GENETICS

Supporting Information
http://www.genetics.org/cgi/content/full/genetics.109.116178/DC1

Developmental Timing of DNA Elimination Following Allopolyploidization in Wheat

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DOI: 10.1534/genetics.109.116178

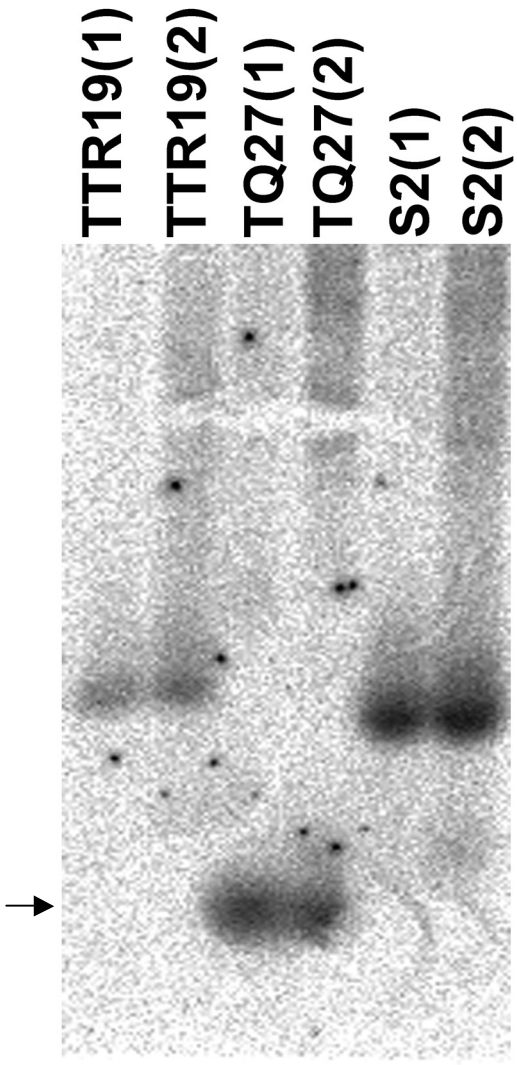

FIGURE S1.—Southern blot validation of the elimination of the TQ27 allele in S2 generation. S2(1) was derived from a cross between TTR19(1) and TQ27(1), while S2(2) was derived from a cross between TTR19(2) and TQ27(2). Genomic DNA was digested with *DraI*. The arrow indicates the TQ27 band.

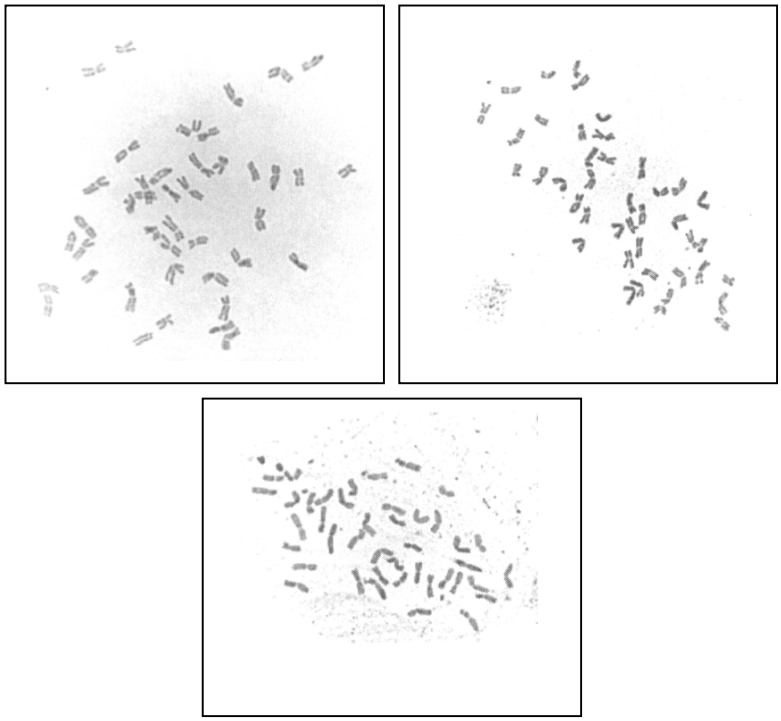

FIGURE S2.—Examples of somatic chromosome number in newly formed allohexaploids. In all individuals 2n=42. For chromosome number count, root tips were cut and subjected to ~24 h cold treatment for cell division arrest. Those root tips were treated with 1% acetocarmine solution for ~48 h. Before squashing, root tips were placed on a preparative slide in a solution containing 1% acetocarmine and 1N HCl (ratio of 5:1, respectively) and briefly heated. Finally, root tips were squashed in a preparative slide in a drop of 1% acetocarmine.

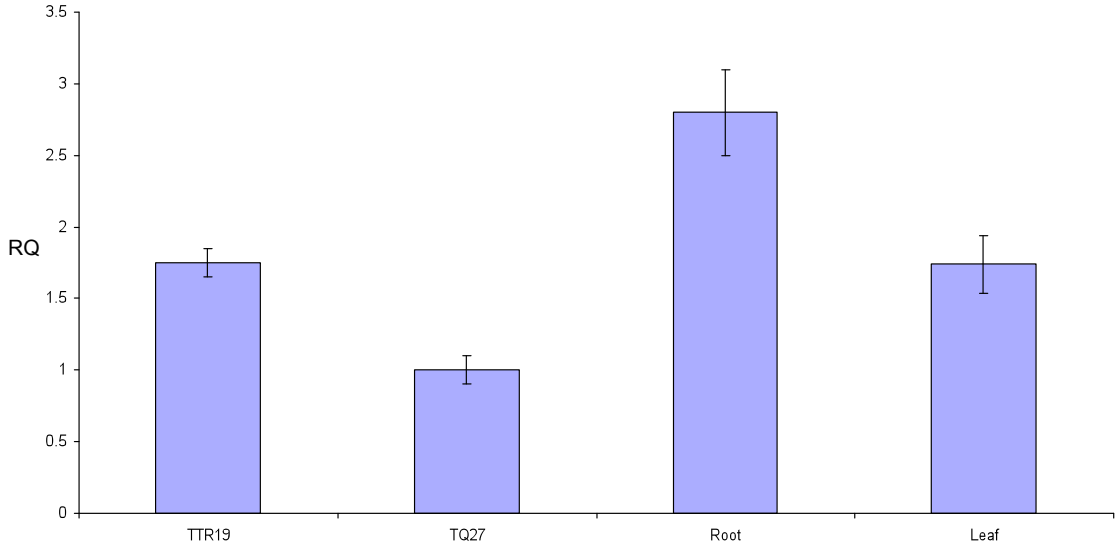

FIGURE S3.—Quantitative PCR analysis of the eliminated sequence in the parental lines, and 4 weeks old roots and leaves of S2. Relative quantity (RQ) of the sequence (mean ± standard error, n=3) shows that the elimination of the sequence occurred on leaf but not in root of S2 generation. A single copy gene *VRN1* was used as a reference. Details on qPCR conditions and primer sequences are available upon request.