Table S1: Primers for *RabE* cloning and mutagenesis

Primer	Sequence
rabE-5'	5'- <u>GAATTC</u> ATGGCGGTTGCGCCGGCAAG-3'
rabE-3'	5'- <u>GGATCC</u> GAGCAATCATACTC CTA AAC-3'
Q74L-for	5'-CACTGCTGGTC <u>T</u> AGAACGTTTC-3'
Q74L-rev	5'-GAAACGTTCT <u>A</u> GACCAGCAGTG-3'
S29N-for	5'-GTGGGGAAGA A TTGTTTGTTAC-3'
S29N-rev	5'-GTAACAAACAA <u>T</u> 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'-CCAACAAGGTCTCTTCTCTCTC-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'

_

	PM1 PM2
AtRabE1b/1-216	MAAPPARARADYDYLIKLLLI <mark>GDSGVGKSC</mark> LLLRFSDGSFTTSFIT <mark>TI</mark> GIDFKIR
AtRabElc/1-216	MAAPPARARADYDYLIKLLLI <mark>GDSGVGKSC</mark> LLLRFSDGSFTTSFIT <mark>TI</mark> GIDFKIR
AtRabEla/1-216	MAAPPARARADYDYLIKLLLI <mark>GDSGVGKSC</mark> LLLRFSDGSFTTSFIT <mark>TI</mark> GIDFKIR
AtRabEld/1-216	MAVAPARARSDYDYLIKLLLI <mark>GDSGVGKSC</mark> LLLRFSDDTFTTSFIT <mark>TI</mark> GIDFKIR
AtRabEle/1-218	MAVAPARARSDYDYLIKLLLI <mark>GDSGVGKSC</mark> LLLRFSDDTFTTSFIT <mark>TI</mark> GIDFKIR
SpYpt2/1-200	MST-KSYDYLIKLLLI <mark>GDSGVGKSC</mark> LLLRFSEDSFTPSFIT <mark>TI</mark> GIDFKIR
HsRab8a/1-207	MAKTYDYLFKLLLI <mark>GDSGVGKTC</mark> VLFRFSEDAFNSTFIS <mark>TI</mark> GIDFKIR
DmRab8/1-207	MAKTYDYLFKLLLI <mark>GDSGVGKTC</mark> ILFRFSEDAFNTTFIS <mark>TI</mark> GIDFKIR
ScSec4p/1-215	MSGLRTVSASSGNGKSYDSIMKILLIGDSGVGKSCLLVRFVEDKFNPSFITTIGIDFKIK
	PM3
AtRabE1b/1-216	TIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQ
AtRabElc/1-216	TIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQ
AtRabEla/1-216	TIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQ
AtRabEld/1-216	TVELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLVYDVTDESSFNNIRNWMKNIEQ
AtRabEle/1-218	TVELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLVYDVTDESSFNNIRNWMKNIEQ
SpYpt2/1-200	TIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLLYDVTDKKSFDNVRTWFSNVEQ
HsRab8a/1-207	TIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEE
DmRab8/1-207	TIELDNKKIKLQIWDTAGQERFRTITTAYYRGAMGIMLVYDITQEKSFENIKNWIRNIEE
ScSec4p/1-215	TVDINGKKV <u>KLQLWDTAGQERFRTI</u> TTA <u>YYRGAM</u> GIIL <u>VYDVTD</u> ERTFTNIKQWFKTVNE
	*
	G2 G3
AtRabE1b/1-216	HASDNVNKILVG <mark>NKAD</mark> MDESKRAVPKSKGQALADEYGIKFFE <mark>TSAK</mark> TNLNVEEVFFSIAK
AtRabElc/1-216	HASDNVNKILVGNKADMDESKRAVPTAKGOALADEYGIKFFE <mark>TSAK</mark> TNLNVEEVFFSIGR
N D 1 D1 (1 01C	······································
AtRabela/1-216	HASDSVNKILV <mark>GNKAD</mark> MDESKRAVPKSKGQALADEYGMKFFE <mark>TSAK</mark> TNLNVEEVFFSIAK
AtRabEla/1-216 AtRabEld/1-216	HASDSVNKILVG <mark>N</mark> KADMDESKRAVPKSKGQALADEYGMKFFE <mark>TSAK</mark> TNLNVEEVFFSIAK HASDNVNKILVG <mark>N</mark> KADMDESKRAVPTAKGQALADEYGIKFFE <mark>TSAK</mark> TNLNVENVFMSIAK
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218	HASDSVNKILV <mark>GN</mark> KADMDESKRAVPKSKGQALADEYGMKFFE <mark>TSAK</mark> TNLNVEEVFFSIAK HASDNVNKILVG <mark>NKAD</mark> MDESKRAVPTAKGQALADEYGIKFFE <mark>TSAK</mark> TNLNVENVFMSIAK HASDSVNKILV <mark>GN</mark> KADMDESKRAVPTSKGQALADEYGIKFFE <mark>TSAK</mark> TNQNVEQVFLSIAK
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200	HASDSVNKILV <mark>GN</mark> KADMDESKRAVPKSKGQALADEYGMKFFE <mark>TSAK</mark> TNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFE <mark>TSAK</mark> TNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFE <mark>TSAK</mark> TNQNVEQVFLSIAK HASENVYKILIG <mark>NKCD</mark> CED-QRQVSFEQGQALADELGVKFLE <mark>ASAK</mark> TNVNVDEAFFTLAR
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207	HASDSVNKILV <mark>GN</mark> KADMDESKRAVPKSKGQALADEYGMKFFE <mark>TSAK</mark> TNLNVEEVFFSIAK HASDNVNKILV <mark>GN</mark> KADMDESKRAVPTAKGQALADEYGIKFFE <mark>TSAK</mark> TNLNVENVFMSIAK HASDSVNKILV <mark>GN</mark> KADMDESKRAVPTSKGQALADEYGIKFFE <mark>TSAK</mark> TNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207	HASDSVNKILV <mark>GN</mark> KADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtRabElb/1-216	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNUNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtRabElb/1-216 AtRabElc/1-216	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNUNVEQVFLSIAK HASDSVNKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK
AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtrabElb/1-216 AtrabElc/1-216 AtrabEla/1-216	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNUNVEQVFLSIAK HASDSVNKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMILGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK
AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtrabElb/1-216 AtrabElc/1-216 AtrabEla/1-216 AtrabEld/1-216	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILUGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMILGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK DIKQRLADTDSRAEPATIKISQTDQA-AGAGQATQKSACCGS- DIKQRLSDTDSRAEPATIKISQTDQA-AGAGQATQKSACCGT- DIKQRLADTDARAEPQTIKINQSDQG-AGTSQATQKSACCGT- DIKQRLADTDARAEPQTIKINQSDQG-AGTSQATQKSACCGT- DIKORLTETDTKAEPOGIKITKODTAASSSTAEKSACCSYV
AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtrabElb/1-216 AtrabElc/1-216 AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMILGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK DIKQRLADTDSRAEPATIKISQTDQA-AGAGQATQKSACCGS- DIKQRLSDTDSRAEPATIKISQTDQA-AGAGQATQKSACCGT- DIKQRLADTDARAEPQTIKINQSDQG-AGTSQATQKSACCGT- DIKQRLTETDTKAEPQGIKITKQDT-AASSSTAEKSACCSYV DIKORLTESDTKAEPOGIKITKODANKASSSSTNEKSACCSYV
AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtrabElb/1-216 AtrabElc/1-216 AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK DIKQRLADTDSRAEPATIKISQTDQA-AGAGQATQKSACCGS- DIKQRLADTDSRAEPATIKISQTDQA-AGAGQATQKSACCGT- DIKQRLADTDARAEPQTIKINQSDQG-AGTSQATQKSACCGT- DIKQRLTETDTKAEPQGIKITKQDT-AASSSTAEKSACCSYV DIKQRLTESDTKAEPQGIKITKQDANKASSSSTNEKSACCSYV EIKKQKIDAENEFSNQANNVDLG-NDRTVKRCC
AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtrabElb/1-216 AtrabElc/1-216 AtrabEla/1-216 AtrabEld/1-216 AtrabEle/1-218 SpYpt2/1-200 HsRab8a/1-207	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASENVYKILIGNKCDCD-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMILGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK DIKQRLADTDSRAEPATIKISQTDQA-AGAGQATQKSACCGS- DIKQRLSDTDSRAEPATIKISQTDQA-AGAGQATQKSACCGT- DIKQRLADTDARAEPQTIKINQSDQG-AGTSQATQKSACCGT- DIKQRLTETDTKAEPQGIKITKQDT-AASSSTAEKSACCSYV DIKQRLTESDTKAEPQGIKITKQDANKASSSSTNEKSACCSYV EIKKQKIDAENEFSNQANNVDLG-NDRTVKRCC DIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFFRCVLL-
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtRabElb/1-216 AtRabEla/1-216 AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCD-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK DIKQRLADTDSRAEPATIKISQTDQA-AGAGQATQKSACCGS- DIKQRLSDTDSRAEPATIKISQTDQA-AGAGQATQKSACCGT- DIKQRLADTDARAEPQTIKINQSDQG-AGTSQATQKSACCGT- DIKQRLTETDTKAEPQGIKITKQDT-ASSSTAEKSACCSYV DIKQRLTESDTKAEPQGIKITKQDANKASSSSTNEKSACCSYV EIKKQKIDAENEFSNQANNVDLG-NDRTVKRCC DIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFFRCVLL- DIKAKTEKRMEANNPPKGGHQLKPMDSRTKDSWLSRCSLL-
AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215 AtRabElb/1-216 AtRabElc/1-216 AtRabEla/1-216 AtRabEld/1-216 AtRabEle/1-218 SpYpt2/1-200 HsRab8a/1-207 DmRab8/1-207 ScSec4p/1-215	HASDSVNKILVGNKADMDESKRAVPKSKGQALADEYGMKFFETSAKTNLNVEEVFFSIAK HASDNVNKILVGNKADMDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNLNVENVFMSIAK HASDSVNKILVGNKADMDESKRAVPTSKGQALADEYGIKFFETSAKTNQNVEQVFLSIAK HASENVYKILIGNKCDCED-QRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLAR HASADVEKMILGNKCDVND-KRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLAR NASADVEKMLLGNKCELTD-KRQVSKERGEQLAIEYGIKFMETSAKASINVEEAFLTLAS HANDEAQLLLVGNKSDMET-RVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAK

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.





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 1x10⁶ 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 5×10^5 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 1×10^5 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 = $50 \mu m$.



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 1×10^8 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.