

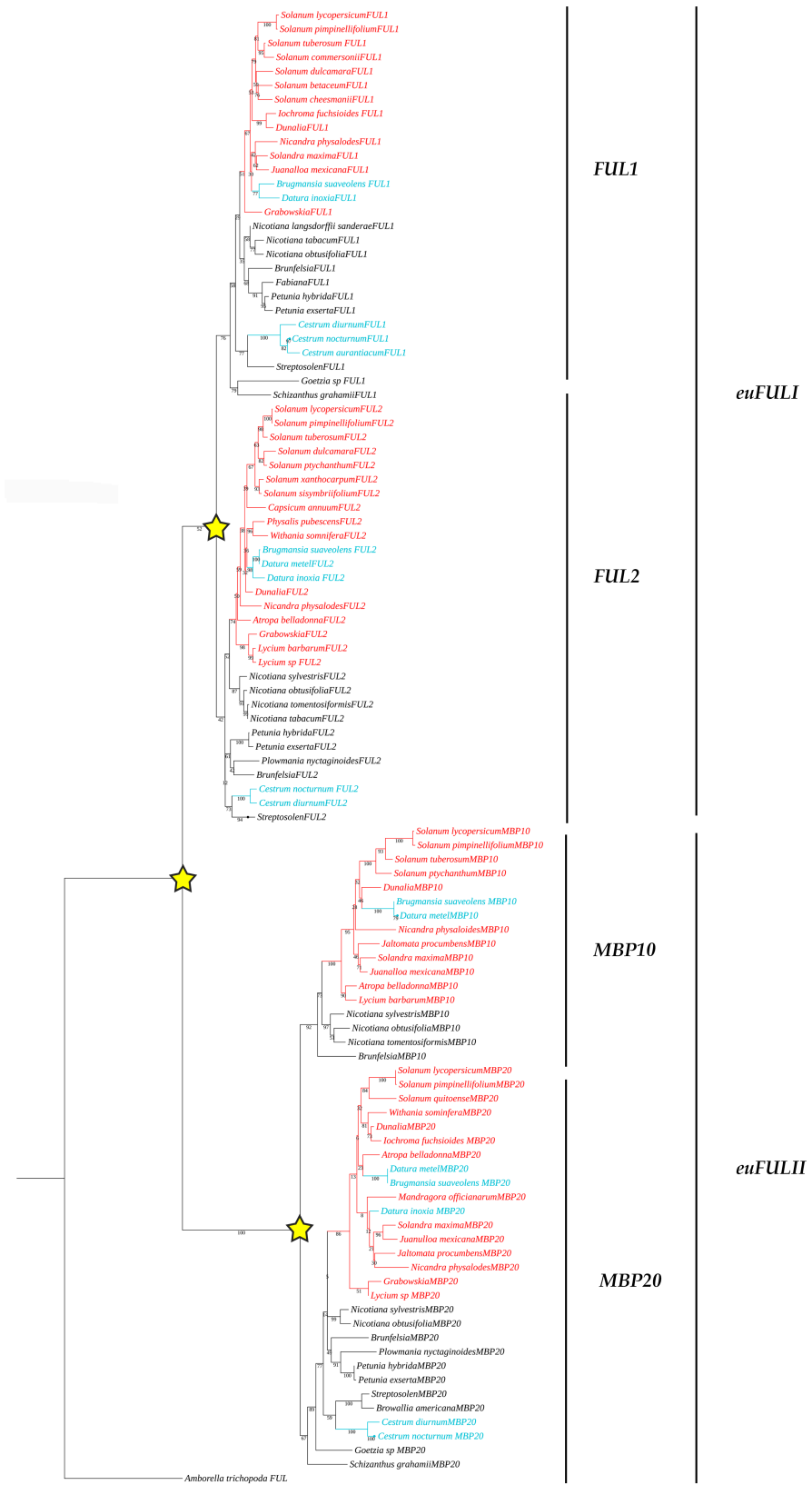
SUPPLEMENTARY MATERIAL

**Anatomical and genetic basis underlying convergent evolution of
fleshy and dry dehiscent fruits in *Cestrum* and *Brugmansia*
(Solanaceae)**

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Colombia .

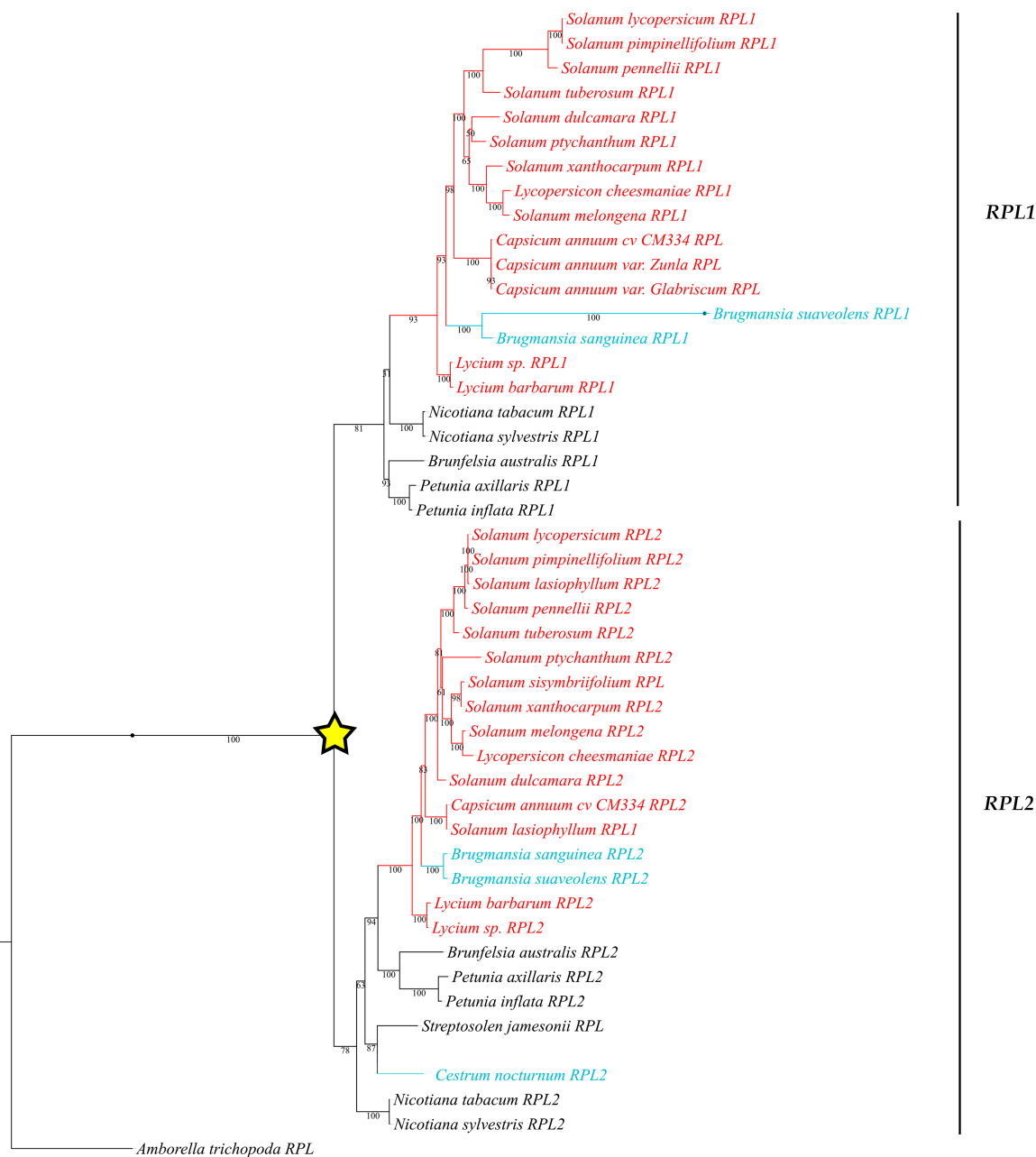
*Corresponding author: lucia.pabon@udea.edu.co



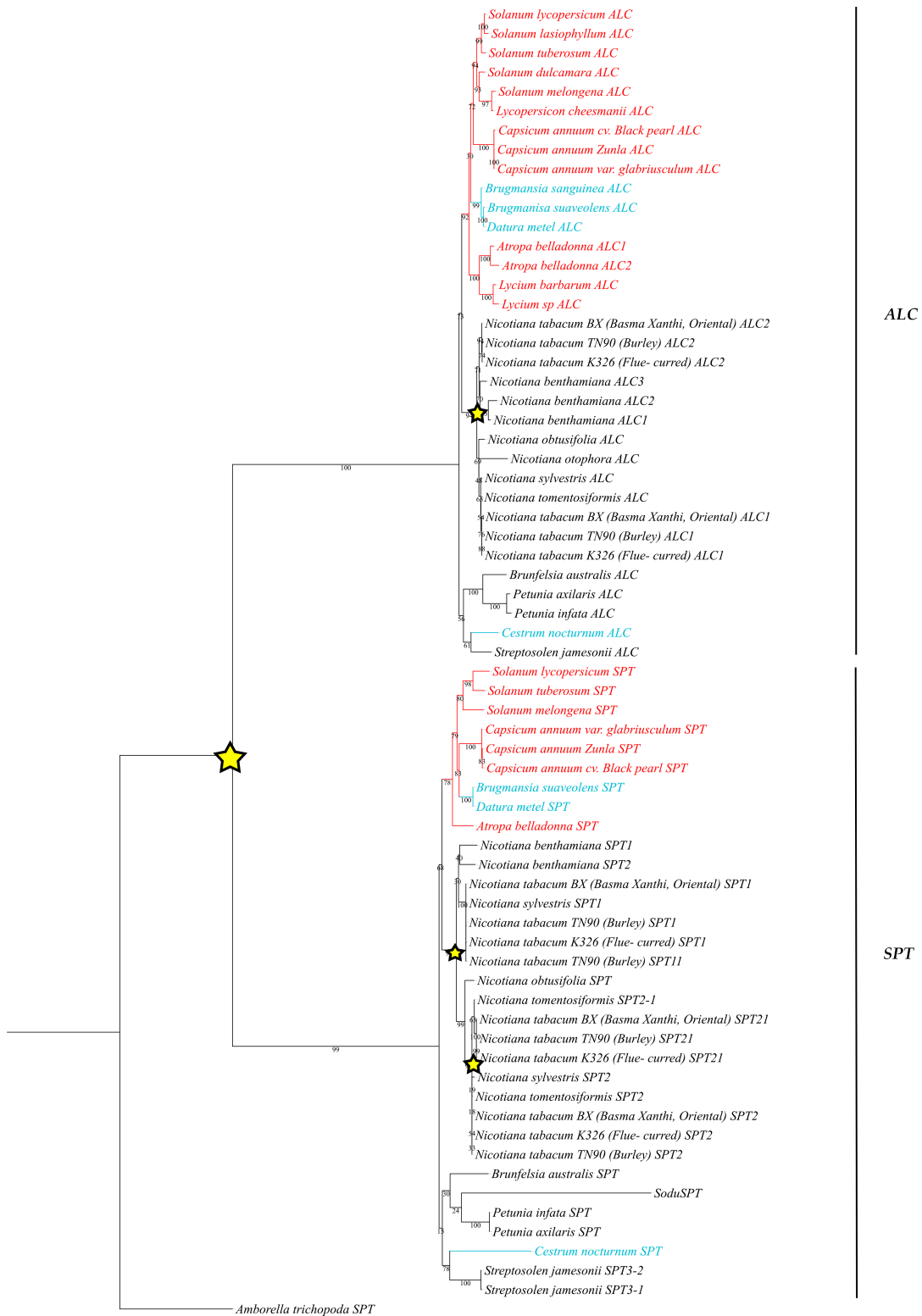
Suppl. Fig. S1. Maximum likelihood tree of *FRUITFULL* genes in Solanaceae. Outgroup used corresponds to the *Amborella trichopoda FUL* (*AmtrFUL*). Duplication events are labelled with stars. Genes belonging to species with dry dehiscent fruits are labeled in black, those belonging to species with fleshy fruits are labeled in red, and those belonging to the target species *Cestrum nocturnum*, indicating an independent origin of fleshy fruits and species from the Daturae tribe (*Brugmansia* and *Datura*), indicating phylogenetic reversals to dry dehiscent fruits, are labeled in light blue. Branch numbers indicate BS supports.



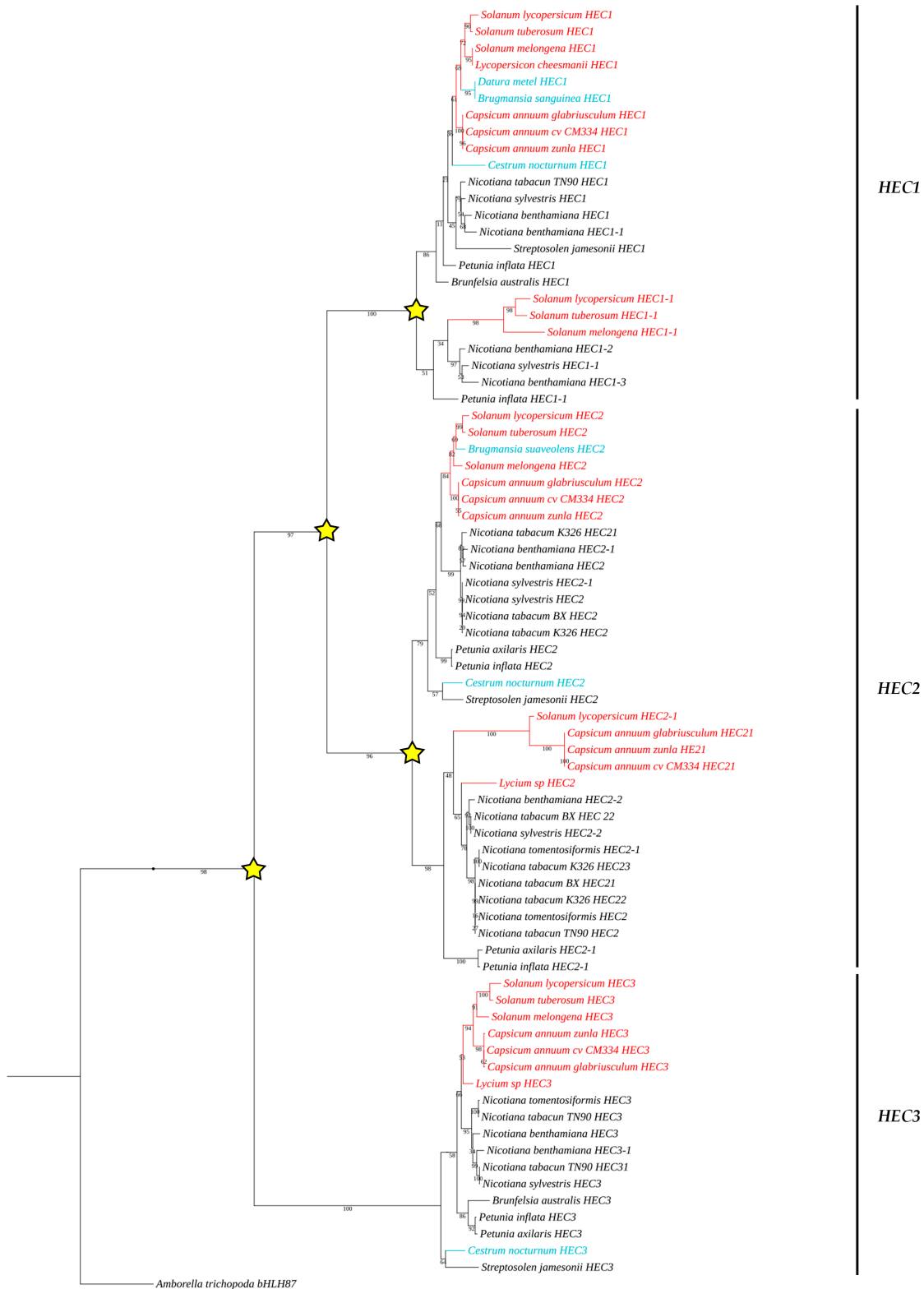
Suppl. Fig. S2. Maximum likelihood tree of AGAMOUS/SHATTERPROOF genes in Solanaceae. Outgroup used corresponds to the *Amborella trichopoda* AG (*AmtrAG*). Duplication events are labelled with stars. Colors follow the conventions specified in the Suppl. Fig. S1. legend. Branch numbers indicate BS supports.



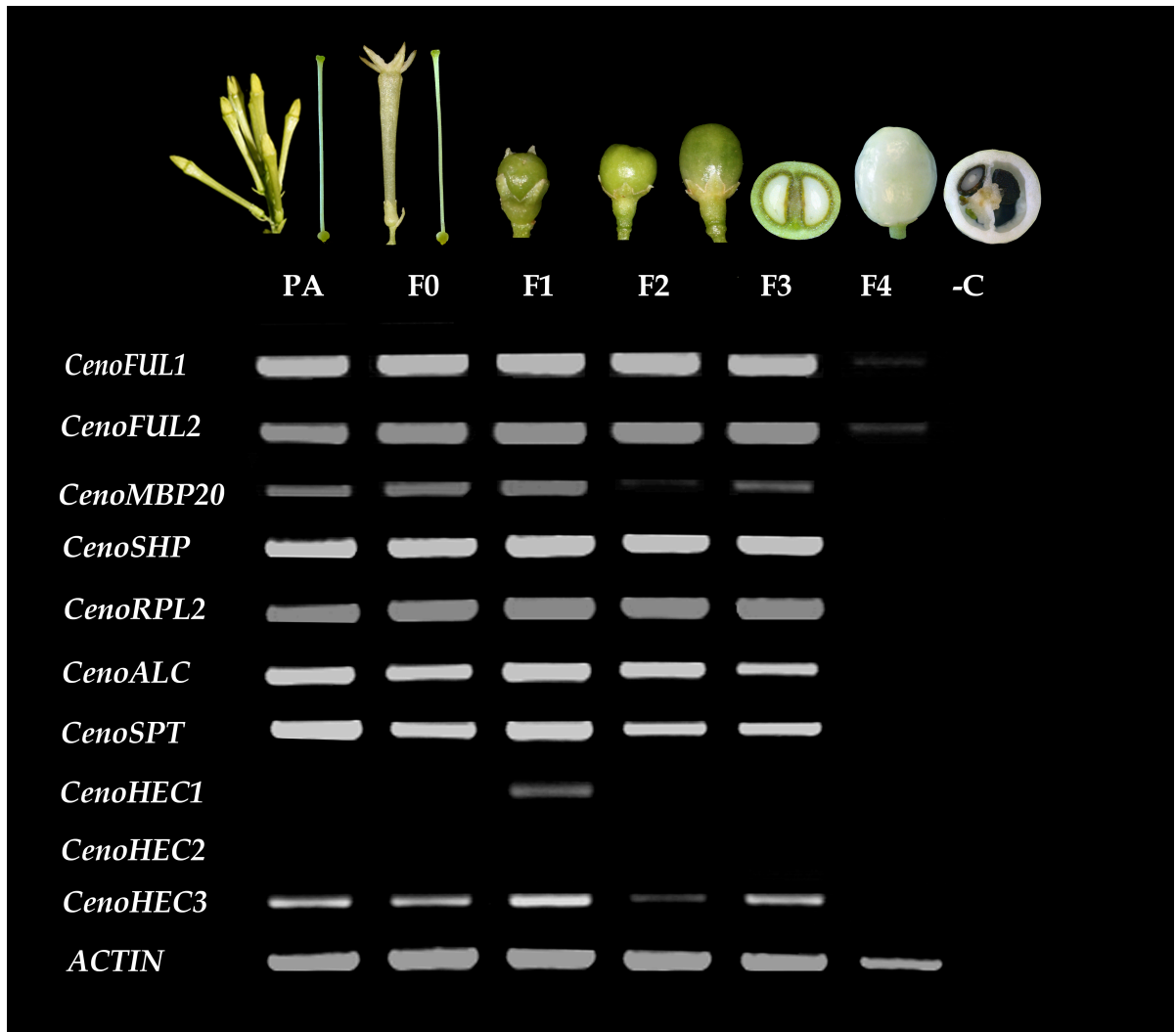
Suppl. Fig. S3. Maximum likelihood tree of *REPLUMLESS* genes in Solanaceae. Outgroup used corresponds to the *Amborella trichopoda RPL* (*AmtrRPL*). Duplication events are labelled with stars. Colors follow the conventions specified in the Suppl. Fig. S1. legend. Branch numbers indicate BS supports.



Suppl. Fig. S4. Maximum likelihood tree of ALCATRAZ/SPATULA genes in Solanaceae. Outgroup used corresponds to *Amborella trichopoda* SPATULA (*AmtrSPT*). Duplication events are labelled with stars. Colors follow the conventions specified in the Suppl. Fig. S1. legend. Branch numbers indicate BS supports.



Suppl. Fig. S5. Maximum likelihood tree of *HECATE/INDEHISCENT* genes in angiosperms. Outgroup used corresponds to *Amborella trichopoda* bHLH87 (*AmtrbHLH87*). Duplication events are labelled with stars. Colors follow the conventions specified in the Suppl. Fig. S1. legend. Branch numbers indicate BS supports.



Suppl. Fig. S6. Expression analyses of the fruit GRN genes in *Cestrum nocturnum* after 35 amplification cycles. PA, ovary in preanthesis; F, fruit developmental stages; -C indicates the amplification reaction loaded without cDNA.

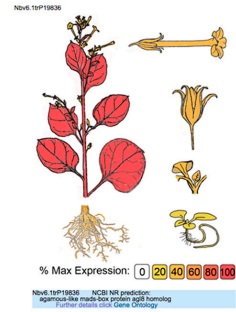
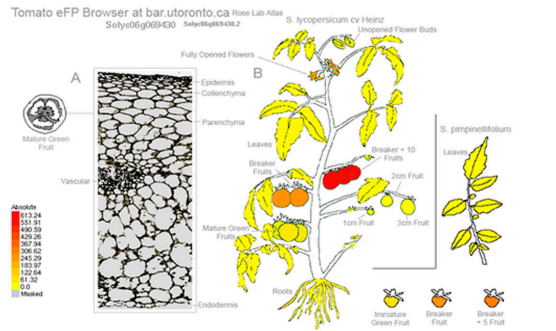


Suppl. Fig. S7. Sepal development and maturation in *Alkekengi officinarum* showing parenchyma degradation in between the primary and secondary vascular traces.

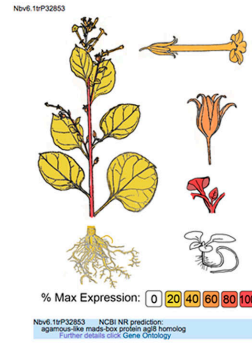
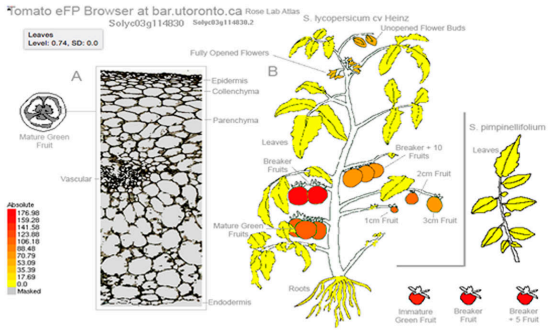
Solanum lycopersicum

Nicotiana benthamiana

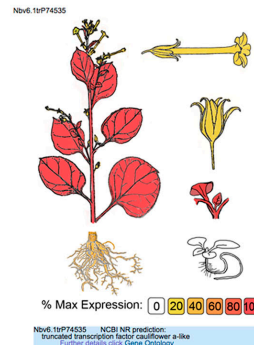
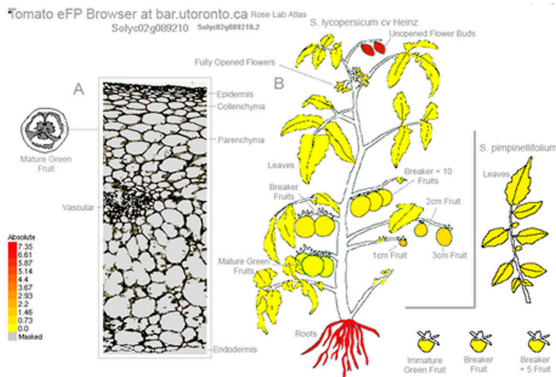
FUL1 (euFUL1)



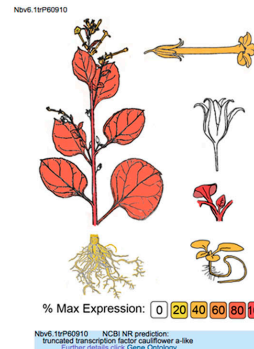
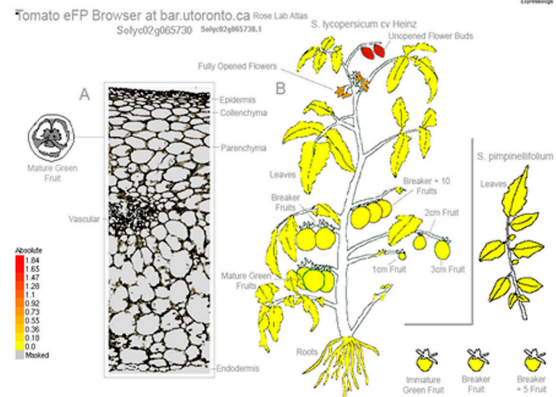
FUL2 (euFUL1)



MBP20 (euFULII)



MBP10 (euFULII)

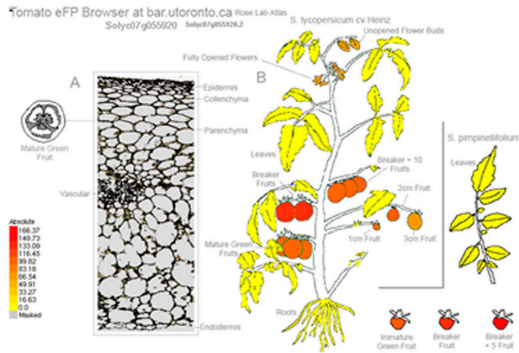


Suppl. Fig. S8. Expression profiles of *FRUITFULL* genes in *Solanum lycopersicum*, from eFP Browser (http://bar.utoronto.ca/efp2/Tomato/Tomato_eFPBrowser2.html), and *Nicotiana benthamiana*, from the Gene Expression ATLAS (<http://sefapps02.qut.edu.au/atlas/tREX6.php>).

Solanum lycopersicum

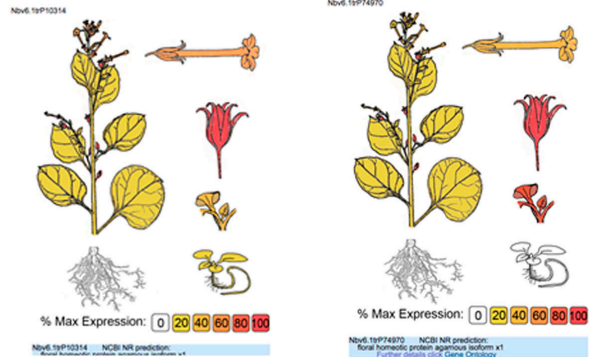
Nicotiana benthamiana

SHP

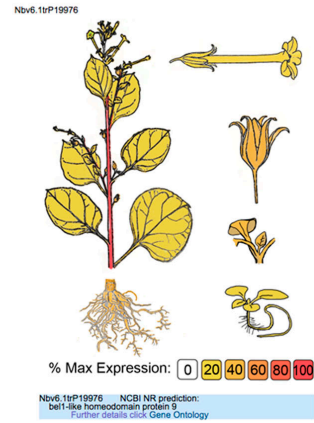
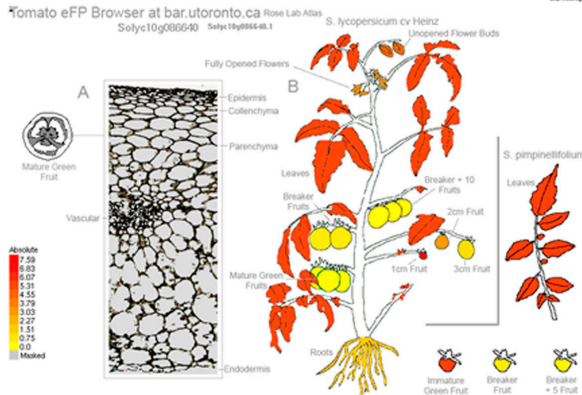


NibeSHP1

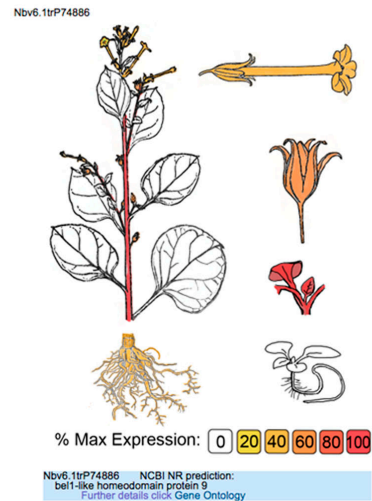
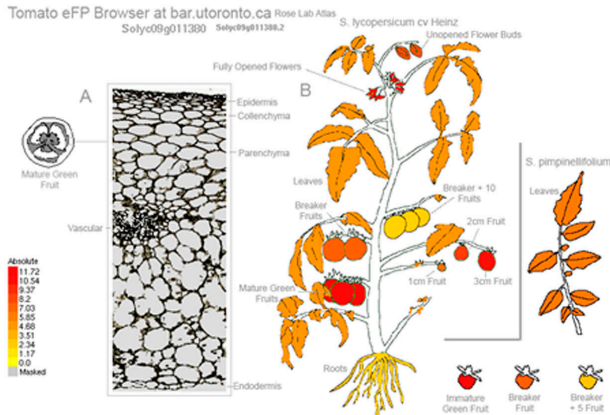
NibeSHP2



RPL1



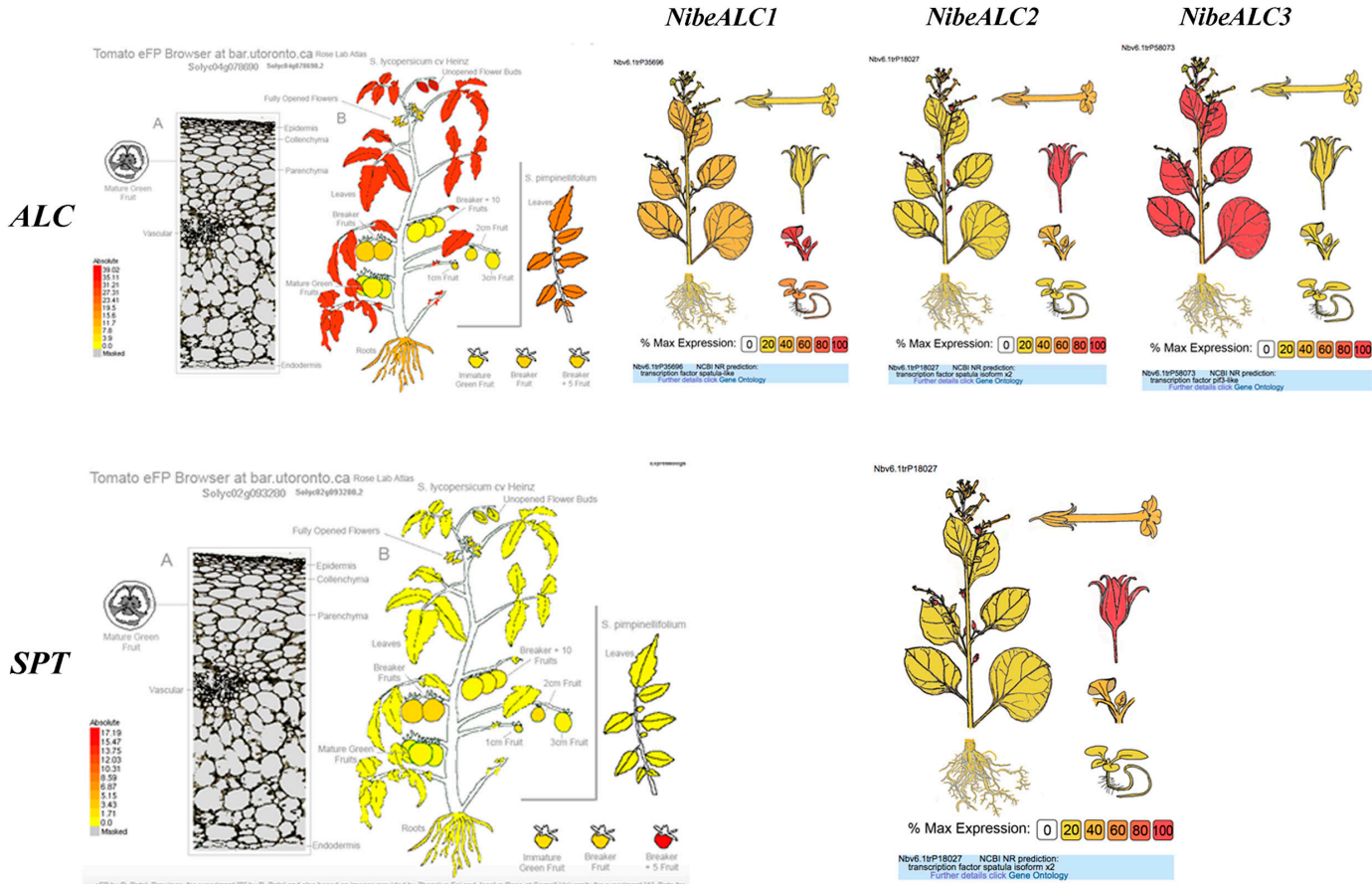
RPL2



Suppl. Fig. S9. Expression profiles of *SHATTERPROOF* and *REPLUMLESS* genes in *Solanum lycopersicum*, from eFP Browser (http://bar.utoronto.ca/efp2/ Tomato/ Tomato_eFPBrowser2.html), and *Nicotiana benthamiana*, from the Gene Expression ATLAS (<http://sefapps02.qut.edu.au/atlas/tREX6.php>).

Solanum lycopersicum

Nicotiana benthamiana

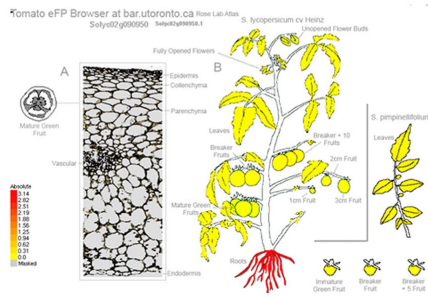


Suppl. Fig. S10. Expression profiles of *ALCATRAZ/SPATULA* genes in *Solanum lycopersicum*, from eFP Browser (http://bar.utoronto.ca/efp2/Tomato/Tomato_eFPBrowser2.html), and *Nicotiana benthamiana*, from the Gene Expression ATLAS (<http://sefapps02.qut.edu.au/atlas/tREX6.php>).

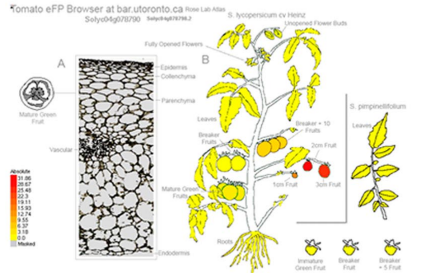
Solanum lycopersicum

Nicotiana benthamiana

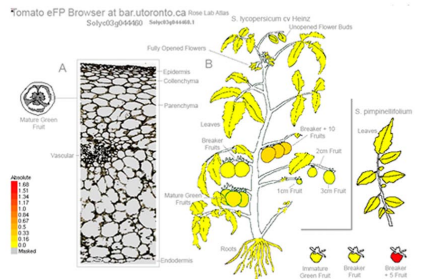
HEC1



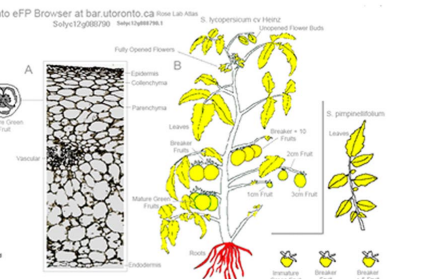
HEC1-1



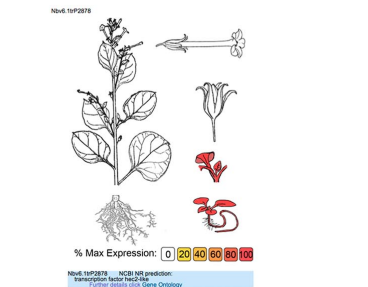
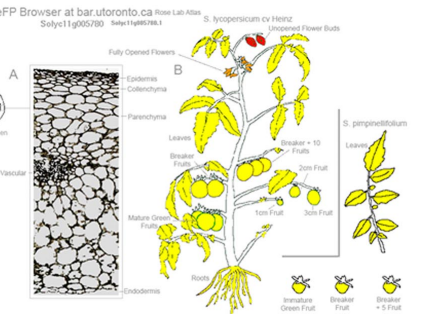
HEC2



HEC2-1



HEC3



NibeHEC1-1



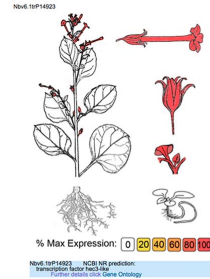
NibeHEC1-2



NibeHEC2-1



NibeHEC2-2



Suppl. Fig. S11. Expression profiles of *HECATE1/2/3* genes in *Solanum lycopersicum*, from eFP Browser (http://bar.utoronto.ca/efp2/Tomato/Tomato_eFPBrowser2.html), and *Nicotiana benthamiana*, from the Gene Expression ATLAS (<http://sefapps02.qut.edu.au/atlas/TREX6.php>).