

Supporting Information

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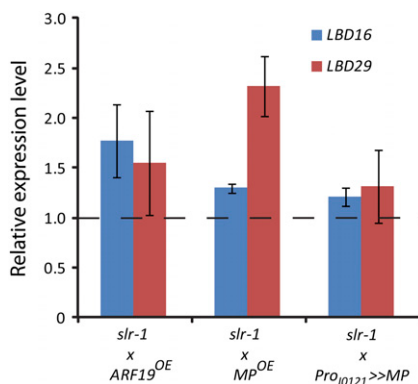


Fig. S1. Quantitative RT-PCR expression analysis of *LBD16* and *LBD29* in *slr-1*x*ARF19*^{OE}, *slr-1*x*Pro*_{J0121}>>*MP* and *slr-1*x*MP*^{OE} (roots from seedlings 10 days after germination, segregating F2 population) compared with the control expression level (dashed line). Data are mean \pm SEM of different independent crosses ($n \geq 2$). No statistically significant differences for values compared with control or with the other transgenic lines as determined by Student's *t* test ($P < 0.05$). The following primers were used to quantify the gene expression levels: *LBD16*, 5'-AGCCGCCGGAGATCTAAGACA-3'/5'-CACTAGTTTGTGCCACGTCATAAAC-3'; *LBD29*, 5'-GAAGTTCTGGGACGGTTCAACAC-3'/5'-GGTTTCGTTGTGTAAGTACTCTCTG-3'.