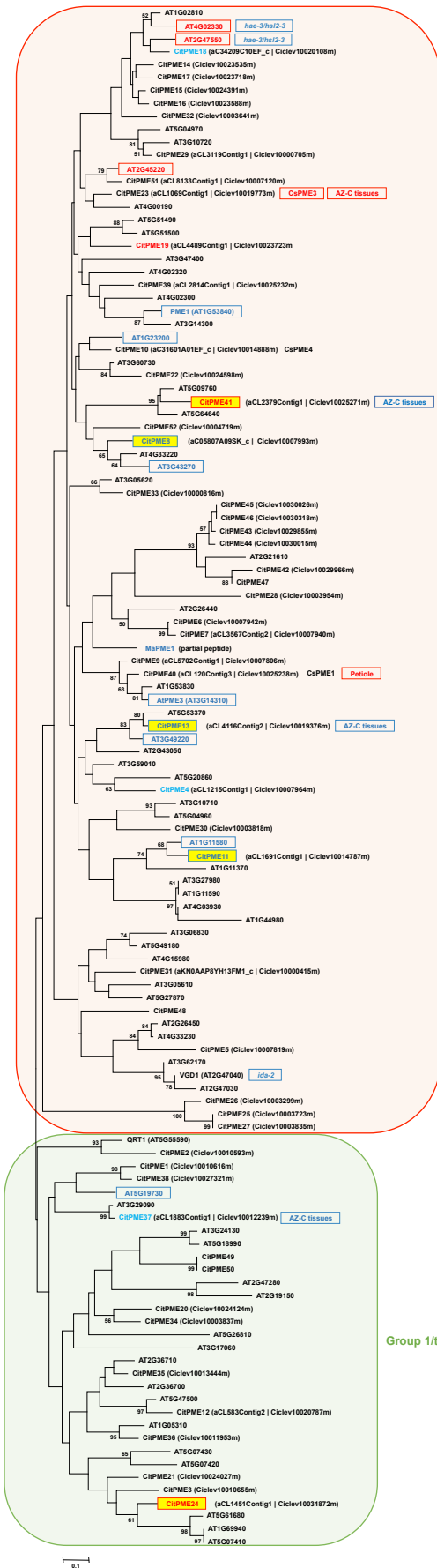


Figure S3. Phylogenetic relationships between carbohydrate esterases (CEs): pectin-methylesterases (CE8s) and pectin-acetylerases (CE13s).

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 exclusively in AZ-C cells
CitXXXXX	Up-regulated exclusively in fruit rind cells
CitXXXXX	Up-regulated in both AZ-C and fruit rind cells
CitXXXXX	Down-regulated exclusively in AZ-C cells
CitXXXXX	Down-regulated exclusively 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 <i>Arabidopsis thaliana</i>
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 <i>ida-2</i> plants (Liu et al, 2013)
hae-3/hsl2-3	Down-regulated in receptacles of <i>hae-2/hsl2-3</i> double mutant plants (Niederhuth et al, 2013)



Group 2/type I

Group 1/type II

Figure S3A. Phylogenetic relationships between carbohydrate esterases (CEs): pectin-methylesterases (PMEs, CE8s). The phylogenetic tree shows the degree of similarity between the PMEs 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://www.ch.embnet.org/software/ClustalW-XXL.html>) 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. Accession numbers for the sequences of PME proteins regulated during organ abscission in different plant species are shown. *Arabidopsis thaliana* (Lashbrook and Cai, 2008): AT1G11580, AT1G23200, AT2G45220, AT2G47550, AT3G14310 (AtPME3), AT3G43270, AT3G49220, AT4G02330 and AT5G19730. Banana [*Musa acuminata*] (Mbéguié-A-Mbéguié et al., 2009): MaPME1 (ACQ85264). Orange [*Citrus sinensis*] (Nairn et al., 1998): CsPME3 (U82997).

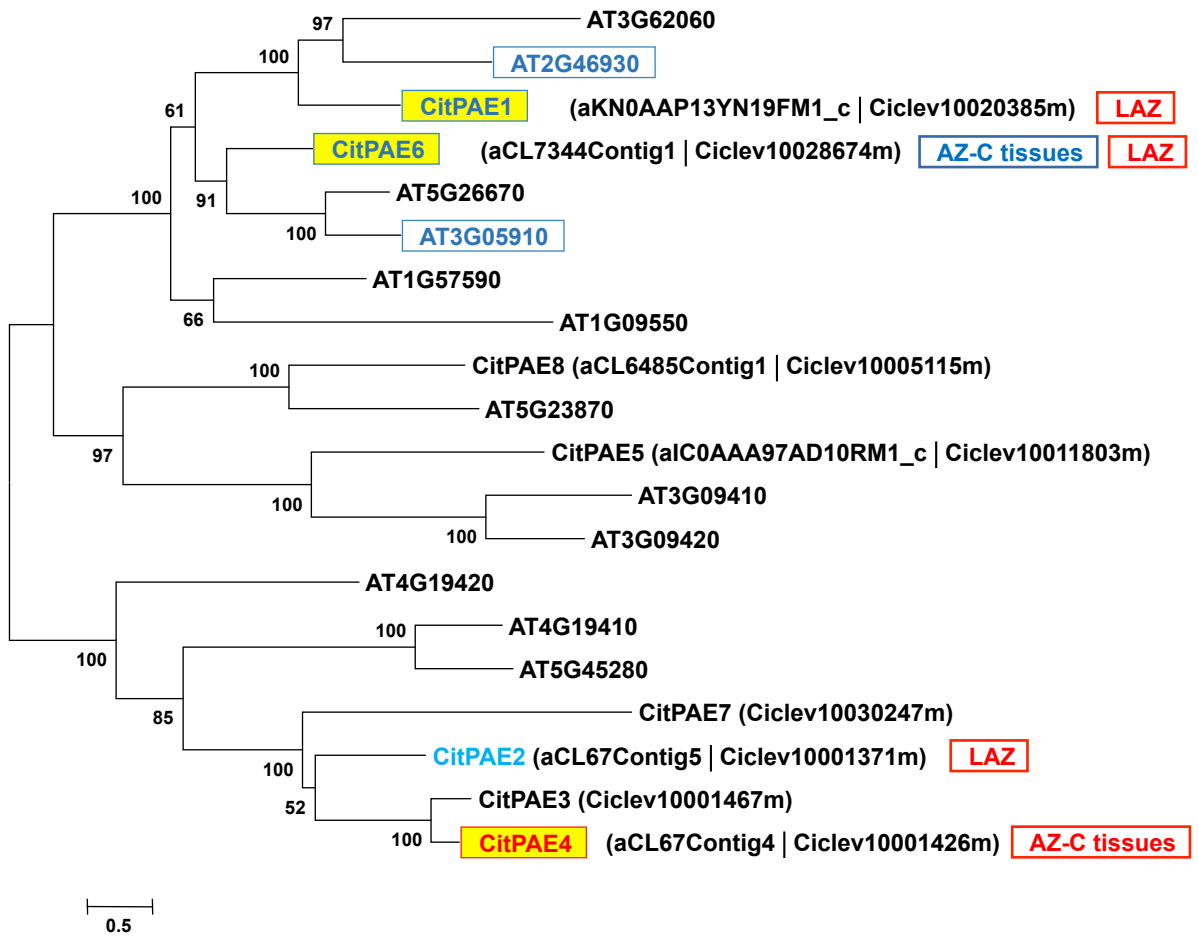


Figure S3B. Phylogenetic relationships between carbohydrate esterases (CEs): pectin-acetyl esterases (PAEs, CE13s). The phylogenetic tree shows the degree of similarity between the PAEs annotated in the genome of *Arabidopsis thaliana* (TAIR) and in the *Citrus clementina* haploid genome (Wu et al., 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://www.ch.embnet.org/software/ClustalW-XXL.html>) 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. Accession numbers for the sequences of PAE proteins regulated during organ abscission in *Arabidopsis thaliana* (Lashbrook and Cai, 2008): AT2G46930 and AT3G05910.

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