

(A)

	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)

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1
LWD1 (1) MGTSSDPIDGSDDEQKRS-EIYTYEAPWHIYAMNNSVRR-DKKYRLAITSLLLEQYNNRVEIVQLDESNGEIRSDPNLSFEHPYPPTKTIIFIPD-KEQRPDLLATSSD
LWD2 (1) MVTSSDQIQNGSEEGSKRS-EIYTYEAPWHIYAMNNSVRR-DKKYRLAITSLLLEQYNNRVEIVQLDESNGEIRSDPNLSFEHPYPPTKTIIFIPD-KEQRPDLLATSSD
TTG1 (1) -----MDNSAPDLSRSSETAVIYDSDPYLYAFSSLRSSSGHRIVYGSFLEDPYNNRIDLISFDSDSMTVKPLPNLSFEHPYPPTKTIIFIPD-KEQRPDLLATSSD
Consensus (1) M TSSD IQNGSDEQ KRS EIYTYEAPW IYAMNNSVRR DKKYRLAITSLLLEQYNNRVEIVQLDESNGEIRSDPNLSFEHPYPPTKTIIFIPD KEQRPDLLATSSD

111
LWD1 (107) FLRLWRIADDSRVVELKSQLNSKNSEFCGPLTSFDWNEAEPRIIGTSSIDTTCTIWDIEREVVDTQLIAHDKEVVDIAWGGVGVFASVSDGGSVRFDLRDKEHSTIIY
LWD2 (107) FLRLWRISDDSEYVELKSQLSSDKNSEFCGPLTSFDWNEAEPRIIGTSSIDTTCTIWDIEREVVDTQLIAHDKEVVDIAWGGVGVFASVSDGGSVRFDLRDKEHSTIIY
TTG1 (104) FLRLWRINEDSSTVEPIVYLNNSKTSEFCAPLTSFDWNOVEPKRIGTCSIDTTCTIWDIEREVVDTQLIAHDKEVVDIAWGGVGVFASVSDGGSVRFDLRDKEHSTIIY
Consensus (111) FLRLWRIADD SRVELKSQLNS KNSEFCGPLTSFDWNEAEPRIIGTSSIDTTCTIWDIEREVVDTQLIAHDKEVVDIAWGGVGVFASVSDGGSVRFDLRDKEHSTIIY

221
LWD1 (217) ESSEPDTPVRLGNKQDPRYMATIIMDSAKVYVLDIRFALPYVELQRHQASVNAIAWAPSSCHIQTAGDSSQAL IWDISSMGQHVEGGLDPIIAYTAGAEIEQLQWS
LWD2 (217) ESGEPSTPLVRLSNKQDPRYMATIIMGSAKIVVLDIRFALPYVELQRHQASVNAIAWAPSSSHICSAAGDSSQAL IWDISSMGQHVEGGLDPIIAYTAGAEIEQLQWS
TTG1 (214) ESPQPDTPVRLAWNKQDPRYMATIIMDSAKVYVLDIRFALPYVELQRHQASVNAIAWAPSSCKHICSGGDDTQAL IWEIPTVAG--PNCIDPMSVYSAGSEINQLQWS
Consensus (221) ES EPDTPVRLAWNKQDPRYMATIIMDSAKVYVLDIRFALPYVELQRHQASVNAIAWAPSS HICSAAGDSSQAL IWDISSMGQHVEGGLDPIIAYTAGAEIEQLQWS

331
LWD1 (327) SSQPDWVAIAFSNKLIQLRV
LWD2 (327) SSQPDWVAIAFSNKLIQLRV
TTG1 (322) SSQPDWVIGIAFANKLIQLRV
Consensus (331) SSQPDWVAIAFSNKLIQLRV

350
LWD1 (327) SSQPDWVAIAFSNKLIQLRV
LWD2 (327) SSQPDWVAIAFSNKLIQLRV
TTG1 (322) SSQPDWVIGIAFANKLIQLRV
Consensus (331) SSQPDWVAIAFSNKLIQLRV

WD1
WD2
WD3
WD4
WD5
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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.