O. rufipogon*) and (A) five rice accessions (RWG4, RWG50, RWG79, RWG87, RWG92) with a 71-bp deletion and (B) five rice accessions (RWG21, RWG22, RWG47, RWG54, RWG70) with a 36-bp insertion. Sequence and location of 3 markers are shown with an A/T SNP, 18-bp and 71-bp deletions, TTC/CGG, and 36-bp insertion variant site.