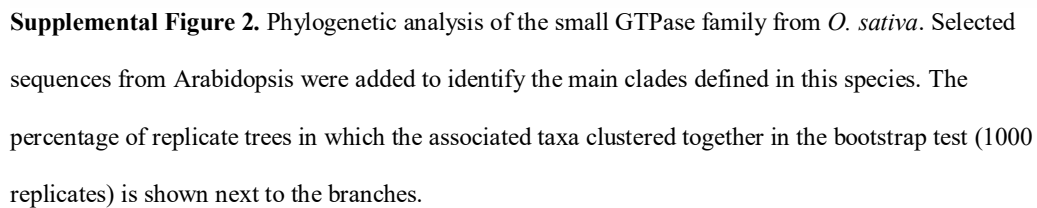
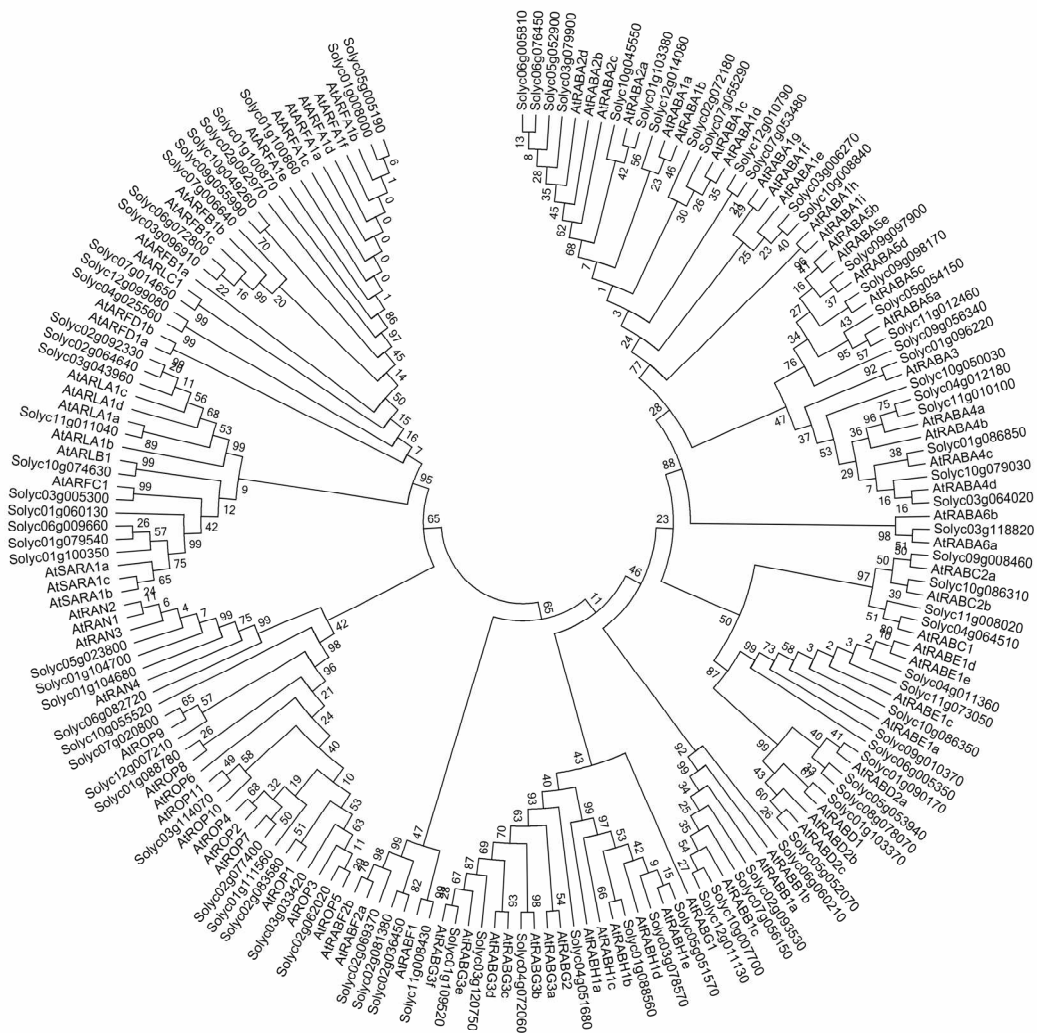


Supplemental Figure 1. Phylogenetic analysis of the small GTPase family from *A. thaliana*. The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. Circular dots indicate reduced (blue) or increased (red) levels of mRNA in aerial tissue compared with the root.

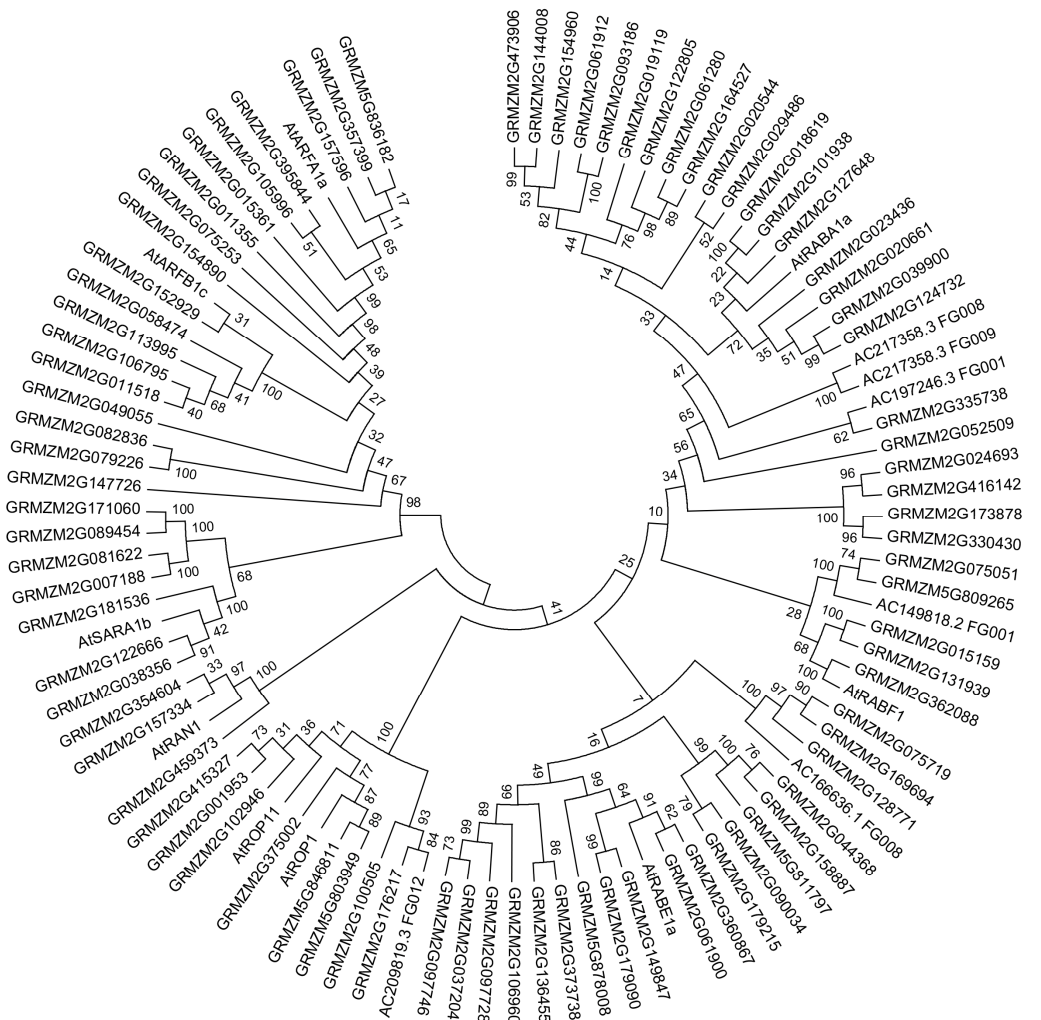


Supplemental Figure 2. Phylogenetic analysis of the small GTPase family from *O. sativa*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

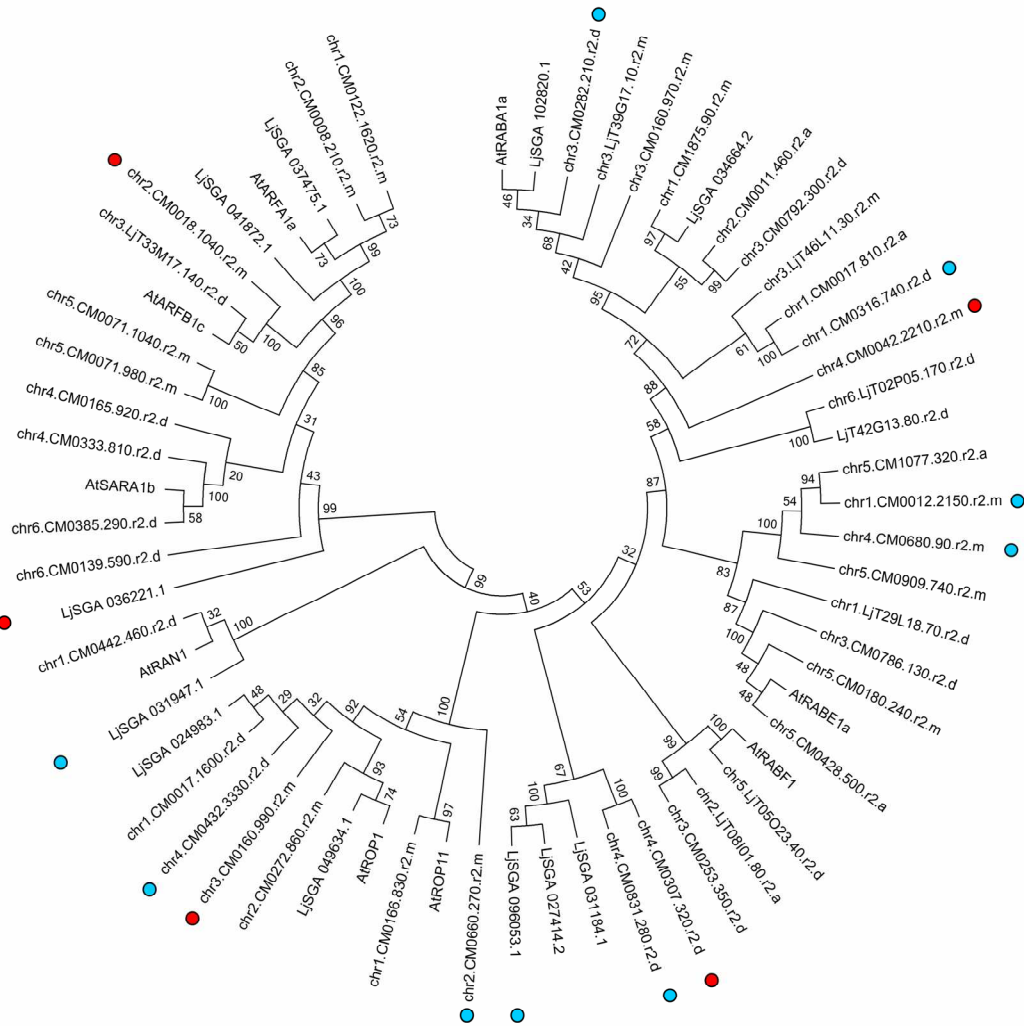


Supplemental Figure 3. Phylogenetic analysis of the small GTPase family from *S. lycopersicum*.

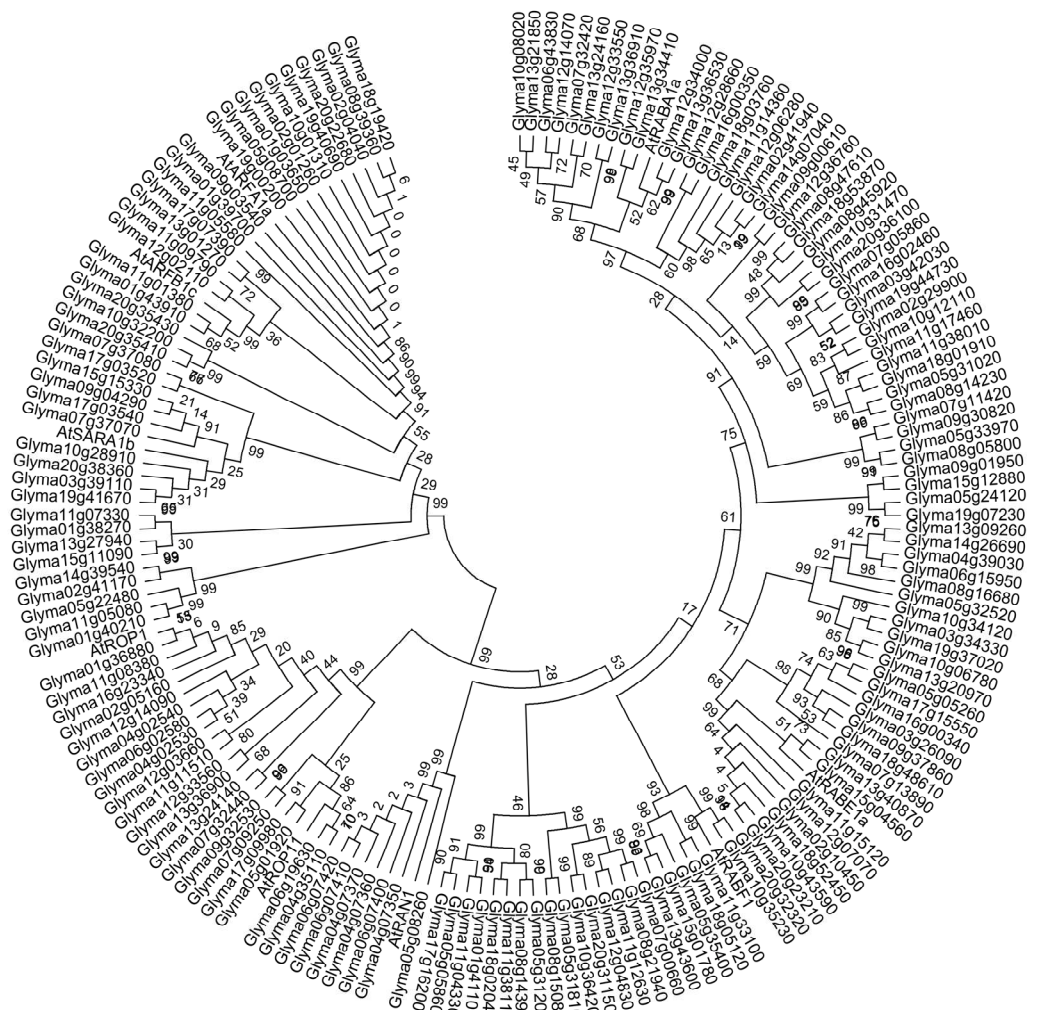
Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



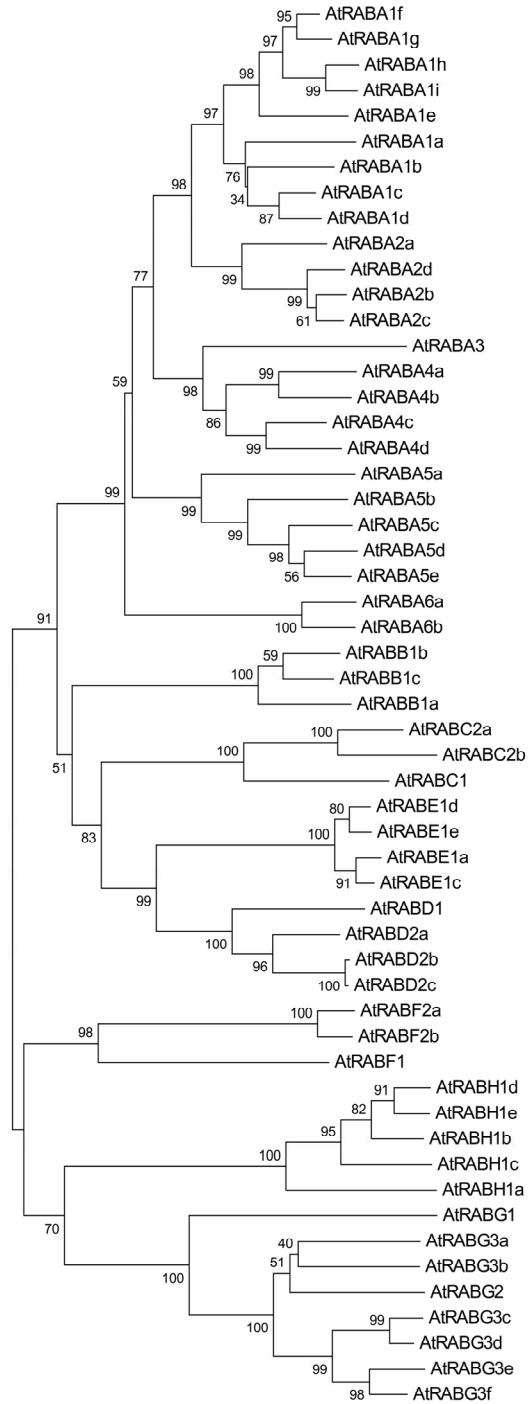
Supplemental Figure 4. Phylogenetic analysis of the small GTPase family from *Z. mays*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



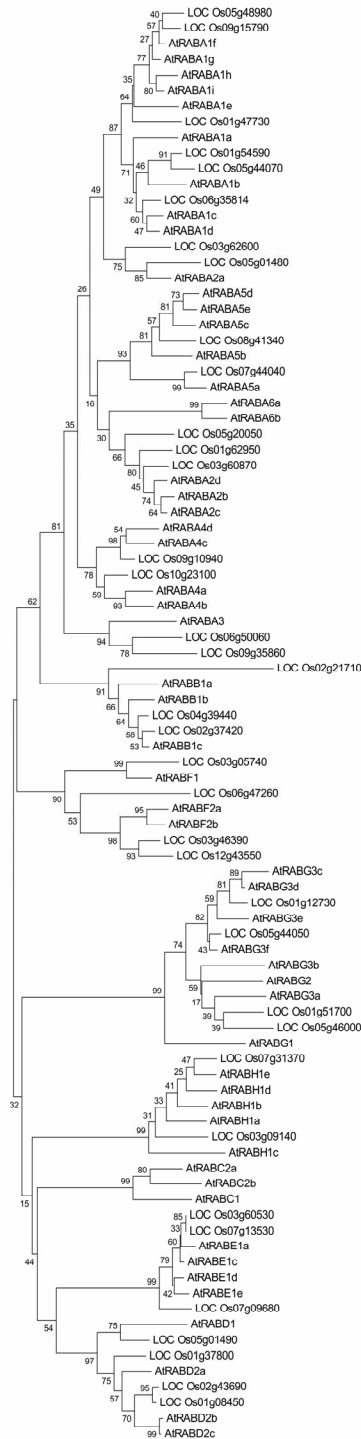
Supplemental Figure 5. Phylogenetic analysis of the small GTPase family from *L. japonicus*. Selected sequences from *Arabidopsis* were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. Circular dots indicate reduced (blue) or increased (red) levels of mRNA in nodule tissue compared with the root.



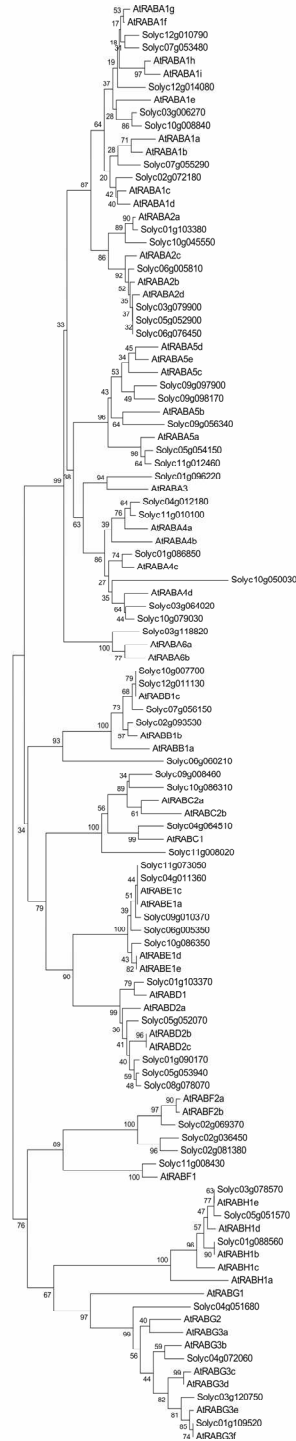
Supplemental Figure 8. Phylogenetic analysis of the small GTPase family from *G. max*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



Supplemental Figure 9. Phylogenetic analysis of the Rab small GTPase family from *A. thaliana*. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

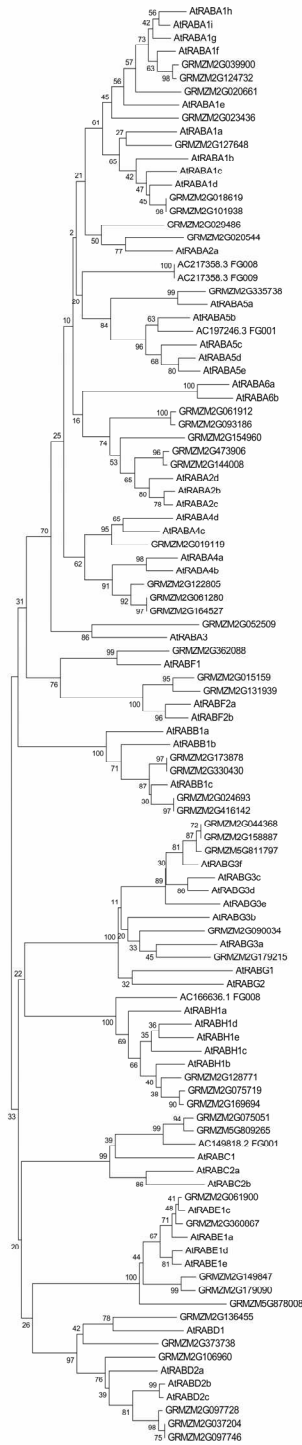


Supplemental Figure 10. Phylogenetic analysis of the Rab small GTPase family from *O. sativa*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

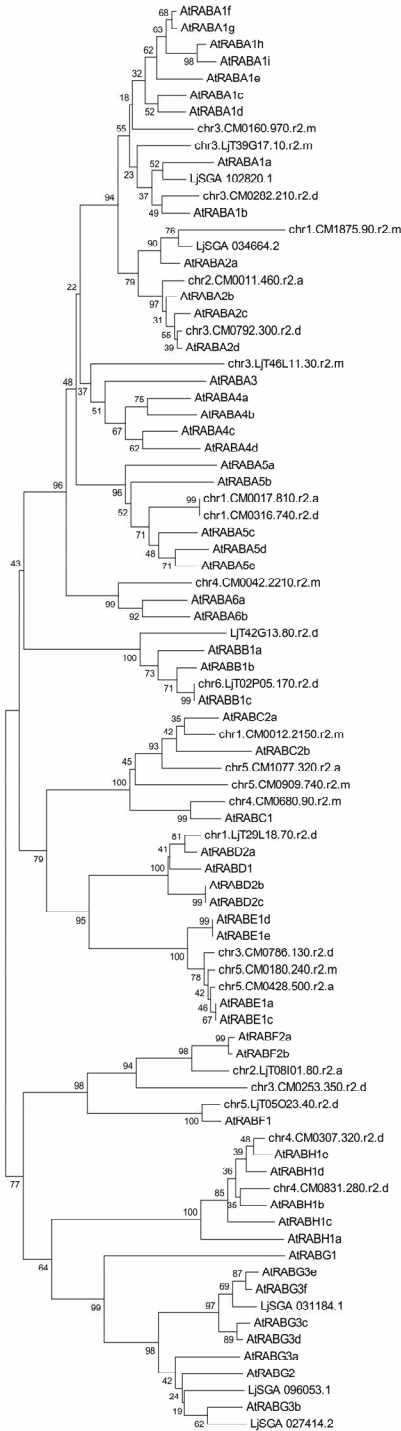


Supplemental Figure 11. Phylogenetic analysis of the Rab small GTPase family from *S. lycopersicum*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

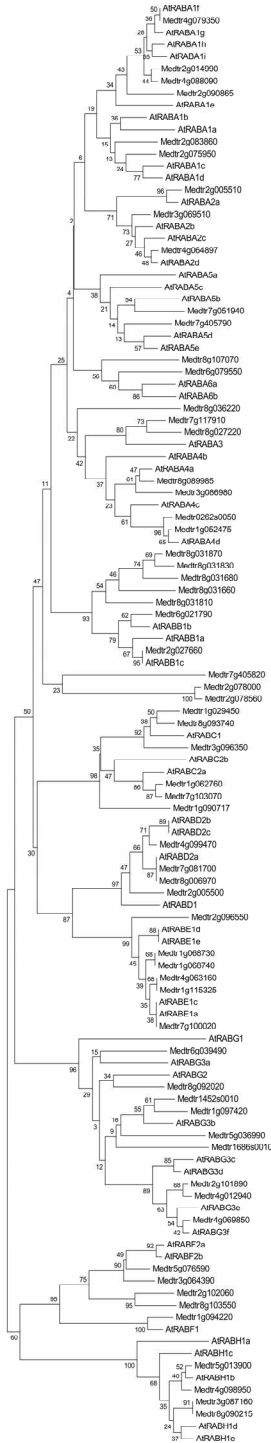


Supplemental Figure 12. Phylogenetic analysis of the Rab small GTPase family from *Z. mays*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



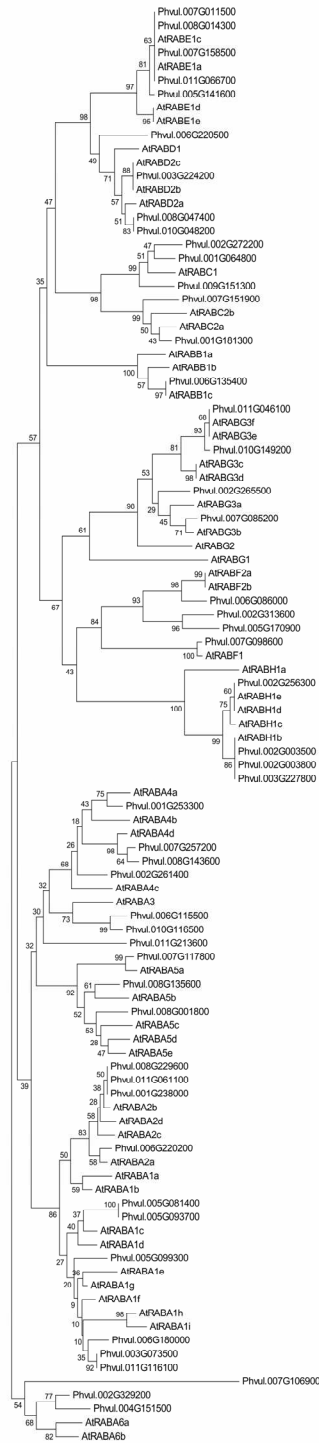
Supplemental Figure 13. Phylogenetic analysis of the Rab small GTPase family from *L. japonicus*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



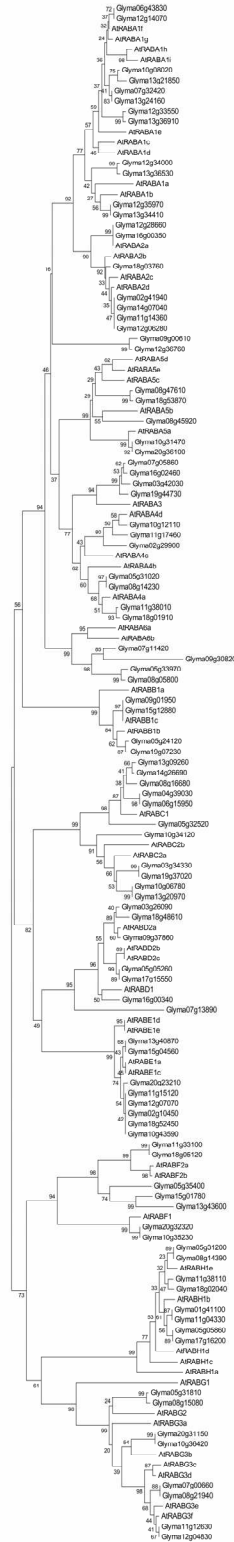
Supplemental Figure 14. Phylogenetic analysis of the Rab small GTPase family from *M. truncatula*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



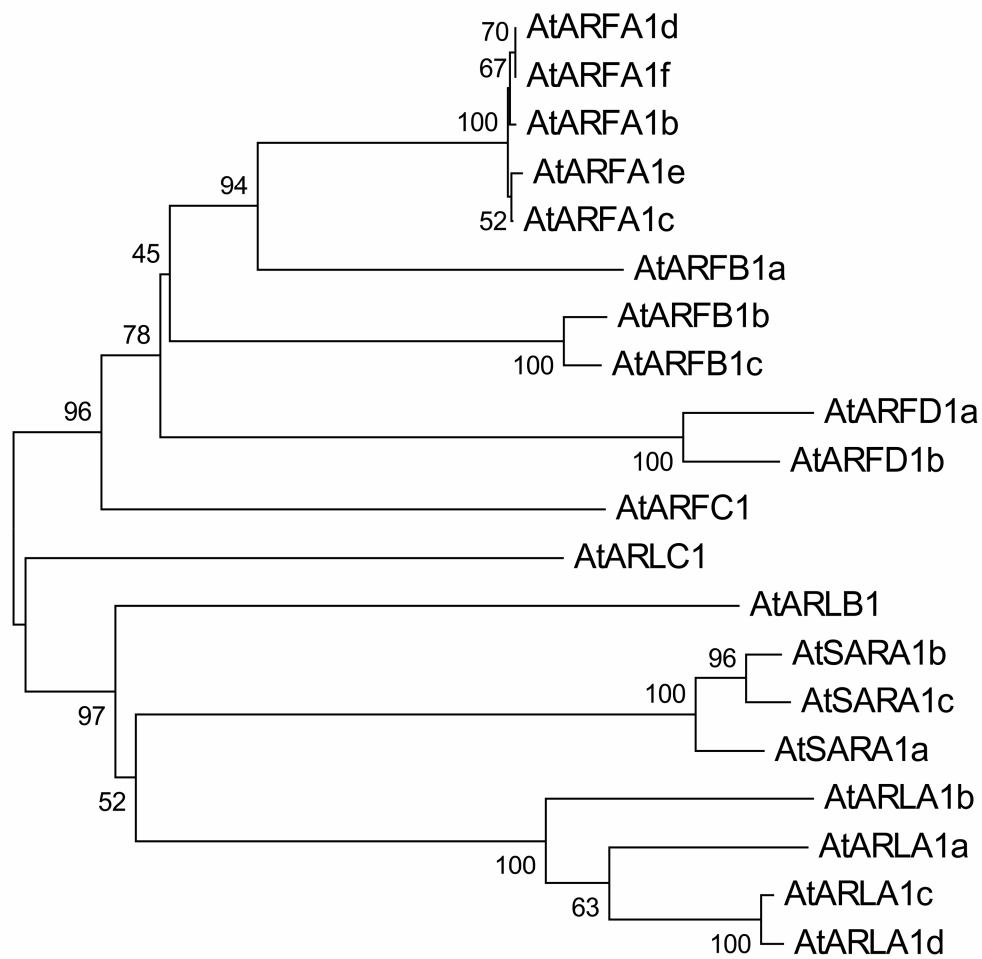
Supplemental Figure 15. Phylogenetic analysis of the Rab small GTPase family from *P. vulgaris*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

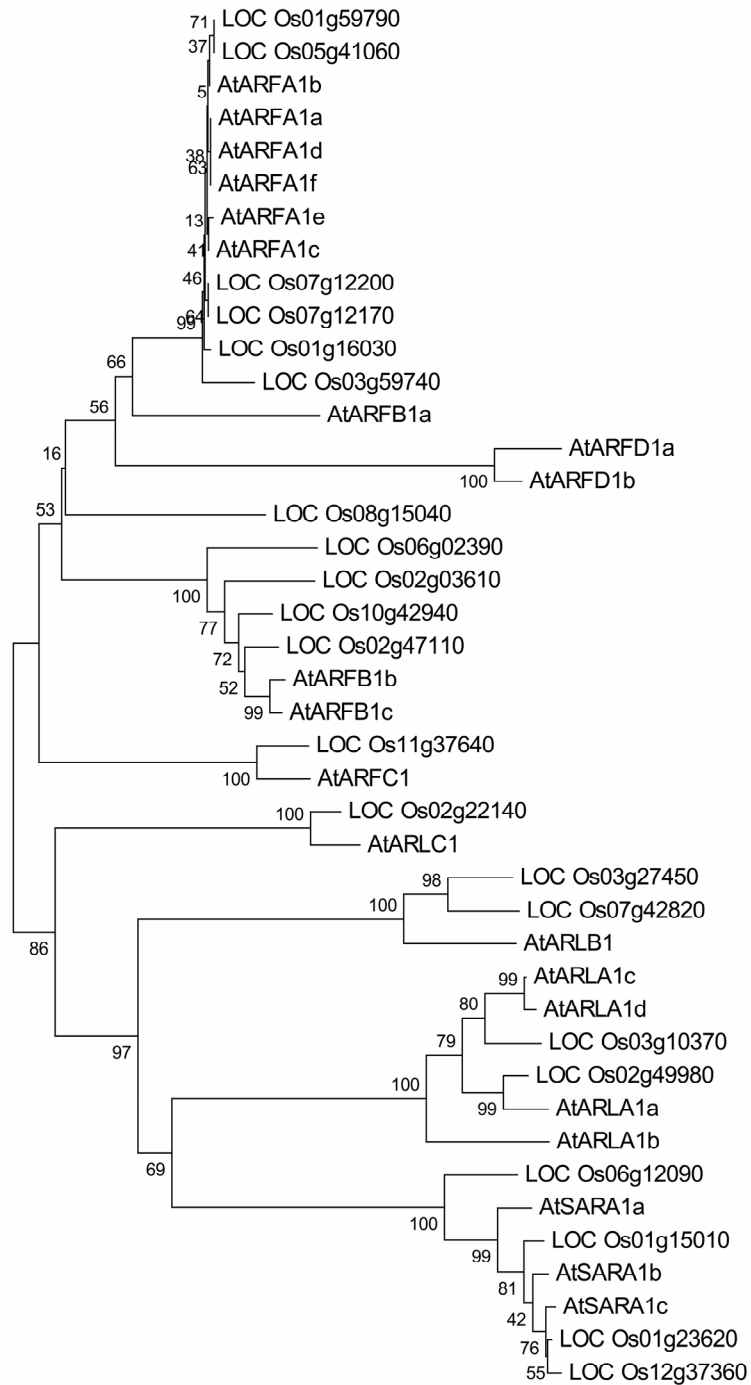


Supplemental Figure 16. Phylogenetic analysis of the Rab small GTPase family from *G. max*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage

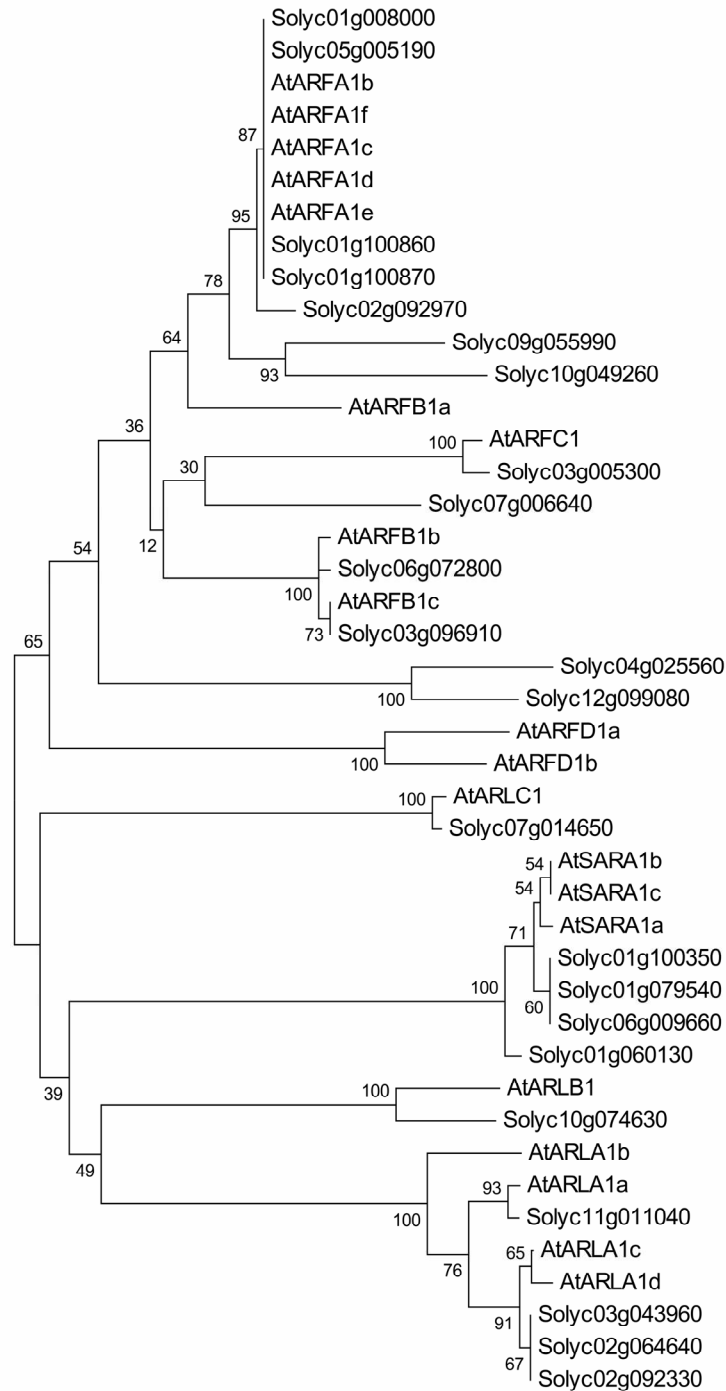
of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



Supplemental Figure 17. Phylogenetic analysis of the Arf small GTPase family from *A. thaliana*. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

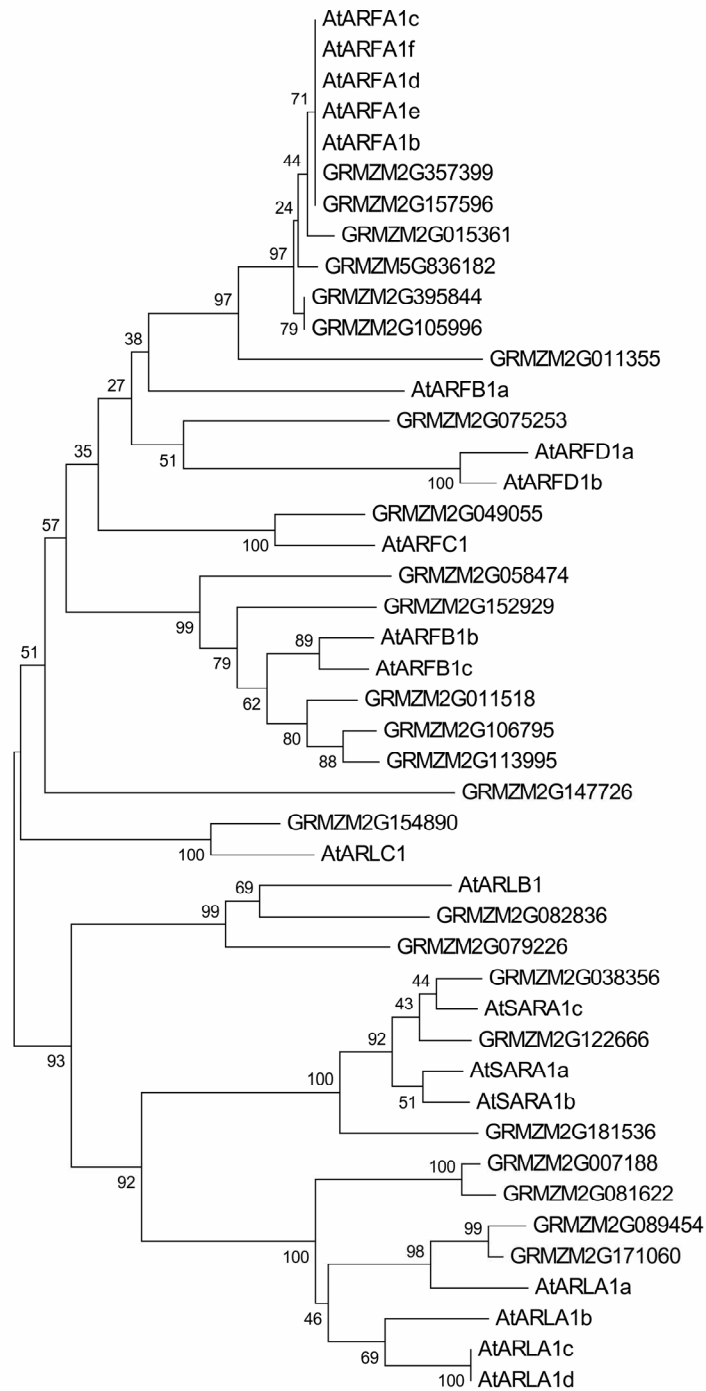


Supplemental Figure 18. Phylogenetic analysis of the Arf small GTPase family from *O. sativa*. Selected sequences from *Arabidopsis* were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

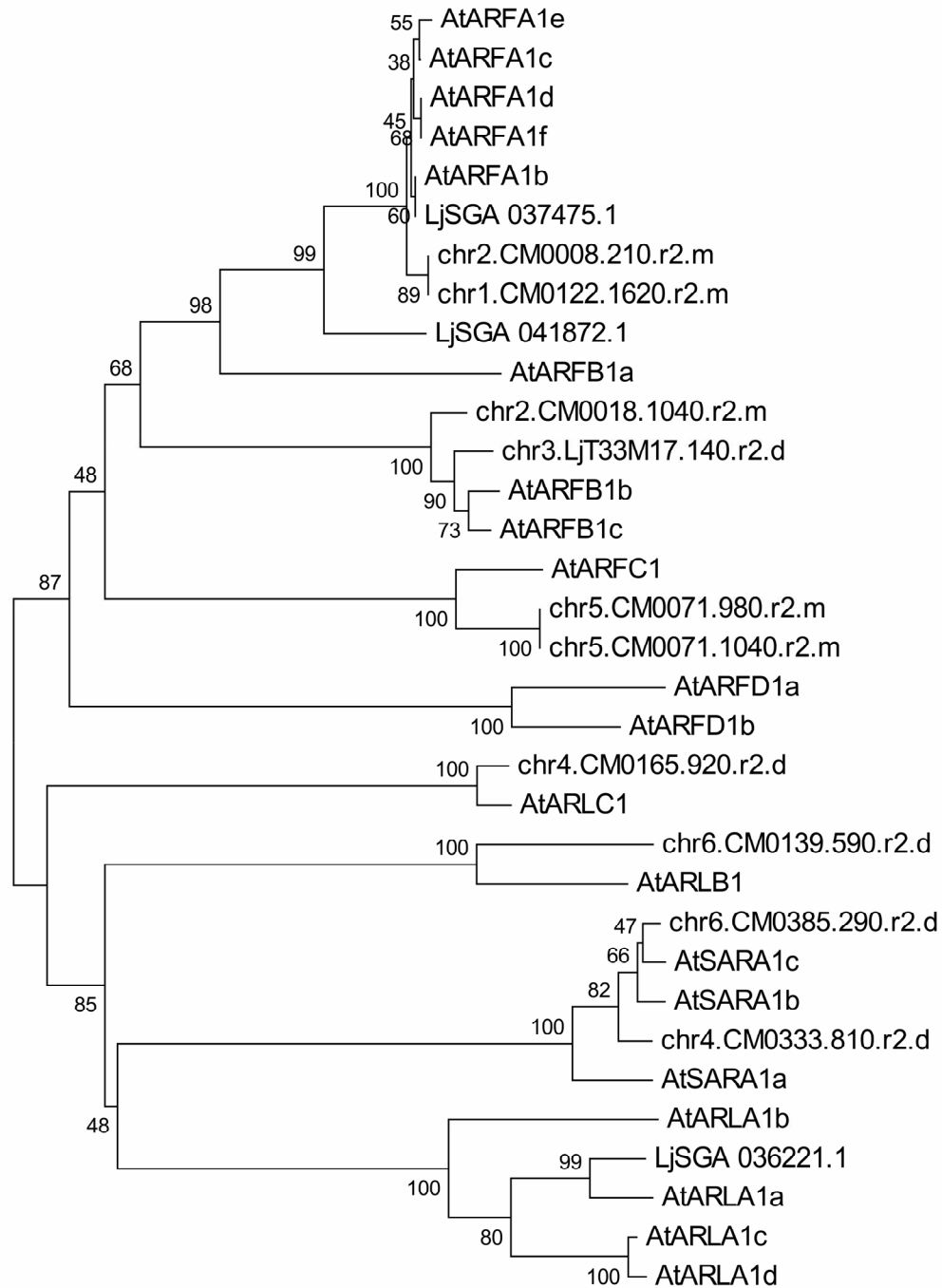


Supplemental Figure 19. Phylogenetic analysis of the Arf small GTPase family from *S. lycopersicum*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

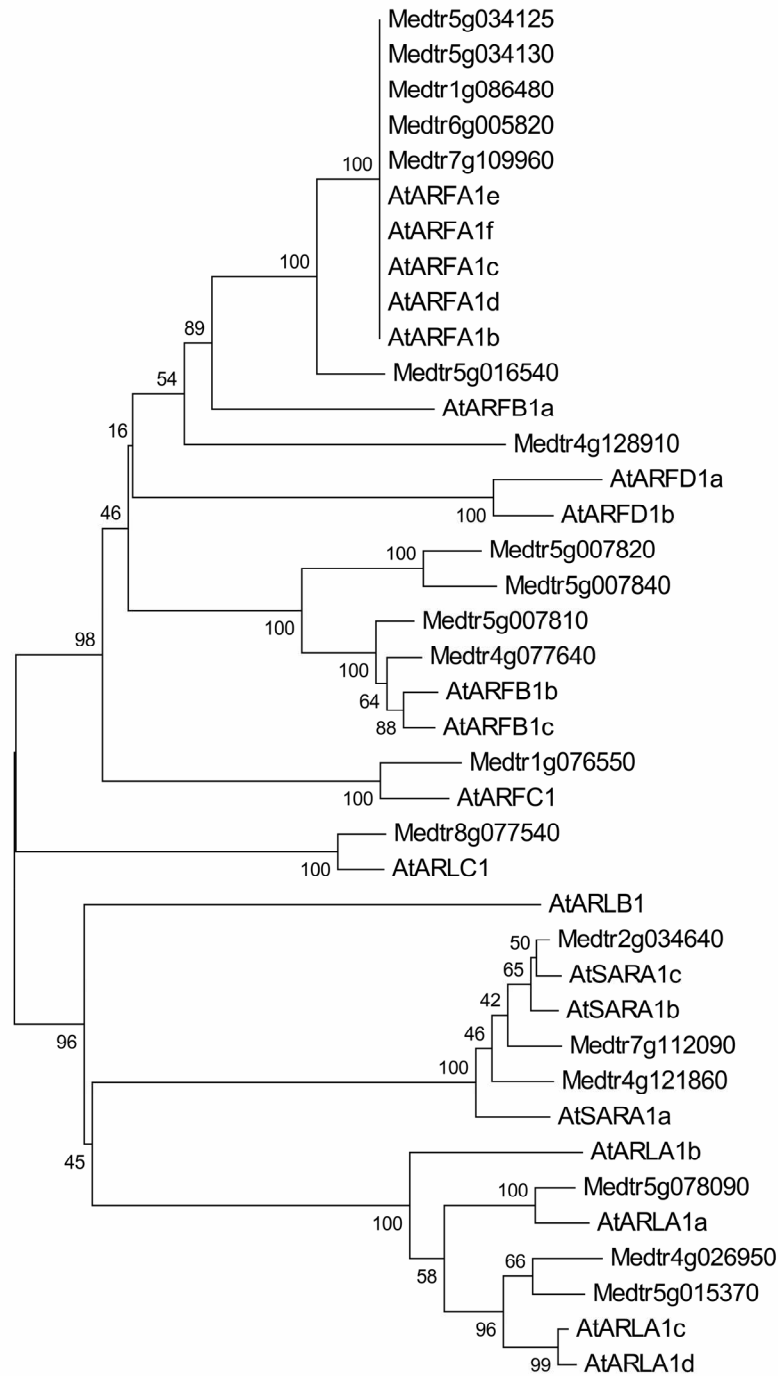


Supplemental Figure 20. Phylogenetic analysis of the Arf small GTPase family from *Z. mays*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



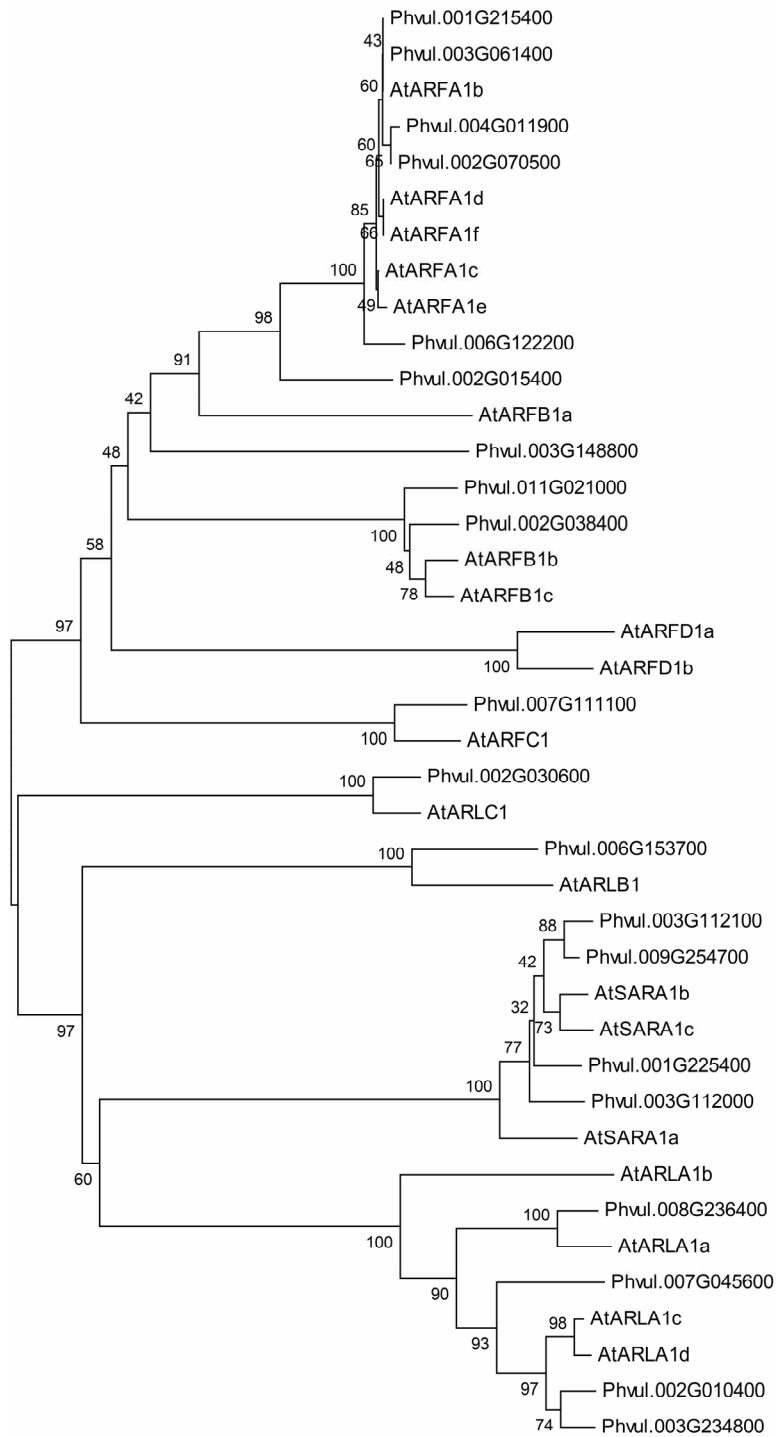
Supplemental Figure 21. Phylogenetic analysis of the Arf small GTPase family from *L. japonicus*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



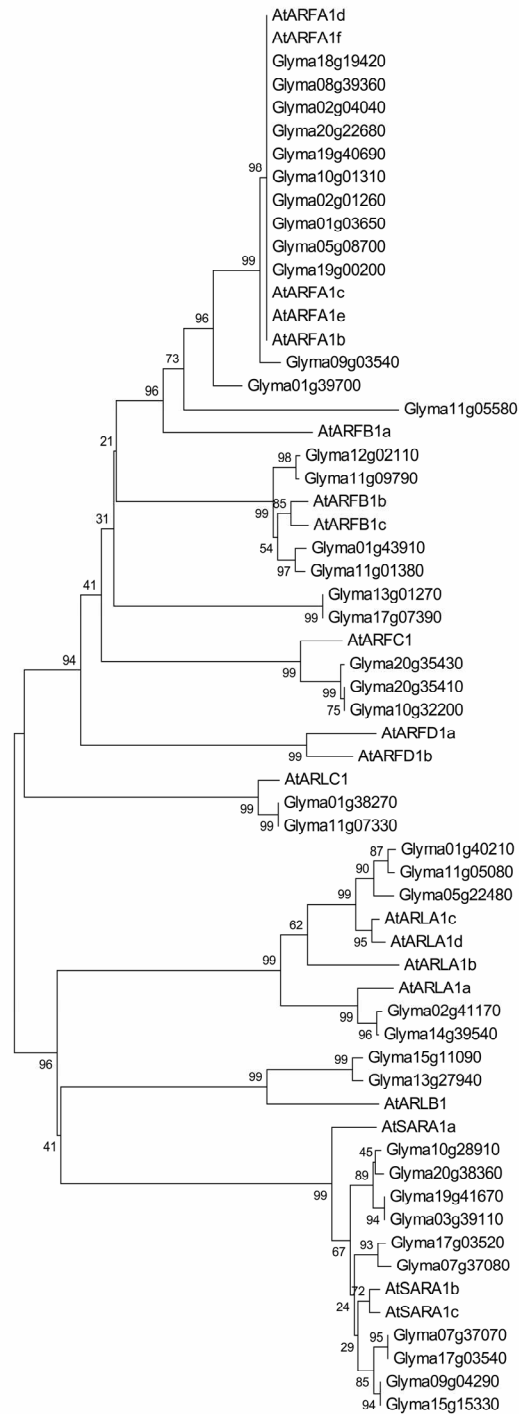
Supplemental Figure 22. Phylogenetic analysis of the Arf small GTPase family from *M. truncatula*.

Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.

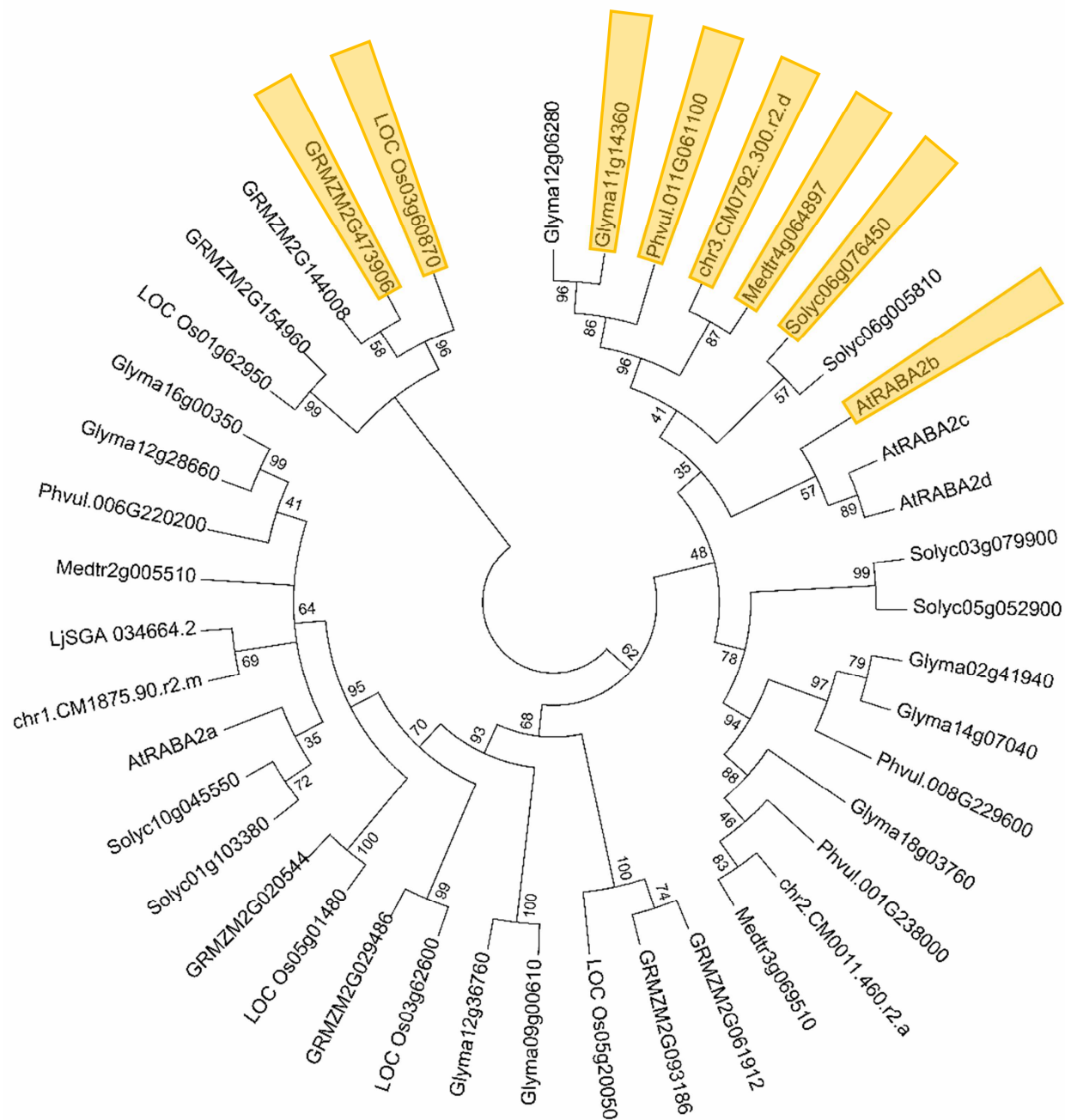


Supplemental Figure 23. Phylogenetic analysis of the Arf small GTPase family from *P. vulgaris*.

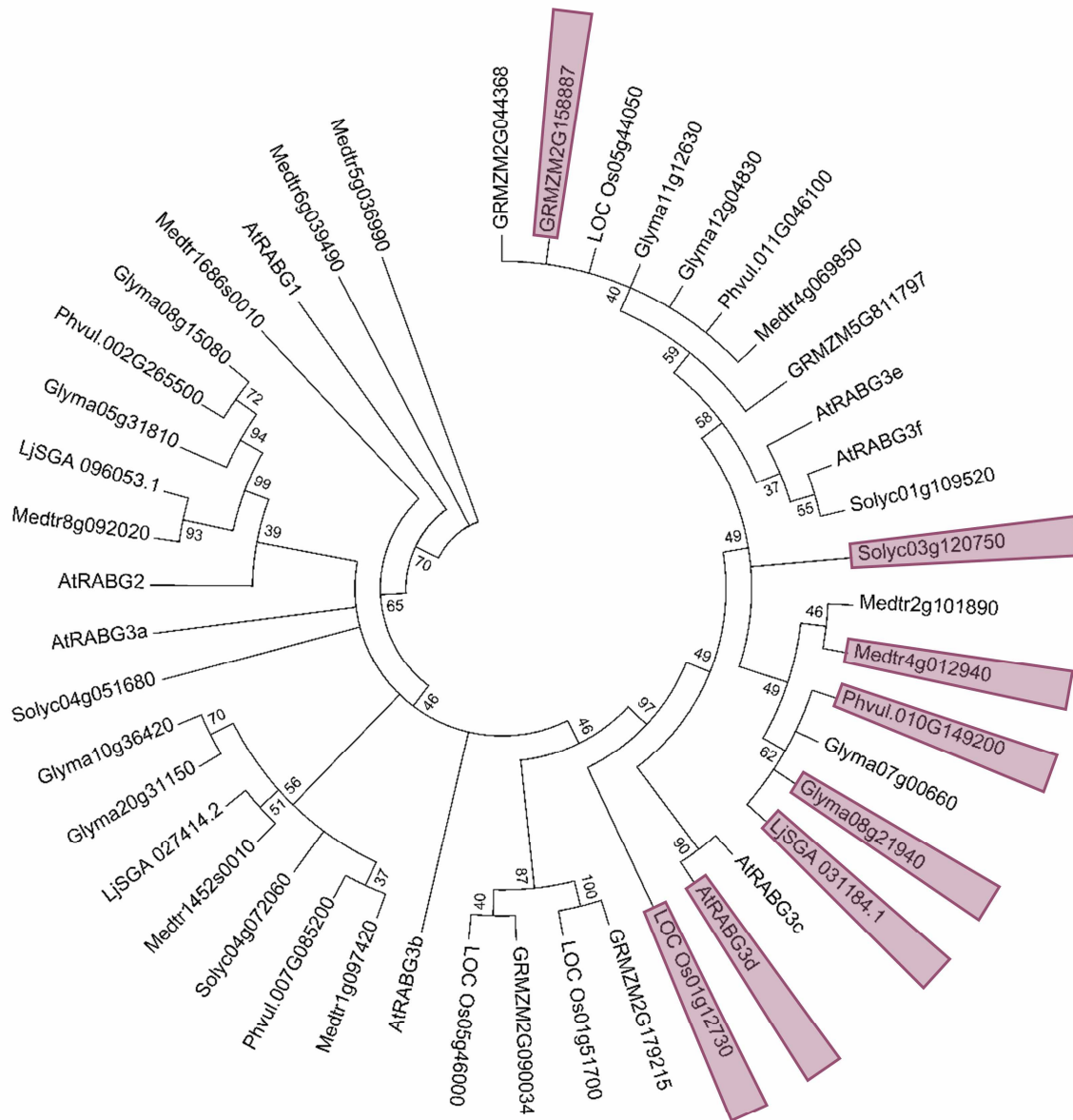
Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



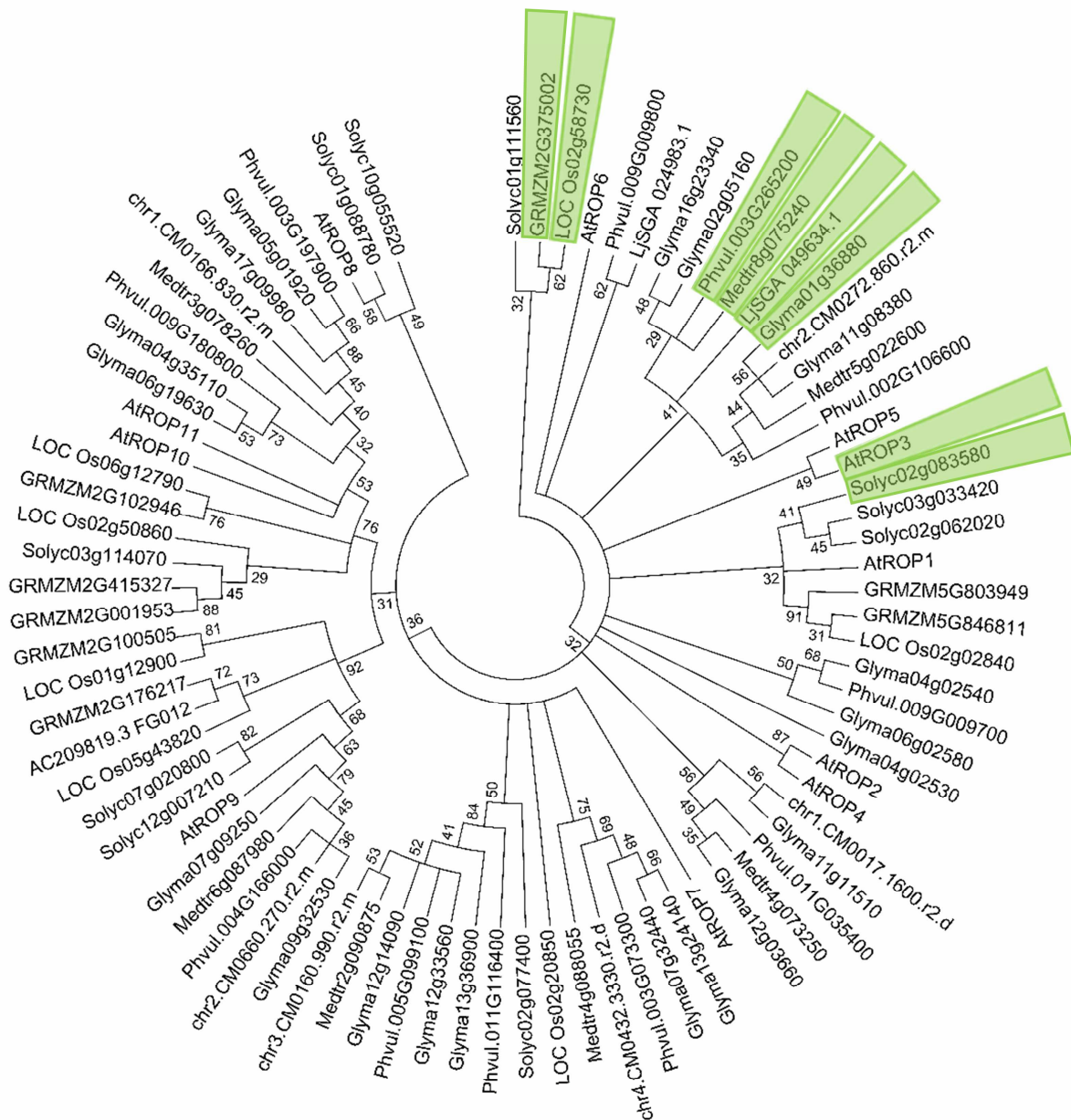
Supplemental Figure 24. Phylogenetic analysis of the Arf small GTPase family from *G. max*. Selected sequences from Arabidopsis were added to identify the main clades defined in this species. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches.



Supplemental Figure 25. Phylogenetic analysis of the RABA2 subfamily from legume and non-legume species. The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. Yellow boxes indicate *P. vulgaris* RABA2 (Phvu 011G061100) and proteins with the highest sequence identity used in multiple sequence alignment shown on Figure 2.



Supplemental Figure 28. Phylogenetic analysis of the RABG subfamily from legume and non-legume species. The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. Violet boxes indicate *M. truncatula* RAB7 (Medtr4g012940) and proteins with the highest sequence identity used in multiple sequence alignment shown on Figure S31.



Supplemental Figure 29. Phylogenetic analysis of the ROP small GTPase family from legume and non-legume species. The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. Green boxes indicate *L. japonicus* ROP6 (*LjSGA_049634*) and proteins with the highest sequence identity used in multiple sequence alignment shown on Figure S32.

M.truncatula	1	MGLTFTKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL	RDAV
P.vulgaris	1	MGLTFTKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL	RDAV
G.max	1	MGLTFTKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL	RDAV
L.japonicus	1	MGL	SFTKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL
A.thaliana	1	MGL	SFAKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL
S.lycopersicum	1	MGLTFTKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL	RDAV
Z.mays	1	MGLTFTKLF	SRLFSKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL	RDAV
O.sativa	1	MGLTFTKLF	SRLFAKKEMRIL	MVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVEARDELHRMLNEDEL	RDAV
M.truncatula	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
P.vulgaris	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
G.max	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
L.japonicus	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
A.thaliana	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
S.lycopersicum	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
Z.mays	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	
O.sativa	121	LLVFANKQDLP	NAMNAAEITDKLGLHSLRQRHWYIQSTCATSGEGLYEGLDWLSNNIANKA	-----	

Supplemental Figure 30. Multiple sequence alignment of *M. truncatula* ARFA1 (Medtr5g034130) and proteins with the highest sequence identity from *P. vulgaris* (Phvul.003G061400), *G.max* (Glyma01g03650), *L. japonicus* (chr2.CM0008.210.r2.m), *A.thaliana* (At1g10630), *S. lycopersicum* (Solyc05g005190), *Z. mays* (GRMZM2G015361) and *O. sativa* (LOC_Os05g41060). Black boxes indicate identical residues and gray ones indicate conservative substitutions. Alignments were generated with Clustal Omega in MEGA7 and formatted with Boxshade. The sequence from *Z. mays* is truncated at its C terminus.

M. truncatula	1	MASRRRMLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQFEDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVKSFENLNHWREEFLLIQASPSDPENFFF
P. vulgaris	1	MASRRRMLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQFEDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVKSFENLNHWREEFLLIQASPSDPENFFF
G. max	1	MASRRRMLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQFEDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVKSFENLNHWREEFLLIQASPSDPENFFF
L. japonicus	1	MASRRRMLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQFEDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVKSFENLNHWREEFLLIQASPSDPENFFF
A. thaliana	1	MSSRRRVLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQIDDRIFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVKSFENLNHWREEFLLIQASPSDPENFFF
S. lycopersicum	1	MASRRRMLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQFEDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVKSFENLNHWREEFLLIQASPSDPENFFF
Z. mays	1	MASRRRVLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQFEDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVSMKSFENLNHWREEFLLIQASPSDPENFFF
O. sativa	1	MASRRRMLLKVIILGDSGVGKTSLMNQYVNRKFSNQYKATIGADFLTKEVQIDDRIFTLQIWDTAGQERFQSLGVAFYRGADCCVLVDVNVTKSPERLNSWRREEFLLIQASPSDPENFFF
M. truncatula	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGNIPYFETSAKEGFNVAAAFQCIAKNALKNEPEEEMYLPTIDVGNNGGRQQRSTGCEC
P. vulgaris	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGNIPYFETSAKEGFNVAAAFQCIAKNALKNEPEEEMYLPTIDVGGGGRQQRSTGCEC
G. max	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGNIPYFETSAKEGFNVAAAFQCIAKNALKNEPEEEMYLPTIDVGGGGRQQRSTGCEC
L. japonicus	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGNIPYFETSAKEGFNVAAAFQCIAKNALKNEPEEEMYLPTIDVGGGGRQQRSTGCEC
A. thaliana	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGNIPYFETSAKEGFNVAAAFQCIATKNAFKNEPEEEMYLPTIDVAG-GQQQRSTGCEC
S. lycopersicum	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKG-IPYFETSAKEGFNVAAAFQCIAKNALKNEPEEEMYLPTIDVA-GGNQPRSTGCEC
Z. mays	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGIDGTVNEDAFQCIIVKNALKNEPEEELVLPDIDVGVGGNRAQRSGCC-
O. sativa	121	VVLGNKIDVDGGNSRVVSEKKAKAWCASKGNIPYFETSAKEGFNVAAAFQCIARNALKNEPEEEMYLPTIDVGGAGRQQRSSTGCEC

Supplemental Figure 31. Multiple sequence alignment of *M. truncatula* RAB7 (MtRAB7A1, Medtr4g012940) and proteins with the highest sequence identity from *P. vulgaris* (Phvul.010G149200), *G. max* (Glyma08g21940), *L. japonicus* (LjSGA_031184.1), *A. thaliana* (At1g52280), *S. lycopersicum* (Solyc03g120750), *Z. mays* (GRMZM2G158887) and *O. sativa* (LOC_Os01g12730). Black boxes indicate identical residues and gray ones indicate conservative substitutions. Alignments were generated with Clustal Omega in MEGA7 and formatted with Boxshade.



Supplemental Figure 32. Multiple sequence alignment of *L. japonicus* ROP6 (LjSGA_049634) and proteins with the highest sequence identity from *M. truncatula* (Medtr8g075240), *P. vulgaris* (Phvul.003G265200), *G. max* (Glyma.01g36880), *A. thaliana* (AT2G17800), *S. lycopersicum* (Solyc02g083580), *Z. mays* (GRMZM2G375002) and *O. sativa* (LOC_Os02g58730). Black boxes indicate identical residues and gray ones indicate conservative substitutions. Alignments were generated with Clustal Omega in MEGA7 and formatted with Boxshade. Red arrows indicate amino acid substitutions in legumes versus non-legumes. The conserved domains of ROPs are indicated by blue lines.