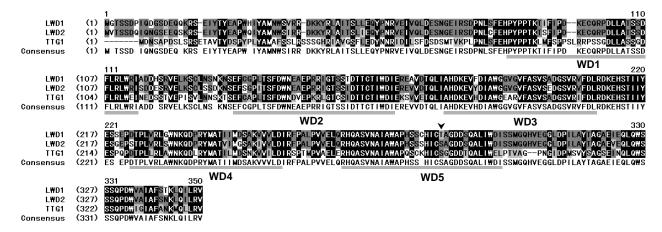
	LWD1 (346 a.a.)	LWD2 (346 a.a.)	TTG1 (341 a.a.)
LWD1	-		
LWD2	91.3% (94.2%)	-	
TTG1	60.3% (74.3%)	58.6% (73.7%)	-

(B)



Supplemental Figure S6. Sequence comparison of Arabidopsis LWD1, LWD2 and TTG1

(A) Pair-wise comparison of amino acid identity (similarity) for LWD1, LWD2 and TTG1. The identity or similarity was determined by use of Vector NTI AlignX. (B) Amino acid sequence alignment of LWD1, LWD2 and TTG1. Amino acid sequences of LWD1, LWD2 and TTG1 were aligned by use of Vector NTI AlignX. Identical amino acids are shaded in black. The dark grey shading represents positions with conserved amino acids. The light grey shading represents positions with similar amino acids. The 5 WD repeats are marked according to positions in LWD1 and LWD2. The position for S282, T285 and S285 of TTG1, LWD1 and LWD2, respectively, is marked with a triangle.