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# Author Correction: Candidate gene mapping identifies genomic variations in the fire blight susceptibility genes *HIPM* and *DIPM* across the *Malus* germplasm

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This Article contains a typographical error in the Materials and methods section under subheading ‘Association between fire blight susceptibility and genomic variations’.

“The SNP genotype file was phased with Beagle v5.1<sup>53</sup> and converted from the IUPAC ambiguity codes to a dominant genetic model, where ‘1’ represents the homozygous SNP states and ‘0’ represents the heterozygous sites.”

should read:

“The SNP genotype file was phased with Beagle v5.1<sup>53</sup> and converted from the IUPAC ambiguity codes to an additive genetic model, where ‘1’ represents the homozygous SNP states and ‘0’ represents the heterozygous states.”



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