Supplemental methods

Amino acid sequence alignment

AlignX in NTI (Invitrogen), a tool of InforMax Vector NTI advanced 8.0 based on the Clustal W algorithm (Thompson et al., 1994), was used to generate the sequence alignment shown in Supplemental Figure S1. The positions of the 5 WD repeats were marked according to criteria used in a previous report (Neer et al., 1994). WD3 and WD5 of the LWD1/LWD2 protein have one mismatch in the consensus core repeat sequence, WD2 has two mismatches, and WD1 and WD4 have three to six mismatches.

Northern blot analyses

An amount of 6 to 9 μg of RNA was denatured at 65 ^{o}C for 10 min, separated by 1% formaldehyde-agarose gel and transferred to a nylon membrane (Nytran supercharged, Schleicher & Schuell, Dassel, Germany). DIG-11-UTP (DIG RNA labeling mix, Roche, Penzberg, Germany) was incorporated into LWD1 or LWD2 probes (shown in Supplemental Figure S1) by PCR. The primer sets used in the probe synthesis were, for LWD1, LWD1(+334~+354)-S and LWD1(+830~+807)-AS; and for LWD2, LWD2-*Xba*I-2-S and LWD2-*Sma*I-2-AS. The detailed primer sequences are listed in the Supplemental Primer Table. The hybridization and signal detection were performed as suggested in the DIG System User's Guide (Roche).

Absolute quantitation of LWD1 and LWD2 transcripts

Plasmids harboring *LWD1* or *LWD2* genomic fragments of known concentration (equivalent to 10^3 to 10^6 transcript molecules) were used as templates in the quantitative PCR reactions to construct a standard curve for the derivation of the *LWD1* and *LWD2* transcript amount.

Neer EJ, Schmidt CJ, Nambudripad R, Smith TF (1994) The ancient regulatory-protein family of WD-repeat proteins. Nature **371:** 297-300

Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res **22:** 4673-4680