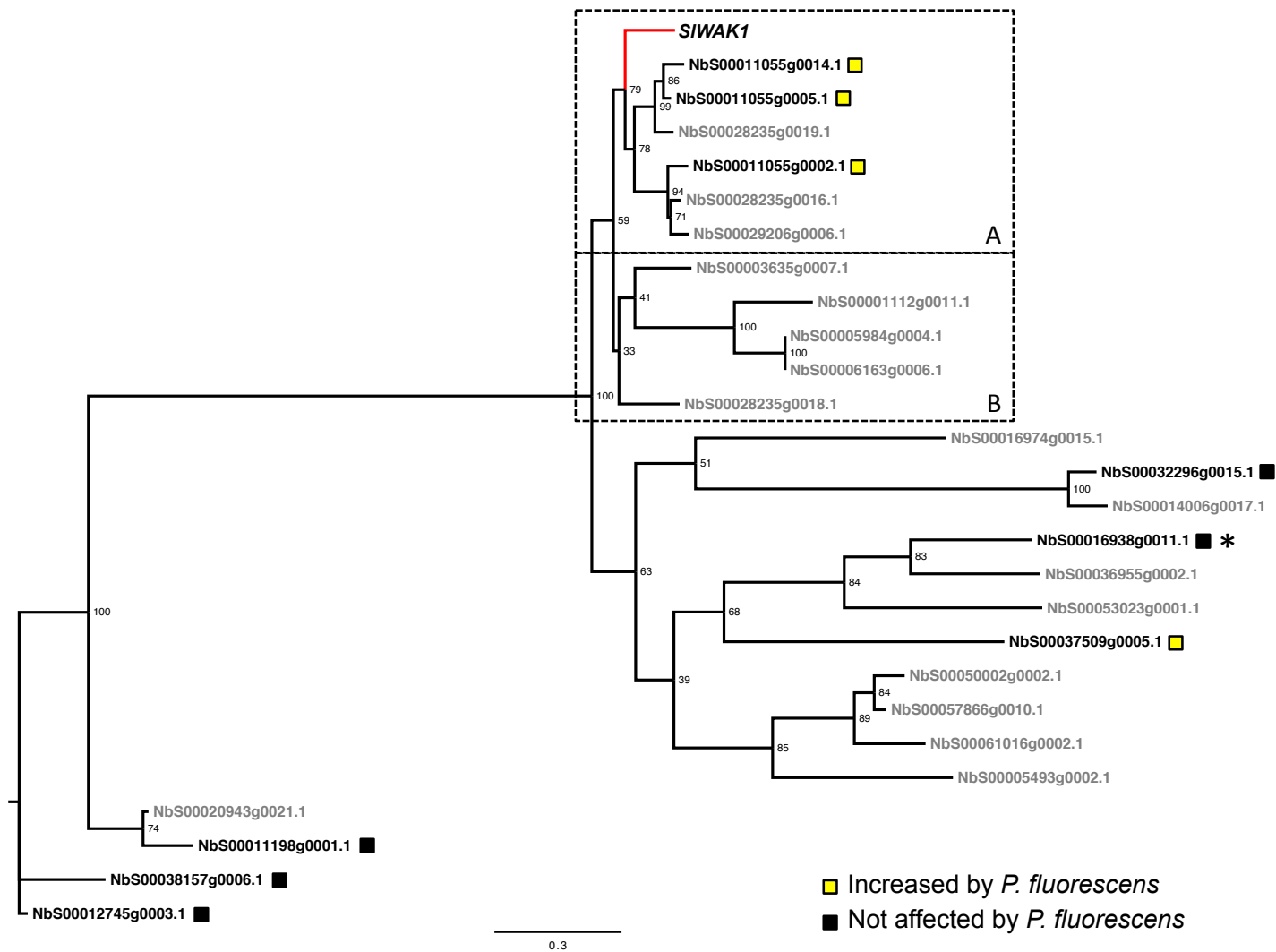




Additional file 10: Figure S5. Phylogenetic analysis of *WAK* and *WAKL* nucleotide sequences from *N. benthamiana* including *SIWAK1* for the identification of putative VIGS construct targets and off-targets. The analysis was performed with PhyML method with a bootstrap of 100 replicates using Seaview program [4]. Bold black font indicates expressed genes with ≥ 3 RPKM in either mock or *P. fluorescens* (10^8 cfu/mL) treatments. Color-coded squares represent the effect of *P. fluorescens* infiltration using ≥ 2 -fold difference and a p-value < 0.05 as cut-offs. The genes considered to be possible targets of *SIWAK1* VIGS construct are included in clusters A and B and further described in Additional file 9: Table S5. Asterisk indicates predicted VIGS non-target gene tested by qPCR (Figure 5).