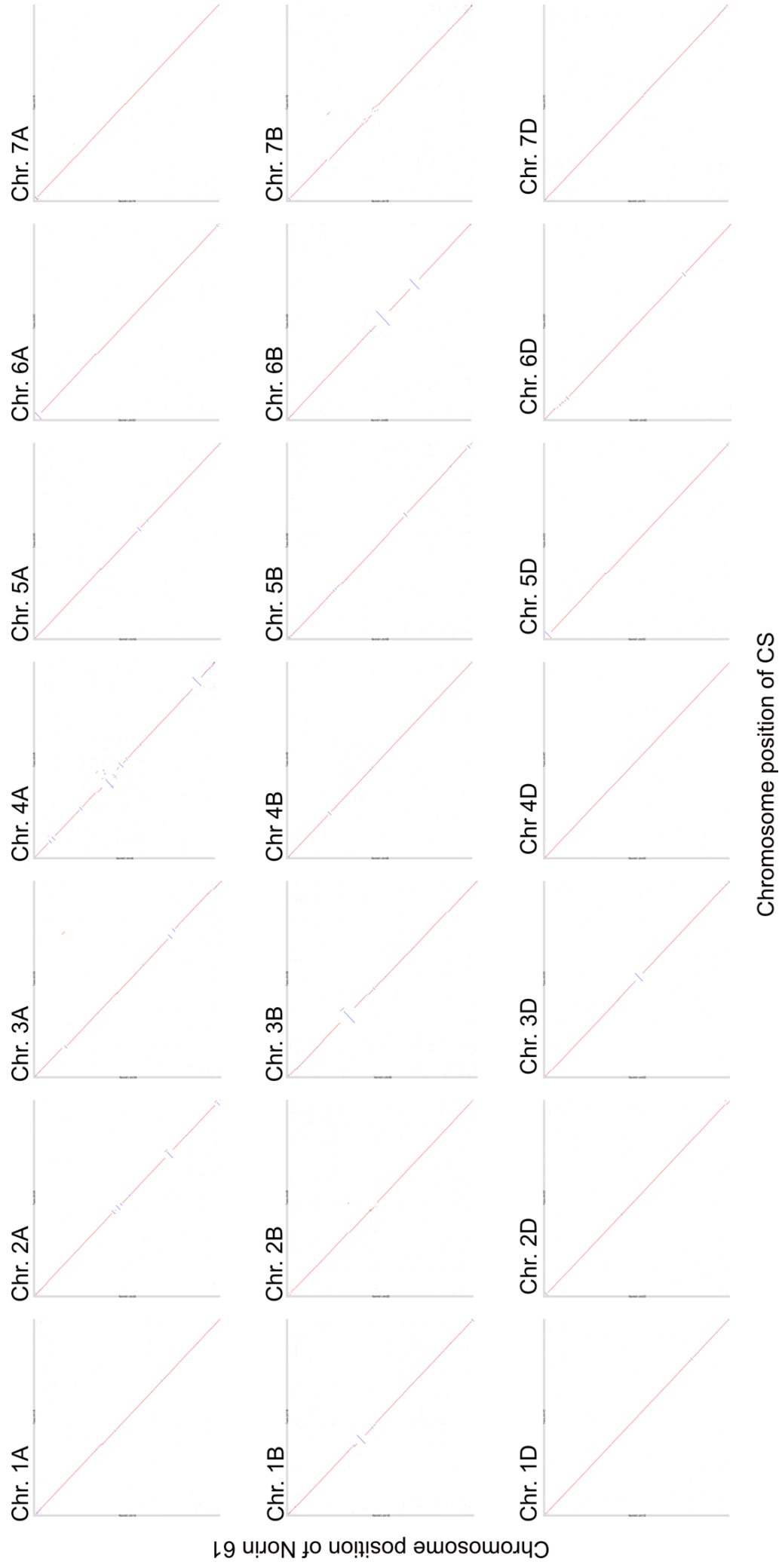
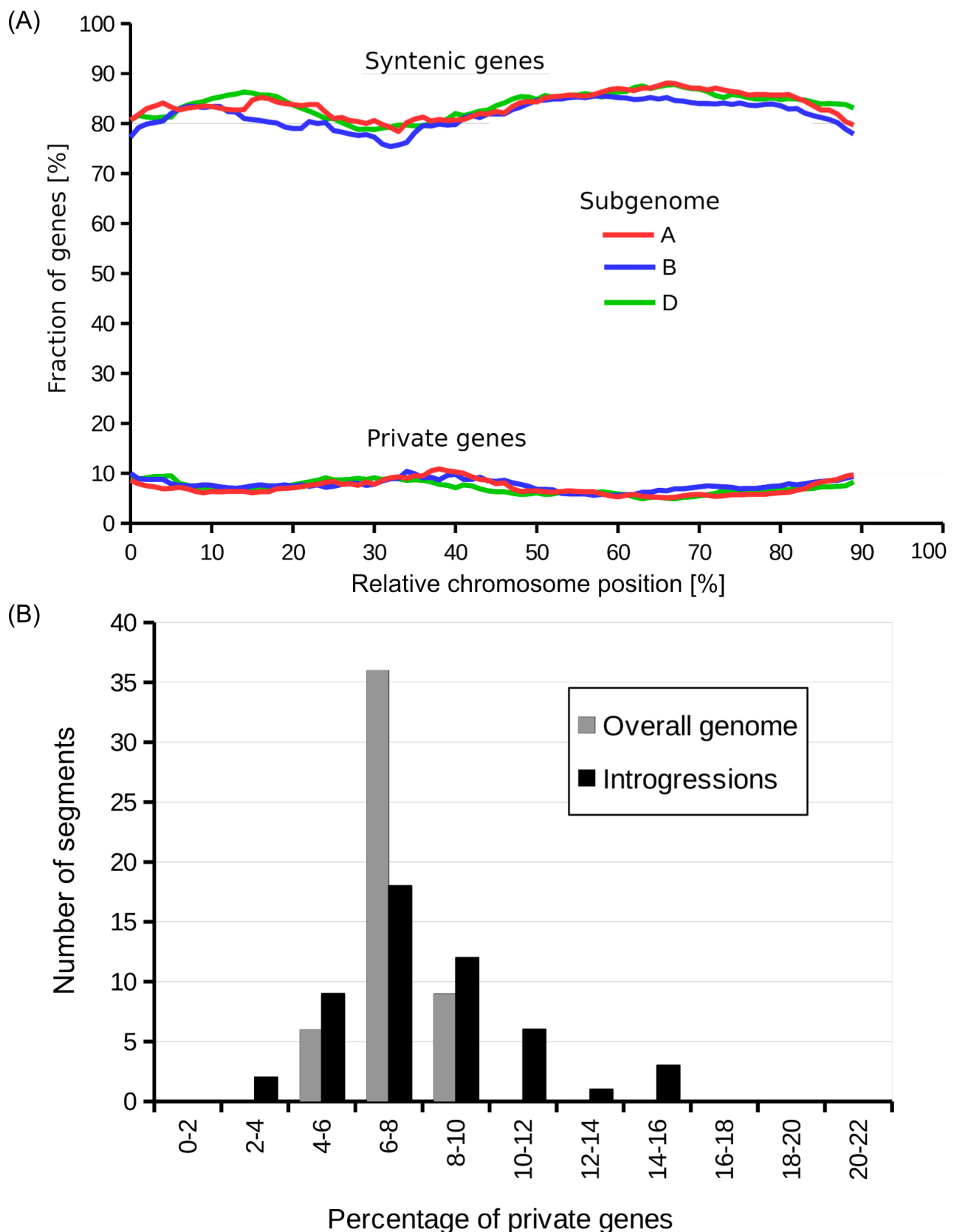


**Supplementary Fig. S1** Hi-C contact map of the 21 Norin 61 pseudomolecules. For each chromosome, the strongest diagonal signal depicts the distance between reads along the pseudomolecule for the whole set of read pairs. The opposite (and weaker) diagonal is a consequence of the Rabl configuration that chromosomes of large genomes assume during interphase. With the two chromosome arms juxtaposed, a smaller fraction of the Hi-C read pairs originates from regions belonging to the two different arms. Subgenome compartments were observed and were consistent with those described by Concia et al. (2020).

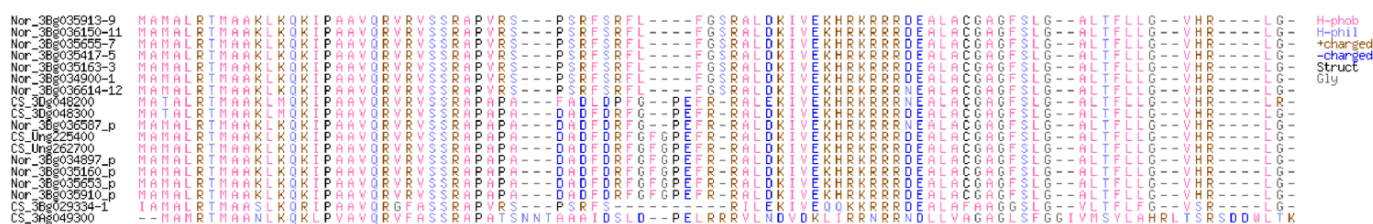


**Supplementary Fig. S2** Homoeologous chromosome alignment between Norin 61 and Chinese Spring (CS). Red and blue lines denote alignments in the same and opposite orientation, respectively.

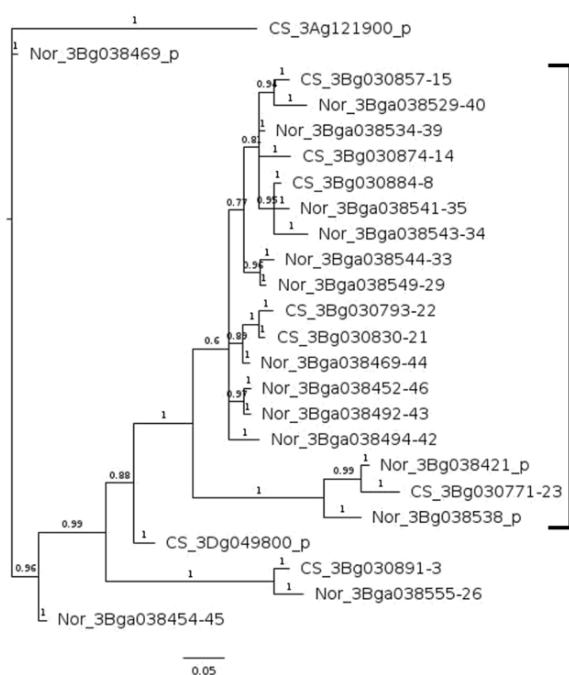


**Supplementary Fig. S3** Analysis of syntenic and private genes in Norin 61 chromosomal introgressions. (A) The overall content of syntenic and private genes between Norin 61 and Chinese Spring along wheat subgenomes. To normalize the different lengths of chromosomes, gene content was calculated along sliding windows corresponding to 10% of chromosome lengths with sliding steps corresponding to 1% of chromosomes lengths. Syntenic and private genes are defined in Materials and Methods. (B) Percentage of private genes in Norin 61 chromosomal introgressions. The x-axis indicates the range of percentages of private genes per introgression, while the y-axis shows the number of introgressions per range (e.g. there are 2 introgressions that have between 2 and 4% of private genes). Data for Norin 61 chromosomal introgressions are shown in black. For comparison, the genomic average of corresponding chromosomal regions is shown in gray. As in (A), all chromosome lengths were normalized. Note that 10 Norin 61 introgressions have a higher content of private genes than any of the control segments.

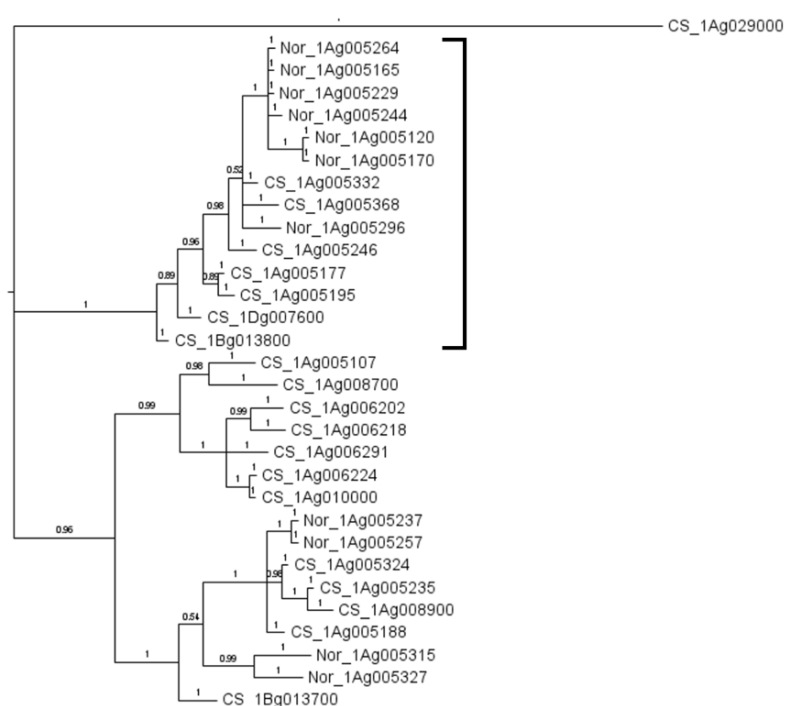
(A)



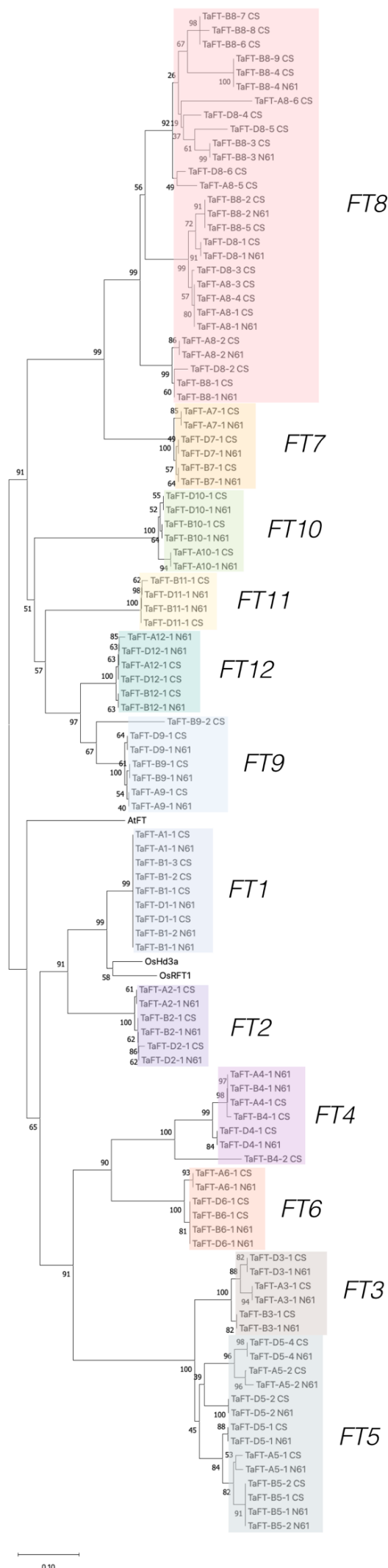
(B)



(C)

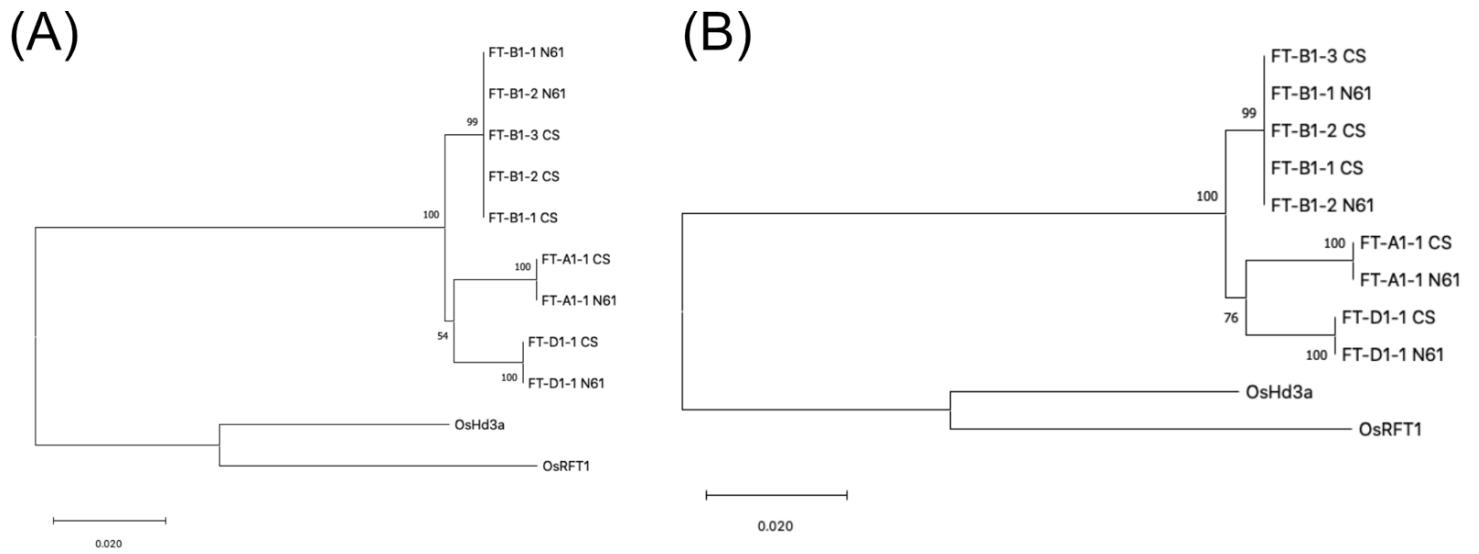


**Supplementary Fig. S4** Characteristics of gene families that are expanded in Norin61 compared to CS. (B) and (C) show phylogenetic trees of gene families that contain high numbers of private genes in Norin 61. Statistical support for each clade is indicated on the branches leading to the clades. (A). Multiple sequence alignment of family 3B\_25-46-1. Amino acids are colored according to their biochemical characteristics (H-phob: hydrophobic, H-phil: hydrophilic, +charged: positively charged, -charged: negatively charged, Struct: structural amino acid [proline and cysteine], Gly: glycine). (B) Phylogenetic tree of family 3B\_25-46-2. A large and well-supported clade (indicated by a black bracket) contains 11 Norin 61 genes from the region of the introgression. In contrast, the corresponding region in Chinese Spring contains only 6 homoeologs. (C) Phylogenetic tree of family 3B\_25-46-1 members found on 1A. One clade is expanded in Norin 61 (indicated by a black bracket).



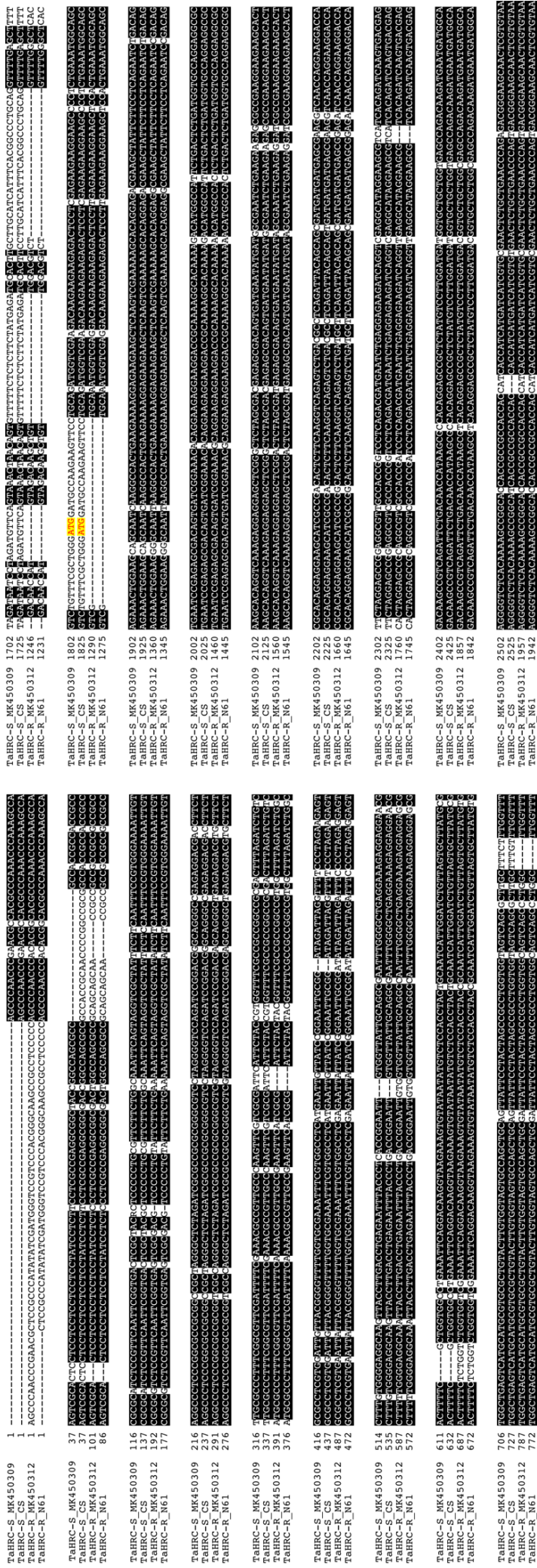
### Supplementary Fig. S5

Phylogenetic tree of 108 *FT* homoeologs. Neighbor-joining tree based on 111 amino acid positions for which all sequences have data without gaps. The bootstrap values are shown on the branches. N61 and CS stand for Norin 61 and Chinese Spring, respectively.



**Supplementary Fig. S6** Phylogenetic tree of 11 nucleotide sequences of *FTI* subfamily sequences. The *OsHd3* and *OsRFT1* genes were used as outgroups. (A) Neighbor-joining tree and (B) Maximum-likelihood tree based on 530 positions for which all sequences have data without gaps. The bootstrap values are shown on the branches. N61 and CS stand for Norin 61 and Chinese Spring, respectively.





**Supplementary Fig. S7 *TaHRC*.** Alignment of the *TaHRC* alleles of CS and Norin 61 compared with resistant allele (*TaHRC-R*: MK450312) and susceptible allele (*TaHRC-S*: MK450309) reported by Su et al. (2019). Norin 61 has the deletion of the ATG start codon as the *TaHRC-R* allele. In the region upstream of the ATG start codon alignment was difficult because the susceptible allele of CS is highly divergent from the resistant alleles (Su et al. 2019). The black boxes indicate the sequences conserved between the four alleles. White regions show the single-nucleotide polymorphisms between resistant and susceptible alleles.

(A)

```
Tamyb10-A1_CS      1 -----
Tamyb10-A1_N61    1 GGGATATGGGGAGGAAGCCATGCTGCGCCAAGGAGGGCTGAACAGAGGGCGTGGACGGCAATGGAGGACGACATCCTGGTCTCTACATCAACGATCA

Tamyb10-A1_CS      1 -----
Tamyb10-A1_N61    101 CGGCGAGGGCAAGTGGGGAAGCCTTCCCAAACGAGCTGGTAGGTTACAAACACCATCGTATCTAGTCTTTTGCTCTTCGCCGAACATTGCATCAATACAT

Tamyb10-A1_CS      1 -----TGC GTGCGATTTTCTCTTAGTTGACCGATCTCTCTCCAAGCTCTTTCTAGCCATTGCAACTGAAACAAAGAGTGTATGTGTGCGT
Tamyb10-A1_N61    201 ACATTTATCGATTATGCGTGCGATTTTCTCTTAGTTGACCGATCTCTCTCCAAGCTCTTTCTAGCCATTGCAACTGAAACAAAGAGTGTATGTGTGCGT

Tamyb10-A1_CS      87 ATGCTTGAAGAAGCCAGGTGGCTGAAACAAGGAATGCGGCAAGAGAGAGGGCAGGGGGACATCACTAGTTTAGCATAGCTCGAGATGGTCTGTTGAGTT
Tamyb10-A1_N61    301 ATGCTTGAAGAAGCCAGGTGGCTGAAACAAGGAATGCGGCAAGAGAGAGGGCAGGGGGACATCACTAGTTTAGCATAGCTCGAGATGGTCTGTTGAGTT

Tamyb10-A1_CS      187 GTTAACGGCGTGTGAGATGTTGTGTGCAAGGCTGAATCGCTGCGGTAAAGAGCTGCCGGTGCCTGAGTCAACTACCTCCGGCCGGGGATCAAGAGAGGC
Tamyb10-A1_N61    401 GTTAACGGCGTGTGAGATGTTGTGTGCAAGGCTGAATCGCTGCGGTAAAGAGCTGCCGGTGCCTGAGTCAACTACCTCCGGCCGGGGATCAAGAGAGGC

Tamyb10-A1_CS      287 AACATCTCCAACGACGAAGAGGAGCTCATCGTCAGGCTCCACGGGCTCCTAGGCAACAGGTGCACATCTATGTTGTTTTCTTTTCATTTGCATCGTGCAC
Tamyb10-A1_N61    501 AACATCTCCAACGACGAAGAGGAGCTCATCGTCAGGCTCCACGGGCTCCTAGGCAACAGGTGCACATCTATGTTGTTTTCTTTTCATTTGCATCGTGCAC

Tamyb10-A1_CS      387 ATTTTCCGTTGTGTAGATGATCAAGCATTGTATATTGTTGTTTACTTACACTTACACTTACACTTGCAATTTACATGCATATTCCTAATGTAATACGTAGT
Tamyb10-A1_N61    601 ATTTTCCGTTGTGTAGATGATCAAGCATTGTATATTGTTGTTTACTTACACTTACACTTACACTTGCAATTTACATGCATATTCCTAATGTAATACGTAGT

Tamyb10-A1_CS      487 ATATAGTGTGAACGAAGATGTACAAGTCGGTCTTTGGTCTGTGGAGGAGTATTAATTAGTCACACTTGCTTGACAAAAATTTAGTATTAGTAATAAACACCA
Tamyb10-A1_N61    701 ATATAGTGTGAACGAAGATGTACAAGTCGGTCTTTGGTCTGTGGAGGAGTATTAATTAGTCACACTTGCTTGACAAAAATTTAGTATTAGTAATAAACACCA

Tamyb10-A1_CS      587 AGGTCATGCTAATACCTTTCCGTTGGAATTTTCATTTTCTTTTCCCTACATGGGAGACAGAGAGAGATGTATGATCAGACAAAGTAGGCCAATGCCTGCT
Tamyb10-A1_N61    801 AGGTCATGCTAATACCTTTCCGTTGGAATTTTCATTTTCTTTTCCCTACATGGGAGACAGAGAGAGATGTATGATCAGACAAAGTAGGCCAATGCCTGCT

Tamyb10-A1_CS      687 AAATGAATATAGGATCCAGTTATCATGATCACCTGTACACACCTACTATCCATATCAGTCAGCGTGCATGTTCCCAATTAGCCATGCCCGAAGAAAAAGA
Tamyb10-A1_N61    901 AAATGAATATAGGATCCAGTTATCATGATCACCTGTACACACCTACTATCCATATCAGTCAGCGTGCATGTTCCCAATTAGCCATGCCCGAAGAAAAAGA

Tamyb10-A1_CS      787 ACAACCTCTTGCTGACAGCCTGAATGCGTGTCCCTAGCCCCAAGAGGTAAACGAGTTATTCGGTCAGCAAAAGTTGATGATGACATGCATTCAATCATGCA
Tamyb10-A1_N61    1001 ACAACCTCTTGCTGACAGCCTGAATGCGTGTCCCTAGCCCCAAGAGGTAAACGAGTTATTCGGTCAGCAAAAGTTGATGATGACATGCATTCAATCATGCA

Tamyb10-A1_CS      887 TGCATGCATGCACAACCACTCTGATCTACTACAACAATCTACACCATAACTTGAAAAGGCTCCCATGGCGCTAGGTCTAGAACGAAATGCCACTCCCTCC
Tamyb10-A1_N61    1101 TGCATGCATGCACAACCACTCTGATCTACTACAACAATCTACACCATAACTTGAAAAGGCTCCCATGGCGCTAGGTCTAGAACGAAATGCCACTCCCTCC

Tamyb10-A1_CS      987 CGGATTTGGCACAACAACCACTGCTAATCGATCTACACCATGACTTGAAAAGGCTCTGACCTACAACAACCAACGCACTCTGTGAGACTGTACATATGCA
Tamyb10-A1_N61    1201 CGGATTTGGCACAACAACCACTGCTAATCGATCTACACCATGACTTGAAAAGGCTCTGACCTACAACAACCAACGCACTCTGTGAGACTGTACATATGCA

Tamyb10-A1_CS      1087 GAAGCTGCAGCTAAACCTTGTGAGGCGCAAGTAAATAGGGCCAGCTAGAATTTCGCTACTGCTAATCAATTGCAAGTGCTTACTAATTCAGGGTCAGCATGT
Tamyb10-A1_N61    1301 GAAGCTGCAGCTAAACCTTGTGAGGCGCAAGTAAATAGGGCCAGCTAGAATTTCGCTACTGCTAATCAATTGCAAGTGCTTACTAATTCAGGGTCAGCATGT

Tamyb10-A1_CS      1187 GATAACAGTTGACGTGGCCCGTGGCAGGTGGTGCCTGATCGCGGGGCGGCTGCCGGGGCGAACAGACAATGAGATCAAGAACTACTGGAACACCACCCTG
Tamyb10-A1_N61    1401 GATAACAGTTGACGTGGCCCGTGGCAGGTGGTGCCTGATCGCGGGGCGGCTGCCGGGGCGAACAGACAATGAGATCAAGAACTACTGGAACACCACCCTG

Tamyb10-A1_CS      1287 AGCAAGAGGATGCTGCAGTCCCACGGCGCCGGCTGCTCGAACACCACCGCAGGCCAAGCCGCGCTGCCGCCGAGGCCGGCGGAGGCCAGGCCCCGC
Tamyb10-A1_N61    1501 AGCAAGAGGATGCTGCAGTCCCACGGCGCCGGCTGCTCGAACACCACCGCAGGCCAAGCCGCGCTGCCGCCGAGGCCGGCGGAGGCCAGGCCCCGC

Tamyb10-A1_CS      1387 CCGAGGGCACGAGCAGCAGTCCGATACGGACCAAGGCGCTGCGGTGCACCAACACGGTGTGGCGGTAGCAGAGGGTTTCCACGAGCAGGGCGTGCGGC
Tamyb10-A1_N61    1601 CCGAGGGCACGAGCAGCAGTCCGATACGGACCAAGGCGCTGCGGTGCACCAACACGGTGTGGCGGTAGCAGAGGGTTTCCACGAGCAGGGCGTGCGGC

Tamyb10-A1_CS      1487 GCCGGAGCACGTGCGCCGAGGAGGATCAGCTGGGGGACTGCCTGTCGATCGGCTCGATCGACCTTGATCTGGAGGGCATCGAGCTGGGCTTCATGATGAGC
Tamyb10-A1_N61    1701 GCCGGAGCACGTGCGCCGAGGAGGATCAGCTGGGGGACTGCCTGTCGATCGGCTCGATCGACCTTGATCTGGAGGGCATCGAGCTGGGCTTCATGATGAGC

Tamyb10-A1_CS      1587 CCGTGGAGCGGCGCCGACGGCTTGGGCGGTGAGCATTTTCGGTGCACCGGGGACTGAGGCTGATGATCTGGAGGAGCTGCTCGGACTGGGAGGAGACGGCG
Tamyb10-A1_N61    1801 CCGTGGAGCGGCGCCGACGGCTTGGGCGGTGAGCATTTTCGGTGCACCGGGGACTGAGGCTGATGATCTGGAGGAGCTGCTCGGACTGGGAGGAGACGGCG

Tamyb10-A1_CS      1687 ACGGCCATGGTGGCCTCGGGGACCTGGAGTTGGCGTGGCTTTGATAG
Tamyb10-A1_N61    1901 ACGGCCATGGTGGCCTCGGGGACCTGGAGTTGGCGTGGCTTTGATAG
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**Supplementary Fig. S8** Sequence alignments of *Tamyb10* alleles of Chinese Spring (CS) (CS RefSeq v1.0) and Norin 61. (A) Alignment of the *Tamyb10-A1* alleles. CS has the recessive allele (*Tamyb10-A1a*) with a large deletion including the start codon and two single-nucleotide polymorphisms indicated by red characters; one is in the second intron and the other is a synonymous substitution in the third exon. Norin 61 has the dominant allele (*Tamyb10-A1b*).



(B)

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Tamyb10-B1_CS      1  ATGGGGAGGAAGCCATGCTGCGCCAAGGAGGGCCTGAACAGAGGGGCATGGACGGCAATGGAGGACGAGATCCTGGTCTCCTACATCAACGATCACGGCG
Tamyb10-B1_N61     1  ATGGGGAGGAAGCCATGCTGCGCCAAGGAGGGCCTGAACAGAGGGGCATGGACGGCAATGGAGGACGAGATCCTGGTCTCCTACATCAACGATCACGGCG

Tamyb10-B1_CS      101 AGGGCAAGTGGGGAAGCCTTCCCAAACGAGCTGGTAGGTTACAGTACACACACCATCGTCTCTAATCTTTGCTTTTCTCTGAACATTACATCAATACATA
Tamyb10-B1_N61     101 AGGGCAAGTGGGGAAGCCTTCCCAAACGAGCTGGTAGGTTACAGTACACACACCATCGTCTCTAATCTTTGCTTTTCTCTGAACATTACATCAATACATA

Tamyb10-B1_CS      201 CATTGTCTATTATGCGTGCGATTTTCTTGAAGTTGACCGATCTCTCCTCCGAACCTCTTTCTAGCCATTGCAACTGAAACAAAGAGTGTGTGTGTGTGTG
Tamyb10-B1_N61     201 CATTGTCTATTATGCGTGCGATTTTCTTGAAGTTGACCGATCTCTCCTCCGAACCTCTTTCTAGCCATTGCAACTGAAACAAAGAGTGTGTGTGTGTGTG

Tamyb10-B1_CS      301 AGTATGCTTGAAGAAGCGCGCGGCCAGGTGGCTGAAACAAGGAATGCGGCAAAAGAGAGAGATCACTGGTTTAGCATAGCTCGAGATGGTCGTGCTTACT
Tamyb10-B1_N61     301 AGTATGCTTGAAGAAGCGCGCGGCCAGGTGGCTGAAACAAGGAATGCGGCAAAAGAGAGAGATCACTGGTTTAGCATAGCTCGAGATGGTCGTGCTTACT

Tamyb10-B1_CS      401 GAGACGTTGTGTGCAGGGCTGAATCGGTGCGGAAAGAGCTGCCGGCTGCGGTGGCTCAACTACCTCCGGCCGGGGATCAAGAGAGGCAACATCTCCGACG
Tamyb10-B1_N61     401 GAGACGTTGTGTGCAGGGCTGAATCGGTGCGGAAAGAGCTGCCGGCTGCGGTGGCTCAACTACCTCCGGCCGGGGATCAAGAGAGGCAACATCTCCGACG

Tamyb10-B1_CS      501 ACGAAGAGGAGCTCATCGTCAGGCTCCACAGGCTCCTAGGCAACAGGTGCACATAGATCTATGTTGTTTTCCTTTTCATTTGCACCGTACCATGCGCATTT
Tamyb10-B1_N61     501 ACGAAGAGGAGCTCATCGTCAGGCTCCACAGGCTCCTAGGCAACAGGTGCACATAGATCTATGTTGTTTTCCTTTTCATTTGCACCGTACCATGCGCATTT

Tamyb10-B1_CS      601 TCTCTTGTGTAGATGATCAAGCATGTATATTGTTGTTTACTTGCGGTTACACTTGCATTTACATGCATATTCCCAATGTGATATATAGTGTGAACGAAG
Tamyb10-B1_N61     601 TCTCTTGTGTAGATGATCAAGCATGTATATTGTTGTTTACTTGCGGTTACACTTGCATTTACATGCATATTCCCAATGTGATATATAGTGTGAACGAAG

Tamyb10-B1_CS      701 GTGTACAAGTTGGTCTTTGGTCATGGAGGAGTATTAATTAATTAGTCACAGTTGTTTCACAAAAAATATTGGTAATAAACACCAAGGTCATGCTAATGAC
Tamyb10-B1_N61     701 GTGTACAAGTTGGTCTTTGGTCATGGAGGAGTATTAATTAATTAGTCACAGTTGTTTCACAAAAAATATTGGTAATAAACACCAAGGTCATGCTAATGAC

Tamyb10-B1_CS      801 CTTTCCGTTGGAGTTTCACTCTCTTTTTCCCTACATGGAAGACAGAGAGAGATGTATGATCAGGCAAAAGTAGGCCAACGCCTGCTAAATGAATATAGGAT
Tamyb10-B1_N61     801 CTTTCCGTTGGAGTTTCACTCTCTTTTTCCCTACATGGAAGACAGAGAGAGATGTATGATCAGGCAAAAGTAGGCCAACGCCTGCTAAATGAATATAGGAT

Tamyb10-B1_CS      901 CCAGTTATCATGATCACCTGTACACACCTACTATCCATATCAGTCAGCGTGCATGTTCCCAATTTCAGCCATGCCTGAAGAAAAGAACAACCTCTTGCTGA
Tamyb10-B1_N61     901 CCAGTTATCATGATCACCTGTACACACCTACTATCCATATCAGTCAGCGTGCATGTTCCCAATTTCAGCCATGCCTGAAGAAAAGAACAACCTCTTGCTGA

Tamyb10-B1_CS      1001 CAGCCTGAGTGCGTGTCCCTAGCCCCAAGAGGTAAACGAGTTATTTCGGTCAGCAAAAGTTGATGATGACATGCATTTCATTCATGCATGCATGCATGCACAA
Tamyb10-B1_N61     1001 CAGCCTGAGTGCGTGTCCCTAGCCCCAAGAGGTAAACGAGTTATTTCGGTCAGCAAAAGTTGATGATGACATGCATTTCATTCATGCATGCATGCATGCACAA

Tamyb10-B1_CS      1101 CCACTCTGATCTACAACAACAATCTACTACACCATAAATTGAAAAGGCTCCCATGGAGCTAGGTCTAGAACGAAATGCCACTCCCTCCCAGATGTGGCAG
Tamyb10-B1_N61     1101 CCACTCTGATCTACAACAACAATCTACTACACCATAAATTGAAAAGGCTCCCATGGAGCTAGGTCTAGAACGAAATGCCACTCCCTCCCAGATGTGGCAG

Tamyb10-B1_CS      1201 TGTGGCACAACAGCCACTGTTAATCAATCTACACCATAAATTGAAAAGGCTCTGAGCTACAACAATAACCACTCTGTCACTCAGACTGTCACGTATGCA
Tamyb10-B1_N61     1201 TGTGGCACAACAGCCACTGTTAATCAATCTACACCATAAATTGAAAAGGCTCTGAGCTACAACAATAACCACTCTGTCACTCAGACTGTCACGTATGCA

Tamyb10-B1_CS      1301 AAAGCAGCAGCTAACCTTGTGAGGCGCAAGTAAATTAACAGGGCCAGCTAGAATTTCGCTACTGCTAATCAATTGCAAGTGCTTGCTAATTCAGGGTCAG
Tamyb10-B1_N61     1301 AAAGCAGCAGCTAACCTTGTGAGGCGCAAGTAAATTAACAGGGCCAGCTAGAATTTCGCTACTGCTAATCAATTGCAAGTGCTTGCTAATTCAGGGTCAG

Tamyb10-B1_CS      1401 CATGTAATAACAGTTGACGTGGCCTGTGGGCAGGTGGTCGCTGATCGCGGGGCGGCTGCCGGGGCGAACAGACAATGAGATCAAGAACTACTGGAACACC
Tamyb10-B1_N61     1401 CATGTAATAACAGTTGACGTGGCCTGTGGGCAGGTGGTCGCTGATCGCGGGGCGGCTGCCGGGGCGAACAGACAATGAGATCAAGAACTACTGGAACACC

Tamyb10-B1_CS      1501 ACGCTGAGCAAGAGGAACCTGCAGTCTCACGGCGCCGGCTGCTCCAACCACCCACAGGCCAAGCC-----GCCGGCGGCGAGGGCGC
Tamyb10-B1_N61     1501 ACGCTGAGCAAGAGGAACCTGCAGTCTCACGGCGCCGGCTGCTCCAACCACCCACAGGCCAAGCCCCCGCCGCCGCCGCCGAGGCCGGCGGCGAGGGCGC

Tamyb10-B1_CS      1582 ACGCCCTGCCCCAGGGGACGAGCAGCAGCCGATACGGACCAAGGCGCTGCGGTGCACCACCACGGTGTGGCGGCAGCAGAGGGGGTTACGAGCAGGG
Tamyb10-B1_N61     1601 ACGCCCTGCCCCAGGGGACGAGCAGCAGCCGATACGGACCAAGGCGCTGCGGTGCACCACCACGGTGTGGCGGCAGCAGAGGGGGTTACGAGCAGGG

Tamyb10-B1_CS      1682 CCGTGCGGCGCCGGAGCACGTCGCGGAGGAGGATCAGCTGGGTGACTGCCTGTCCATCGGCTCGATCGACCTCGATCTGGAGGGCATCGAGCTGGGCTTC
Tamyb10-B1_N61     1701 CCGTGCGGCGCCGGAGCACGTCGCGGAGGAGGATCAGCTGGGTGACTGCCTGTCCATCGGCTCGATCGACCTCGATCTGGAGGGCATCGAGCTGGGCTTC

Tamyb10-B1_CS      1782 ATGA
Tamyb10-B1_N61     1801 ATGA
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**Supplementary Fig. S8 (B)** Alignment of *Tamyb10-B1* alleles. CS has the recessive allele (*Tamyb10-B1a*) with a 19-bp deletion (highlighted in yellow) and Norin 61 has the dominant *Tamyb10-B1b* allele.

(C)

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Tamyb10-D1_CS      1 ATGGGGAGGAAGCCATGCTGCGCCAAGGAAGGCCTGAACAGAGGGGCATGGACGGCAATGGAGGACGAGATCCTGGTCTCCTACATCAACGATCACGGTG
Tamyb10-D1_N61     1 ATGGGGAGGAAGCCATGCTGCGCCAAGGAAGGCCTGAACAGAGGGGCATGGACGGCAATGGAGGACGAGATCCTGGTCTCCTACATCAACGATCACGGTG

Tamyb10-D1_CS     101 AGGGCAAGTGGGGGAGCCTCCCCAAACGAGCTGGTAGGTTACTCACACCATCGTCTCTAATCTATGCTCTTCTCCGAACATTACATCAATACATACAATT
Tamyb10-D1_N61     101 AGGGCAAGTGGGGGAGCCTCCCCAAACGAGCTGGTAGGTTACTCACACCATCGTCTCTAATCTATGCTCTTCTCCGAACATTACATCAATACATACAATT

Tamyb10-D1_CS     201 GTCGATTATGCGCGCGATTTTCTTTAAGTCGATCGATATCTCCTCCAAACTCTTTCTTGCCATTGCAACTGAAACAAAGAGTGTGTGTGTGTGCGGTAT
Tamyb10-D1_N61     201 GTCGATTATGCGCGCGATTTTCTTTAAGTCGATCGATATCTCCTCCAAACTCTTTCTTGCCATTGCAACTGAAACAAAGAGTGTGTGTGTGTGCGGTAT

Tamyb10-D1_CS     301 GCTTGAAGAAGCCAGGTGACTGAAACAAGGAATGCGGCAAGAGTGAGATCACTGGTTTAGCTTTAGCATAGCTCGAGATGGTGTGTGACGGCGTGTGA
Tamyb10-D1_N61     301 GCTTGAAGAAGCCAGGTGACTGAAACAAGGAATGCGGCAAGAGTGAGATCACTGGTTTAGCTTTAGCATAGCTCGAGATGGTGTGTGACGGCGTGTGA

Tamyb10-D1_CS     401 GATATTGTGTTCAGGGCTGAATCGCTGCGGAAAGAGCTGCCGGTGCGGTGGCTCAACTACCTCCGGCCGGGGATCAAGAGAGGCAACATCTCCGACGAC
Tamyb10-D1_N61     401 GATATTGTGTTCAGGGCTGAATCGCTGCGGAAAGAGCTGCCGGTGCGGTGGCTCAACTACCTCCGGCCGGGGATCAAGAGAGGCAACATCTCCGACGAC

Tamyb10-D1_CS     501 GAAGAGGAGCTCATCGTCAGGCTTCACGGGCTCCTAGGCAACAGGTGCACATCTATGTTGTTTTCTTTTCGTTTGTCATCGTGCACATTTCTGTTGTGTAC
Tamyb10-D1_N61     501 GAAGAGGAGCTCATCGTCAGGCTTCACGGGCTCCTAGGCAACAGGTGCACATCTATGTTGTTTTCTTTTCGTTTGTCATCGTGCACATTTCTGTTGTGTAC

Tamyb10-D1_CS     601 ATGATCAAGCACTGTATGTGTTTTACTTTACACTTACACTTGCACTTTACATGCATATTCCTAATGTAATACGGGGTACGTAGTATATAGTGTGAACGAAG
Tamyb10-D1_N61     601 ATGATCAAGCACTGTATGTGTTTTACTTTACACTTACACTTGCACTTTACATGCATATTCCTAATGTAATACGGGGTACGTAGTATATAGTGTGAACGAAG

Tamyb10-D1_CS     701 ATGTACAAGTGGGTCTTTGGTCGTGGAGGAGTATTAATTAGTCAACACTTGCTTGACAAAAATTTAGTACTAGTAATAAACACCAAGGTCATGCTAATACCT
Tamyb10-D1_N61     701 ATGTACAAGTGGGTCTTTGGTCGTGGAGGAGTATTAATTAGTCAACACTTGCTTGACAAAAATTTAGTACTAGTAATAAACACCAAGGTCATGCTAATACCT

Tamyb10-D1_CS     801 TTCCGTGGGAATTTCAATTTCTTTTTCCCTACATGGAAGACAGAGAGAGATGTATGATCAGACAAAGTAGGCCAACACCTTCTAAACGTATATAACTTCT
Tamyb10-D1_N61     801 TTCCGTGGGAATTTCAATTTCTTTTTCCCTACATGGAAGACAGAGAGAGATGTATGATCAGACAAAGTAGGCCAACACCTTCTAAACGTATATAACTTCT

Tamyb10-D1_CS     901 AATCAATATGATCAAGTTATCATGATCACCTGTACACACCTACTATCCATATCAGTCAGCATGCATGTTCCCAATTACGCCATGCCCGAAGAAAAAGAAC
Tamyb10-D1_N61     901 AATCAATATGATCAAGTTATCATGATCACCTGTACACACCTACTATCCATATCAGTCAGCATGCATGTTCCCAATTACGCCATGCCCGAAGAAAAAGAAC

Tamyb10-D1_CS     1001 ACCTCTTGCTGACAGCCTGAATGCGTGTCTCTACCCCAAGAGGTAAACGAGTTATTCCGGTCAGCAAAGTTGATGATGACGTGCATTAATTCACCTTCATGC
Tamyb10-D1_N61     1001 ACCTCTTGCTGACAGCCTGAATGCGTGTCTCTACCCCAAGAGGTAAACGAGTTATTCCGGTCAGCAAAGTTGATGATGACGTGCATTAATTCACCTTCATGC

Tamyb10-D1_CS     1101 ATGCATGCACAACCACTCTGATCTACTACAAGAATCTACACCATAACTTGAAAAAGGCTCCCATGGAGGTCTAGAACGAAATGCCACTCCCTCCCTCCCAG
Tamyb10-D1_N61     1101 ATGCATGCACAACCACTCTGATCTACTACAAGAATCTACACCATAACTTGAAAAAGGCTCCCATGGAGGTCTAGAACGAAATGCCACTCCCTCCCTCCCAG

Tamyb10-D1_CS     1201 ATGTGGCACAACAACCACTGCTAATCAATCTACACCATGACTTGAAAAGGCTCTGATCTACGACAACCACTCTGTCACTGAGTGTCAACATATGCAGA
Tamyb10-D1_N61     1201 ATGTGGCACAACAACCACTGCTAATCAATCTACACCATGACTTGAAAAGGCTCTGATCTACGACAACCACTCTGTCACTGAGTGTCAACATATGCAGA

Tamyb10-D1_CS     1301 AGCTGCAGCTAACCTTGTCAGGCGCAAGTAAATAGGGCCAGCTAGAAATTCGCTACTGCTAATCAATTGCATGTGCTTAGCTAATAGTAGTAATAATCCA
Tamyb10-D1_N61     1301 AGCTGCAGCTAACCTTGTCAGGCGCAAGTAAATAGGGCCAGCTAGAAATTCGCTACTGCTAATCAATTGCATGTGCTTAGCTAATAGTAGTAATAATCCA

Tamyb10-D1_CS     1401 GCGTCAGATAACAGTGACCGTGGCCCGTGGCAGGTGGTTCGCTGATCGCGGGGCGGCTGCCGGGGCGAACAGACAATGAGATCAAGAACTACTGGAACACC
Tamyb10-D1_N61     1401 GCGTCAGATAACAGTGACCGTGGCCCGTGGCAGGTGGTTCGCTGATCGCGGGGCGGCTGCCGGGGCGAACAGACAATGAGATCAAGAACTACTGGAACACC

Tamyb10-D1_CS     1501 ACGCTGAGCAAGAGGAACAGCAGTCCCACGGCGCCGGCTGCTCGAACCACCCGAGGCCAAGCCGCTGCCGCCGGCGCCGAGGCCGGTGGCGAGGCAC
Tamyb10-D1_N61     1501 ACGCTGAGCAAGAGGAACAGCAGTCCCACGGCGCCGGCTGCTCGAACCACCCGAGGCCAAGCCGCTGCCGCCGGCGCCGAGGCCGGTGGCGAGGCAC

Tamyb10-D1_CS     1601 AGGCCCTGCCGGAGGGGACGAGCAGCAGTCCGATACGGACCAAGGCGCTGCGGTGCACCACCACGGTGTGGCGGCAGCAGAGGGGTTTCACGAGCAGGG
Tamyb10-D1_N61     1601 AGGCCCTGCCGGAGGGGACGAGCAGCAGTCCGATACGGACCAAGGCGCTGCGGTGCACCACCACGGTGTGGCGGCAGCAGAGGGGTTTCACGAGCAGGG

Tamyb10-D1_CS     1701 CCGTGCGGCGCCGGAGCACGTTGCGGCGGAGGATCAGCTGGGGGACTGCCTGTGTCATCGGCTCGATCGACCTCGACCTGGAGGGCATCGAGCTGGGCTTC
Tamyb10-D1_N61     1701 CCGTGCGGCGCCGGAGCACGTTGCGGCGGAGGATCAGCTGGGGGACTGCCTGTGTCATCGGCTCGATCGACCTCGACCTGGAGGGCATCGAGCTGGGCTTC

Tamyb10-D1_CS     1801 ATGATGAGCCCGTGGAGCGGCGGCGCCGACGGCGTGGGTGATCAGCATTTTCGGTGTCCCGGGGCTGAGGCTGATGGTCTGGAGGAGCTGCTCGGGCTGG
Tamyb10-D1_N61     1801 ATGATGAGCCCGTGGAGCGGCGGCGCCGACGGCGTGGGTGATCAGCATTTTCGGTGTCCCGGGGCTGAGGCTGATGGTCTGGAGGAGCTGCTCGGGCTGG

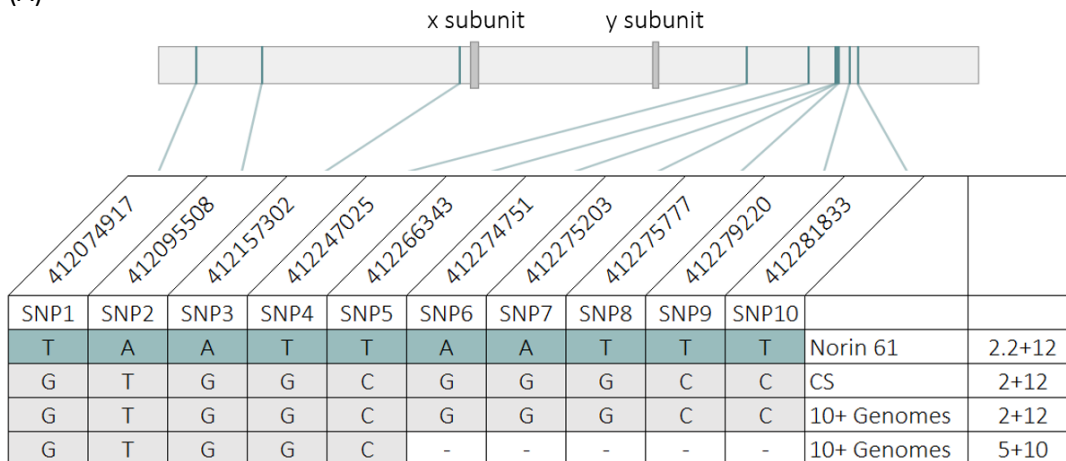
Tamyb10-D1_CS     1901 GCGTGGCCGGAGGAGGCGGCGACGGCCATGGCGGACTCGGGGACCTGGAGTTGGCGTGGCTTTGCTAG
Tamyb10-D1_N61     1901 GCGTGGCCGGAGGAGGCGGCGACGGCCATGGCGGACTCGGGGACCTGGAGTTGGCGTGGCTTTGCTAG
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**Supplementary Fig. S8 (C)** Alignment of *Tamyb10-D1* alleles. Both CS and Norin 61 have the identical dominant allele (*Tamyb10-D1b*).

Rht-D1_CS	1	ATGAAGCGGGAGTACCAGGACGCCGGAGGGAGCGGCGGCGCGGTGGCGGCATGGGCTCGTCCGAGGACAAGATGATGGTGTGCGGCGGCG
Rht-D1_N61	1	ATGAAGCGGGAGTACCAGGACGCCGGAGGGAGCGGCGGCGCGGTGGCGGCATGGGCTCGTCCGAGGACAAGATGATGGTGTGCGGCGGCG
Rht-D1_CS	91	GCGGGGGAGGGGAGGAGGTGGACGAGCTGCTGGCGGCGCTCGGGTACAAGGTGCGCGCCTCCGACATGGCGGACGTGGCGCAGAAGCTG
Rht-D1_N61	91	GCGGGGGAGGGGAGGAGGTGGACGAGCTGCTGGCGGCGCTCGGGTACAAGGTGCGCGCCTCCGACATGGCGGACGTGGCGCAGAAGCTG
Rht-D1_CS	181	GAGCAGCTCGAGATGGCCATGGGGATGGGCGGCGTGGGCGCCGGCGCGCCCCGACGACAGCTTCGCCACCCACCTCGCCACGGACACC
Rht-D1_N61	181	TAGCAGCTCGAGATGGCCATGGGGATGGGCGGCGTGGGCGCCGGCGCGCCCCGACGACAGCTTCGCCACCCACCTCGCCACGGACACC
Rht-D1_CS	271	GTGCACTACAACCCACCGACCTGTCTGCTTTGGGTCGAGAGCATGTGTGCGAGCTCAACGCGCCGCCCGCGCCCTCCCGCCCGCCCCG
Rht-D1_N61	271	GTGCACTACAACCCACCGACCTGTCTGCTTTGGGTCGAGAGCATGTGTGCGAGCTCAACGCGCCGCCCGCGCCCTCCCGCCCGCCCCG
Rht-D1_CS	361	CAGCTCAACGCCTCCACCTCCTCCACCGTCACGGGCGAGCGGCGGTACTTCGATCTCCCGCCCTCCGTGACTCCTCCAGCAGCATCTAC
Rht-D1_N61	361	CAGCTCAACGCCTCCACCTCCTCCACCGTCACGGGCGAGCGGCGGTACTTCGATCTCCCGCCCTCCGTGACTCCTCCAGCAGCATCTAC
Rht-D1_CS	451	GCGCTGCGGCCGATCCCCCTCCCCGGCCGGCGCGACGGCGCCGGCCGACCTGTCCGCGGACTCCGTGCGGGATCCCAAGCGGATGCGCACT
Rht-D1_N61	451	GCGCTGCGGCCGATCCCCCTCCCCGGCCGGCGCGACGGCGCCGGCCGACCTGTCCGCGGACTCCGTGCGGGATCCCAAGCGGATGCGCACT
Rht-D1_CS	541	GGCGGGAGCAGCACCTCGTCGTATCTCTCTCTCGTCGTCTCTCGGTGGGGGCGCCAGGAGCTCTGTGGTGGAGGCTGCCCGCCGGTTC
Rht-D1_N61	541	GGCGGGAGCAGCACCTCGTCGTATCTCTCTCTCTCGTCGTCTCTCGGTGGGGGCGCCAGGAGCTCTGTGGTGGAGGCTGCCCGCCGGTTC
Rht-D1_CS	631	GCGGCCGCGGCCAACGCGACGCCCGCGTGCCTGCTGCTGCTGTCGACACGAGGAGCCGGGATTCGGCTGGTGCACGCGCTGCTGGCG
Rht-D1_N61	631	GCGGCCGCGGCCAACGCGACGCCCGCGTGCCTGCTGCTGCTGTCGACACGAGGAGCCGGGATTCGGCTGGTGCACGCGCTGCTGGCG
Rht-D1_CS	721	TGCGCGGAGGCCGTCGAGCAGGAGAACCTCTCCGCCGCGGAGGCGCTGGTGAAGCAGATACCCCTTGTGGCCGCGTCCAGGGCGGCGCG
Rht-D1_N61	721	TGCGCGGAGGCCGTCGAGCAGGAGAACCTCTCCGCCGCGGAGGCGCTGGTGAAGCAGATACCCCTTGTGGCCGCGTCCAGGGCGGCGCG
Rht-D1_CS	811	ATGCGCAAGGTCGCCGCCTACTTCGGCGAGGCCCTCGCCCGCCGCGTCTTCGGCTTCGCCCCGAGCCGGACAGCTCCCTCCTCGACGCC
Rht-D1_N61	811	ATGCGCAAGGTCGCCGCCTACTTCGGCGAGGCCCTCGCCCGCCGCGTCTTCGGCTTCGCCCCGAGCCGGACAGCTCCCTCCTCGACGCC
Rht-D1_CS	901	GCCTTCGCCGACCTCCTCCACGCGCACTTCTACGAGTCCTGCCCTACCTCAAGTTTCGCGCACTTCACCGCCAACCAGGCCATCCTGGAG
Rht-D1_N61	901	GCCCTTCGCCGACCTCCTCCACGCGCACTTCTACGAGTCCTGCCCTACCTCAAGTTTCGCGCACTTCACCGCCAACCAGGCCATCCTGGAG
Rht-D1_CS	991	GCGTTTCGCCGGCTGCGCGCCGCTGCACGTCGTGCTGCTTCGGCATCAAGCAGGGGATGCAGTGGCCCGCACTTCTCCAGGCCCTCGCCCTC
Rht-D1_N61	991	GCGTTTCGCCGGCTGCGCGCCGCTGCACGTCGTGCTGCTTCGGCATCAAGCAGGGGATGCAGTGGCCCGCACTTCTCCAGGCCCTCGCCCTC
Rht-D1_CS	1081	CGTCCCGGCGGCCCTCCCTCGTTCCGCCTCACCGGCGTCGGCCCCCGCAGCCGGACGAGACCGACGCCCTGCAGCAGGTGGGCTGGAAG
Rht-D1_N61	1081	CGTCCCGGCGGCCCTCCCTCGTTCCGCCTCACCGGCGTCGGCCCCCGCAGCCGGACGAGACCGACGCCCTGCAGCAGGTGGGCTGGAAG
Rht-D1_CS	1171	CTCGCCAGTTTCGCGCACACCATCCGCGTCGACTTCCAGTACCGCGGCTCGTCGCGCCACGCTCGCGGACCTGGAGCCGTTTCATGCTG
Rht-D1_N61	1171	CTCGCCAGTTTCGCGCACACCATCCGCGTCGACTTCCAGTACCGCGGCTCGTCGCGCCACGCTCGCGGACCTGGAGCCGTTTCATGCTG
Rht-D1_CS	1261	CAGCCGGAGGGCGAGGAGGACCCGAACGAGGAGCCGAGGTAATCGCCGTCAACTCAGTCTTCGAGATGCACCGGCTGCTCGCGCAGCCC
Rht-D1_N61	1261	CAGCCGGAGGGCGAGGAGGACCCGAACGAGGAGCCGAGGTAATCGCCGTCAACTCAGTCTTCGAGATGCACCGGCTGCTCGCGCAGCCC
Rht-D1_CS	1351	GGCGCCCTGGAGAAGGTCTTGGGCACCGTGCAGCGCCGTGCGGCCAGGATCGTCACCGTGGTGGAGCAGGAGGCGAATCACAACCTCCGGC
Rht-D1_N61	1351	GGCGCCCTGGAGAAGGTCTTGGGCACCGTGCAGCGCCGTGCGGCCAGGATCGTCACCGTGGTGGAGCAGGAGGCGAATCACAACCTCCGGC
Rht-D1_CS	1441	ACATTCTGGACCGCTTCACCGAGTCTCTGCACTACTACTCCACCATGTTTCGATTCCCTCGAGGGCGGCAGCTCCGGCGGCGGCCATCC
Rht-D1_N61	1441	ACATTCTGGACCGCTTCACCGAGTCTCTGCACTACTACTCCACCATGTTTCGATTCCCTCGAGGGCGGCAGCTCCGGCGGCGGCCATCC
Rht-D1_CS	1531	GAAGTCTCATCGGGGCTGCTGCTGCTCCTGCCGCCGCCGGCACGGACAGGTCATGTCCGAGGTGTACCTCGGCCGGCAGATCTGCAAC
Rht-D1_N61	1531	GAAGTCTCATCGGGGCTGCTGCTGCTCCTGCCGCCGCCGGCACGGACAGGTCATGTCCGAGGTGTACCTCGGCCGGCAGATCTGCAAC
Rht-D1_CS	1621	GTGGTGGCCTGCGAGGGGGCGGAGCGCACAGAGCGCCACGAGACGCTGGGCCAGTGGCGGAACCGGCTGGGCAACGCCGGTTTCGAGACC
Rht-D1_N61	1621	GTGGTGGCCTGCGAGGGGGCGGAGCGCACAGAGCGCCACGAGACGCTGGGCCAGTGGCGGAACCGGCTGGGCAACGCCGGTTTCGAGACC
Rht-D1_CS	1711	GTCCACCTGGGCTCCAATGCCTACAAGCAGGCGAGCACGCTGCTGGCGCTCTTCGCCGGCGGCGACGGCTACAAGGTGGAGGAGAAGGAA
Rht-D1_N61	1711	GTCCACCTGGGCTCCAATGCCTACAAGCAGGCGAGCACGCTGCTGGCGCTCTTCGCCGGCGGCGACGGCTACAAGGTGGAGGAGAAGGAA
Rht-D1_CS	1801	GGCTGCCTGACGCTGGGGTGGCACACGCGCCCGCTGATCGCCACCTCGGCATGGCGCTGGCCGGGCGCGTGA
Rht-D1_N61	1801	GGCTGCCTGACGCTGGGGTGGCACACGCGCCCGCTGATCGCCACCTCGGCATGGCGCTGGCCGGGCGCGTGA

**Supplementary Fig. S9** Comparison of *Rht-1* sequences. Chinese Spring (CS) has the wild-type allele (*Rht-B1a*) and Norin 61 (N61) has the semi-dwarf *Rht-D1b* allele. The yellow box indicates the TAG stop codon introduced by the G to T substitution (shown in red).

### (A) Glu-D1 locus



### (B)

>SNP1\_412074917-in-CSv1\_CS/Norin-61\_x-flanking  
CAGCCCTTCCTTGTGTACAGTAACTTGGATGCCTGCATGCGCTCATTTAAAGAGGAAGTGAAGTGGCTCACCTACAGGGCCAAAAG  
GAAGGAGTATAGTG[G/T]CCTGATTGATTGGGTCAAAGCTTTCAGATGAAGTCTTCTCTCCATTGTAGCTTTTGTATTTCTGTG  
CCTGTTTGTCTTCACTAGGCCTGTATAG

>SNP2\_412095508-in-CSv1\_CS/Norin-61\_x-flanking  
TAGAAATAGTGCAAAAATGATTACAATAGTGATTGATGCCATCATATTGCTGATCCATGAATGGATTAGGCAAGTGTGCTAA  
GTTCCAAAGGAAA[T/A]ACTGTACTCATCTTTATCCTCGTGCTAAAGCGAGCCTTGTGAAGTGTGAGGTTTCATACCGACCA  
TTAGCAAATAGTTATTGCATGCTTTATG

>SNP3\_412157302-in-CSv1\_CS/Norin-61\_x-flanking  
GTTCTGAGCATTGCTTGTATAGTCCATTGCTGGACTGCAATACGGCCCGGATTACTCGGATGGCGCGGTTAGTTTCTGTT  
TGAACACACTCTT[G/A]ACGACACATCTGAAGAGCATCTAGAAAGGCTAATATTCGGGACTATTTATCGTTGCATATCCGCTGTTA  
TATATTGTTAACAATGTATCGCAATTACC

>SNP4\_412247025-in-CSv1\_CS/Norin-61\_y-flanking  
AATCAGGCGATTCAAACGCCTAGAGTTTGTCTCGAAACGCTCTTTCTGTTAGCCAACTTAAACAAGTTTTGCTACTGTAAATTT  
GACTTTAGCCCA[G/T]ATTAGTAAACGAAGCTGTTTCTTTCGCGGTTGAGTTTTGTTGCTTCGTTGATTGATTCTTTTGTCAAA  
CGGAGTTCTTAAGTTGAACCTTCTGTG

>SNP5\_412266343-in-CSv1\_CS/Norin-61\_y-flanking  
AGGATGAAGCCGAAGCCGTCCCGCGCCGCCGCGCATCTGGACGCGCGCGGGCTCCTCCGCGCGCAGCCTGCTCGGGGTG  
GAGGGCAGAAAGCGTCG[C/T]GCCGCCGAGGTCTATTGCGCAGCCGAACGAAGAAGCCAGGGGGCGGGCAGCAGCCACCGAGG  
GGGAAGAGGCGCGCCGAAGGCGGCTCTGTTCCGCA

>SNP6\_412274751-in-CSv1\_CS/Norin-61\_y-flanking  
CGCAGTGCCCTTGCAGCATGAGGGGACGTACTTCGCGCGACGCGCGATTGCCGTTGGCTATGCTGACGCGCGTGGAGTAGTCG  
ATGAGCCAATCTTCC[G/A]GCTTACCGAGCCGTTGTAAGTGGGCGTGTCTGCGGGAGCGAGAACCCTTTGGGGAAGGGCTCGT  
GCGGATGACAGGGGCCAAAGCATGCGCGGCGGAC

>SNP7\_412275203-in-CSv1\_CS/Norin-61\_y-flanking  
CCTTGTCTTTCTTcTGGCGCGCGCGCTCGCAGTCGCGAGCGGGACGTCGCGCGTGTCTCCGCGCTGGGGGATGACTATCAGCA  
CGGGCGCGGCTT[C/G]TGCCTGTTCTGCAGCCGTCGATCAGTGTGATCCGCTTGTATGATAGGGGAGCTCGTCGGCTCC  
CAGCCCATGAGCTCCTTGCAGCCGCTGAG

>SNP8\_412275777-in-CSv1\_CS/Norin-61\_y-flanking  
GTCGTCGAAGACCACACGTCGGAGGGGTAGGCGTCAAGCGACGCGGTGTCGGAGTCGATGAGCATCGGGTCCGTTGGAGCCGAC  
AGACTCCATGTCCGCA[G/T]CAGGCTCGCTGGAGACGTGAAGTTGGTCGAGGAGGCTGACGAGGCGGCTCTCGGGGTAGTCGCT  
GCCTGCGTCGGACGCATGCTCATCGGAGATGCGAGT

>SNP9\_412279220-in-CSv1\_CS/Norin-61\_y-flanking  
ACATAGCACTTGCTGCAAAAACAAGTTAGACGTCCTCTAATTGTTGTTGCAAGTTTTACGTGGCTTGTATAGGTTTCTAGCAAGAAT  
TTTTCTTACCTA[C/T]GTAAACCACAAAGTATTTGCCAATTTCTATTACCTTCATAAGGACCTTTTCATCGAATCCGTTCCGACT  
AAAGTAGGAGAGACAGACACCCGCTA

>SNP10\_412281829-in-CSv1\_CS/Norin-61\_y-flanking  
AGTTTGTGTTGGCCTACTAGATTGATCTTTCTGCAATAGGAGAAGTGTAGGTTTGGGTTCAATCTTGGGTTGCTTTCCAGTGA  
CAGCAGGGGCGAG[C/T]AAGGCACGTATTGATTGTTTCCATCGAGGATAAAAAGATGGGGTTTATACCATATTGCATGAGTTTATCC  
CTCTACATCATGTCATCTTACTTAAAGCA

**Supplementary Fig. S10** (A) Within the 256 kb region around the *x* and *y* subunits of the *Glu-D1* locus, only 10 single nucleotide polymorphisms were identified between the 2+12 allele (CS, Long Reach Lancer, ArinaLrFor, Mace, SY Mattis) and 2.2+12 allele of Norin 61. The 396 bp duplication in the central repeat domain of the 2.2x subunit relative to 2x, was not detected due to the limitations of short sequencing in highly repetitive regions. SNP positions relative to CS v1. (B) The 10 SNPs could be utilized as high throughput molecular markers in breeding programs to differentiate 2.2+12 from 2+12 and 5+10. The 100 bp flanking sequences for each SNP are giving for this purpose, with the CS variant listed before the Norin 61 variant (i.e. CS/Norin-61).