Figure S6. Phylogenetic relationships between Expansins.

Color-coding of proteins regulated by ethylene in AZ-C cells and/or FR cells of Washington Navel maturing fruits or regulated during abscission in AZs in other plant species

CitXXXXX	Up-regulated exclusivelly in AZ-C cells
CitXXXXX	Up-regulated exclusivelly in fruit rind cells
CitXXXXX	Up-regulated in both AZ-C and fruit rind cells
CitXXXXX	Down-regulated exclusivelly in AZ-C cells
CitXXXXX	Down-regulated exclusivelly in fruit rind cells
CitXXXXX	Down-regulated in both AZ-C and fruit rind cells
CitXXXXX	Probe printed in the 20 K citrus microarray (Martínez-Godoy et al, 2008) but without hybridization results
XXXXX	Up-regulated during AZ activation in other plant species
XXXXX	Down-regulated during AZ activation in other plant species
XXXXX	β-glucuronidase (GUS) activity in floral organ AZ cells of *Arabidopsis thaliana*
LAZ	Up-regulated in LAZ-enriched tissues (Agustí et al., 2008; 2012) or preferentially expressed in LAZ cells (Agustí et al., 2009) during ethylene-promoted abscission in citrus leaves
Petiole	Up-regulated in petioles (Agustí et al., 2008) or preferentially expressed in petiolar cortical cells (Agustí et al., 2009) during ethylene-promoted abscission in citrus leaves
AZ-C tissues	Up-regulated in AZ-enriched tissues during ethylene-promoted abscission in orange fruits (Cheng et al, 2015)
AZ-C tissues	Down-regulated in AZ-enriched tissues during ethylene-promoted abscission in orange fruits (Cheng et al, 2015)
ida-2	Down-regulated in receptacles of *ida-2* plants (Liu et al, 2013)
hae-3/hsl2-3	Down-regulated in receptacles of *hae-2/hsl2-3* double mutant plants (Niederhuth et al, 2013)

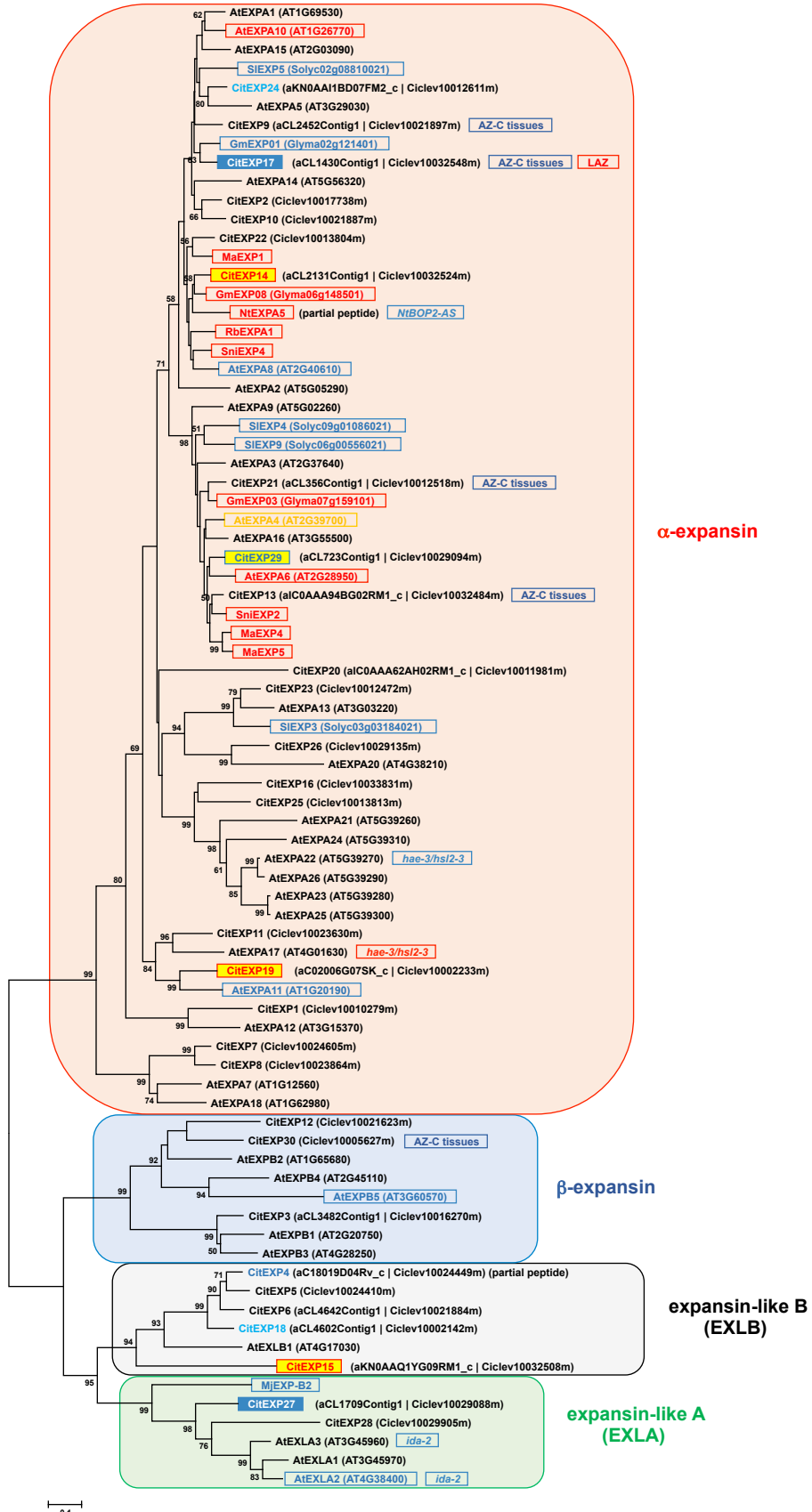

Figure S6. Phylogenetic relationships between expansins (EXPs). The phylogenetic tree shows the degree of similarity between the EXPs annotated in the genome of *Arabidopsis thaliana* (TAIR) and in the *Citrus clementina* haploid genome (Wu et al, 2014; Table S3) and those previously described as related to the abscission process in other plant species. Phylogenetic trees are based on multiple alignments of proteins using the profile alignment function of ClustalW (http://wwwchembnetorg/software/ClustalW-XXLhtml) and were generated with MEGA7 (Kumar et al, 2016) using the neighbor-joining algorithm with 1,000 bootstrap replicates. Only bootstrap supports higher than 50% were considered and are shown in the nodes. Transcripts of NtEXPA5 were down-regulated in the corolla base of tobacco plants over-expressing an antisense-oriented sequence of NtBOP2 ([NtBOP2-AS]; Wu et al, 2012). Accession numbers for the sequences of EXP proteins regulated during organ abscission in AZs of different plant species are shown. *Arabidopsis thaliana* (Cho and Cosgrove, 2000; González-Carranza et al., 2012; Lashbrook and Cai, 2008): AtEXPA4 (AT2G39700), AtEXPA6 (AT2G28950), AtEXPA8 (AT2G40610), AtEXPA10 (AT1G26770), AtEXPA11 (AT1G20190), AtEXPB5 (AT3G60570) and AtEXLA2 (AT4G38400). Elderberry [*Sambucus nigra*] (Belfield et al, 2005): SniEXP2 (AAP48989) and SniEXP4 (AAP48991). Soybean [*Glycine max*] (Tucker et al, 2007): GmEXP1 (Glyma02g121401), GmEXP3 (Glyma07g159101) and GmEXP8 (Glyma06g148501). Banana [*Musa acuminata*] (Mbéguié-A-Mbéguié et al, 2009): MaEXP1 (AAM08930), MaEXP4 (ABN09939) and MaEXP5 (ABN09940). Rose [*Rosa bourboniana*] (Sane et al, 2007): RbEXPA1 (ABC55453). The four o'clock flower [*Mirabilis jalapa*] (Meir et al, 2006): MjEXP-B2 (AAN86683). Tomato [*Solanum lycopersicum*] (Meir et al, 2010): SlEXP3 (SGN-U576599), SlEXP4 (SGN-U580310), SlEXP5 (SGN-U581279) and SlEXP9 (SGN-U580110). GUS activity in floral organ AZs according to González-Carranza et al. (2012).

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