

## Supplemental Table 6

Mutant allele *wp* (top sequence) and *Wp F3H1* (bottom sequence) genomic sequences alignment. EMBOSS pairwise alignment algorithm from EMBL-European Bioinformatics Institute (EBI) was chosen for the alignment of these two sequences differing by a large 5.7 kb insertion.

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EMBOSS_001      1  WpTACACGCACATTCTCCTCAAAGACAACAATGGCACCAACAGCCAAGAC
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EMBOSS_001     51  TCTGACTTACCTGGCCCAGGAGAAAACCTAGAATCGAGCTTCGTTTCGGG
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|
EMBOSS_001    101  ACGAGGAGGAGCGTCCCAAGGTTGCCTACAACGAATTCAGCGACGAGATC
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EMBOSS_001    151  CCAGTGATTTCTCTTGCCGGAATCGACGAGGTGGATGGACGCAGAAGAGA
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EMBOSS_001    201  GATTTGTGAGAAGATCGTGGAGGCTTGCGAGAATTGGGGTATATTCCAGG
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