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Transcriptome-based identification and validation of reference genes for plant-bacteria interaction studies using *Nicotiana benthamiana*

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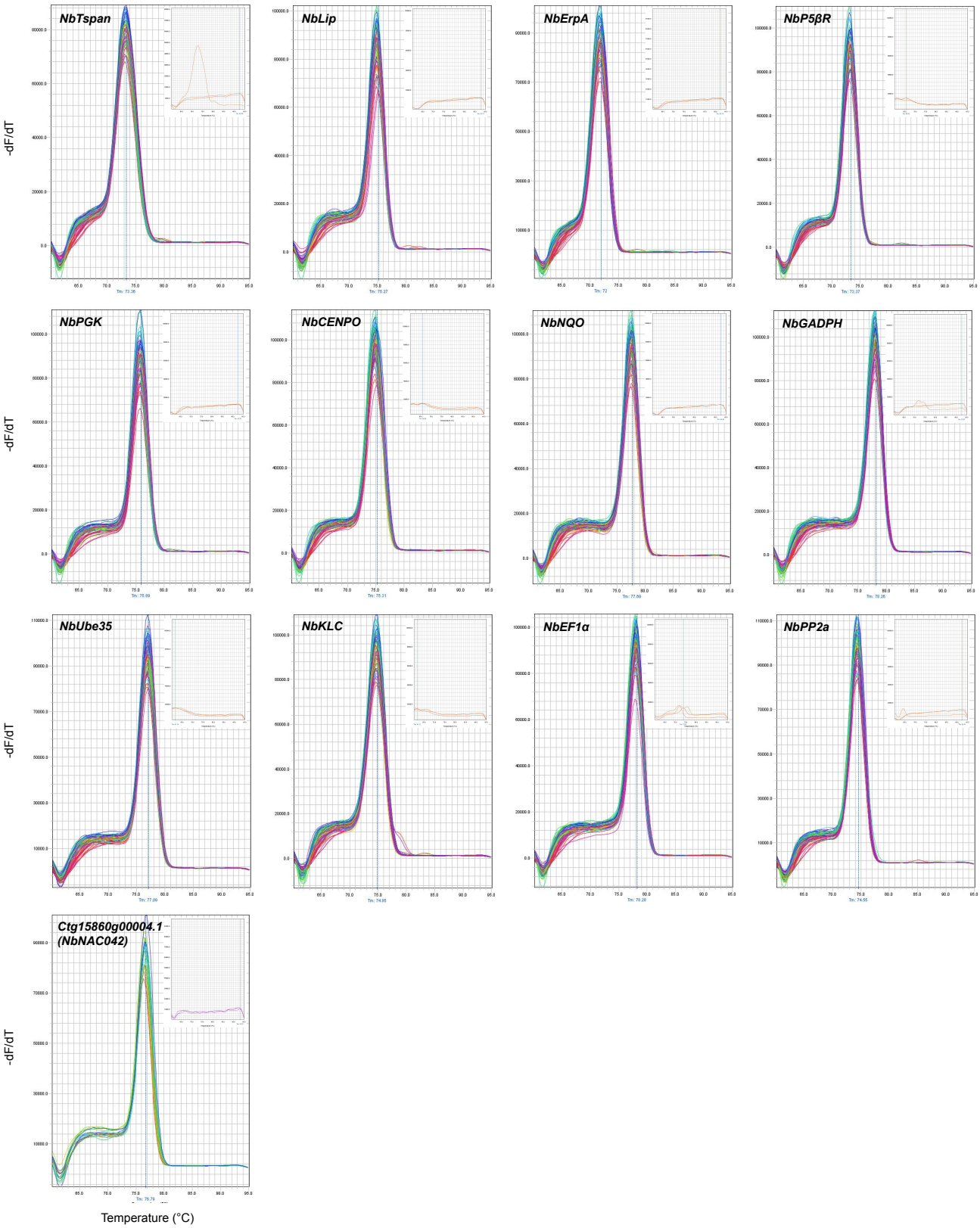
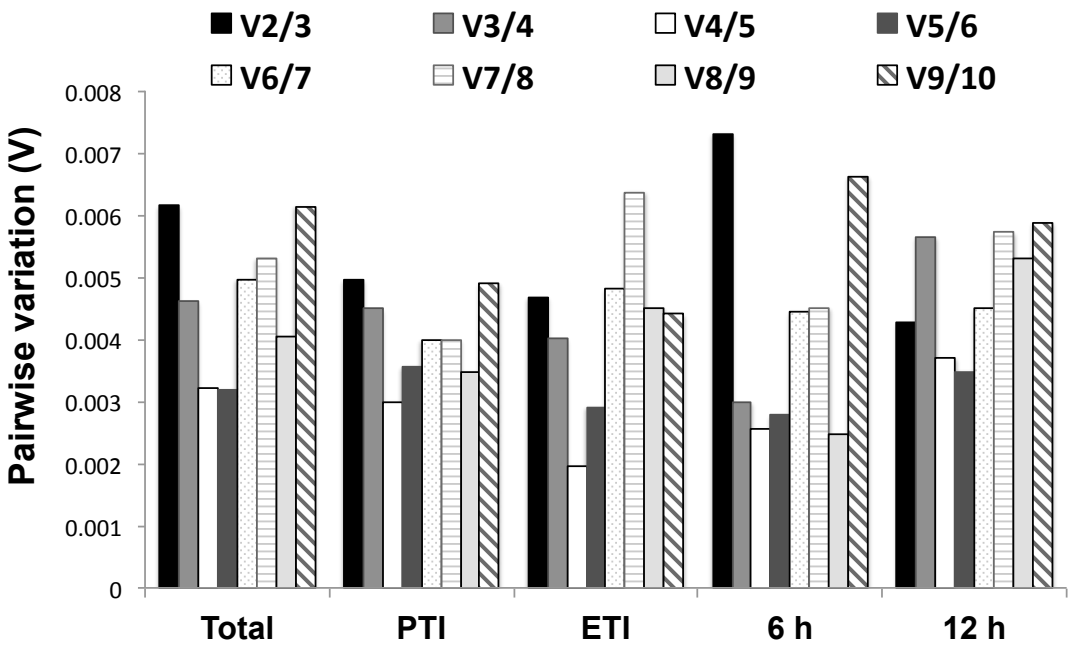


Supplementary Fig. S1: Validation of primer pairs of *N. benthamiana* candidate reference genes for RT-qPCR experiments and *NbNAC042*. PCR amplification specificity was measured by the presence of unique amplicons using melting curve analysis. Negative sample (water templates) melting curves performed for each analyzed gene are shown in a small graph in the upper right corner.



Supplementary Fig. S2: Pairwise variation (Vn/Vn+1) analysis for the determination of the optimal number of reference genes. *N. benthamiana* reference genes were included in the analysis using the final ranking order shown in Table 3. The pairwise variation was calculated considering all the samples together (Total), mock and *P. fluorescens* inoculations (PTI), *Pst* DC3000 and *Pst* DC3000 Δ*hopQ1-1* (ETI), samples taken at 6 hpi (6 h) or samples taken at 12 hpi (12 h).