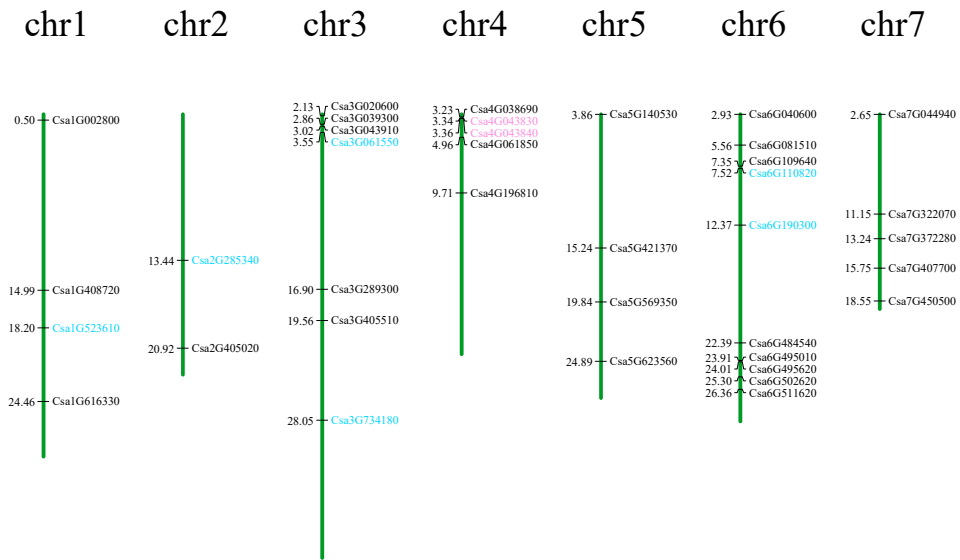
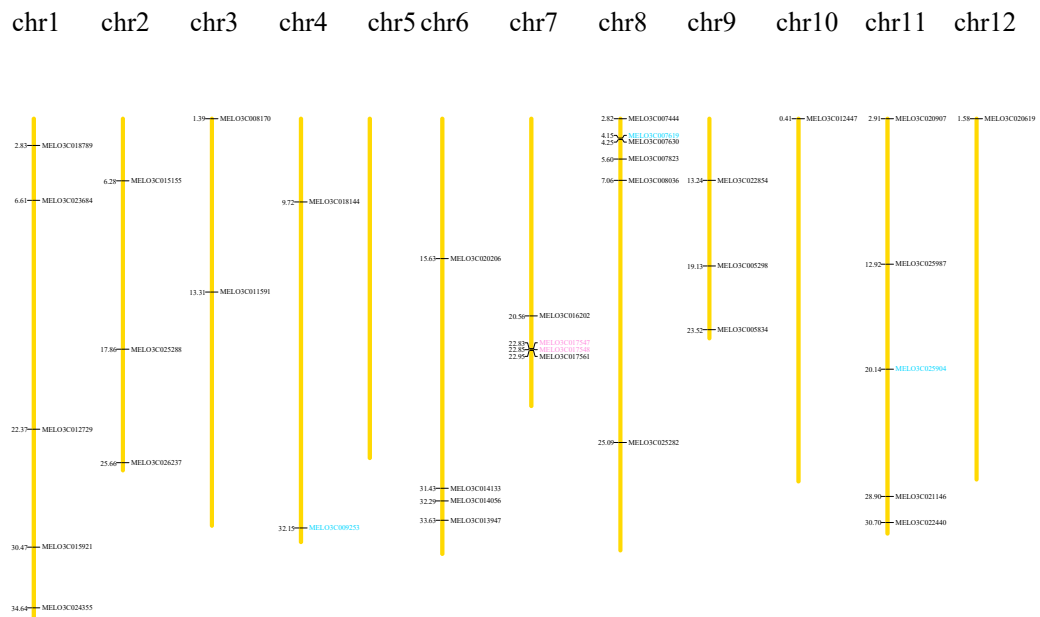


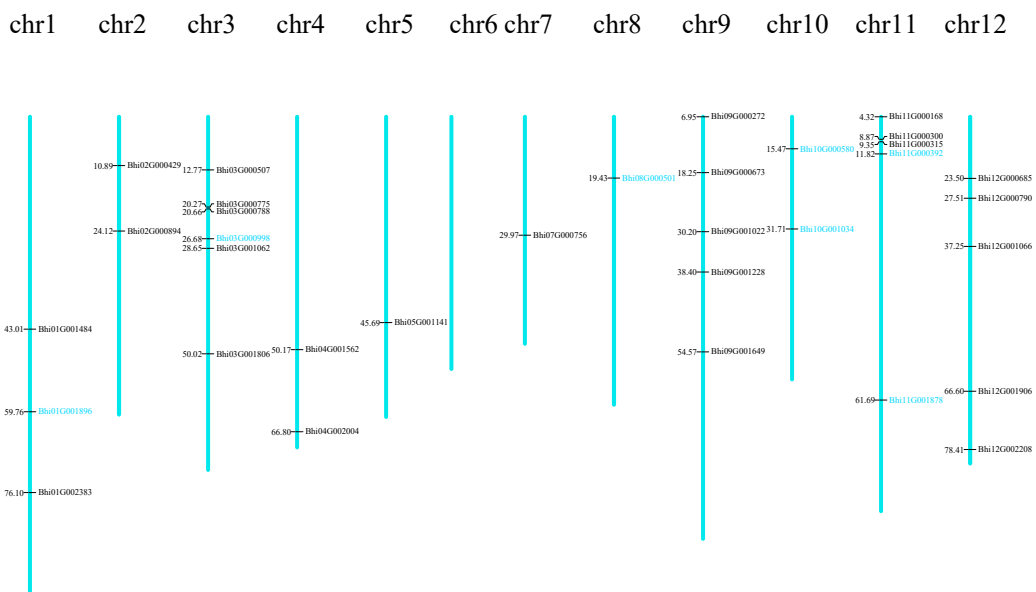
a



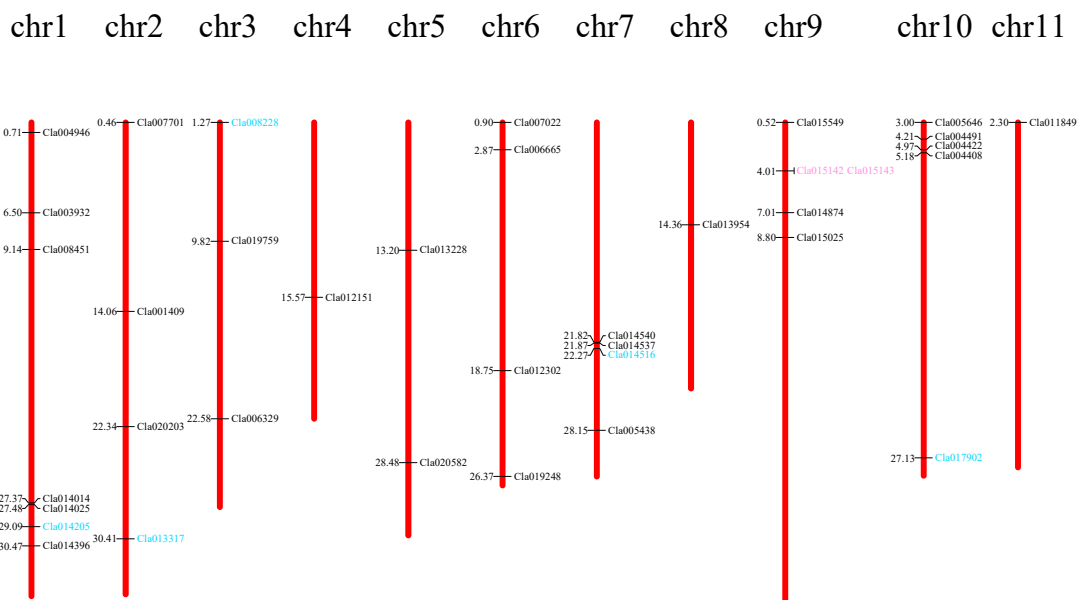
b



C

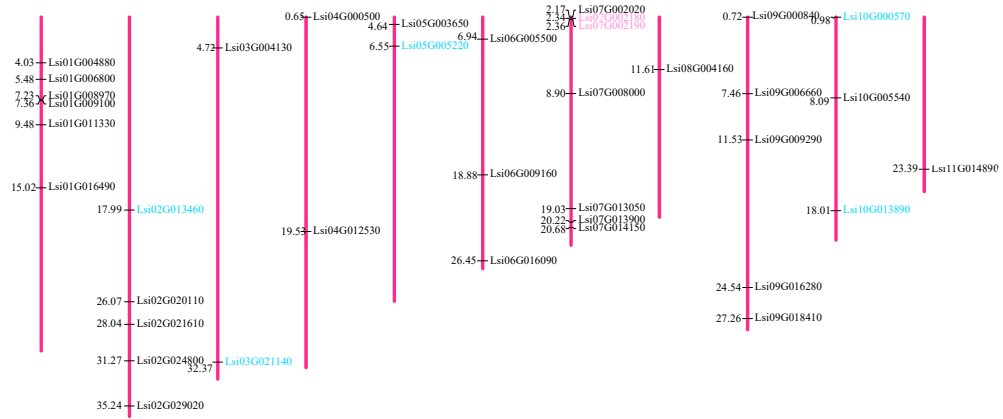


d



e

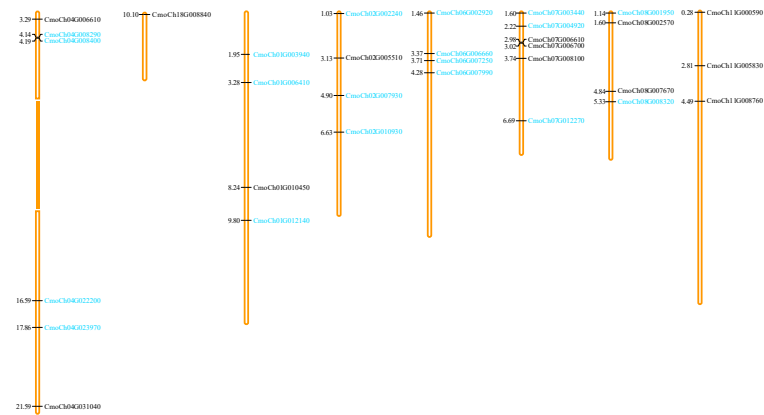
chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chr10 chr11



f

Subgenome A

chr4 chr18 chr1 chr2 chr6 chr7 chr8 chr11 chr12



Subgenome B

chr13 chr16 chr9 chr20 chr15 chr3 chr17 chr14 chr10 chr19 chr5

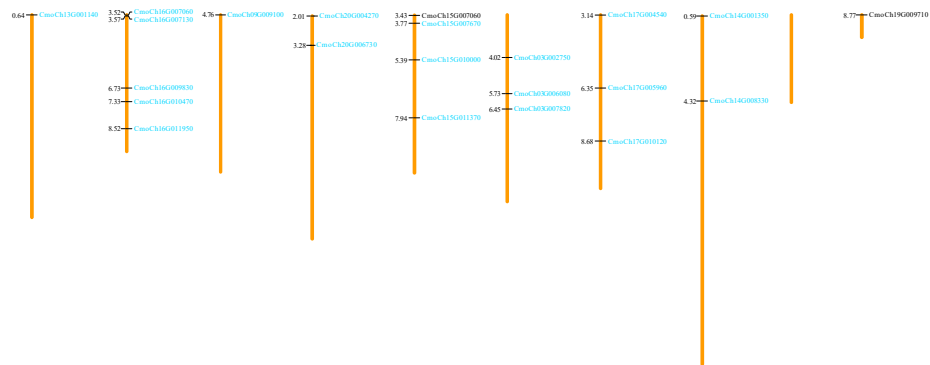


Figure S1. Chromosomal location of *GRAS* genes on six cucurbit crops. (a) cucumber, (b) melon, (c) wax gourd, (d) watermelon, (e) bottle gourd, and (f) pumpkin, respectively. In pumpkin, the chromosomes are assigned to subgenome A (the hollow bars) and subgenome B (the solid bars). The graphical view was drawn from each gene ID and chromosomes information and position of each gene are indicated by line. The magenta font indicated TD *GRAS* genes. The blue font indicated WGD *GRAS* genes.

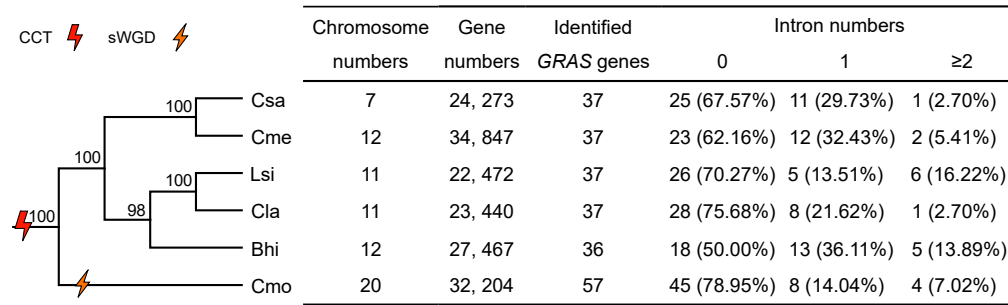













Figure S2. *GRAS* gene numbers and intron number distribution patterns in six cucurbit crops. The left panel shows a species tree of six cucurbit crops, including cucumber (Csa), melon (Cme), watermelon (Cla), bottle gourd (Lsi), wax gourd (Bhi), and pumpkin (Cmo). The abbreviations CCT and sWGD stand for cucurbit-common tetraploidization and specific whole-genome duplication, respectively. The right panel displays the intron number distribution patterns within the *GRAS* genes of the six cucurbit crops.



Figure S3. Phylogenetic tree, *GRAS* gene structure, and *GRAS* protein motifs from six cucurbit crops. (a) Phylogenetic tree of 237 *GRAS* proteins is shown on the left. *GRAS* proteins are categorized into 16 distinct clusters including SCR, SHR, DELLA, SCL32, HAM, LISCL, NSP1, PAT1, Ls, SCL3, DLT, SCL4/7, NSP2, SCLB, RAM1, and RAD1, and are represented by different colored vertical boxes; (b) The horizontal-colored boxes indicated conserved motifs within each protein; (c) CDS/UTR of *GRAS* proteins are shown on the right. A scale of protein/genes length is shown at the bottom.

S. No	Sequences	Width	Logo
1	VHIIDFDIMQGLQWPTLIQALALRPGGPP	29	
2	LFYEVCPLYKFAHFTANQAILEA	23	
3	EYLGREIVNVACEGAERVERHETLG	26	
4	ENGCLVLGWKDRPLVAASAWR	21	
5	LEZTGRRLAEFAESLGVPFEE	21	
6	NGPPFLTRFVEALHYSAJFD	21	
7	LLRLIKSLsPKIVTVVEQEAN	21	
8	PSGDPMQRLAAYFAEALAARL	21	
9	SSSSGSSRLEDSEESGLDLVHLLJAC	26	
10	KWRSRLESAGFKPVPLsSNAF	21	
11	KLEDVTREDLGVRPGEALAVNFAFRLHHMPD ESVSTENPRD	41	

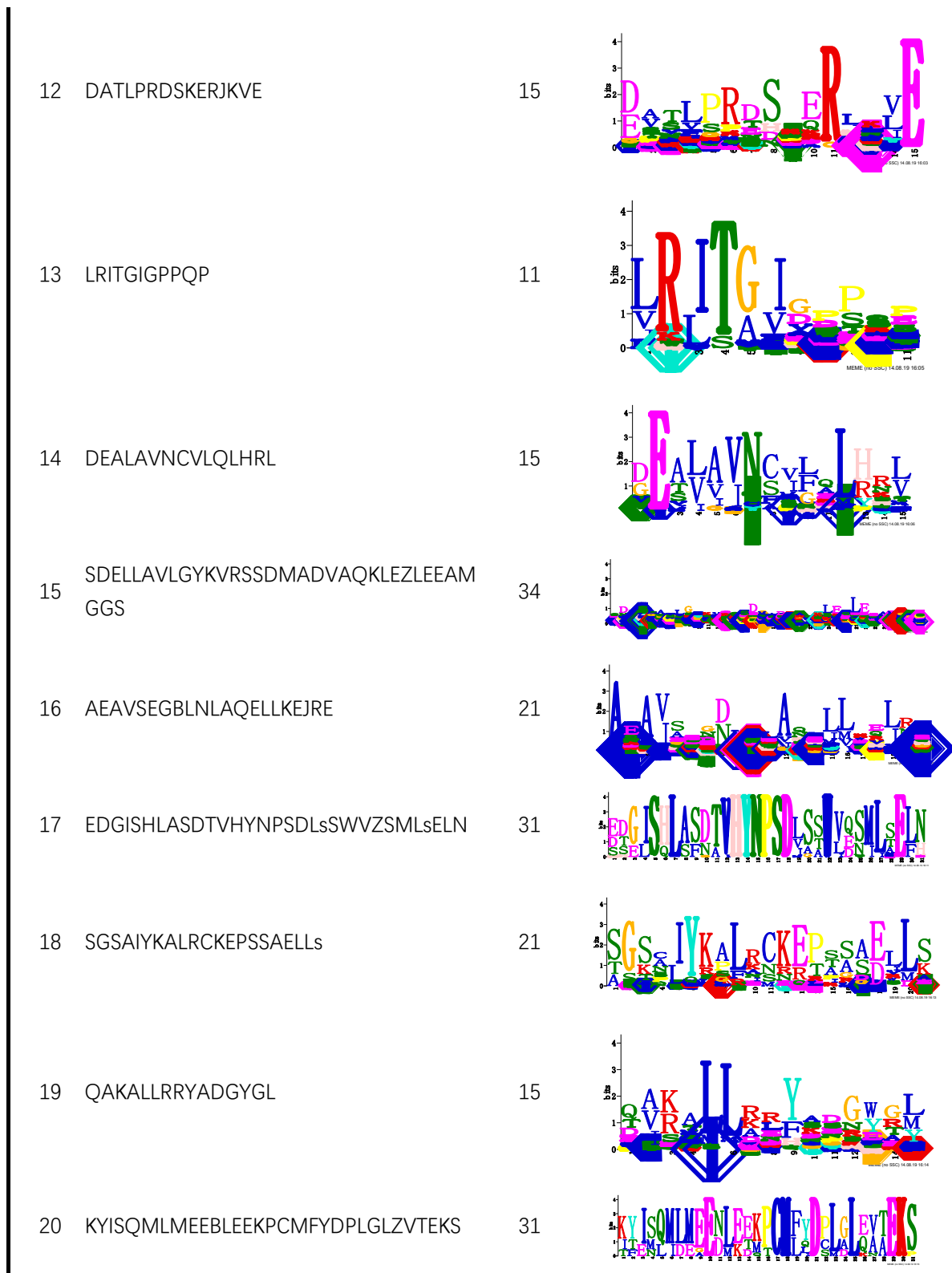


Figure S4. Sequence analysis and weblog of 20 identified motifs of 237 *GRAS* proteins from six cucurbit crops.





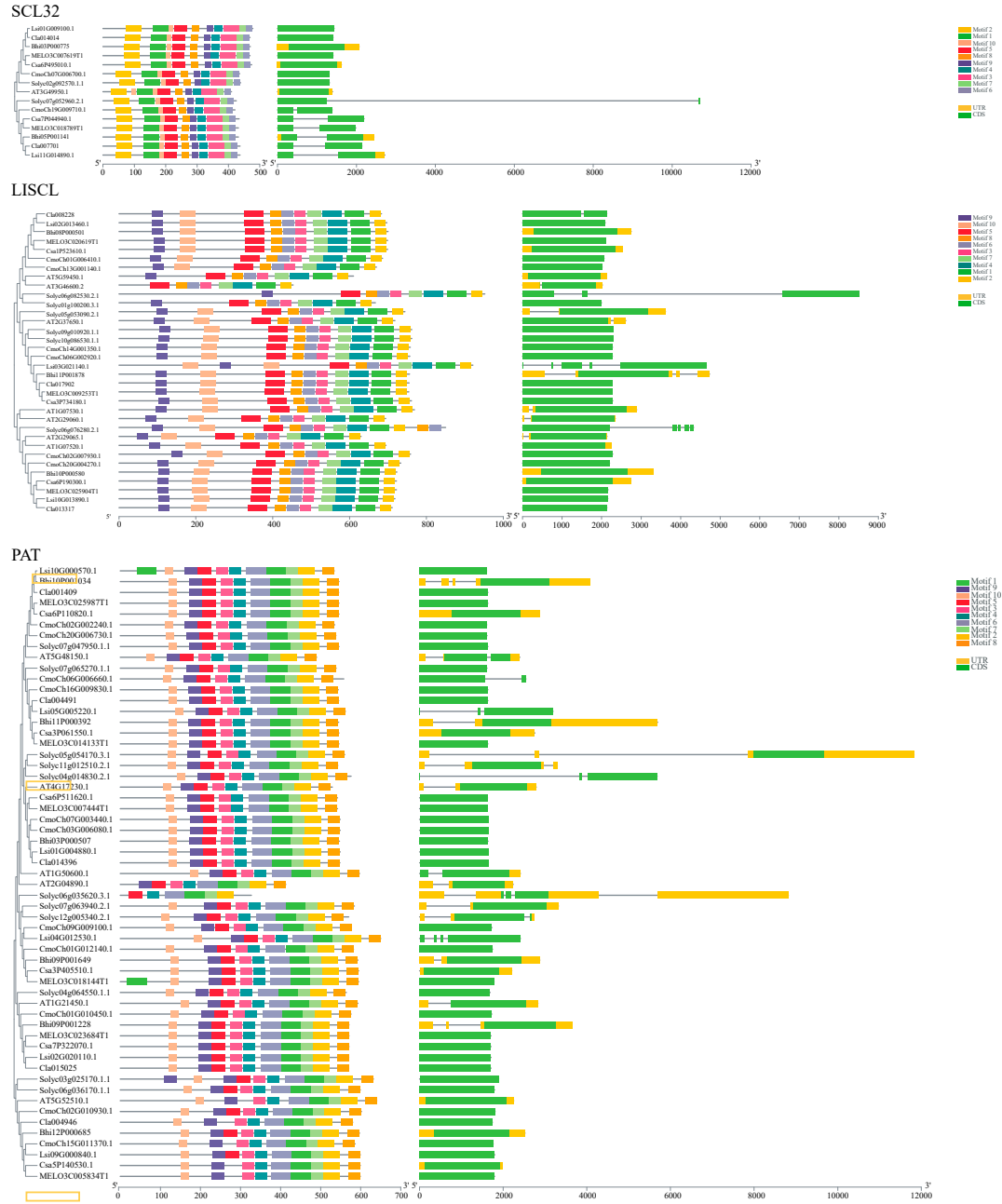


Figure S5. Phylogenetic tree, *GRAS* gene structures and *GRAS* protein motifs from *Arabidopsis*, tomato and six cucurbit crops from different clades. From top to bottom on the figures are, in order, DLT, SCR, Ls, SCLB, NSP2, HAM, SCL4/7, RAM1, RAD1, SCL3, DELLA, SHR, NSP1, SCL32, LISCL, and PAT 1 clades. The neighbor-joining tree of *GRAS* proteins is shown on the left. The horizontal-colored boxes indicate conserved motifs within each protein. CDS/UTR of *GRAS* proteins are shown on the right. A scale of protein/genes length is shown at the bottom.

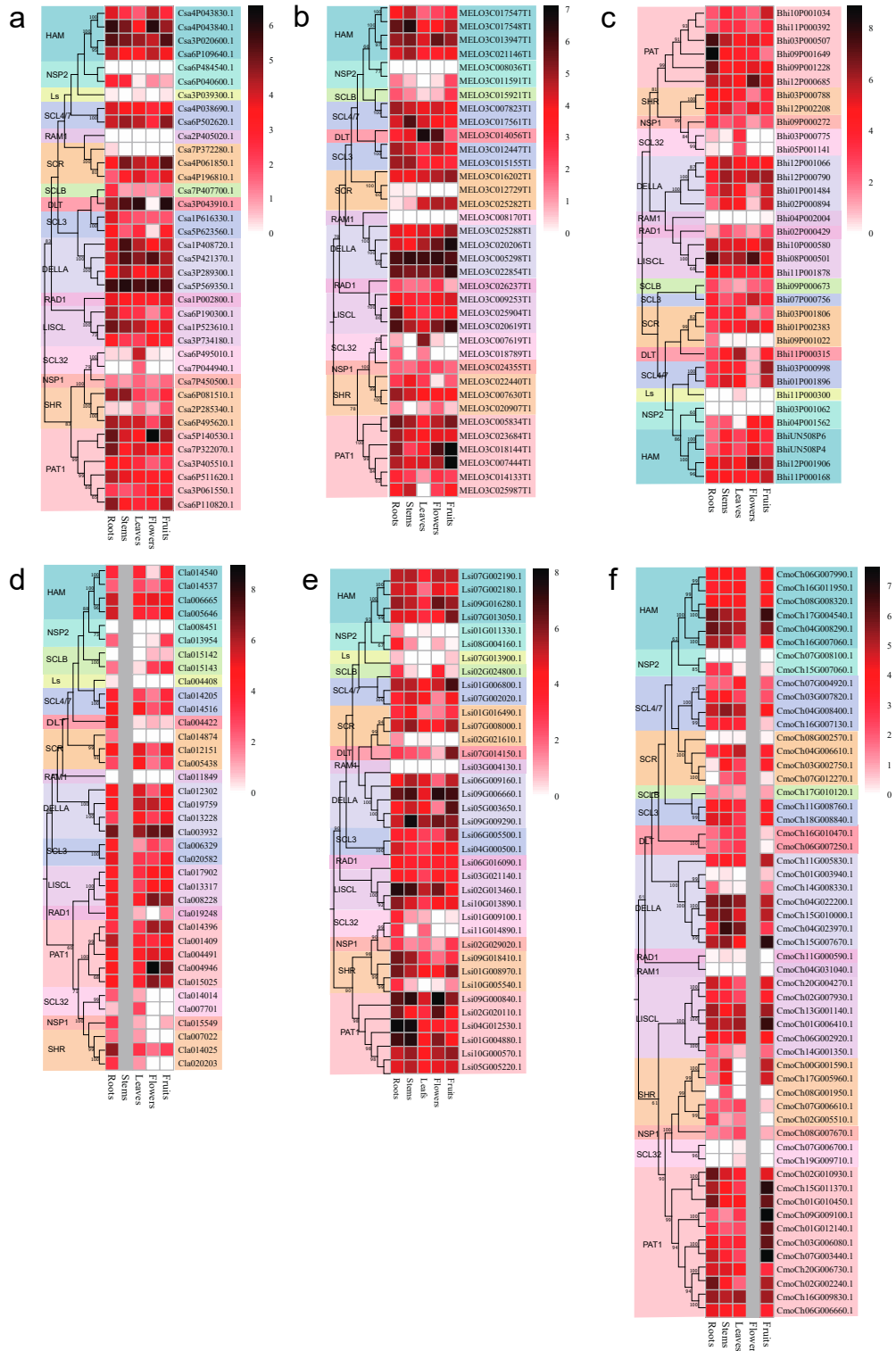
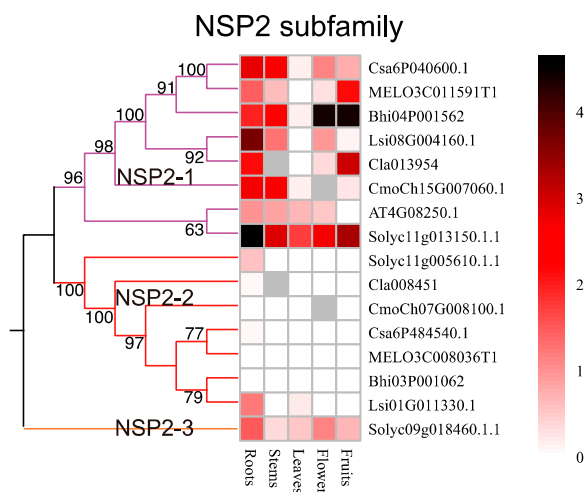
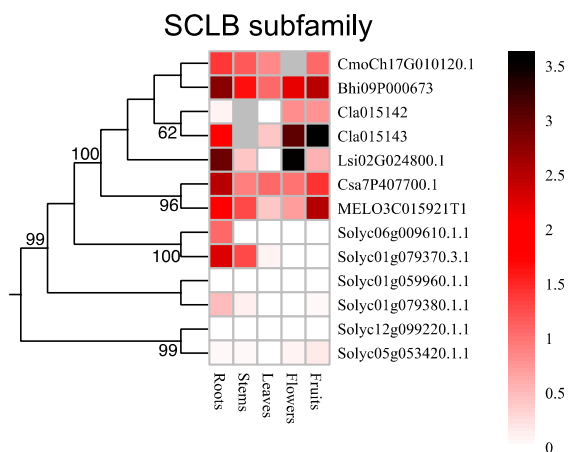
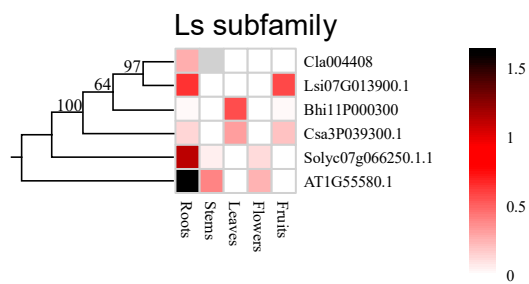
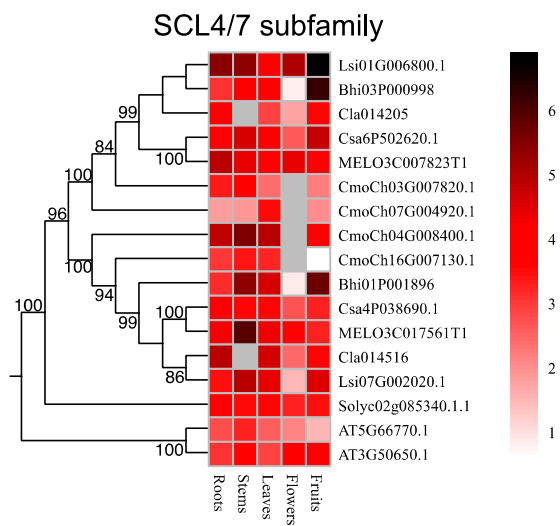
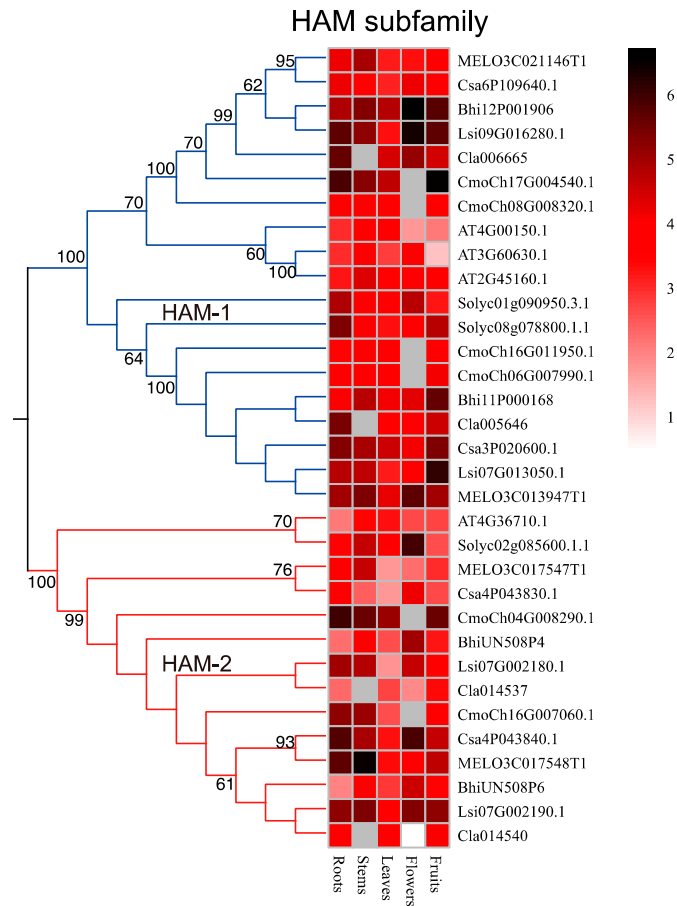
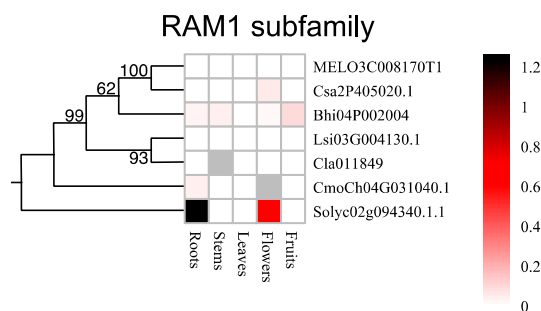
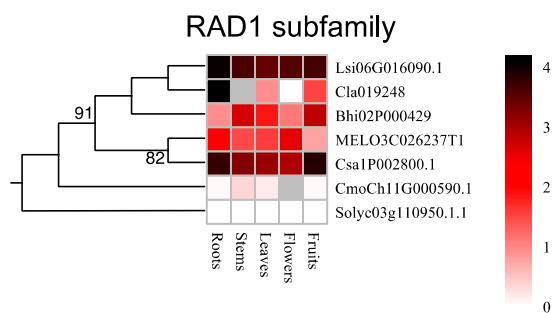
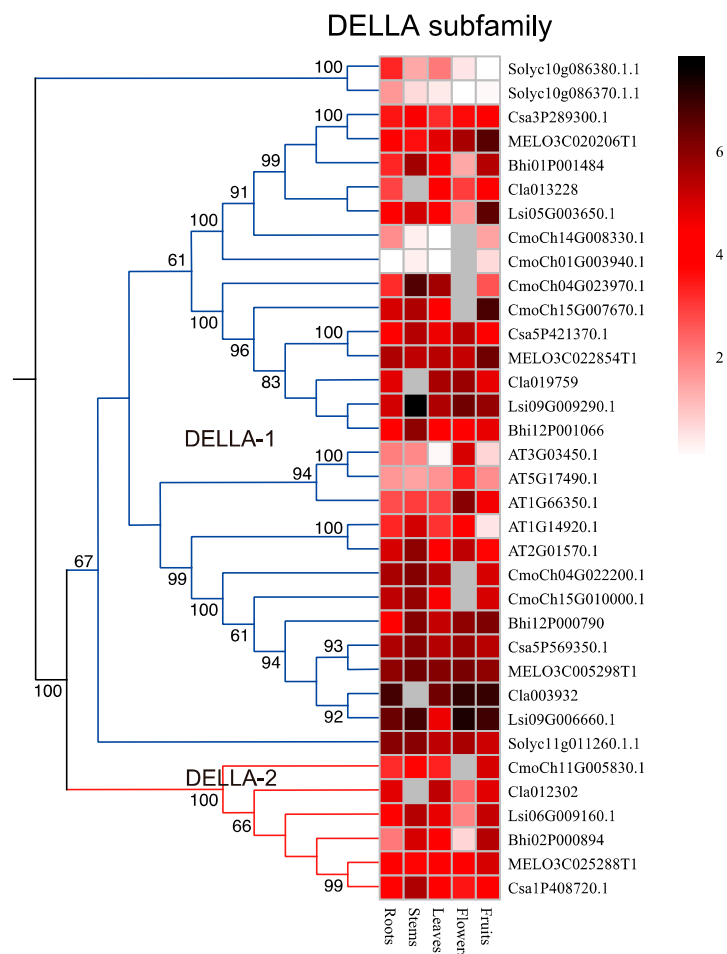
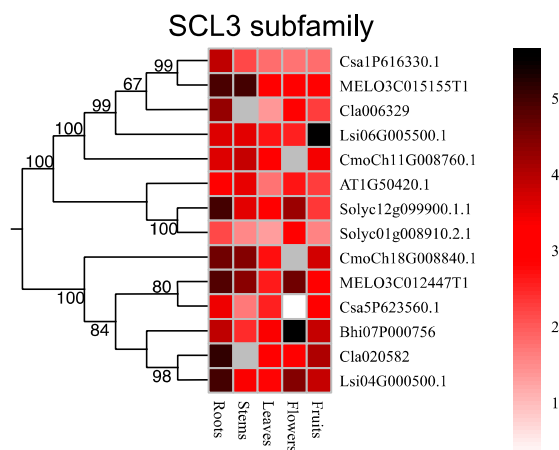
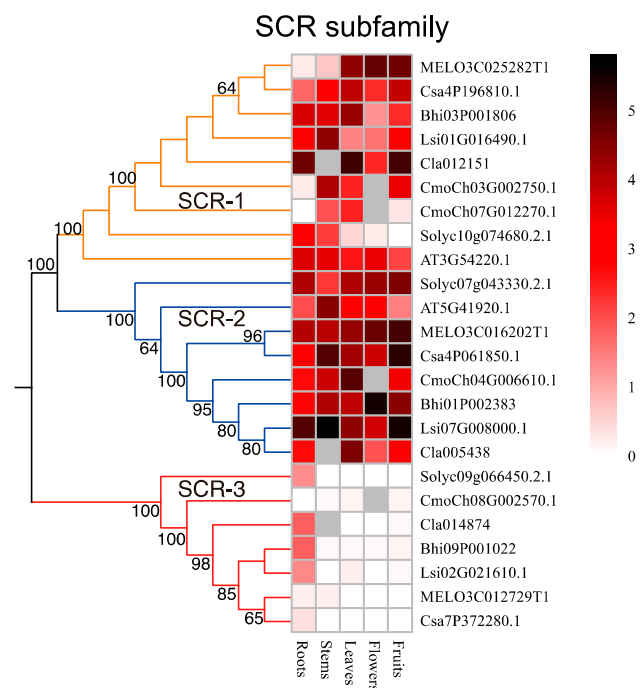
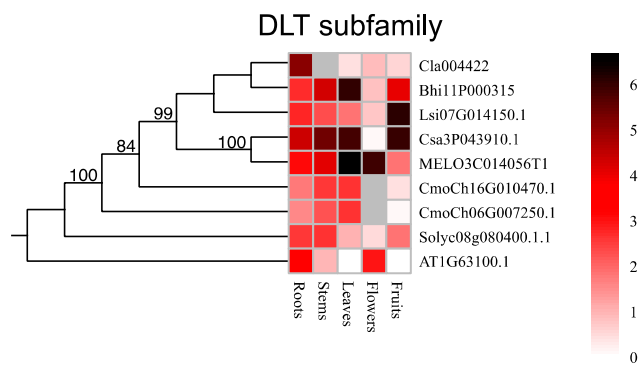


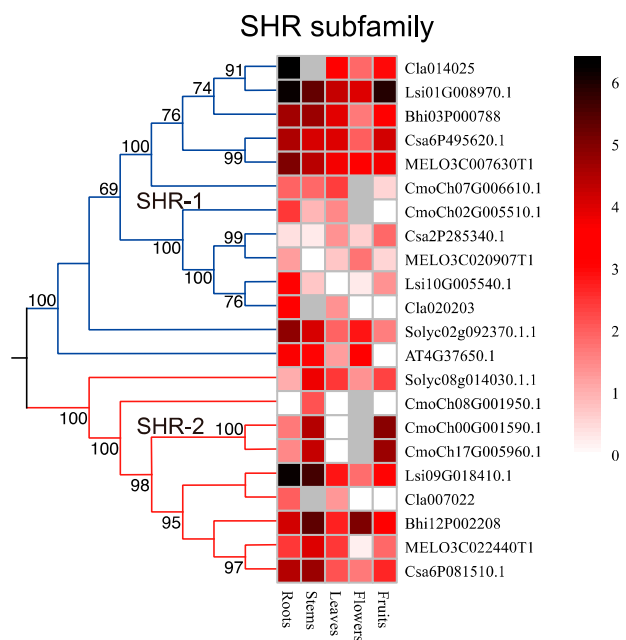
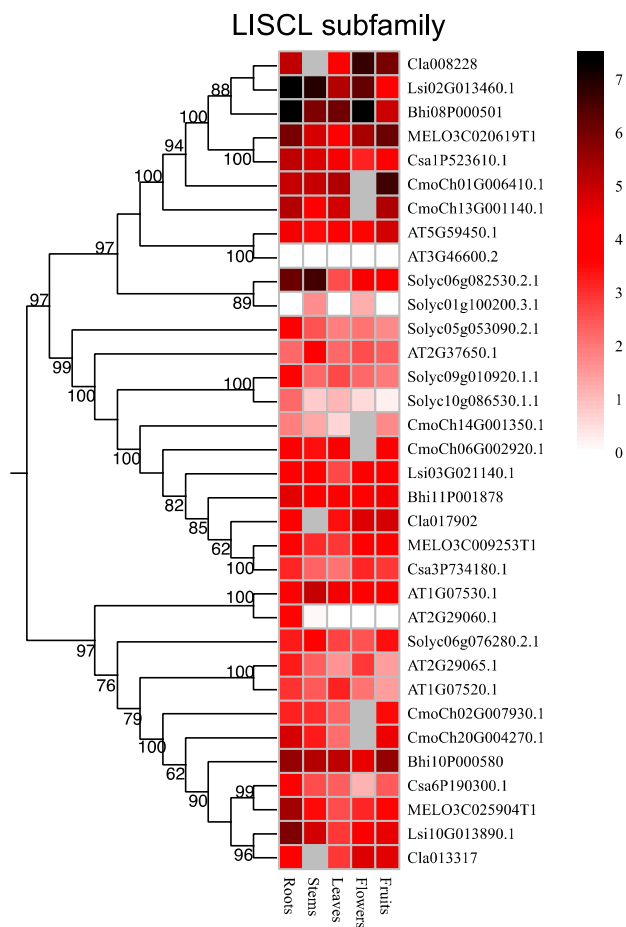
Figure S7. Expression profiles of 237 cucurbit *GRAS* genes in different tissues. (a) cucumber, (b) melon, (c) wax gourd, (d) watermelon, (e) bottle gourd, and (f) pumpkin. Neighbor-joining tree of *GRAS* proteins is shown on the left, and the right is the heatmap. In the heat map, rows represent genes, columns represent different tissues. The color changes from white to black represent the relative expression ($\log_2(\text{FPKM} + 1)$) in different tissues respectively, and the gray color represents missing values.

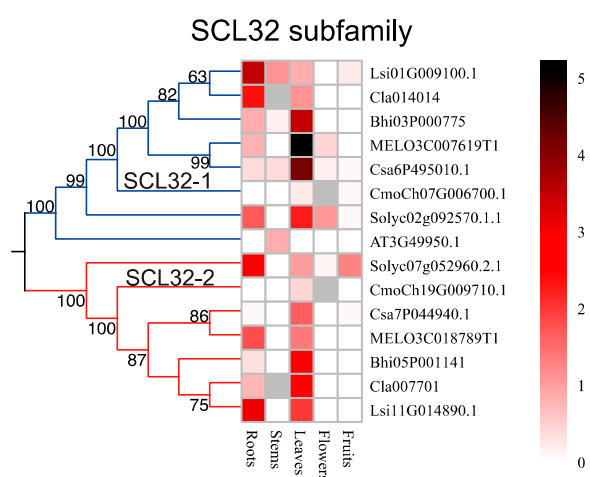
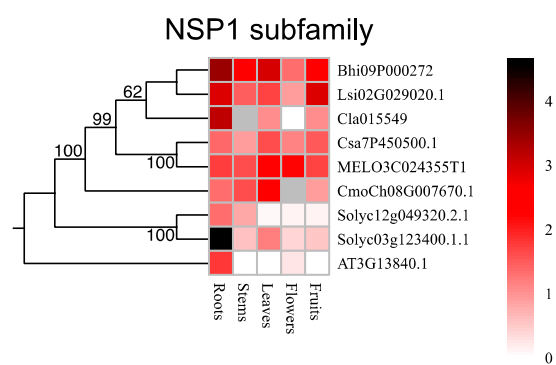












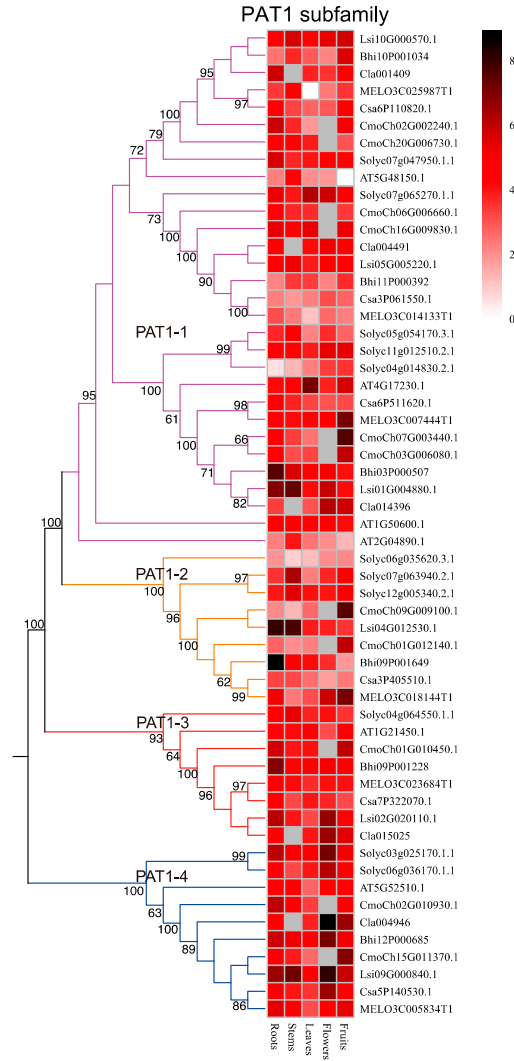


Figure S8. Expression profiles of 318 *GRAS* genes in *Arabidopsis*, tomato and six cucurbit plants from different clades. From top to bottom on the figures are, in order, DLT, SCR, Ls, SCLB, NSP2, HAM, SCL4/7, RAM1, RAD1, SCL3, DELLA, SHR, NSP1, SCL32, LISCL, and PAT1 clades. Neighbor-joining tree of *GRAS* proteins is shown on the left, and the right is the heat map. In the heat map, and columns represent different tissues, while rows represent genes, including roots, stems, leaves, flowers, and fruits. The color changes from white to black represent the relative expression ($\log_2(\text{FPKM} + 1)$) in different tissues respectively.