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Corrigendum: Saturation mapping of a major effect QTL for stripe rust resistance on wheat chromosome 2B in cultivar Napo 63 using SNP genotyping arrays

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A Corrigendum on

Saturation mapping of a major effect QTL for stripe rust resistance on wheat chromosome 2B in cultivar Napo 63 using SNP genotyping arrays

By Wu J, Wang Q, Liu S, Huang S, Mu J, Zeng Q, Huang L, Han D and Kang Z (2017) *Front. Plant Sci.* 8:653. doi: 10.3389/fpls.2017.00653

In the published article, there was an error in **Figure 1** as published. The photos of Avocet S and F₁ were not the original wheat lines. We carefully checked them and found that they are the cultivar Zhengmai 9023 and the offspring of Friedrichswerther, respectively. We got the wrong order number of the materials. The corrected **Figure 1** and its caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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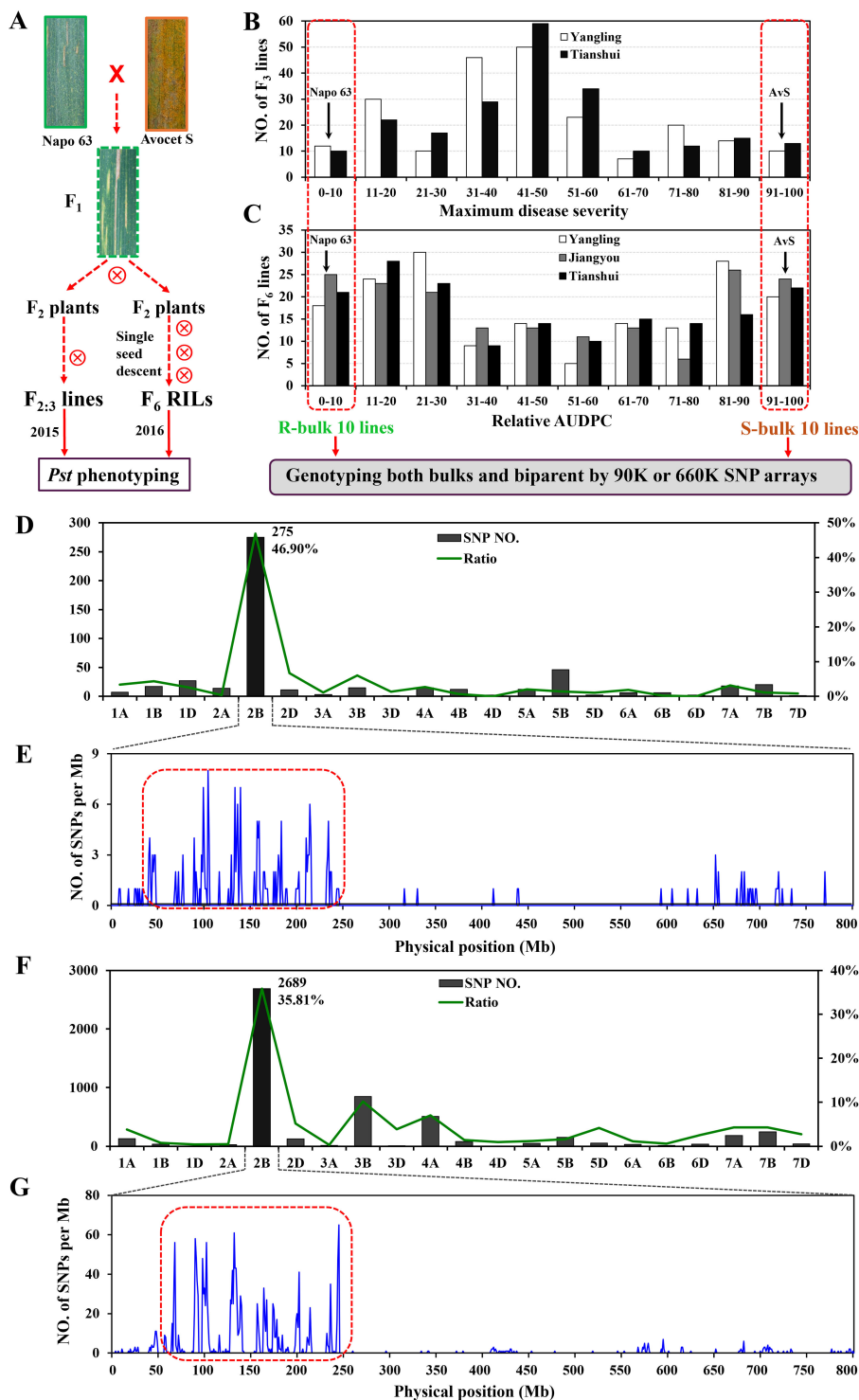


FIGURE 1

Overview of analyses. F_{2:3} lines and F_{5:6} recombinant inbred lines (RILs) were derived from the cross AvS × Napo 63. (A) Phenotypes of AvS, Napo 63 and their progenies across all environments and data collected at heading-flowering stage. (B) Frequency distribution of maximum disease severity (MDS) for 221 F_{2:3} lines grown at Yangling and Tianshui in 2015. (C) Frequency distribution of relative area under the disease progress curve (rAUDPC) for 175 F₆ RILs grown at at Yangling, Jianguou and Tianshui in 2016. Black arrows indicate the parental line means. Distributions of the polymorphic SNPs in each chromosome by 90K (D) and 660K (F) SNP arrays and positions of SNPs in chromosome 2B (E, G). Selected SNPs (in the red dotted boxes) were analysed in KASP assays.