


Tgmw4m



T322	CGTATCATATTTATATATTTTATAGGTAATAAT	<u>AA</u> TACATGAATGCTTATATTTTTT
58-1	CGTATCATATTTATATATTTTATAGGTAATAAT	ACATGAATGCTTATATTTTTT
58-18	CGTATCATATTTATATATTTTATAGGTAATA	AA TACATGAATGCTTATATTTTTT
58-9	CGTATCATATTTATATATTTTATAGGTAATAAT	AT ACATGAATGCTTATATTTTTT
58-4	CGTATCATATTTATATATTTTATAGGTAATAAT	T AA TACATGAATGCTTATATTTTTT
58-6	CGTATCATATTTATATATTTTATAGGTAATAAT	AT ACATGAATGCTTATATTTTTT
58-13	CGTATCATATTTATATATTTTATA	TACATGAATGCTTATATTTTTT
58-21	CGTATCATATTTATATATTTTATAGGTAATAAT	T AA TACATGAATGCTTATATTTTTT
58-7	CGTATCATATTTATATATTTTATAGGTAATAAT	AT AA TACATGAATGCTTATATTTTTT
58-5	CGTATCATATTTATATATTTTATAGGTAATAAT	AT ACATGAATGCTTATATTTTTT
T321	CGTATCATATTTATATATTTTATAGGTAATAAT	AT AA TACATGAATGCTTATATTTTTT
T369	CGTATCATATTTATATATTTTATAGGTAATAAT	CATGAATGCTTATATTTTTT
WT	CGTATCATATTTATATATTTTATAGGTAATAAT	ACATGAATGCTTATATTTTTT
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FIGURE S5.—Unique footprints left behind by *Tgm9* during germinal reversion. Germinal revertants from nine families identified in Figure 7a and two intermediate germinal revertants T321 (*w4-dp*) and T369 (*w4-p*) were selected for determining footprints left behind by *Tgm9* in *DFR2* intron II through PCR by compare to the wild-type *DFR2* (WT) from cv. Williams 82. Nucleotides representing the target site duplication are underlined. Footprint nucleotides left by *Tgm9* germinal excision are in bold font.