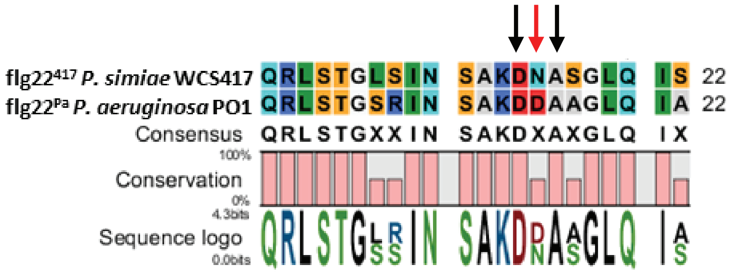
Supplemental Figures 1 and 2



Supplemental Figure 1: **Alignment of flg22 peptides from flagellin of *P. simiae* WCS417 (flg22^{417}) and *P. aeruginosa* PO1 (flg22^{Pa}).** Arrows indicate the amino acids previously shown (Felix et al., 1999) to be required for the induction of immune responses in tomato. Alignment is created using the sequence alignment tool of CLC Main Workbench 6.9.

flg22^{Pa}
Col-0 root / *Ler*-0 root
This study / Beck *et al.* (2014)

flg22^{Pa}
Col-0 root / *Ler*-0 seedling
This study / Zipfel *et al.* (2004)

chitin
Col-0 root / Col-0 root
This study / Wan *et al.* (2008)

Supplemental Figure 2. Venn diagrams of DEGs shared between Arabidopsis responses to flg22^{Pa} or chitin in different studies. Venn diagrams show the overlap between DEGs responding to **(A)** flg22^{Pa}, 0.5 h after treatment of Col-0 roots (RNA-Seq data of this study) or L*er*-0 roots (Beck *et al.,* 2014), **(B)** flg22^{Pa}, 0.5 h after treatment of Col-0 roots (RNA-Seq data of this study) or L*er*-0 seedlings (Zipfel *et al.,* 2004), and **(C)** chitin, 0.5 h after treatment of Col-0 roots (RNA-Seq data of this study versus Wan *et al.,* 2008). In the study of Beck *et al.* (2014), L*er*-0 roots were treated with 10 μM flg22^{Pa}. In the study of Zipfel *et al.* (2004), whole L*er*-0 seedlings were treated with 10 μM flg22^{Pa}. In the study of Wan *et al.* (2008), Col-0 roots were treated with 1 μM chitooctaose. In all cases, DEGs were selected based on FDR <0.05 and log$_2$-fold change >1.