

Figure S1. *drp2b* mutants display increased ROS in response to multiple PAMPs independent of *RbohD* and *FLS2* mRNA levels.

(A) Compared to Col-0 and drp2a-1 (2a-1), peak ROS production (at 10-15 minutes postelicitation) was significantly increased in drp2b-2 (2b-2) after elicitation with 0.1µM of active flg22 (black bars) (P<0.0001). Responses to inactive flg22^{A.tum} (white bars) were not different between genotypes (P>0.5). Data were based on time-course experiment from Figure 1C. (n=24/genotype and treatment). (B) Compared to Col-0 (white bar) and drp2a-1 (2a-1; gray bar), peak ROS production (10-15 minutes post elicitation) was significantly increased in drp2b-2 (2b-2; black bar) after elicitation with 0.1µM elf26 (P<0.005). (n=32/genotype). (C) Using quantitative Real-Time PCR (qRT-PCR) with At2g28390 as the reference gene, mRNA levels of RbohD were not significantly different between drp2b-2 (2b-2; black bar) and Col-0 (white bar). Tissues were cut and prepared exactly as those for ROS experiments in 96-well plates and collected immediately prior to flg22-elicitation (n=3/genotype; P=0.9). (D) Based on experimental design and qRT-PCR as described in (C), mRNA levels of FLS2 were not significantly different between drp2b-2 (2b-2; black bar) and Col-0 (white bar) (P=0.33). (n=3/genotype). For (A - B), luminol-based ROS production is shown as Relative Light Units (RLU). For (A - D), all experiments were done in 4-5 week old leaf tissue and repeated more than three independent times with similar results. Values are mean ± SE. Different letters indicate significant differences while the same letter indicates no significant differences between samples based on Two tailed student's t-test. ROS experiments shown in the same panel were performed in the same 96-well plate at the same time to allow for direct comparison.