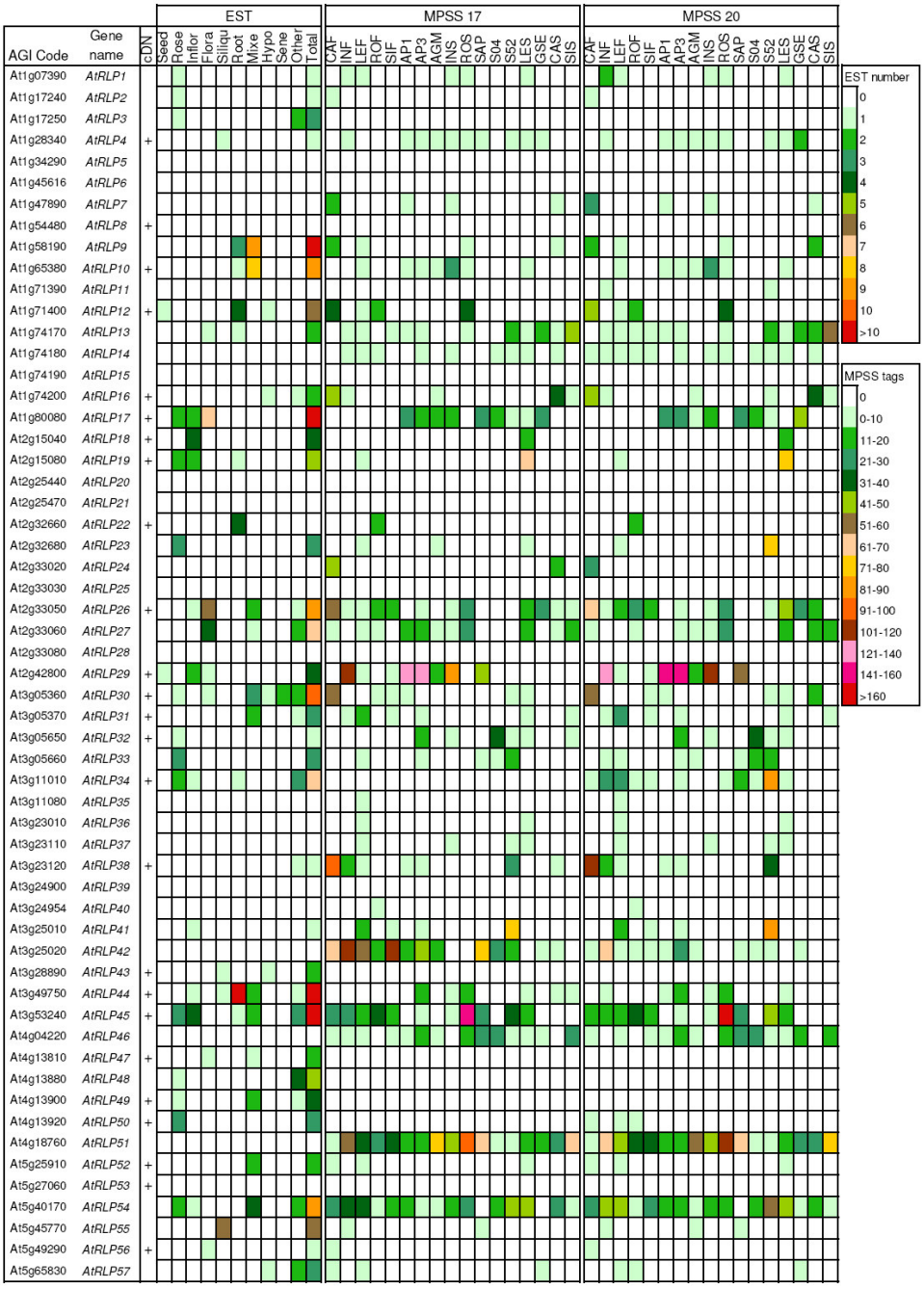

Fig. S1. cDNA, EST and MPSS expression data for *AtRLP* genes. The MPSS (17) and MPSS (20) abbreviations are: CAF/CAS, callus tissue culture; INF, inflorescence; LEF/LES, leaves; ROF/ROF, root; SIF/SIS, silique; AP1, ap1-10 infloresence; AP3, ap3-6 infloresence; AGM, agamous infloresence; INS, infloresence; SAP, sup/ap1 infloresence; S04, leaves, 4 hr after salicylic acid treatment; S52, leaves, 52 hr after salicylic acid treatment; GSE, germinating seedlings.

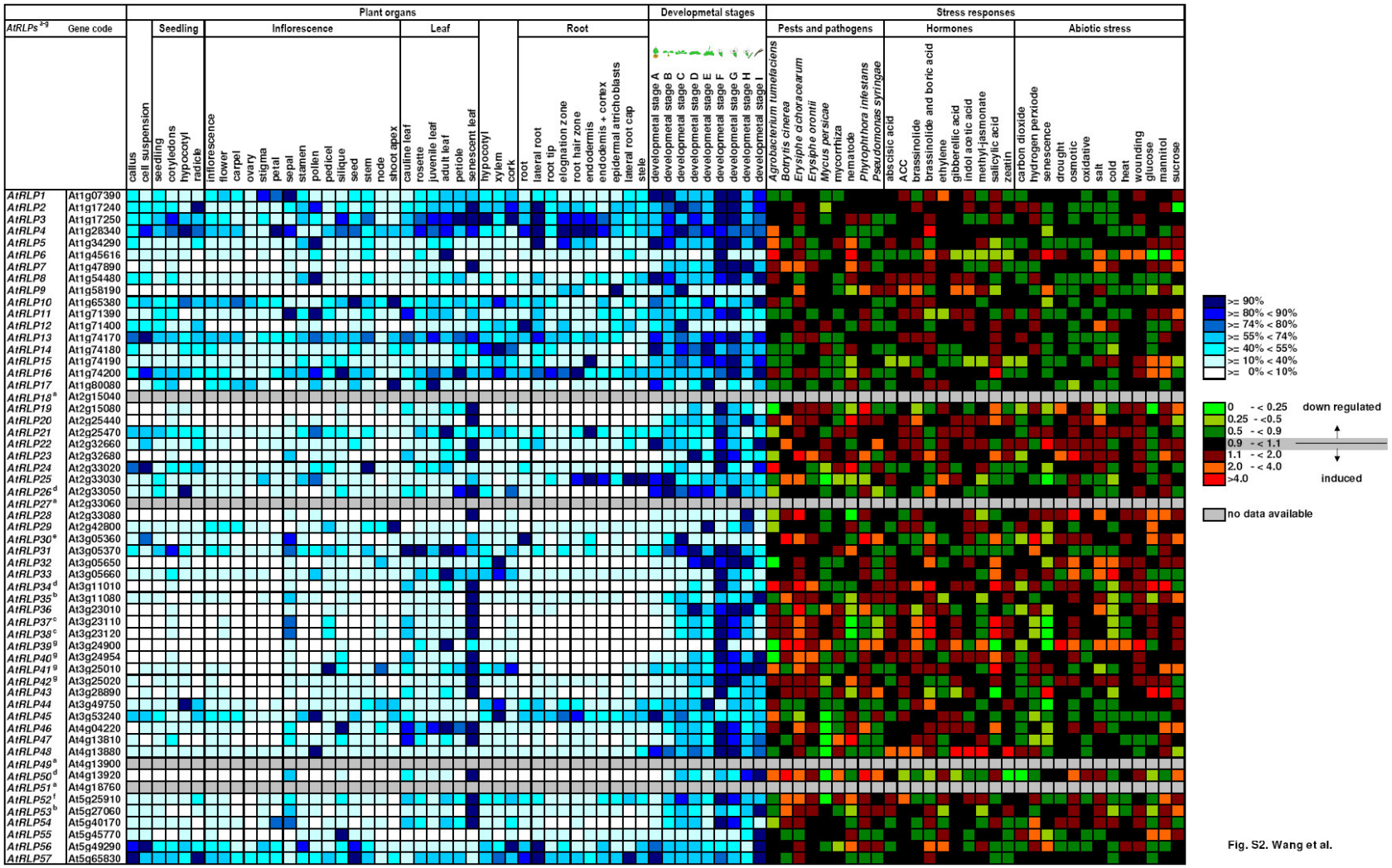

Fig. S2. Wang et al.

Fig. S2. Expression profile of *AtRLP* genes in various organs, growth stages and upon stress responses. The figure was modified from an output of Meta-Analyzer of Genevestigator (Zimmermann et al., 2004).

Heat maps are rendered either in blue-white for gene expression patterns for plant organs and developmental stages or in red-green for gene expression patterns upon stress responses. For the blue-white scheme on the left panel, absolute signal intensities of one gene for all plant organs or for all developmental stages were compared with each other and normalized that the highest signal intensity value obtained the value 100% (dark blue) and the absence of signals obtained value 0% (white).

For the red-green scheme on the right panel, signal intensity values for a gene upon one treatment were compared with the corresponding control and given as linear ratio values. Red, orange and dark red indicate that the signal intensity of the treatment is higher than signal intensity of the corresponding control, and green, lime and bright green mean the opposite. Black indicates no difference in signal intensity between treatment and control.

Plant organs, developmental stages and stress responses are listed on top.

[a] For *AtRLP18*, *AtRLP27*, *AtRLP49* and *AtRLP51* no probesets are present on the Affymetrix ATH1 22k array chip.

[b] *AtRLP35* and *AtRLP53* have the same probeset (254741_at) and thus have the same values.

[c] *AtRLP37* and *AtRLP38* hybridize to the same probeset (257763_s_at) that is representing two or more closely related genes.

[d] *AtRLP26*, *AtRLP34* and *AtRLP50* hybridize to probesets (267596_s_at, 256431_s_at and 254741_s_at, respectively) that are representing two or more closely related genes.

[e] *AtRLP30* hybridizes to two different probesets (265993_at and 259297_at) of which only the data of one (259297_at) was included in the figure.

[f] *AtRLP52* hybridizes to two different probesets (265893_at and 246916_at) of which only the data of one (246916_at) was included in the figure.

[g] *AtRLP39*, *40*, *41* and *42* cross-hybridize to three different probesets (257100_at, 257591_at and 257592_at). In addition, *AtRLP39*, *41* and *42* cross-hybridize to another probeset (257101_at). For *AtRLP39* the data of probeset 257592_at, for *AtRLP40* the data of probeset 257100_at, for *AtRLP41* the data of probeset 257101 and for *AtRLP42* the data of probeset 257591_at were included in the figure.

Abbreviations: ACC: 1-aminocyclopropane-1-carboxylic acid.

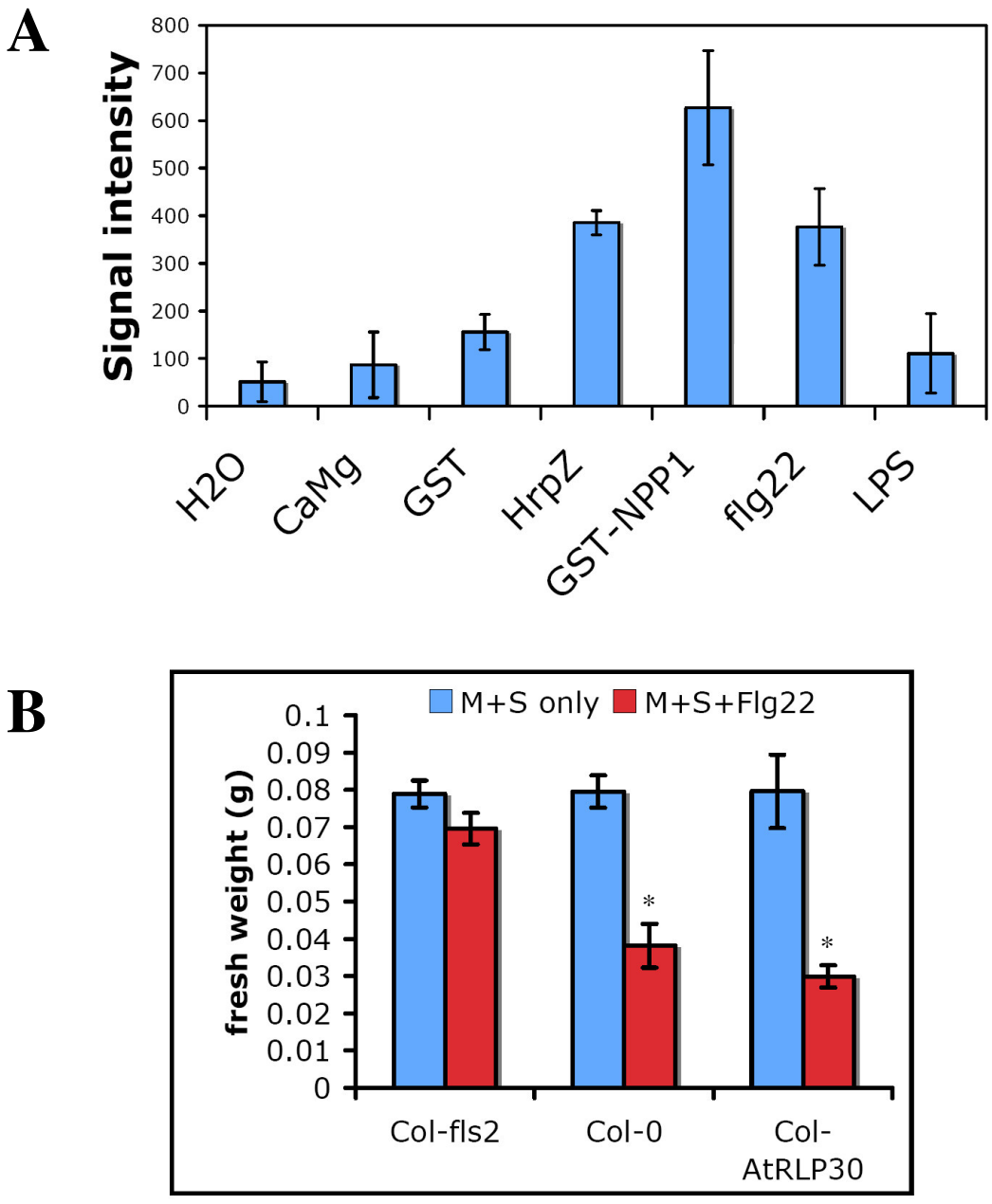

Fig. S3. Expression of *AtRLP30* after PAMP treatment. A, Data obtained using the Genevestigator software derived from the AtGenExpress experiment "Response to bacterial-(LPS, HrpZ, Flg22) and oomycete-(NPP1) derived elicitors". More details of this experiment are available at http://www.arabidopsis.org. Expression level of *AtRLP30* was increased by the PAMPs HrpZ, flg22 and NPP1 when compared to control treatments (H_2O, CaMg and GST). LPS did not increase the level of expression.

Effect of flg22 on seedling growth. The addition of flg22 to MS growth media causes a significant reduction in weight of seedlings that can detect flg22 (Col-0) but not in mutants in the flg22 perception pathway (Col-0 *fls2*). Col-*Atrlp30* shows a wild-type response to flg22, indicating that it is not involved in flg22 perception. Statistically significant differences are indicated by asterisks.