Table S1: Primers for *RabE* cloning and mutagenesis

Primer	Sequence
rabE-5'	5'-GAATTC**ATG**GCGGTTGCGCCGGCAAG-3'
rabE-3'	5'-GGATCCGAGCAATCATACTC**CTA**AAC-3'
Q74L-for	5'-CACTGCTGGTC**T**AGAACGTTTC-3'
Q74L-rev	5'-GAAACGTTCT**A**GACCAGCAGTG-3'
S29N-for	5'-GTGGGGAAGA**A**TTGTTTGTTAC-3'
S29N-rev	5'-GTAACAAACAA**T**TCTTCCCCAC-3'

Restriction sites are underlined (*Eco*RI for rabE-5', *Bam*HI for rabE-3'). Start and stop codons are in bold; single nucleotide changes are in bold and underlined.

Table S2. Gene-specific primers for RT-PCR

Gene	Locus	Forward and Reverse Primers
ACT8	At1g49240	F: 5'-GCTTCATCGGCCGTTGCATTTC-3' R: 5'-GATCCCGTCATGGAAACGATGTCTC-3'
AtRabD1	At3g11730	F: 5'-CTCGGAAACGCAGTCTTCAGC-3' R: 5'-GCTTATTCAAGACACAGCGACATGG-3'
AtRabD2a	At1g02130	F: 5'-GATCTCTGGCTCTGTATCGCTCG-3' R: 5'-GGATATTGCTAGGCTGGTCACGTC-3'
AtRabD2b	At5g47200	F: 5'-CTGAATTGACTGCCGGAGATTCC-3' R: 5'-GATGATCGAAAGAGGAGTGGTGAC-3'
AtRabD2c	At4g17530	F: 5'-CATCACCGACGAAGATCACGG-3' R: 5'-GCGAATTAAGAGGAGCAGCAGC-3'
AtRabE1a	At3g53610	F: 5'-CCGACGATCTATCTTCCCCGAGTAG-3' R: 5'-GACAGGCGTCGTGGACCC-3‘
AtRabE1b	At5g59840	F: 5'-CCAACAAGGTCTCTTCTCTTCTC-3' R: 5'-CAACTTTGGAGCCTTTTGGGAC-3'
AtRabE1c	At3g46060	F: 5'-GTCGTCCGCCATAACCTTC-3' R: 5'-CACTTCACCCCCAAACTTTTTTCG-3'
AtRabE1d	At5g03520	F: 5'-GTTTCTGACGATGGCGGTTGC-3' R: 5'-CAGCAAGCTGACTTCTCGGCTG-3'
AtRabE1e	At3g09900	F: 5'-GGCTGTCTCCGGCGAGAAG-3' R: 5'-CATAGGACGATCCCTTGAATGATGC-3'

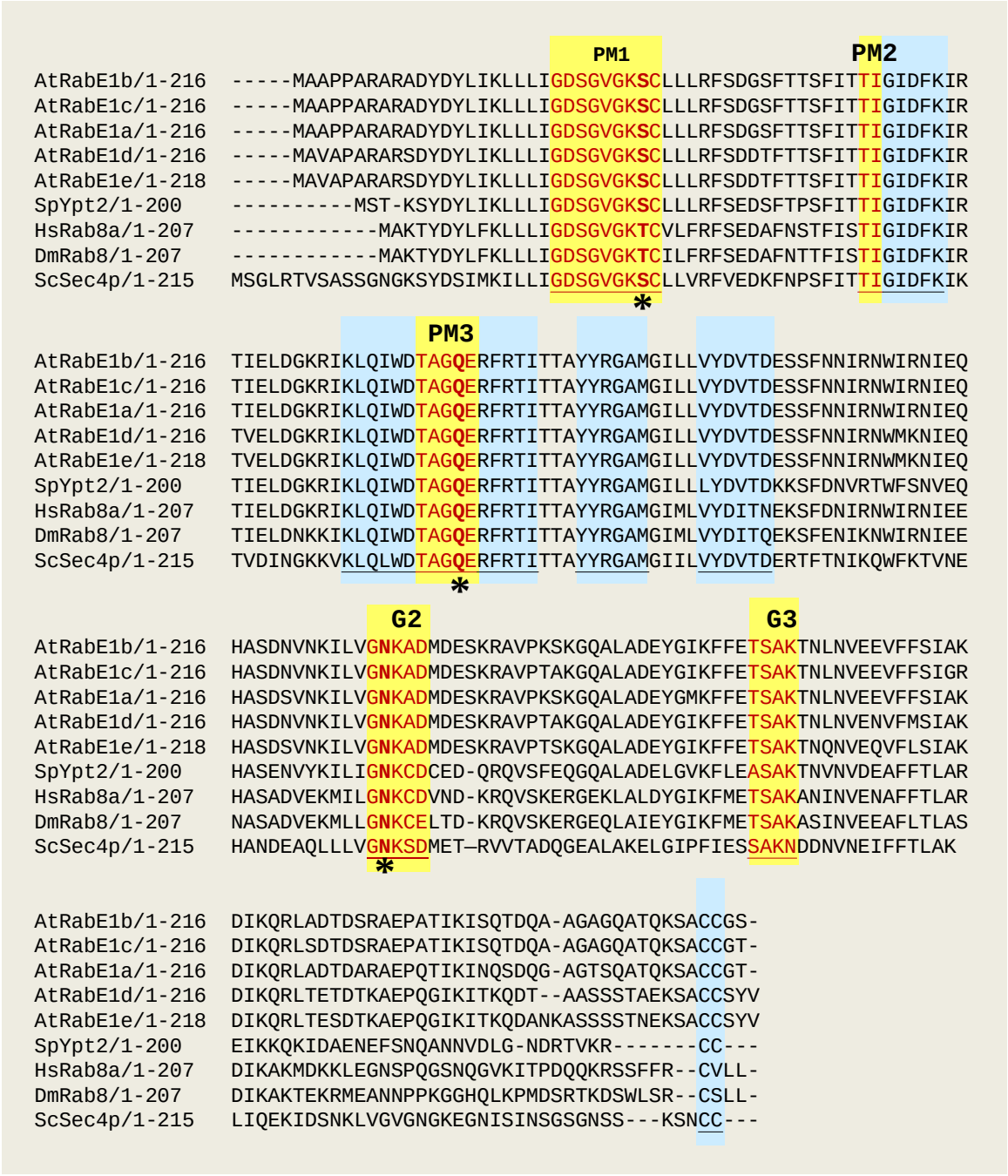

Figure S1: ClustalW alignment of the five Arabidopsis RabE proteins and their closest homologues in other organisms.
Yellow boxes highlight the highly conserved nucleotide-binding domain residues (PM = phosphate/magnesium-binding domain; G = guanine base-binding domain). Blue boxes highlight Rab-specific residues (Stenmark and Olkkonen, 2001). Mutation of the conserved amino acids marked with asterisks is used to create Rab variants that have a higher affinity for GDP than for GTP (S/T in PM1), or that cannot hydrolyze GTP (Q in PM3). Mutating the N in G2 results in Rabs that cannot bind any nucleotide. The two C residues highlighted at the carboxy-terminus represent sites of geranylgeranylation that are critical for membrane targeting.

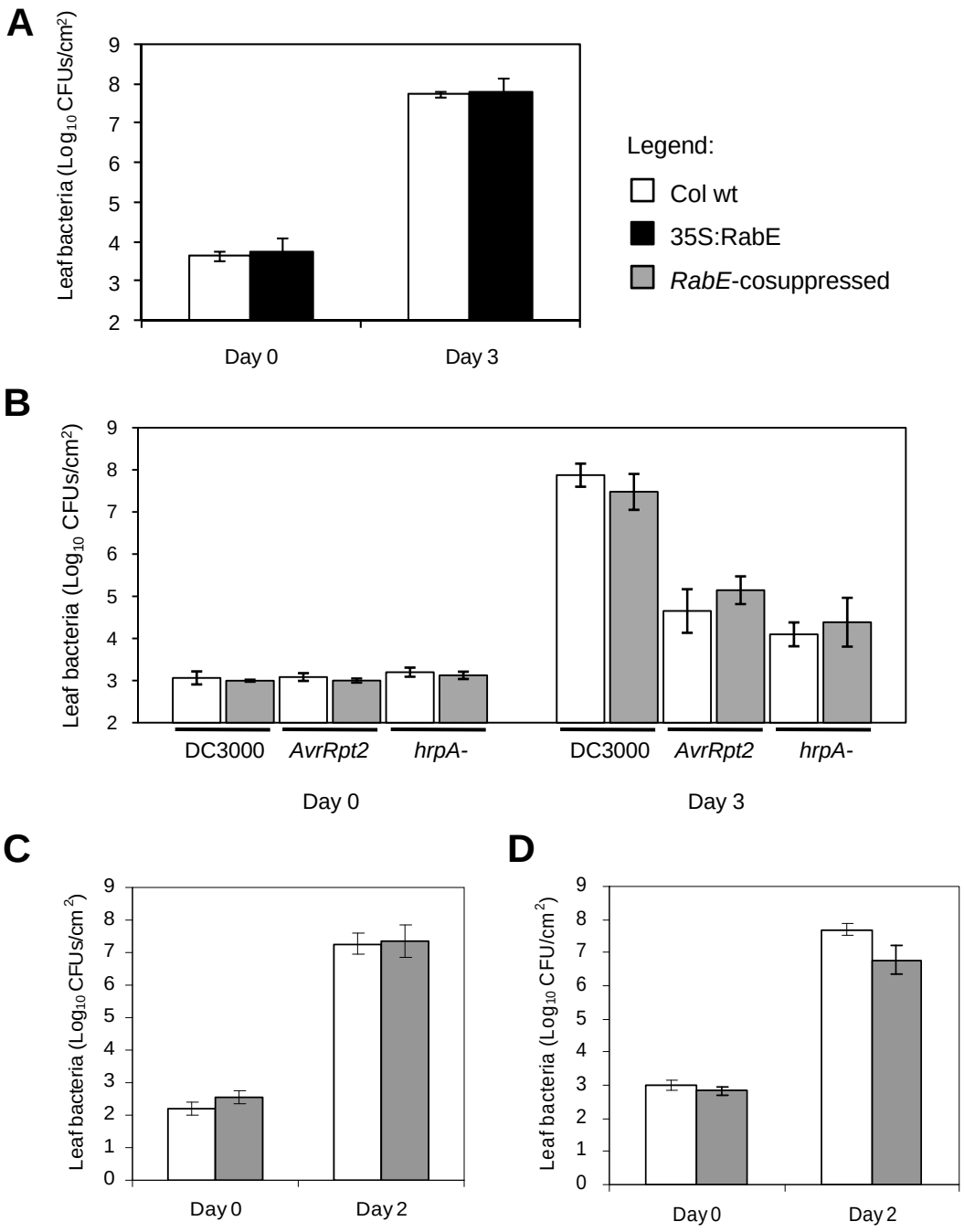

Figure S2: Bacterial multiplication assays.
A, *Pst* DC3000 multiplication in GFP-RabE1d-expressing plants (grey bars) is similar to that in wild-type Arabidopsis (white bars). *Pst* DC3000 was vacuum-infiltrated at a density of $1x10^6$ CFUs/ml.
B, Bacterial multiplication in *RabE*-cosuppressed plants (grey bars) is similar to that in wild-type Arabidopsis (white bars). Bacteria were vacuum-infiltrated at a density of $5x10^5$ CFUs/ml.
C , Young and/or non-stressed RabE-cosuppressed plants (in grey) are as susceptible to *Pst* DC3000 as wild-type (in white), whereas older RabE-cosuppressed plants show a low degree of basal resistance (D). *Pst* DC3000 was syringe-infiltrated at a density of $1x10^5$ CFUs/ml. Error bars represent standard deviation.

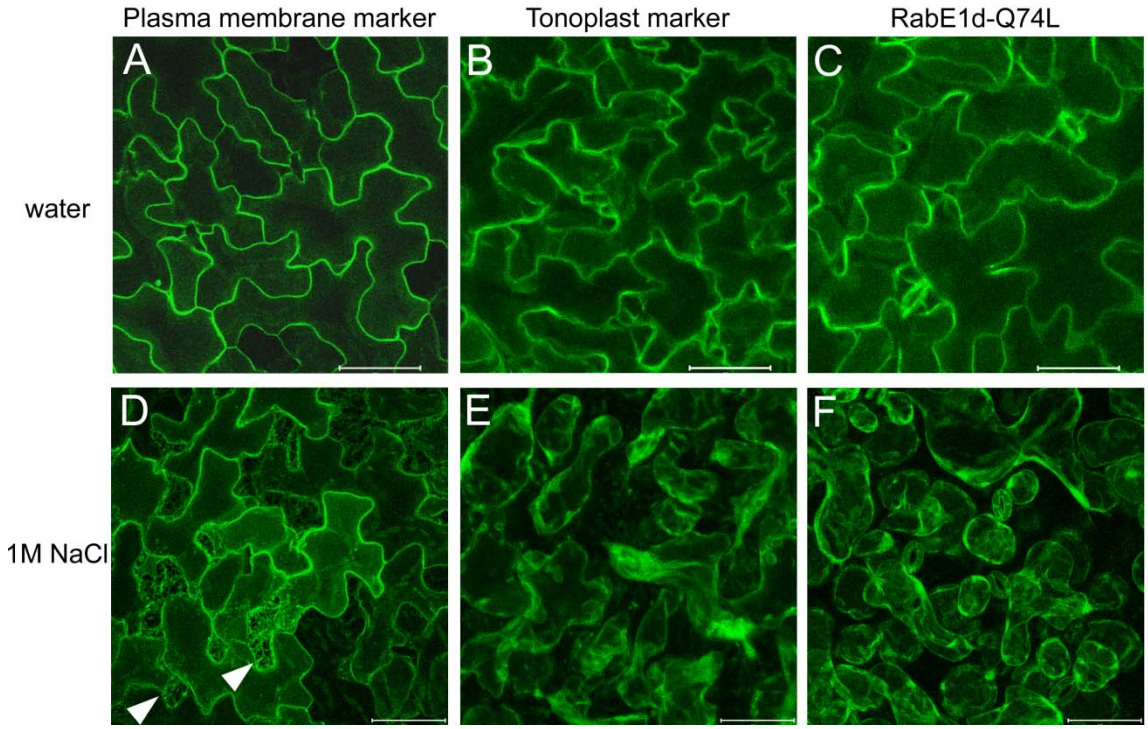

Figure S3: Localization pattern of GFP-RabE1d-Q74L compared to the localization of a PM marker protein and a tonoplast marker protein. A and D, Arabidopsis line Q8, expressing a GFP fusion to the plasma membrane integral protein PIP2A. B and E, Arabidopsis line Q5, expressing a GFP fusion to delta-TIP (Tonoplast Integral Protein), a vacuolar membrane channel protein. C and F, Arabidopsis expressing GFP-RabE1d-Q74L. D-F, samples were plasmolyzed in 1M NaCl. Arrowheads in panel D indicate Hechtian strands visible after plasmolysis in the PM marker-expressing Q8 plants. No Hechtian strands are observed in the tonoplast marker-expressing Q5 line (E) or in RabE-Q74L plants (F).

All images are Z-stacks. Scale bars = 50 μm.

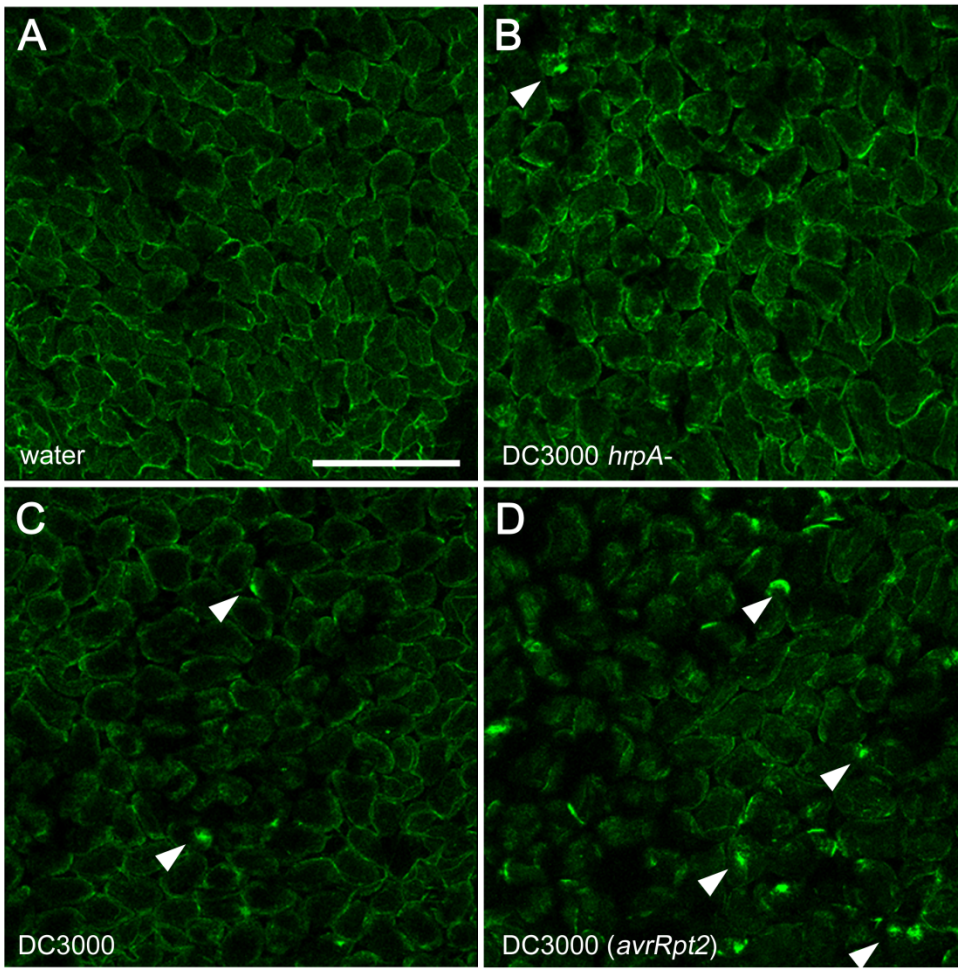

Figure S4. Focal accumulation of GFP-RabE1d in response to bacteria.
Leaves of transgenic GFP-RabE1d Arabidopsis were syringe-inoculated with various strains of *Pst* DC3000 at a density of $1x10^8$ CFUs/ml. Confocal microscope observation 6 h post inoculation revealed focal accumulation of the fluorescent GFP-RabE1d in mesophyll cells. A, no bacteria; B, *Pst* DC3000 *hrpA*$^-$ mutant bacteria, non pathogenic; C, wild-type *Pst* DC3000, virulent; D, *Pst* DC3000 (*avrRpt2*), avirulent. Arrowheads indicate some of the points of accumulation. All images are Z-stacks. Scale bar = 200 μm.