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1                                                                 80
LWD1 (At1g12910) MGTSSDPTIQGSDEEQKRSEIYTYEAPWHIYAMNWSVRRDKKYRLAITSLEQYPNRVEIQLDESNGEIRSDPNLSFEH
LWD2 (At3g26640) MVTSSDQIQNGSEEQSKRSEIYTYEAPWQIYAMNWSVRRDKKYRLAITSLEQYPNRVEIQLDESNGEIRSDPNLCFEH
Consensus      M TSSD IQ GSDEQ KRSEIYTYEAPW IYAMNWSVRRDKKYRLAITSLEQYPNRVEIQLDESNGEIRSDPNL FEH

81                                                                 160
LWD1 (At1g12910) PYPPTKTIFIPDKECQRPDLLATSSDFLRLWRIADDSRVELKSCLSNKNSEFCGPLTSFDWNEAEPRI GTSSITDTC
LWD2 (At3g26640) PYPPTKTSFIPDKECQRPDLLATSSDFLRLWRIADDSRVELKSCLSNKNSEFCGPLTSFDWNEAEPRI GTSSITDTC
Consensus      PYPPTKT FIPDKECQRPDLLATSSDFLRLWRIADDSRVELKSCLSNKNSEFCGPLTSFDWNEAEPRI GTSS DTC
                WD-1                                                                                               WD-2

161                                                                 240
LWD1 (At1g12910) TIWDIEREAVDTQLIAHDKEVFDIAWGGVGVFASVSDGSVRVFDLRDKEHSTIIYESSEPDTPLVRLGWNKQDPRYMAT
LWD2 (At3g26640) TIWDIEREVVDTQLIAHDKEVFDIAWGGVGVFASVSDGSVRVFDLRDKEHSTIIYESGEPSTPLVRLSWNKQDPRYMAT
Consensus      TIWDIERE VDTQLIAHDKEVFDIAWGGVGVFASVSDGSVRVFDLRDKEHSTIIYES EP TPLVRL WNKQDPRYMAT
                WD-3                                                                                               WD-4

241                                                                 320
LWD1 (At1g12910) IIMDSAKIVVLDIRFPALPVVELQRHQASVNAIAWAPHSSCHI CTAGDSSQALIWDI SSMGQHVEGGLDPI LAYTAGAEI
LWD2 (At3g26640) VMGSAKIVVLDIRFPALPVVELQRHQASVNAIAWAPHSSSHI CSAGDSSQALIWDI SSMGQHVEGGLDPI LAYTAGAEV
Consensus      IIM SAKIVVLDIRFPALPVVELQRHQASVNAIAWAPHSS HI CSAGDSSQALIWDI SSMGQHVEGGLDPI LAYTAGAEI
                WD-5

321                                                                 347
LWD1 (At1g12910) EQLQWSSSQPDWVAIAFSTKLQILRV
LWD2 (At3g26640) EQLQWSSSQPDWVAIAFSNKLQILRV
Consensus      EQLQWSSSQPDWVAIAFS KLQILRV

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Supplemental Figure S1. Amino acid sequence alignment of LWD1 and LWD2
LWD1 and LWD2 share 91.4% amino acid identity. Identical amino acids between LWD1 and LWD2 are shaded in black. The grey shading represents positions with similar amino acids. The 5 WD repeats are underlined and numbered.