

Erratum to: Association of allelic variation in two *NPR1*-like genes with *Fusarium* head blight resistance in wheat

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We thank Dr. Anna Gordon from NIAB in Cambridge, UK, for spotting discrepancies in marker designations in Fig. 1. We confounded designations of markers for TDF_076_2A and TDF_076_2D which affects five parts of the manuscript. The authors apologize to the readers of Molecular Breeding for all inconveniences caused by these mistakes. The paper should be modified as follows:

The online version of the original article can be found under doi:[10.1007/s11032-013-0010-2](https://doi.org/10.1007/s11032-013-0010-2).

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1. Under the side heading “Sequence analysis of TDF_076”: The lines “Genetic mapping of these markers showed that TDF_076_INDEL1, TDF_076_INDEL2, TDF_076_SNP1 and TDF_076_SNP12 (T = allele 2) mapped to the long arm of chromosome 2A, while TDF_076_INDEL3, TDF_076_SNP13 and TDF_076_SNP12 (A = allele 2) mapped on the long arm of chromosome 2D (Fig. 1)” should read as “Genetic mapping of these markers showed that TDF_076_INDEL3, TDF_076_INDEL2, TDF_076_SNP1 and TDF_076_SNP12 (T = allele 2) mapped to the long arm of chromosome 2A, while TDF_076_INDEL1 and TDF_076_SNP12 (A = allele 1) mapped on the long arm of chromosome 2D (Fig. 1).”
2. The corrected Fig. 1 is given in this Erratum.
3. In Table 1, SNP13: the haplotype 1 of TDF_076_2D has T and haplotype 2 has A.
4. Under the side heading “Effect of TDF_076, TDF_032 and TDF_102 in a diverse collection of European winter wheat cultivars”: The lines “Genotypes with a combination of haplotype 1 of TDF_076_2A and haplotype 2 of TDF_076_2A had 14.2 % less infected spikelets than genotypes with the negative allele 1 and 3 % more infected spikelets than genotypes with the positive allele 2 of both homoeologous genes” should read as “Genotypes with a combination of haplotype 1 of TDF_076_2A and haplotype 2 of TDF_076_2D had 14.2 % less infected spikelets than genotypes with the negative allele 1 and 3 % more infected

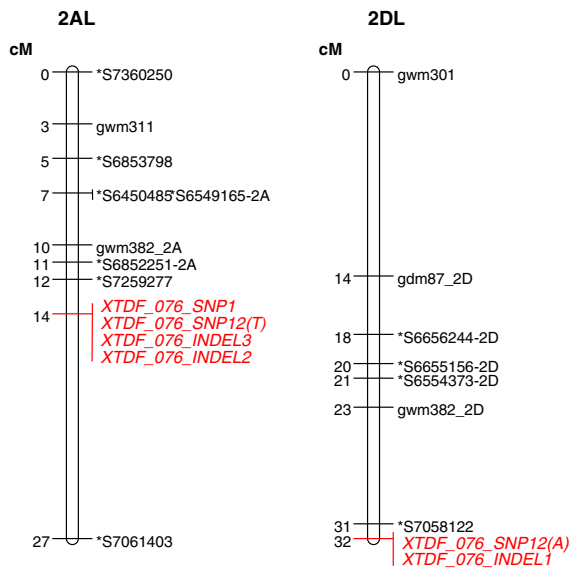


Fig. 1 Genetic map of chromosomes 2AL and 2DL of the Sng3559//Capo/SVP72017 mapping population. The marker loci *XTDF_076* were derived from a *NPR1*-like gene identified in the expression analysis described above. *AFLP markers were assigned to specific chromosomes with nulli-tetrasomic lines

spikelets than genotypes with the positive allele 2 of both homeologous genes.”

- Under the heading “Discussion”, the paragraph starting with “Allelic diversity in both homeologous genes...”: The lines “None of the tested genotypes showed a combination of allele 1 of *TDF_076_2A* and allele 2 of *TDF_076_2D*” should read as “None of the tested genotypes showed a combination of allele 2 of *TDF_076_2A* and allele 1 of *TDF_076_2D*”.