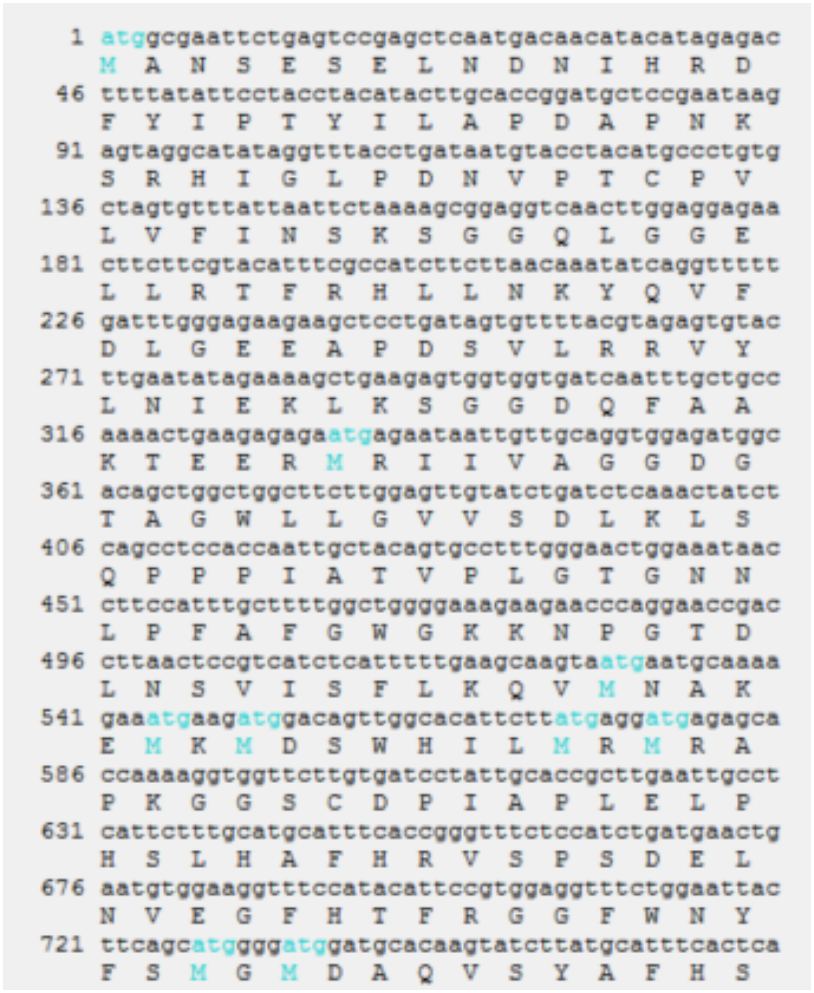
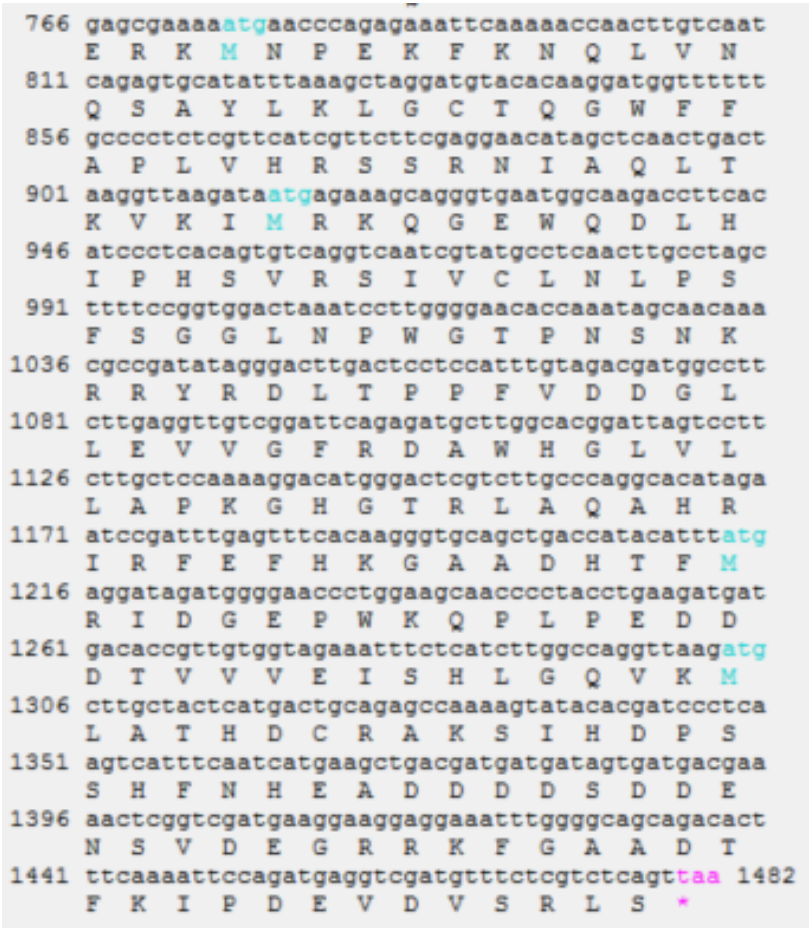
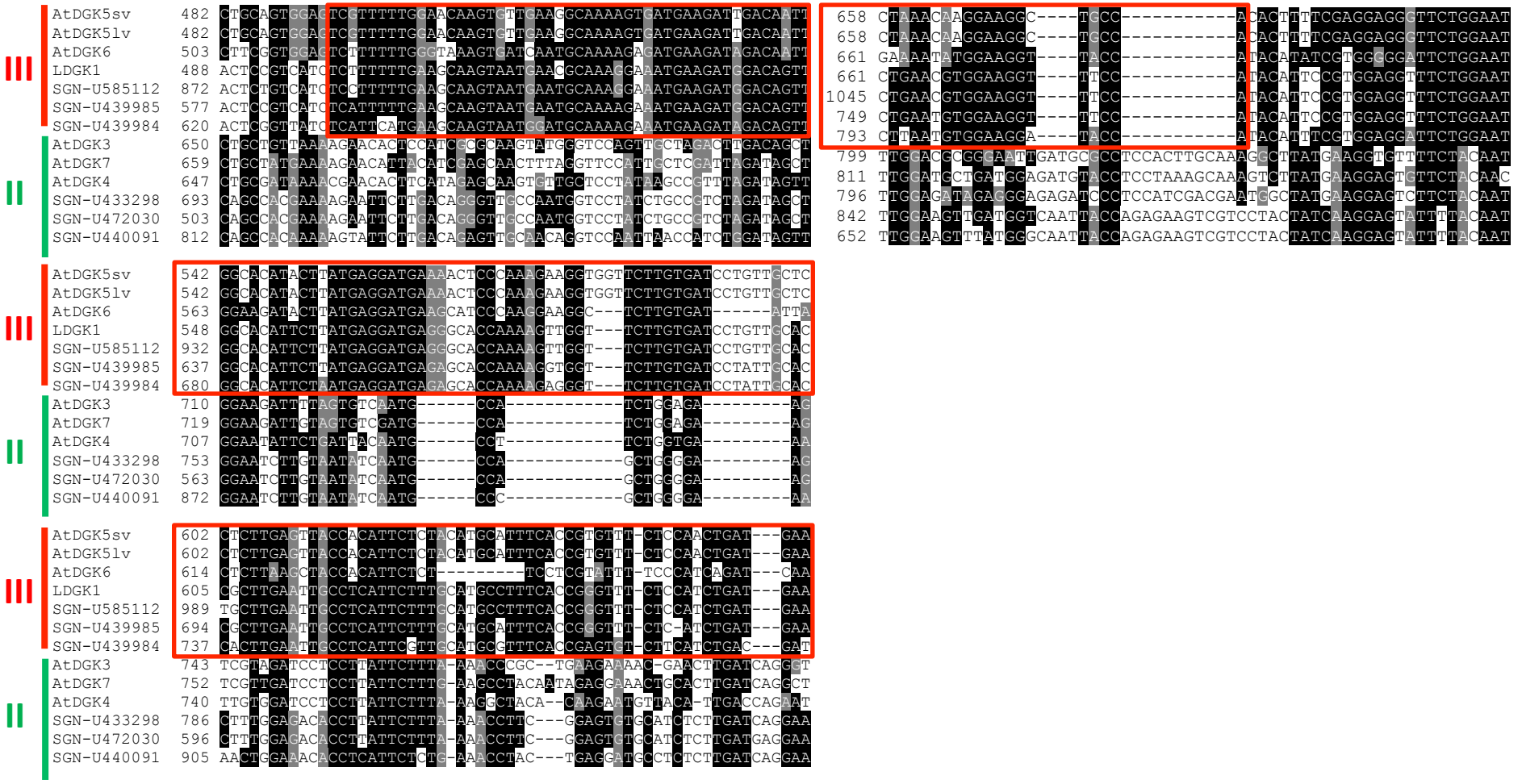
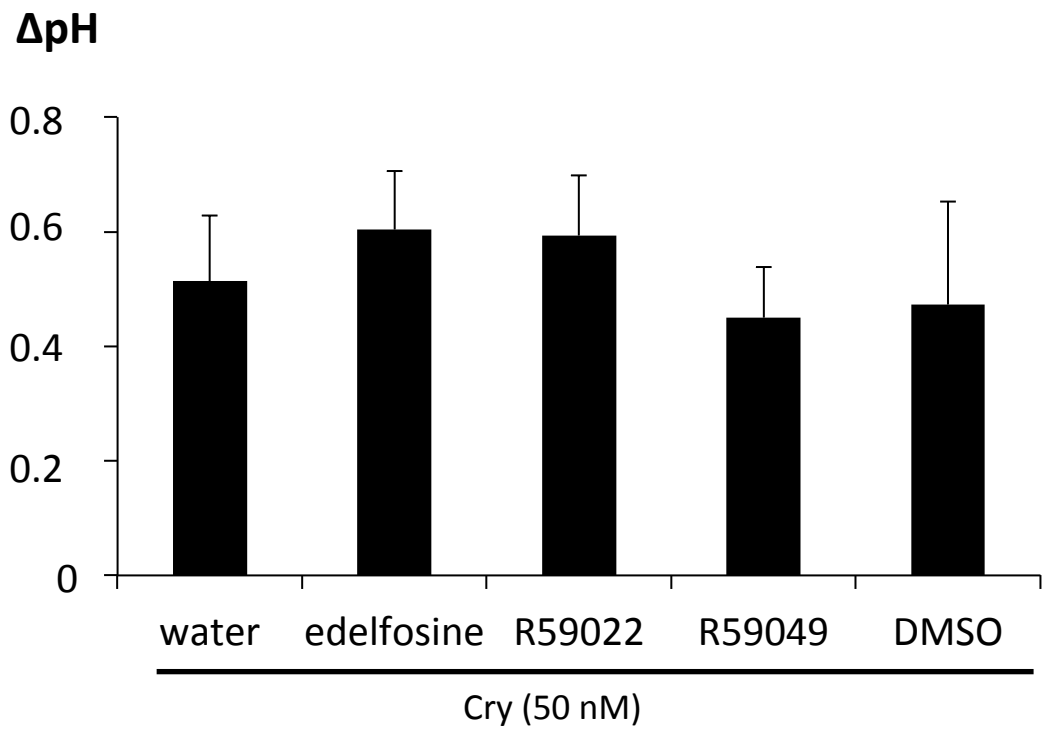




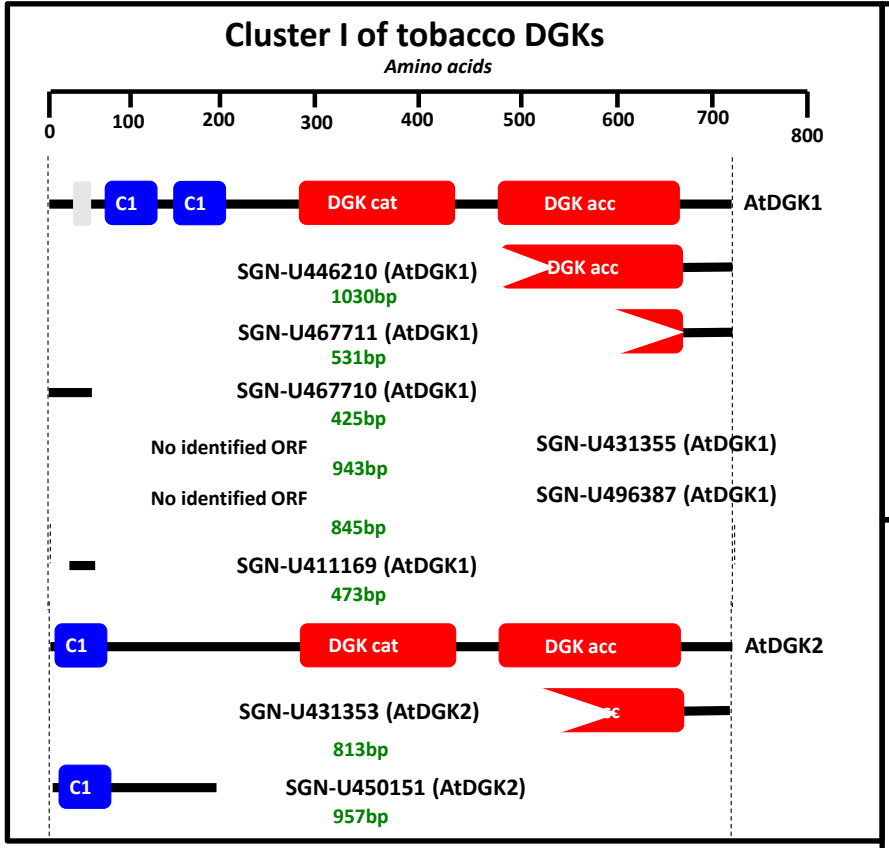
Supporting information figure S1: The translated coding sequence of the tobacco *NtDGK5* gene. The identified nucleic acid sequence was deposited in GenBank under the reference # 1902348. It codes for a 493-amino acid-long protein (55.24kDa), having a predicted pI of 6.75. *In silico* translation was performed using the freeware ORF Finder available at the NCBI website (http://www.ncbi.nlm.nih.gov/gorf/gorf.html).

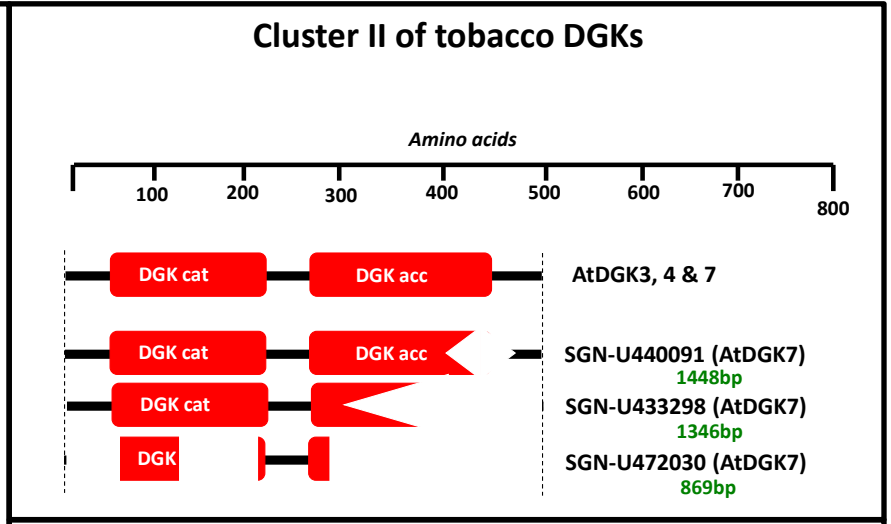


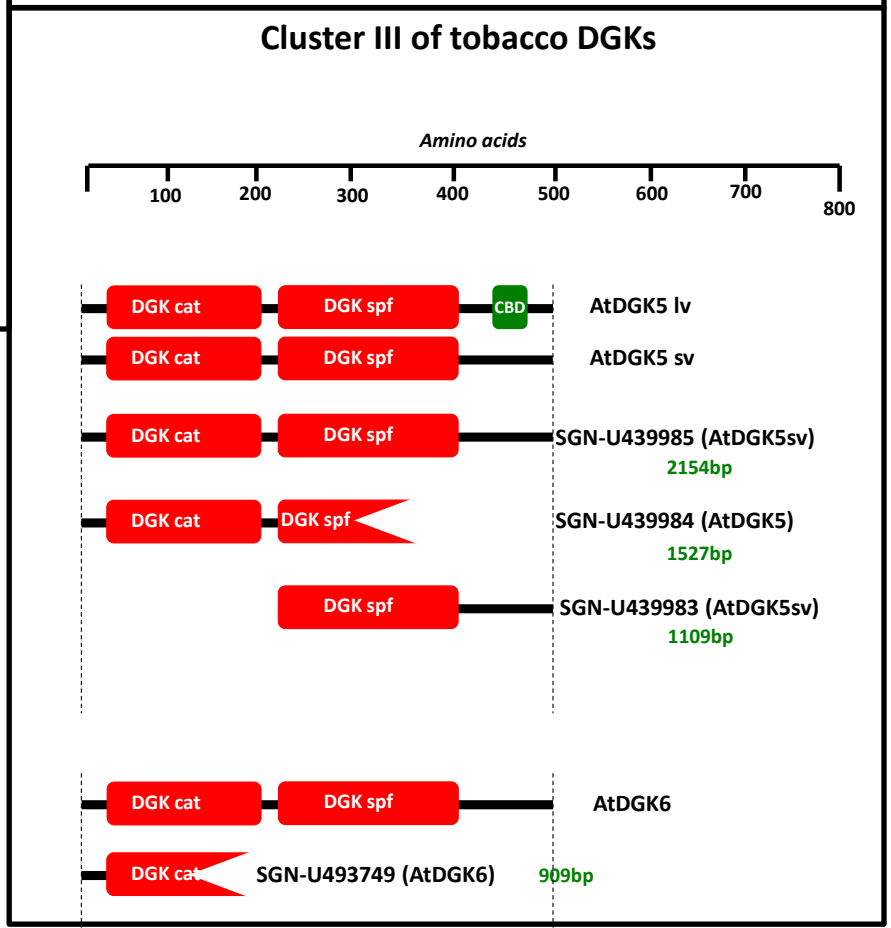
Supporting information figure S2: Partial alignment of plant DGK coding sequences from clusters II and III. This figure shows the nucleic acid coding region used for miRNA design (squared in red), which is highly conserved among cluster III members and divergent with cluster II counterparts. Full-length nucleic acid sequences were aligned using version 2.0.10 of Clustal X (Larkin et al. 2007) and the resulting alignment was processed online at the BoxShade server (http://www.ch.embnet.org/software/BOX_form.html). Roman numbers (II and III) on the right of the alignment indicate DGK cluster.



Supporting information figure S3: Effects of inhibitors on the alkalization triggered by cryptogein. Cells were preincubated 15 min with inhibitors (or DMSO, solvent of the inhibitors) before cryptogein (50 nM) elicitation. Final concentrations of edelfosine, R59022 and R59949 were 25 µM, 75 µM and 75 µM, respectively. R59949 is another DGK inhibitor. Extracellular pH alkalinization was measured and reported as the difference between initial and final (1 hour of cryptogein treatment) pH values. Means +/- SD.







Supporting information figure S4: Topology of the sixteen identified tobacco DGK proteins. Protein structure is depicted for the 3 phylogenetic clusters. DGK nucleic acid sequences were retrieved from the *Solanacea Genomics Network* (SGN) database (https://solgenomics.net/) using the BLAST algorithm and keyword search tool. Known Arabidopsis, rice and tomato DGKs were used as nucleic acid sequence queries. Upon *in silico* translation using ORF Finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html), the resulting polypeptides were compared to their Arabidopsis counterparts and the Conserved Domain Architecture Retrieval Tool (CDART, (Geer et al. 2002)) was used to predict domain location. Within a panel (corresponding to one protein cluster), the closest Arabidopsis relative is followed by orthologous tobacco translated sequences. The latter are referenced by their SGN numbers and the identified part of the protein is presented. The length of the corresponding contigs is also indicated in green. Abbreviations: AtDGK5lv, AtDGK5 long splice variant; AtDGK5sv, AtDGK5 short splice variant; C1, DAG binding domain; CBD, calmodulin-binding domain; DGKcat, DGK catalytic domain; DGKacc, DGK accessory domain. The grey rectangle localized to the N-terminal part of AtDGK1 represents a transmembrane domain.

Supporting information figure S5: Identification of the PA binding domain of NtRBOHD by alignment with the cognate domain of Arabidopsis isoform D. Full length primary amino-acid sequences of RBOHD from *Arabidopsis thaliana* (SwissProt:Q9FIJ0.1) and *Nicotiana tabacum* (GenBank:ABN58915) were aligned using version 2.0.10 of Clustal X (Larkin et al. 2007) and the resulting alignment was then processed online at the BoxShade server (http://www.ch.embnet.org/software/BOX_form.html). Stars indicate the two basic amino-acid residues experimentally proven to be critical for interaction with PA (Zhang *et al.* 2009). Note the conservation of these residues between the two proteins.