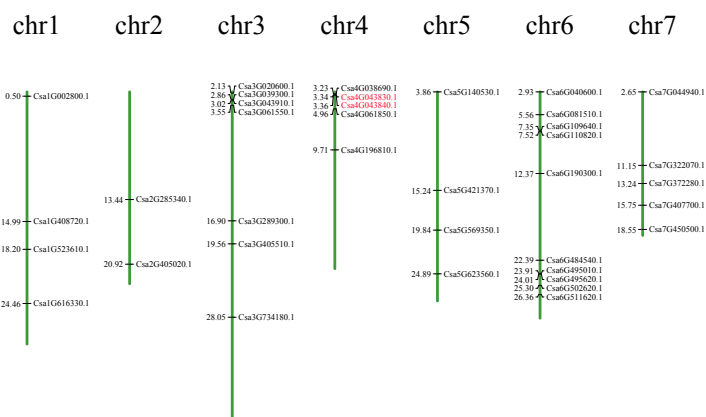
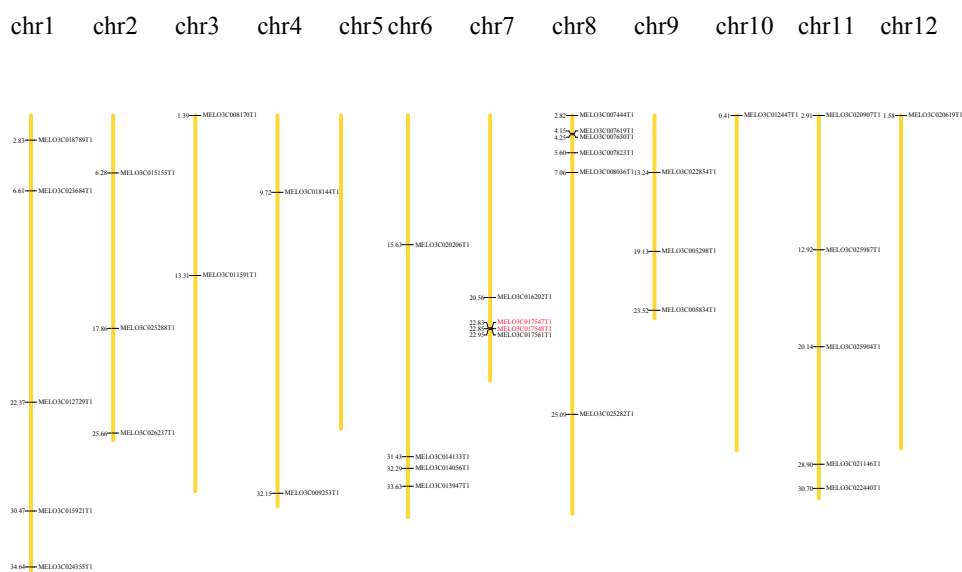


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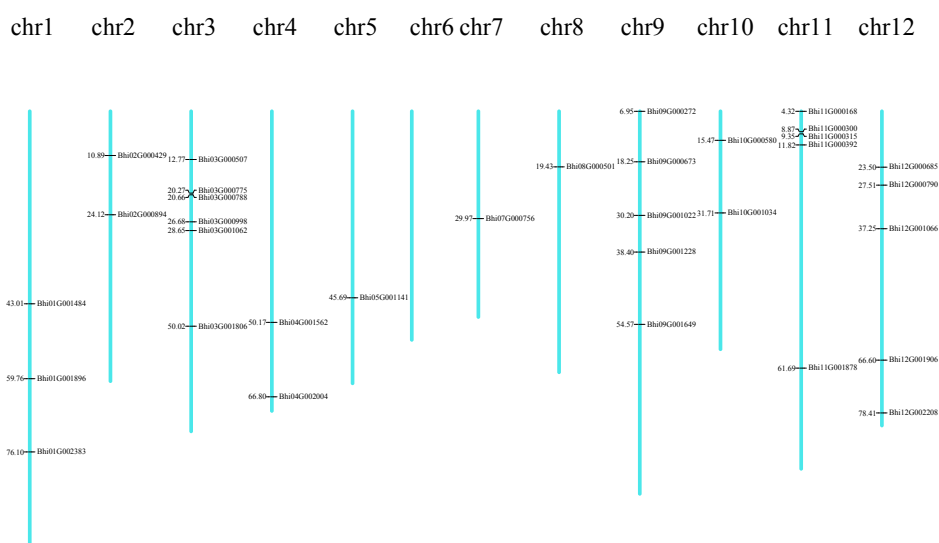


2 b



3

4 c

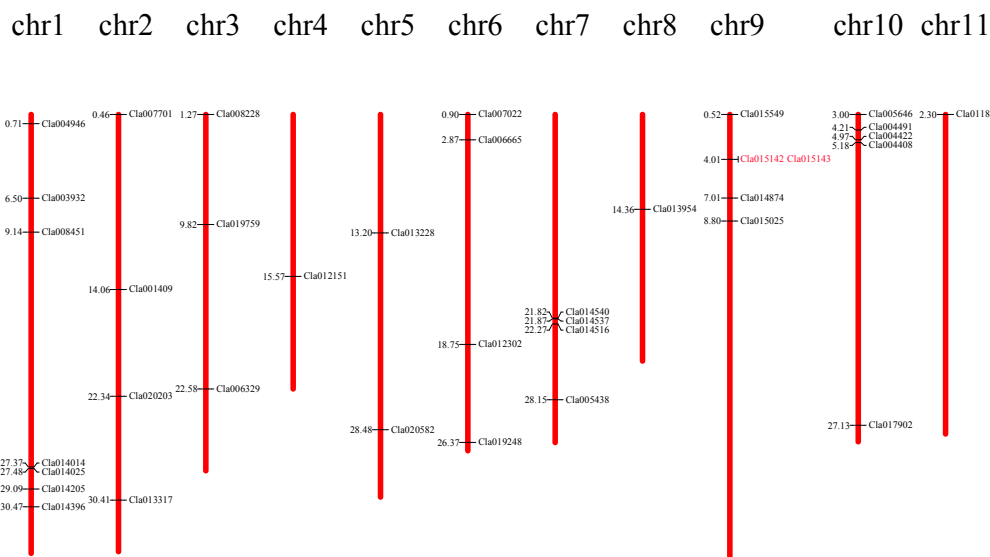


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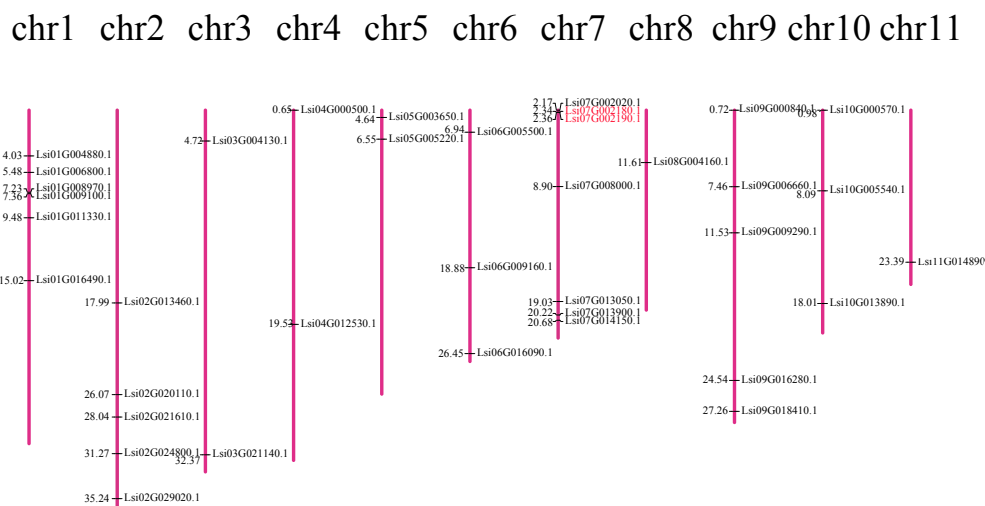
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8 d



9

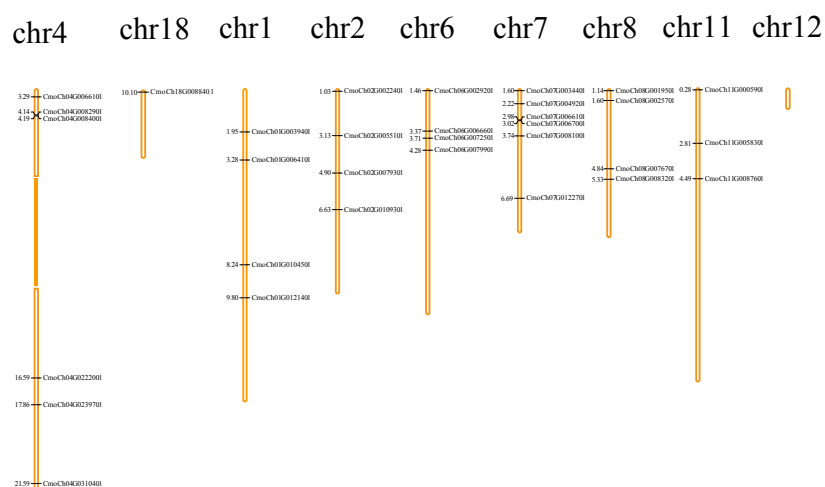
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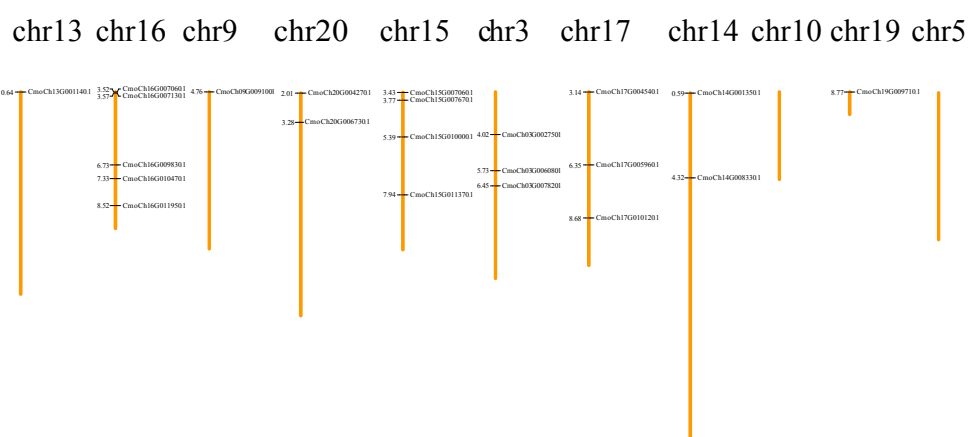
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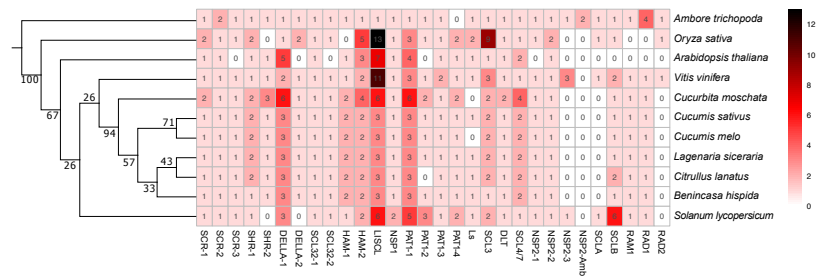
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Subgenome A



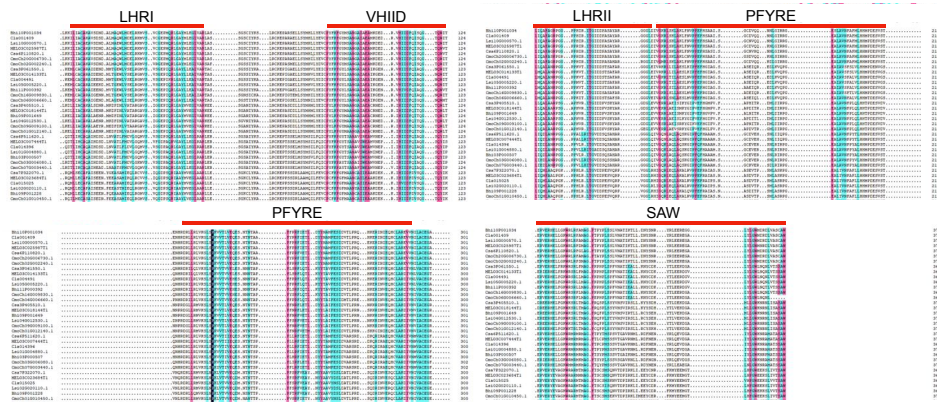
Subgenome B



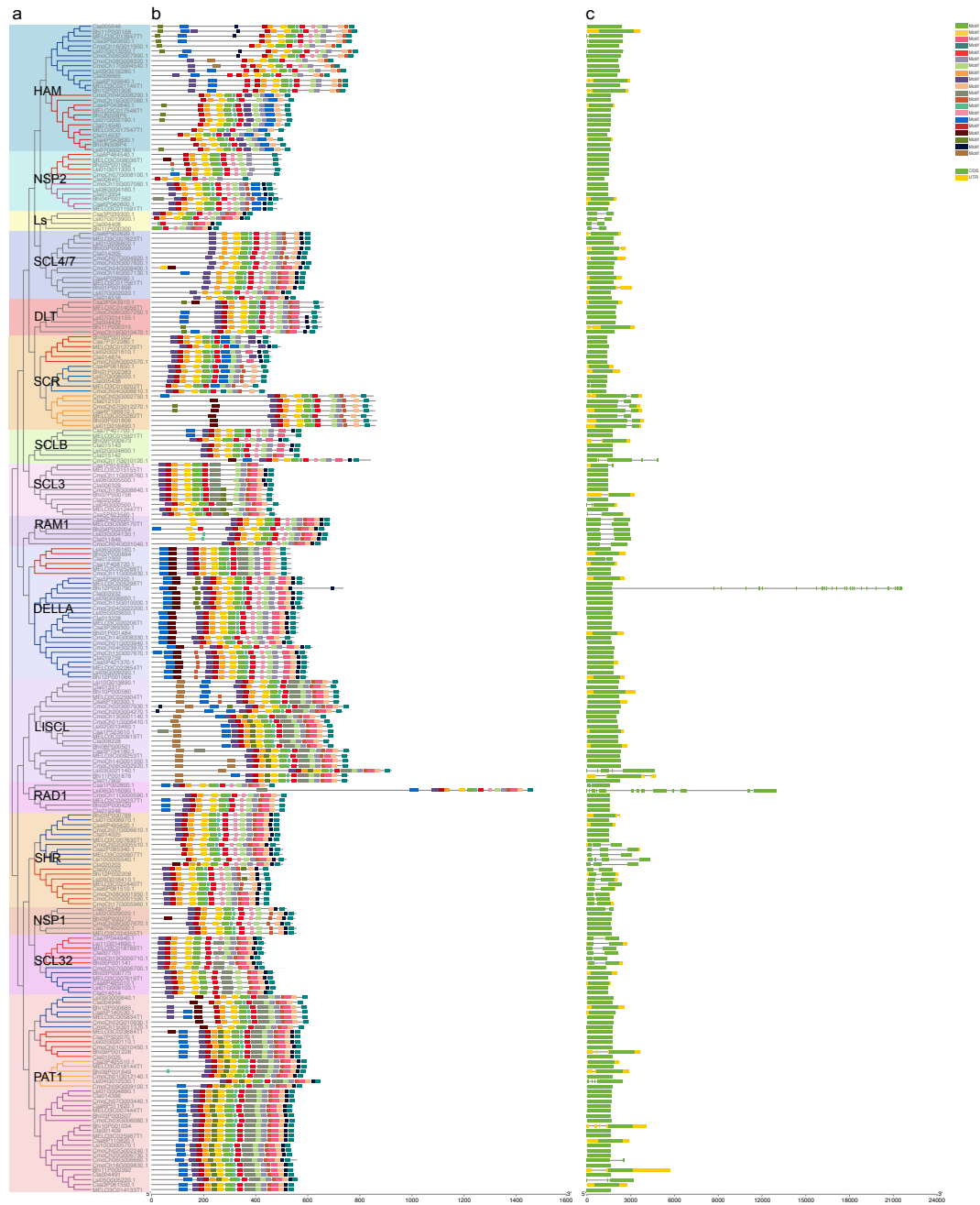


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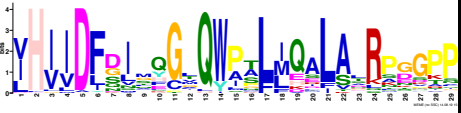
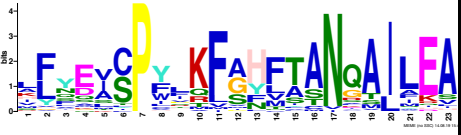
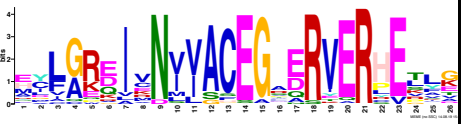
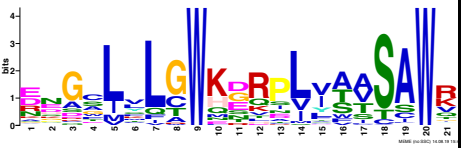
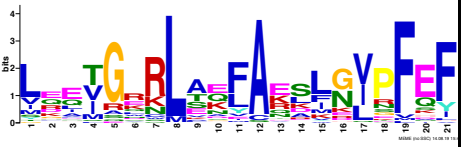
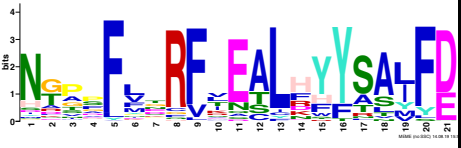
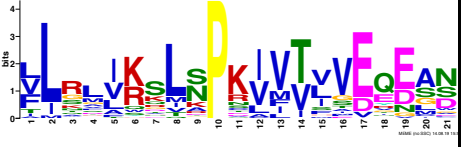
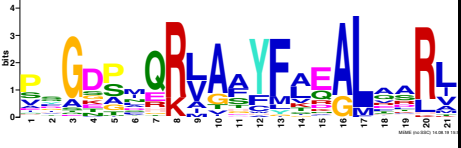
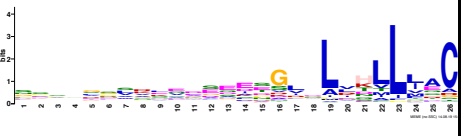
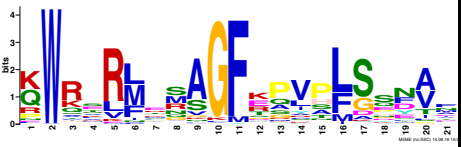
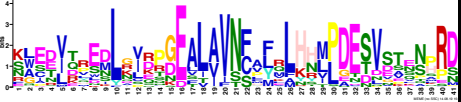
22 **Additional Fig. S2 GRAS genes distribution by orthologous groups (OGs) in *A.trichopoda*,**
 23 ***V.vinifera*, *O. sativa*, *A. thaliana*, *S. lycopersicum* and six Cucurbitaceae species.** Numbers in the
 24 matrix represent the number of genes by OG specified in the header. The gradient color from white to
 25 black illustrates the abundance of genes.

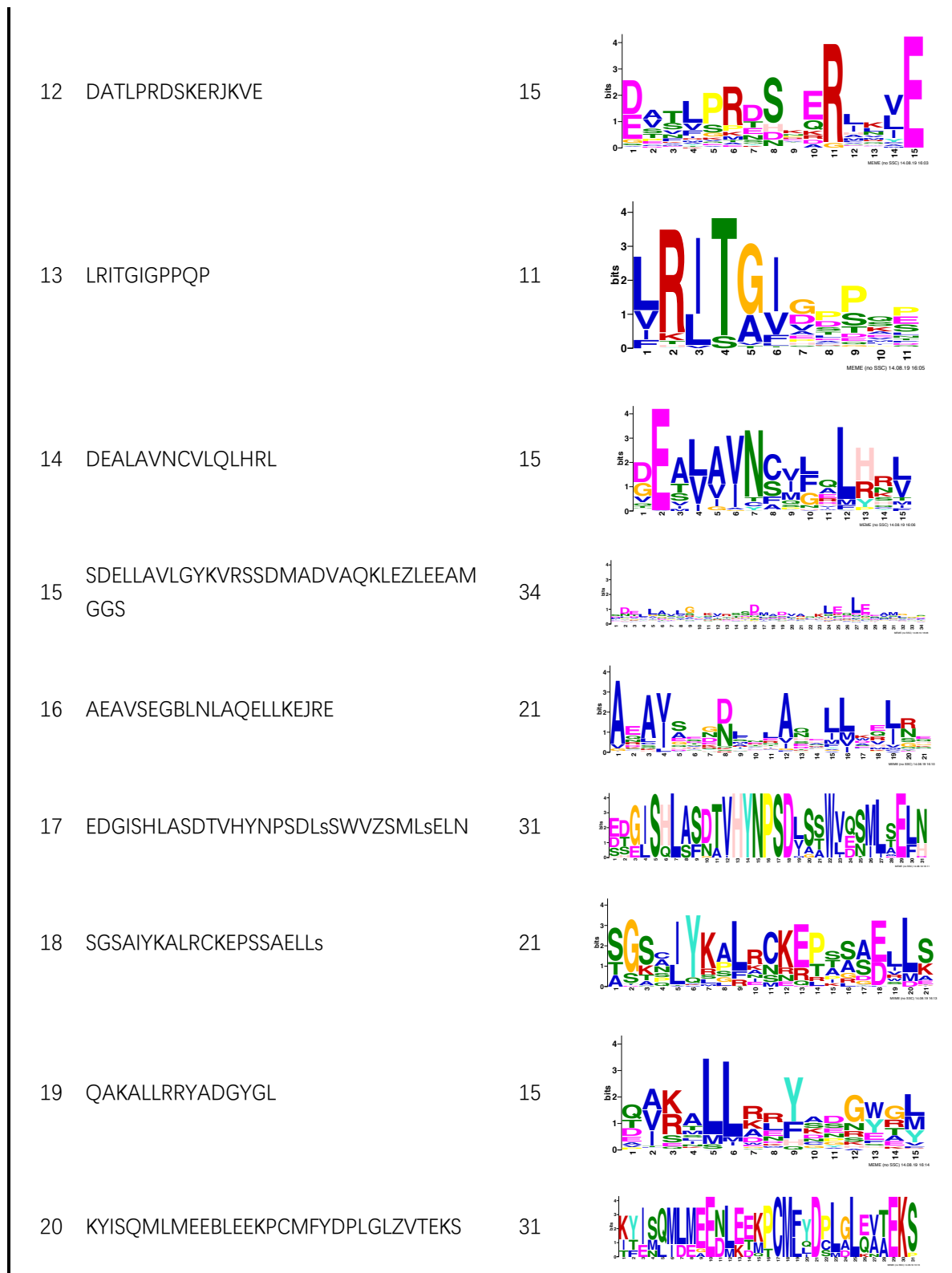


Additional Fig. S3 Multiple alignment of selected GRAS conserved domain sequences in six Cucurbitaceae species by DNAMAN software. Black, pink and blue background color indicate the homology level of amino acid residues is 100%, above 75 and 50%, respectively. Conserved LHRI, VHIID, LHRII, PFYRE and SAW motifs were marked with red line.



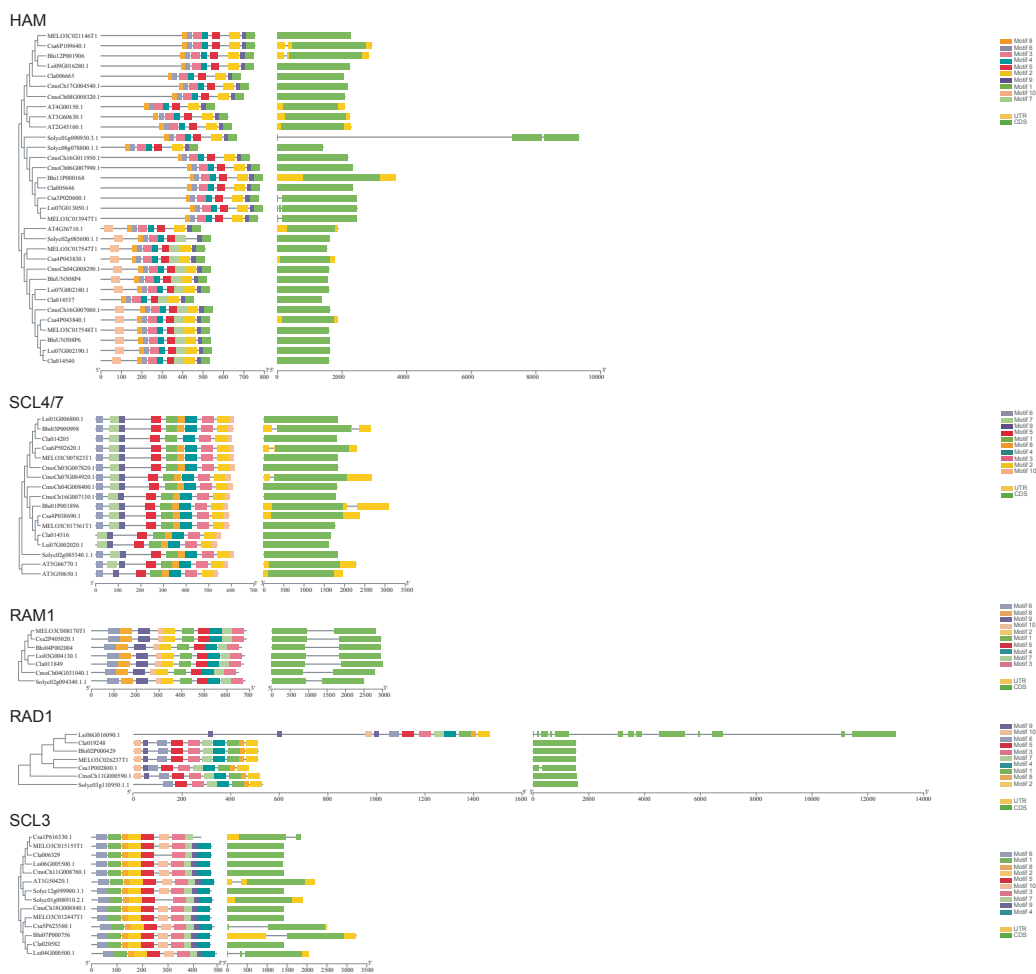
Additional Fig. S4 Phylogenetic tree, *GRAS* gene structure and GRAS protein motifs from six Cucurbitaceae species. **a** Phylogenetic tree of 237 GRAS proteins is shown on the left. GRAS proteins are categorized into 16 distinct clusters including SCR, SHR, DELLA, SCL32, HAM, LISCL, NSP1, PAT1, Ls, SCL3, DLT, SCL4/7, NSP2, SCLB, RAM1 and RAD1, and are represented by different colored vertical boxes. **b** The horizontal-colored boxes indicate 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	LFYEVCPYLKFAHFTANQAILEA	23	
3	EYLGREIVNVACEGAERVERHETLG	26	
4	ENGCLVLGWKDRPLVAASAWR	21	
5	LEZTGRRLAEFAESLGVPFEF	21	
6	NGPPFLTRFVEALHYSAJFD	21	
7	LLRLIKSLsPKIVTVVEQEAN	21	
8	PSGDPMQRLAAYFAEALAARL	21	
9	SSSSGSSRLEDSEESGLDLVHLLJAC	26	
10	KWRSRLESAGFKPVPLsSNAF	21	
11	KLEDVTREDLGVRPGEALAVNFAFRLHHMPD ESVSTENPRD	41	

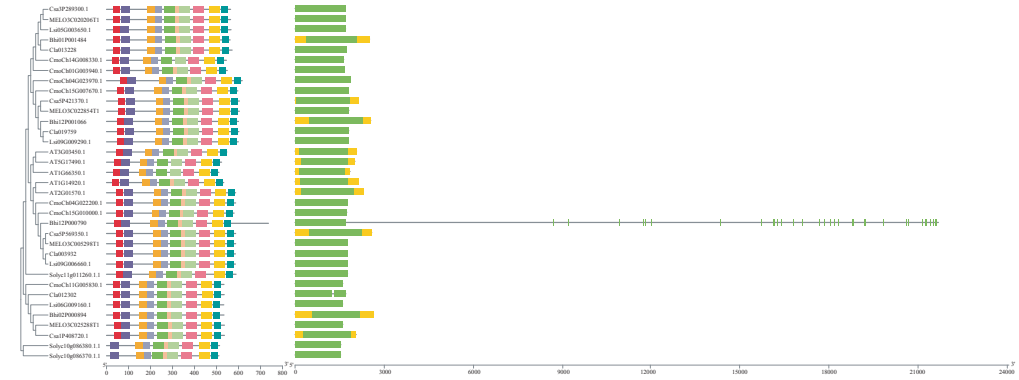


42 **Additional Fig. S5 Sequence analysis and weblog of 20 identified motifs of 237 *GRAS* proteins from**
43 **six Cucurbitaceae species.**

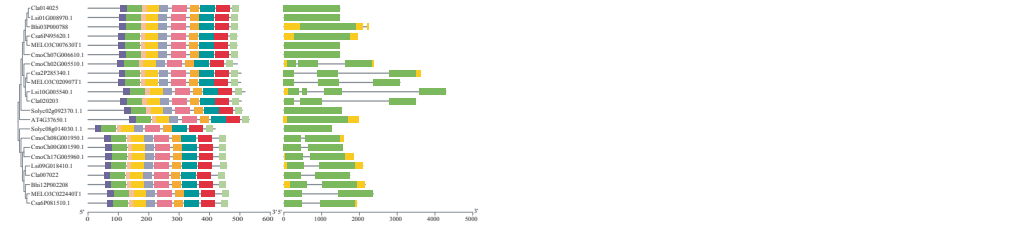




DELLA



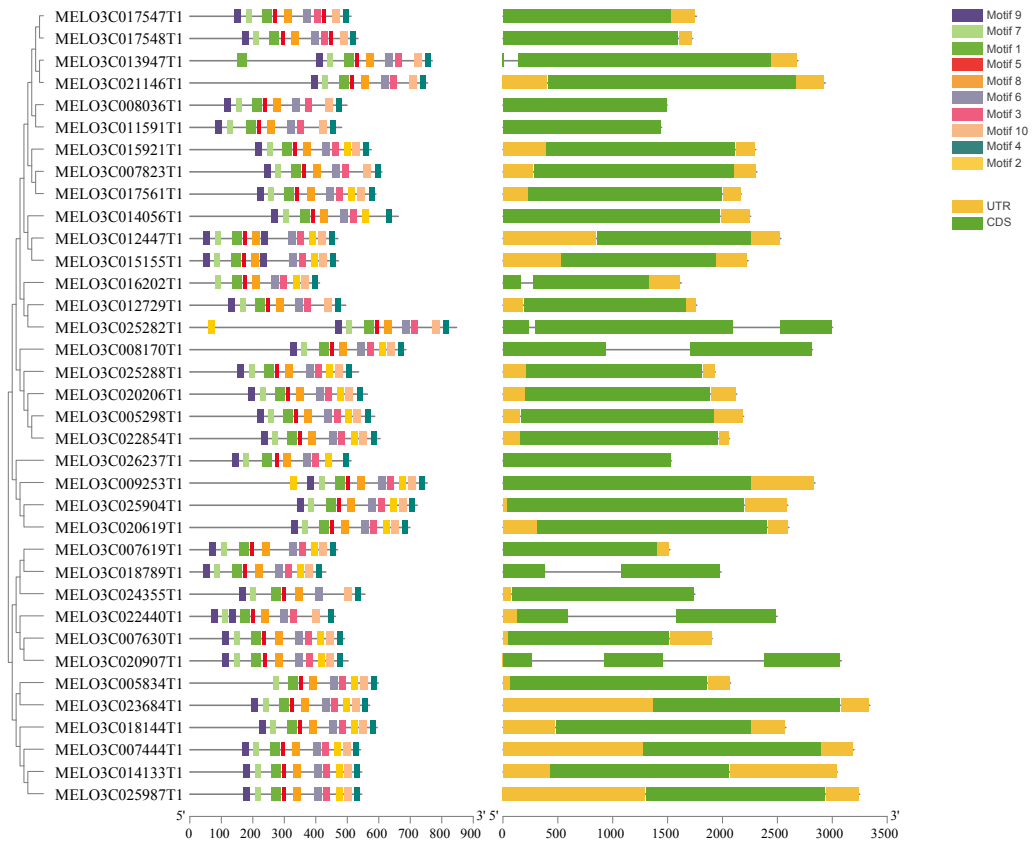
SHR



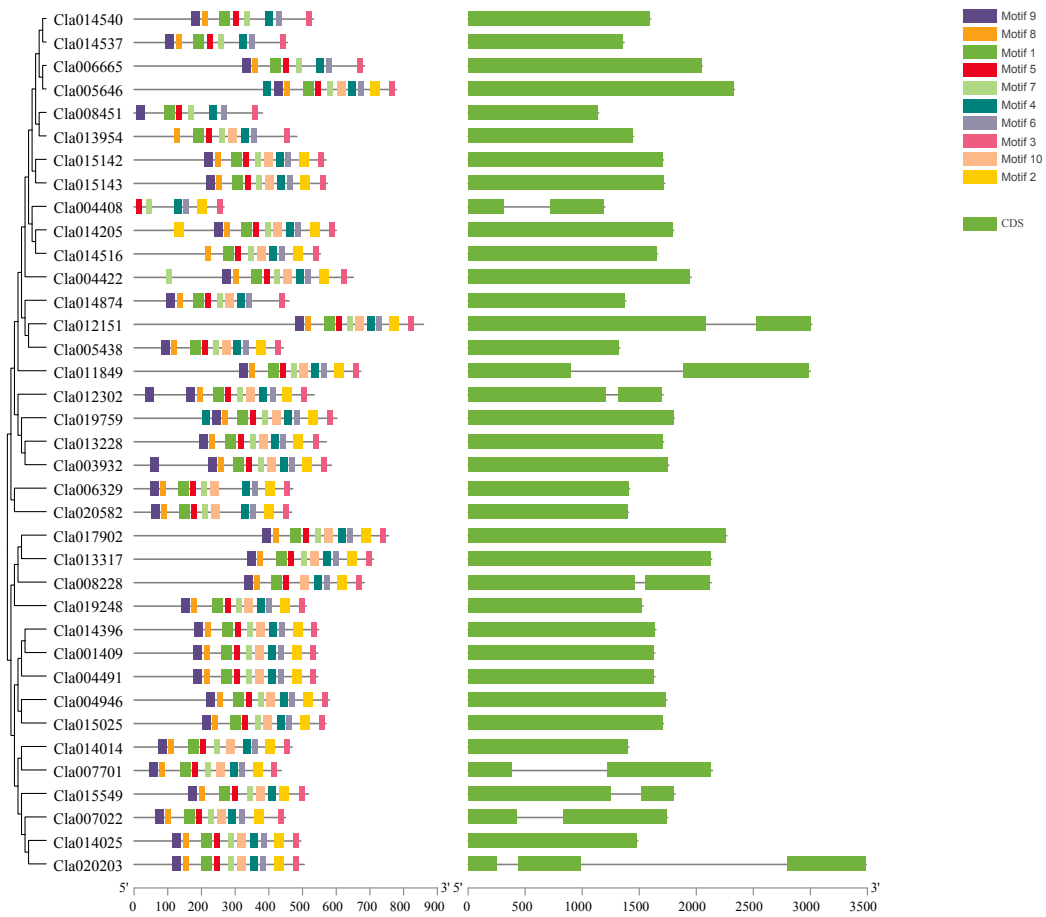
NSP1



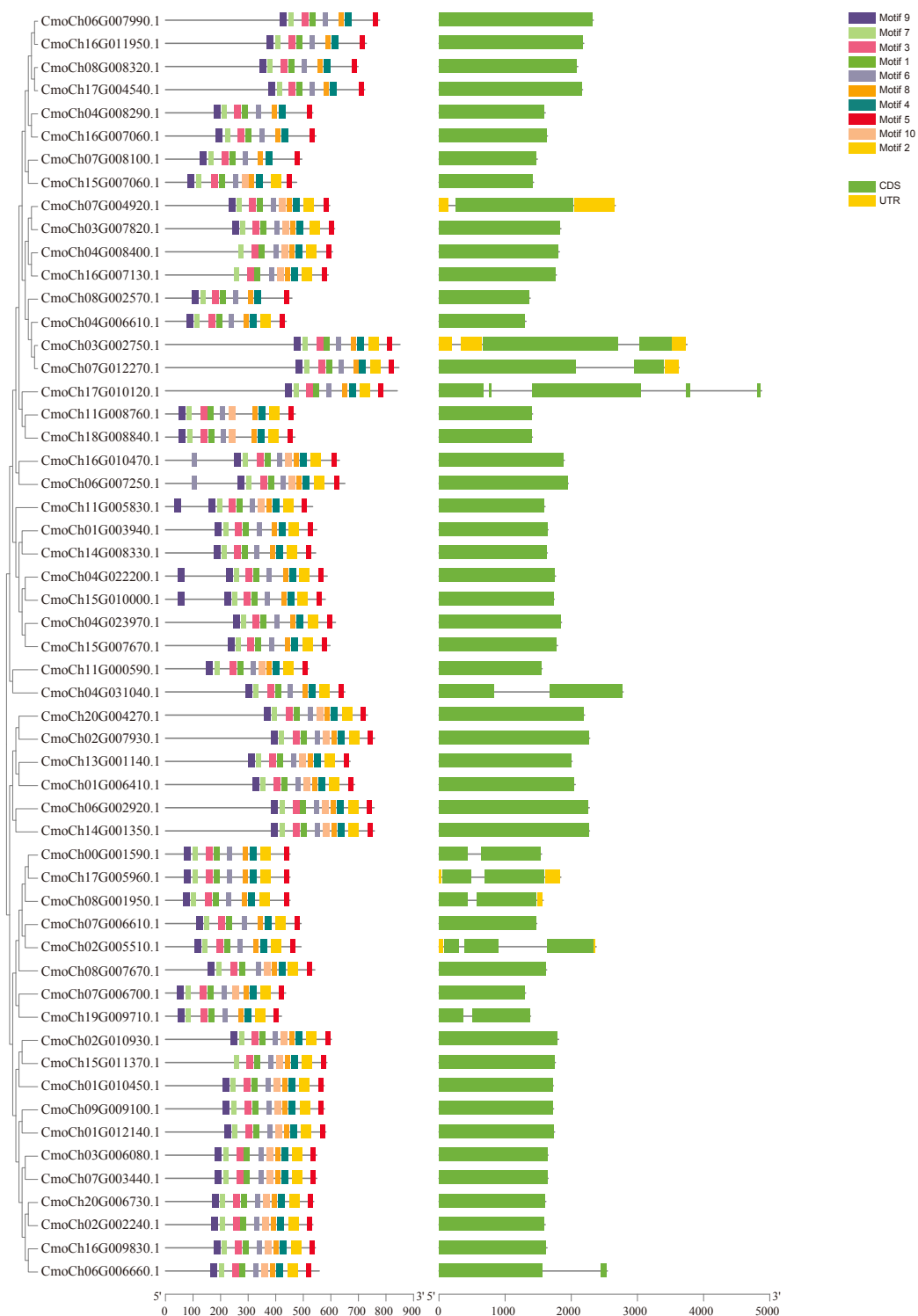












71

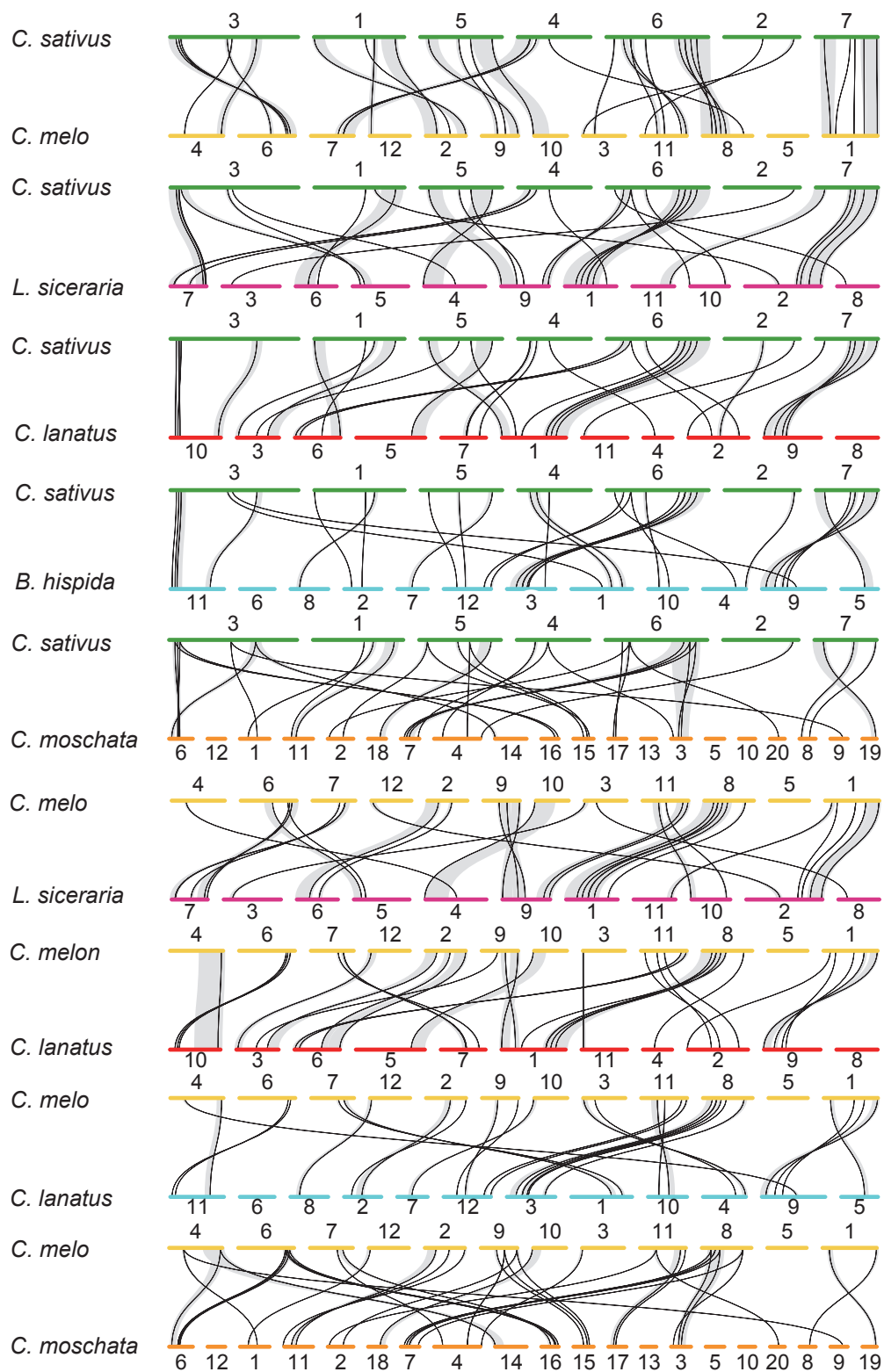
72 **Additional Fig. S7 Phylogenetic tree, *GRAS* gene structures and GRAS protein motifs from six**

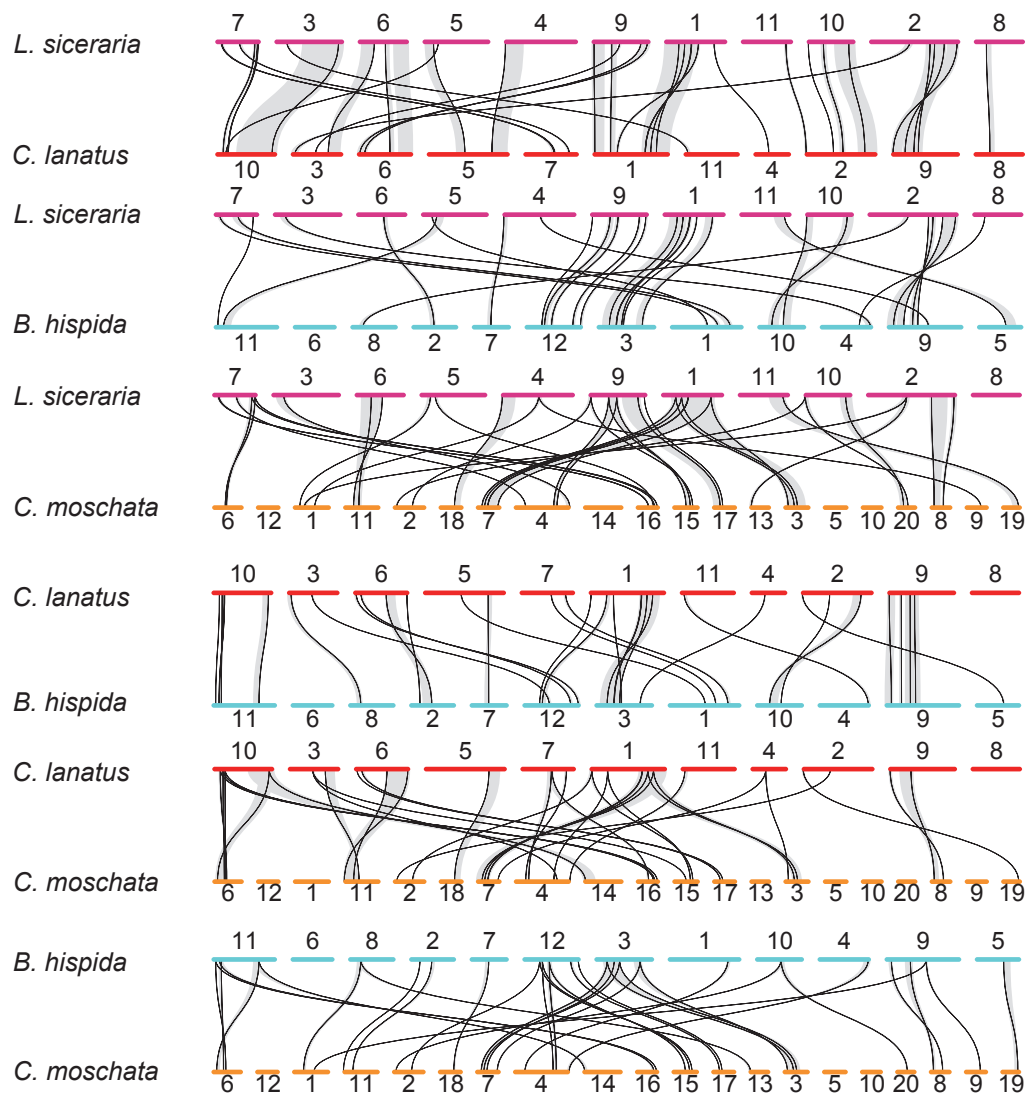
73 ***Cucurbitaceae* species. a, *C. sativus*, b, *C. melo*, c, *B. hispida*, d, *C. lanatus*, e, *L. siceraria* and f, *C.***

74 ***moschata*, respectively. Neighbor-joining tree of GRAS proteins is shown on the left. The horizontal**

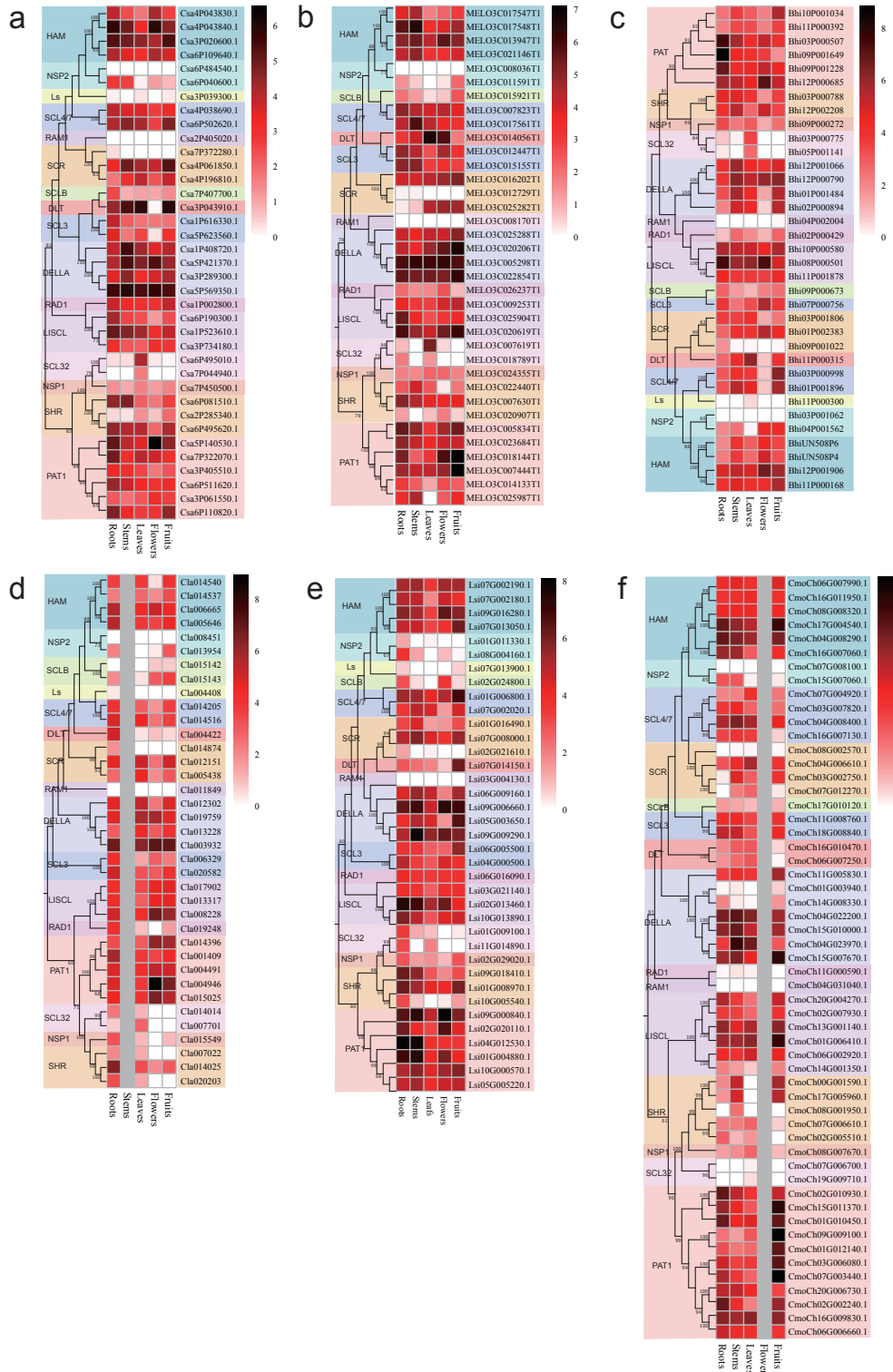
75 **colored boxes indicate conserved motifs within each protein. CDS/UTR of GRAS proteins are shown on**

76 **the right. A scale of protein/genes length is shown at the bottom.**

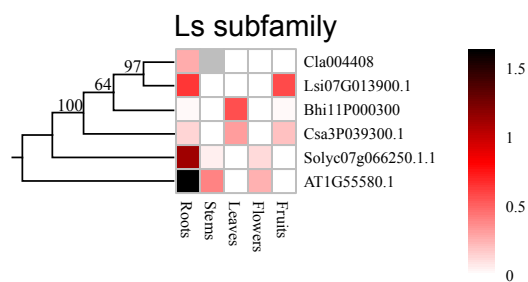




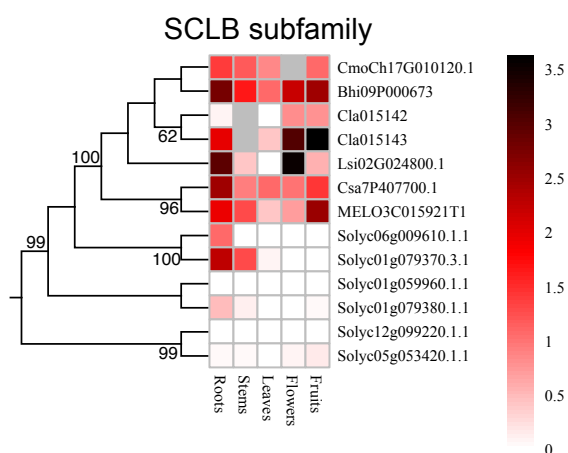
Additional Fig. S8 Synteny analysis of *GRAS* genes between six Cucurbitaceae species. The gray lines in the background represent the genes in the collinear blocks where the *GRAS* genes are located between the genomes of six Cucurbitaceae species, and the black lines represent the *GRAS* collinear genes.



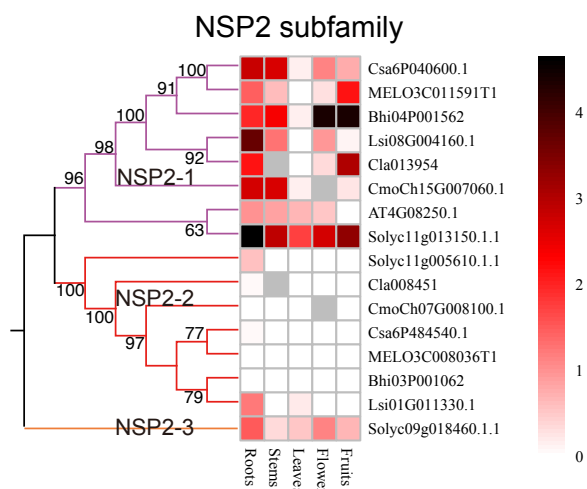
Additional Fig. S9 Expression profiles of 237 Cucurbitaceae GRAS genes in different tissues. **a**, *C. sativus*, **b**, *C. melo*, **c**, *B. hispida*, **d**, *C. lanatus*, **e**, *L. siceraria* and **f**, *C. moschata*. Neighbor-joining tree of GRAS proteins is shown on the left, and the right is the 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.



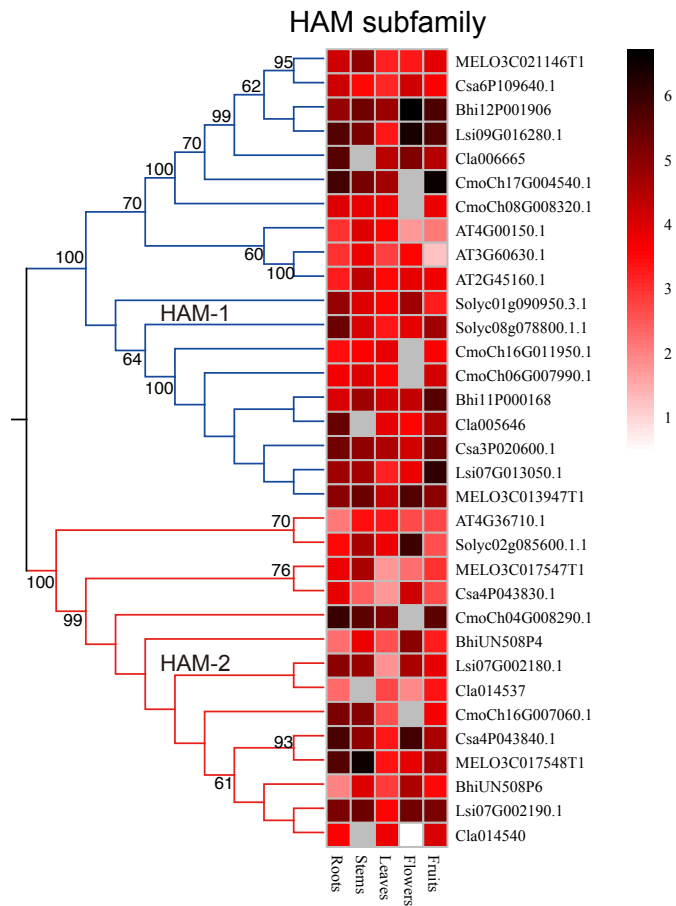
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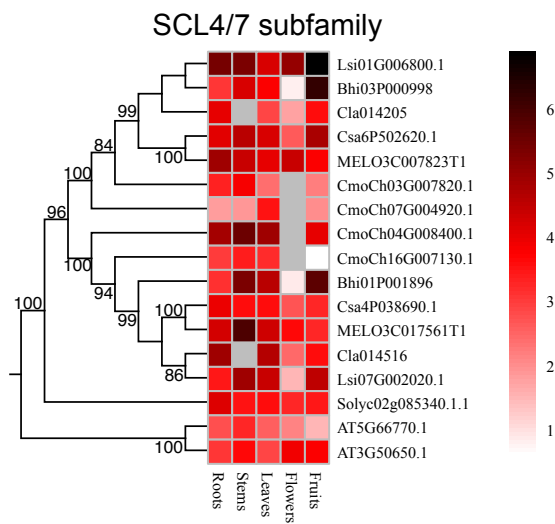
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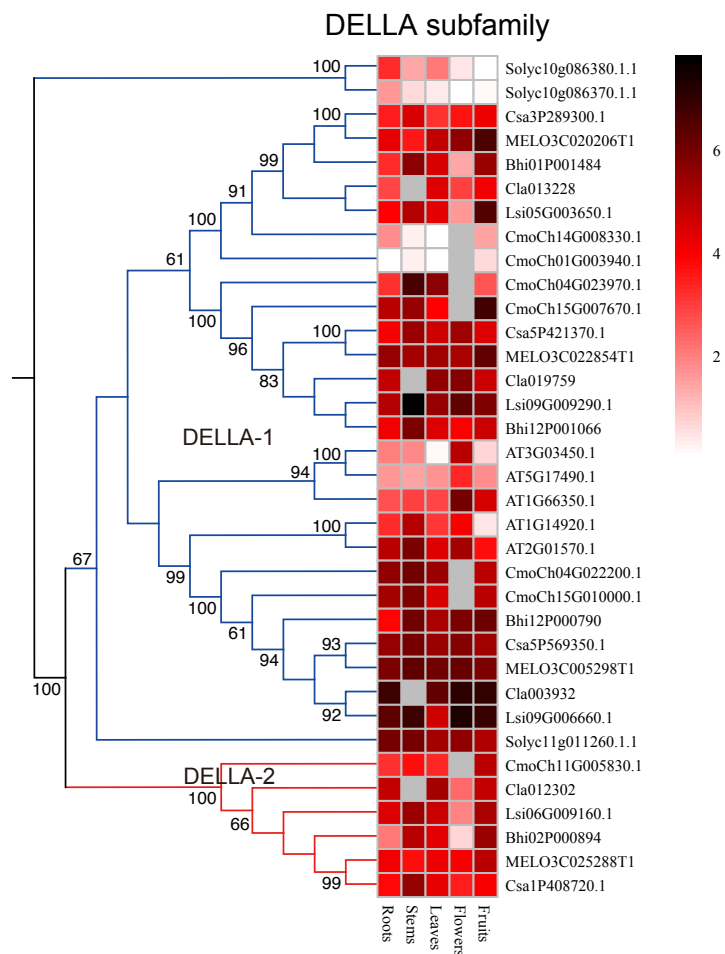
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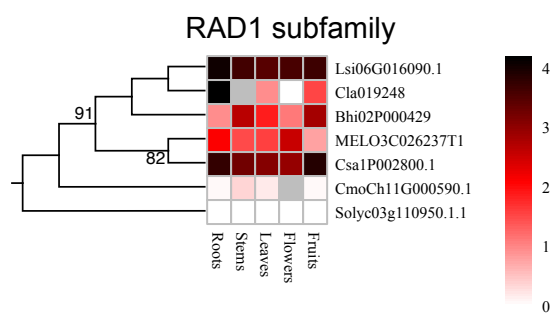
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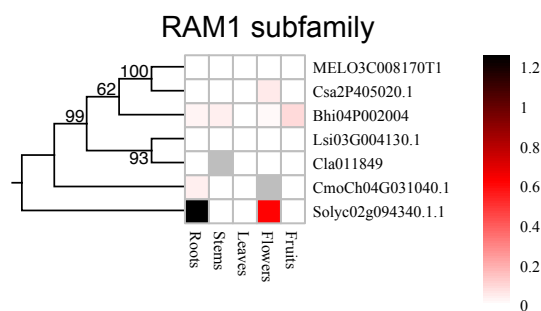
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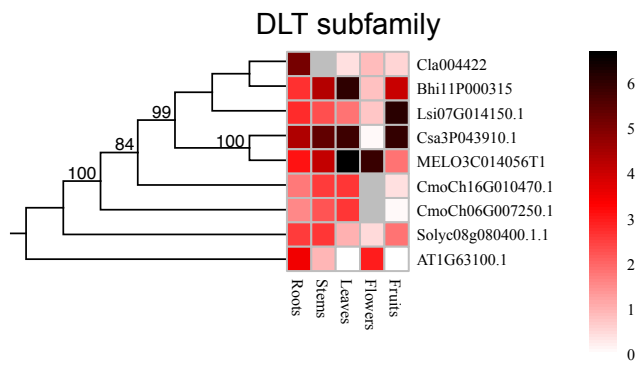
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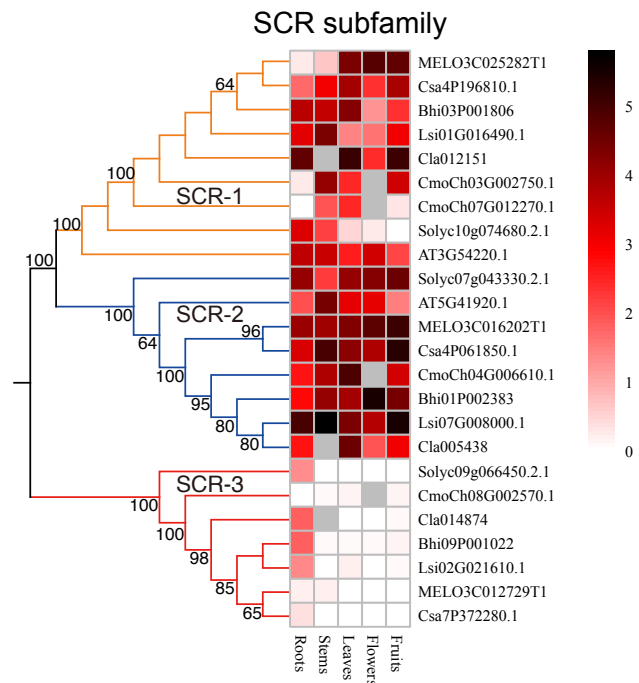
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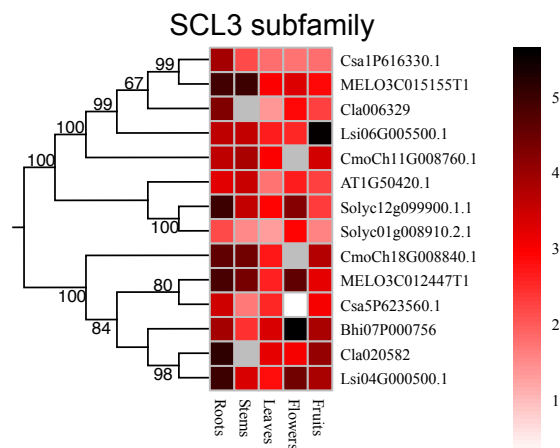
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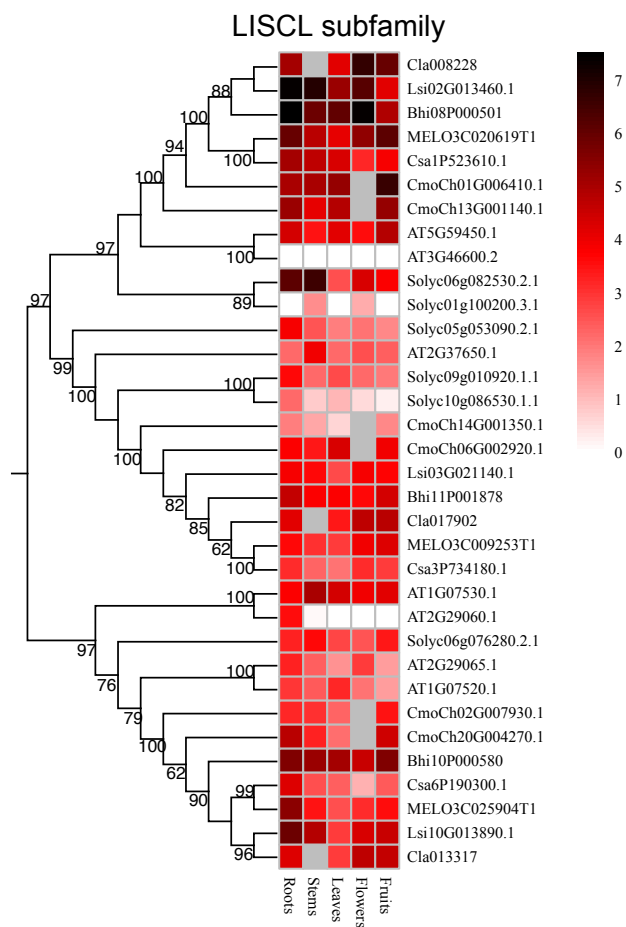
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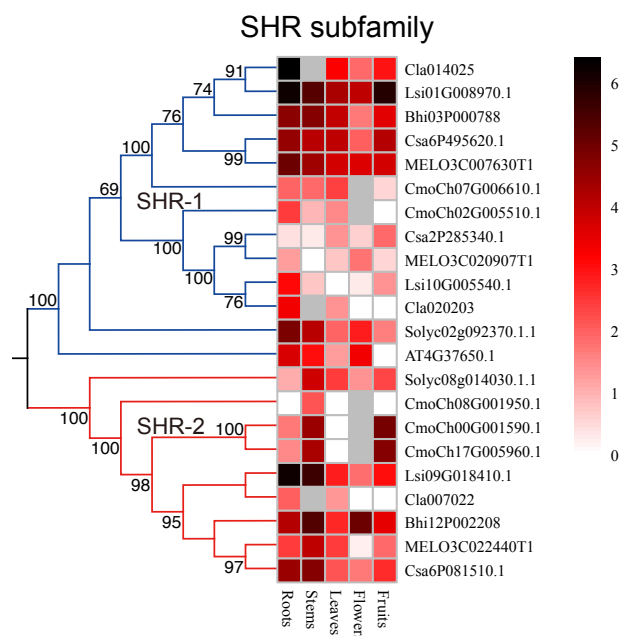
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102

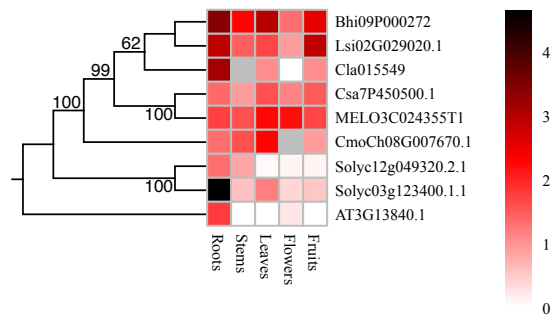


103



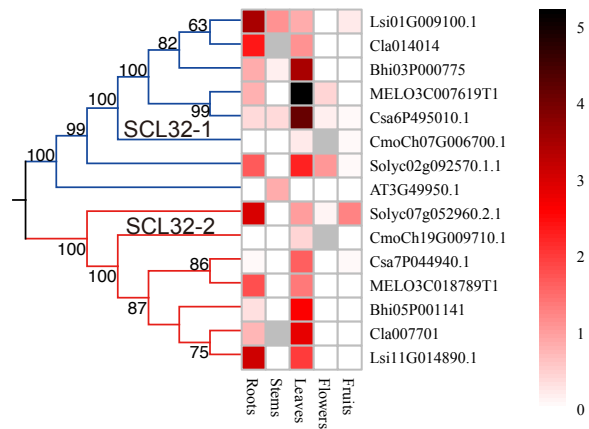
104

NSP1 subfamily

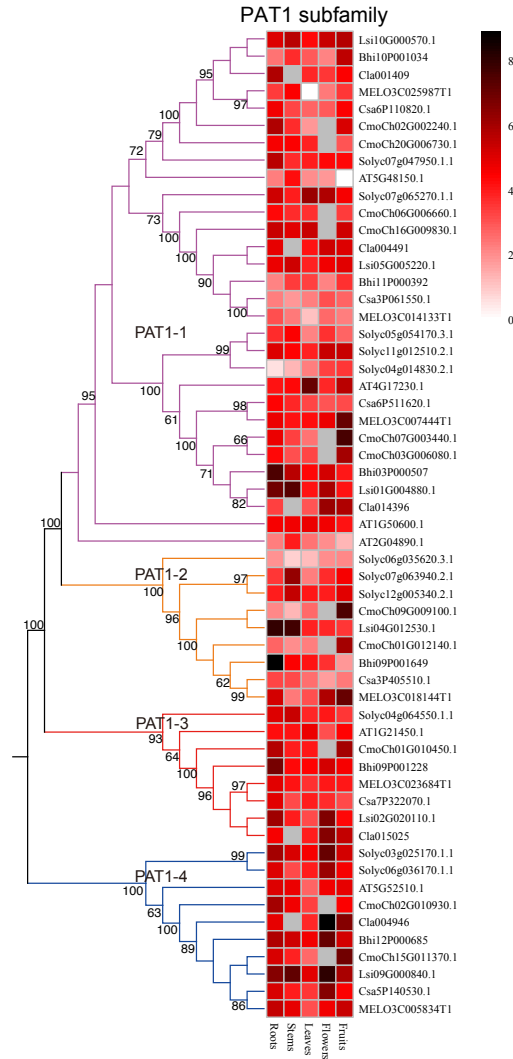


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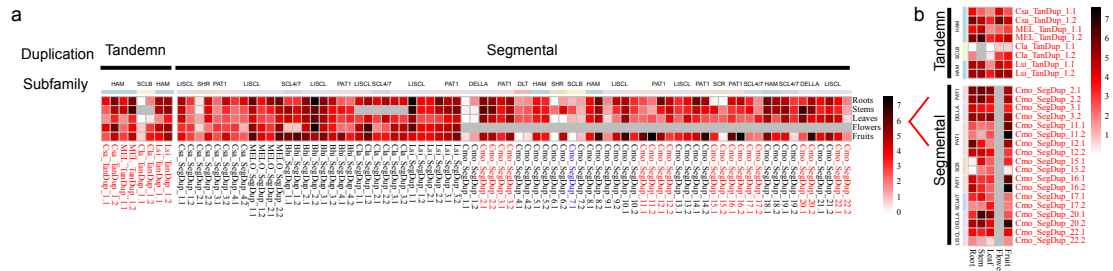
SCL32 subfamily



106



Additional Fig. S10 Expression profiles of 318 *GRAS* genes in *A.thaliana*, *S.lycopersicum* and six Cucurbitaceae 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.



Additional Fig. S11 Expression profiles of duplicated *GRAS* genes in six Cucurbitaceae species. In the heat map, rows represent duplicated genes, while columns represent different tissues, 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, gray color represents missing values. **a** Expression profiles of all duplicated *GRAS* genes in six Cucurbitaceae plants, the red font represented *GRAS* duplicated gene pairs whose identity and coverage were all more than 80%. **b** Expression profiles of duplicated *GRAS* genes whose identity and coverage were all more than 80% in six Cucurbitaceae plants (The marked red genes in **Additional Fig. S11a**).