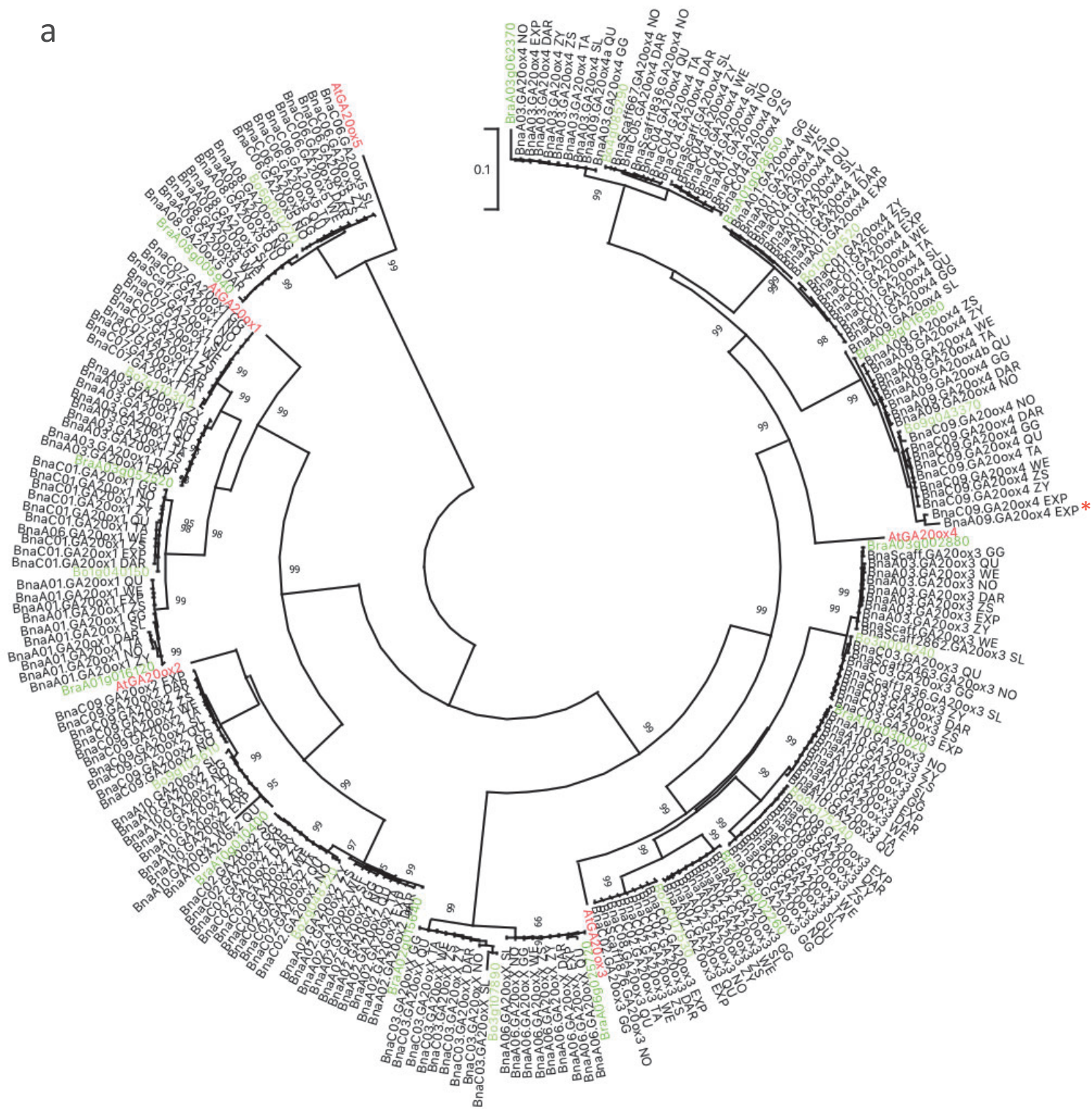


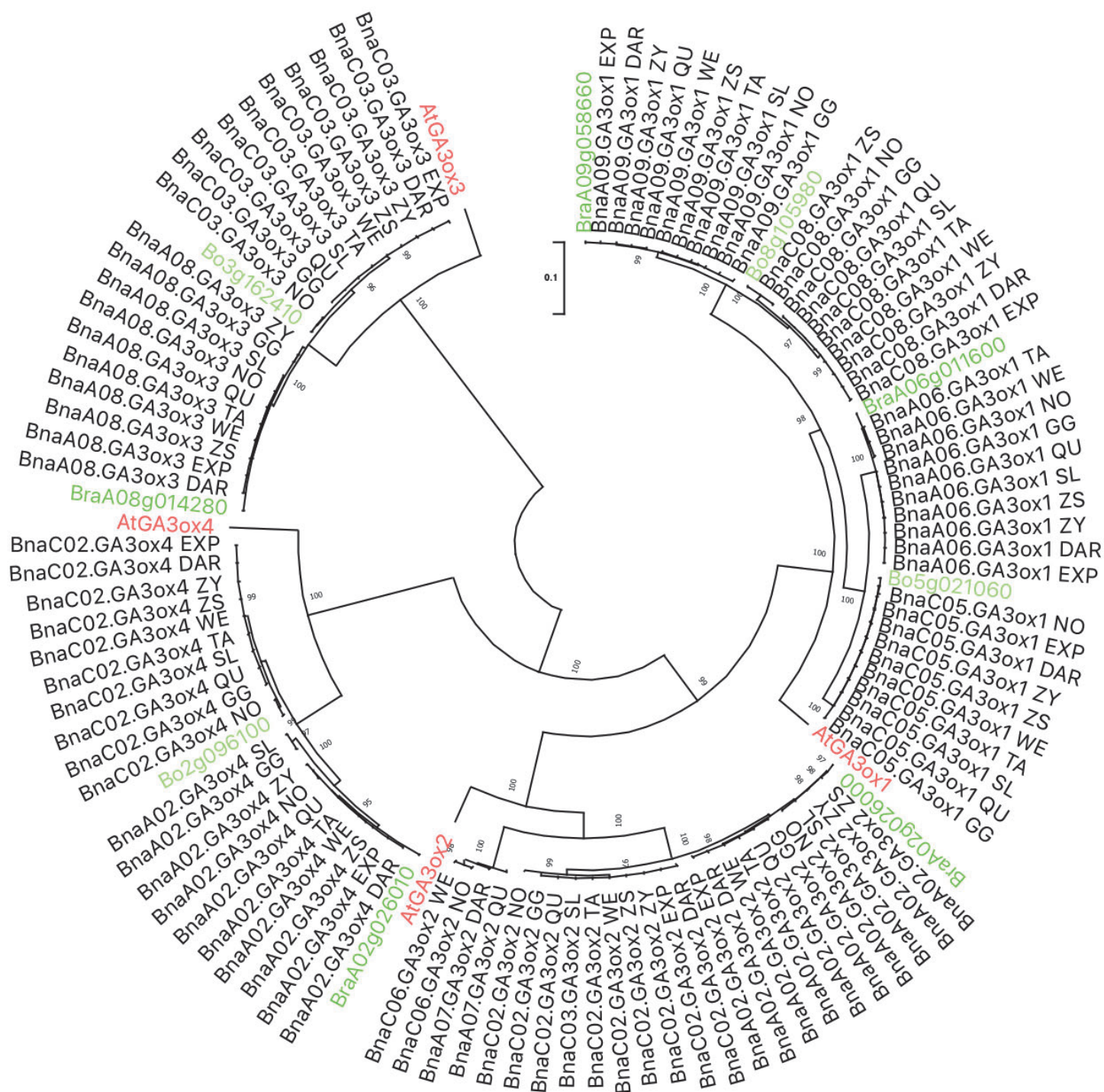
Supplemental Figure 11.1. Phylogenetic trees of genes encoding GA biosynthesis, catabolism, and signaling proteins in 10 accessions of *B. napus*

Phylogenetic trees of *BnaGA2Oox* (a), *BnaGA3ox* (b), Class I and II *BnaGA2ox* (c), Class III *BnaGA2ox* (d), *BnaGID1* (e), *BnaGID2/SLY* (f), and *BnaDELLA* (g) families are shown. Coding sequences (CDSs) of corresponding genes from 10 *B. napus* accessions were used to construct the phylogenetic trees. Gene IDs and protein lengths are shown in Supplemental Table 7.1. Orthologues from *A. thaliana*, *B. rapa*, and *B. oleracea* are included as references. The 3'-extensions of *BnaGA2ox* (BraA05g010560 (711-bp), C03p22380.1_BnaDAR (711-bp), A03p19180.1_BnaDAR (711-bp), BnaC03G0117000NO (792-bp)), were removed prior to constructing phylogenetic trees. CDSs were aligned by ClustalW (Gap open Penalty is 7.0, Gap extension penalty is 6.66 for both pairwise and multiple alignments). Neighbor-joining trees were constructed by using MEGAX (1000 rounds of bootstrap replications were conducted with default settings). Reference genes are highlighted in red (*A. thaliana*), green (*B. rapa*), and pale green (*B. oleracea*). The last 2-3 letters of *B. napus* gene names indicate the accession: Darmor-bzh (DAR), Express617 (EXP), Gangan (GG), No2127 (NO), Quinta (QA), Shengli (SL), Tapidor (TA), Westar (WE), ZS11 (ZS), and Zhenyou7 (ZY).

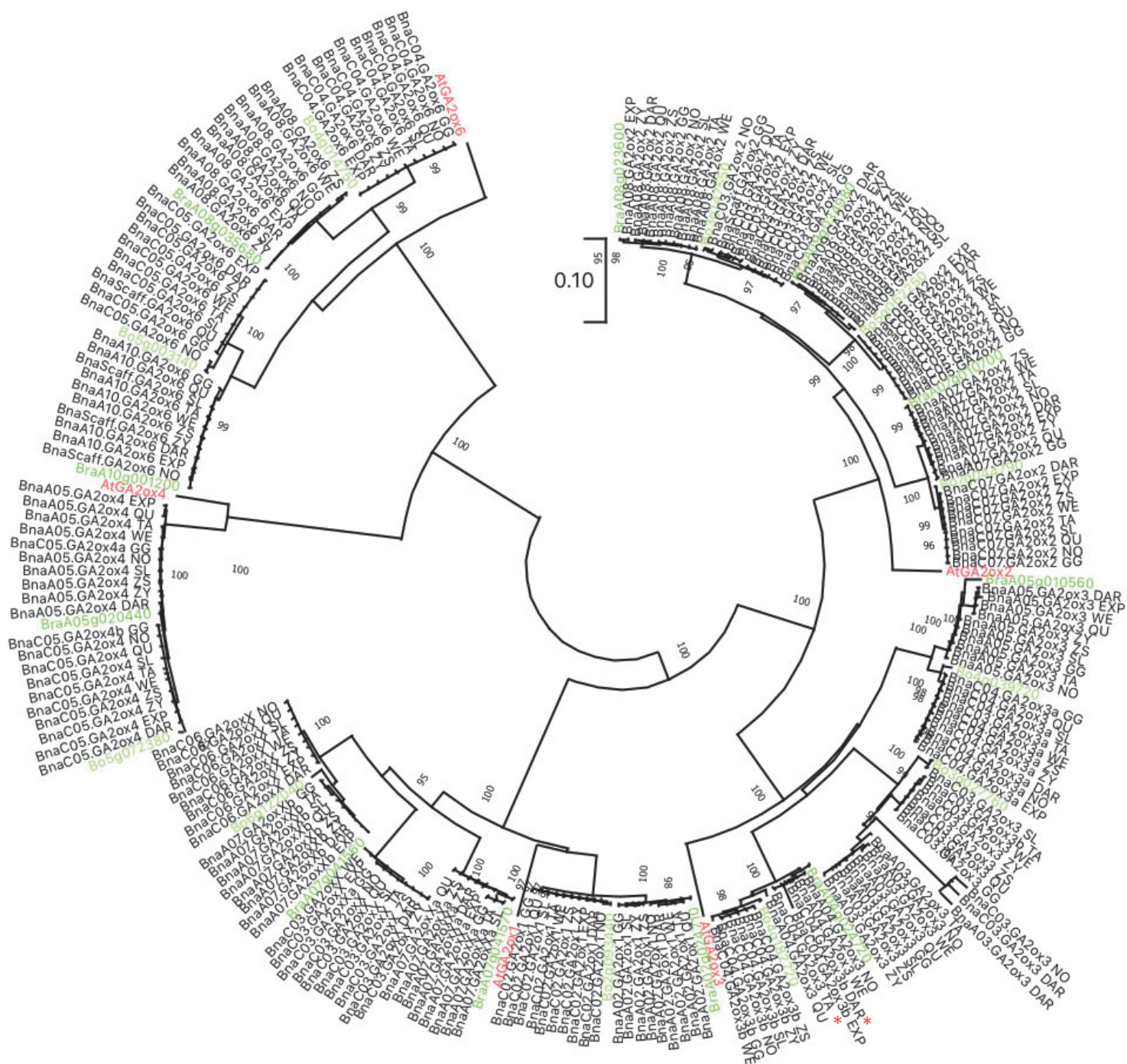
a



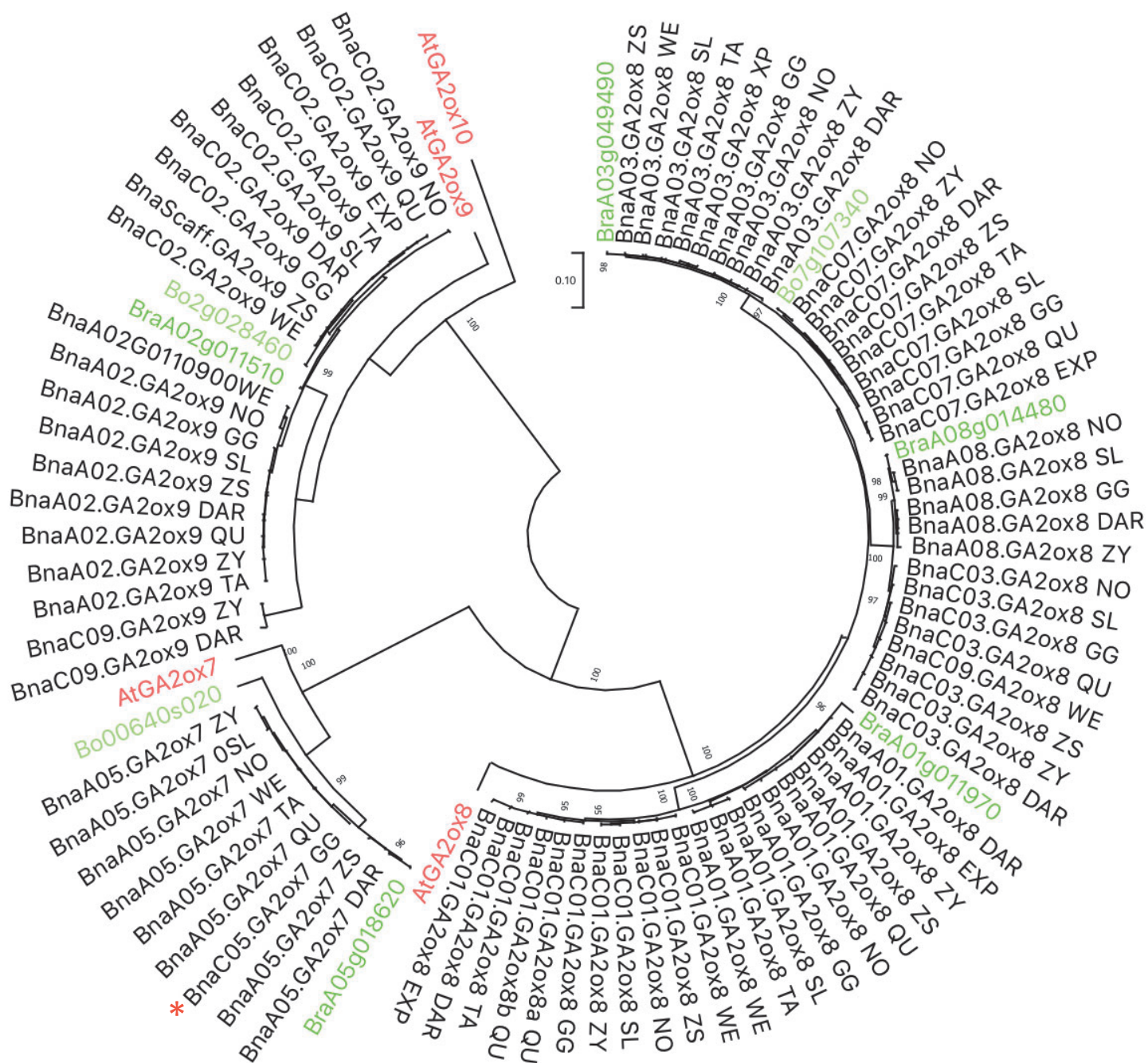
b



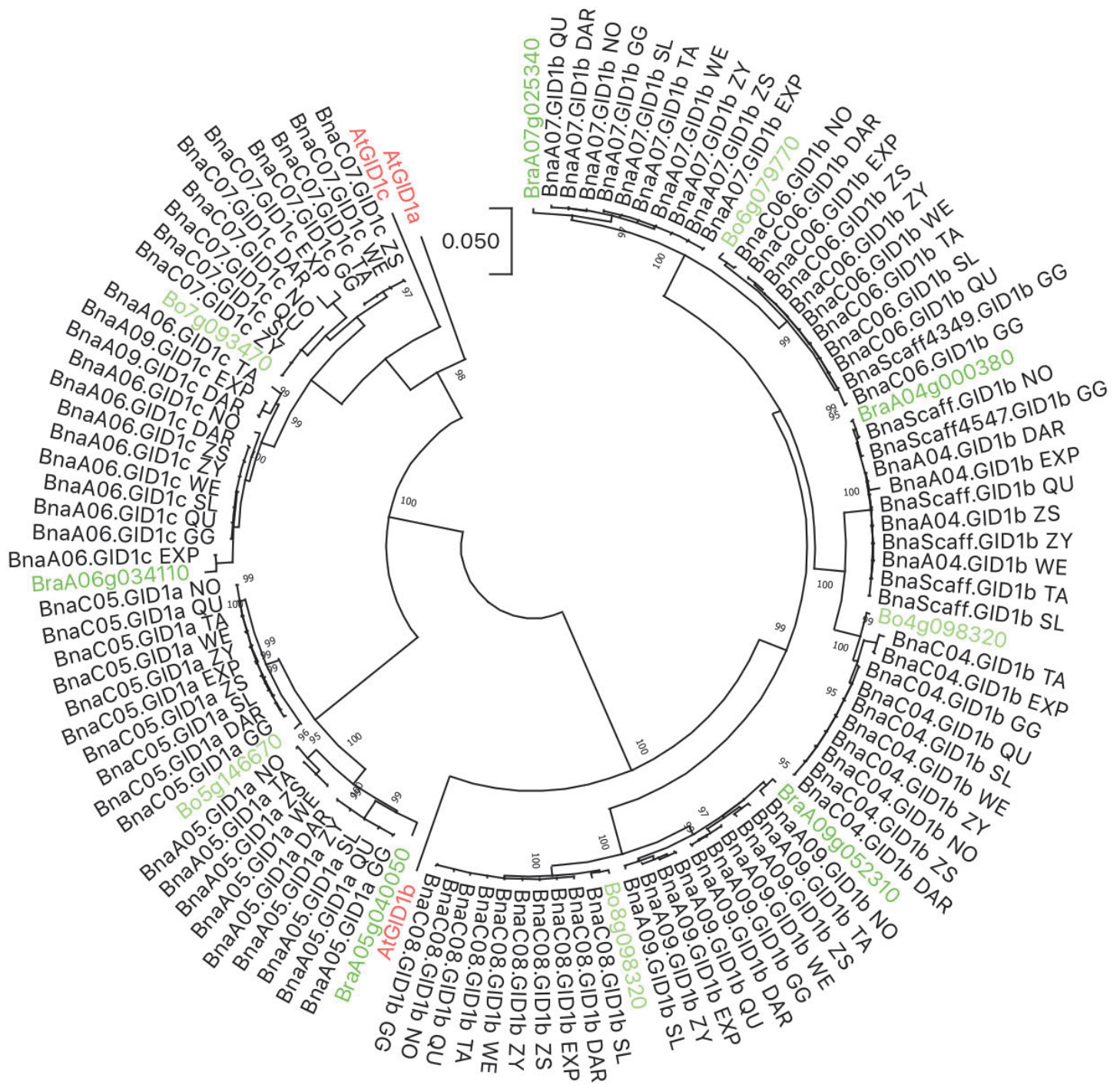
C



d

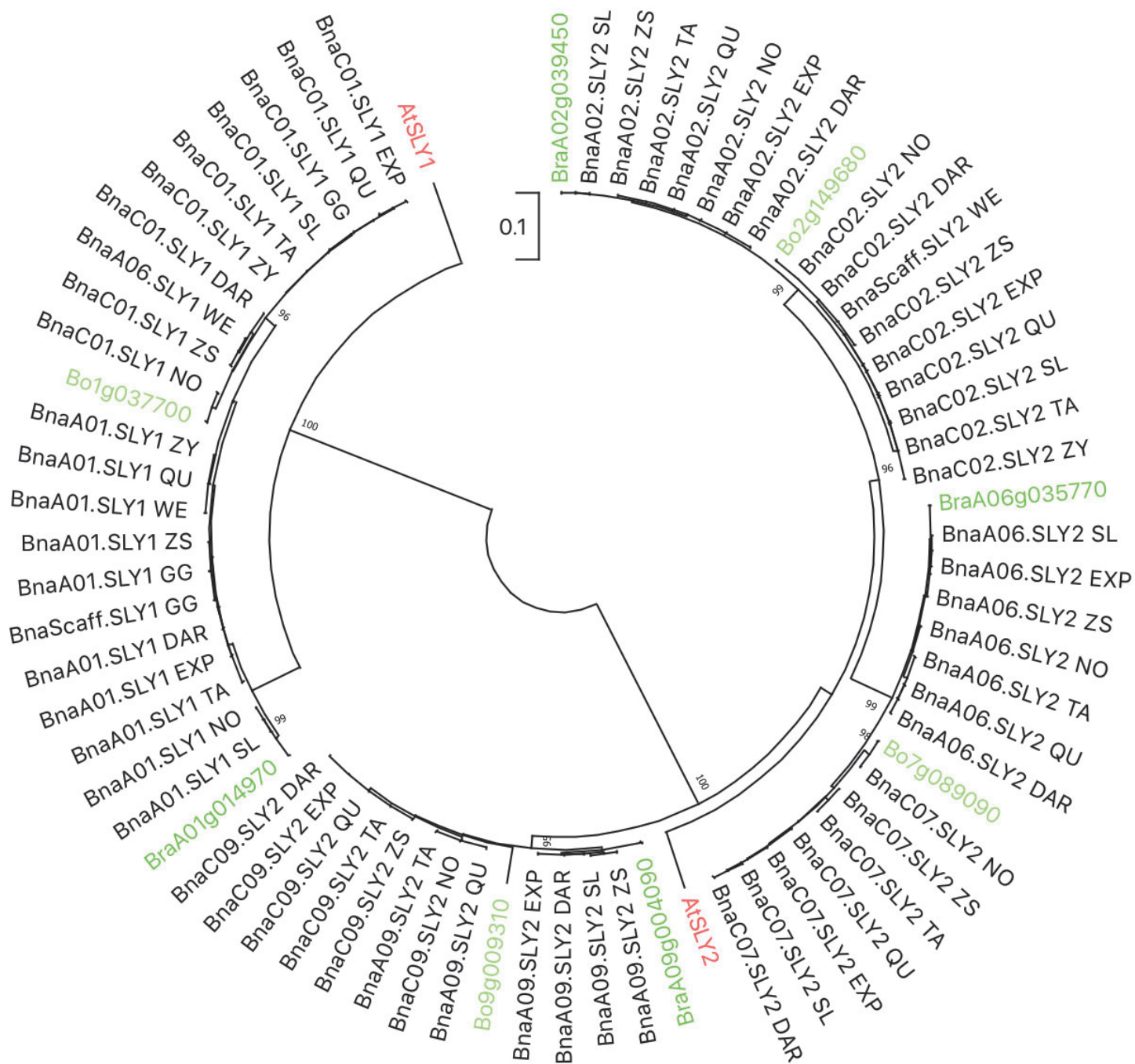


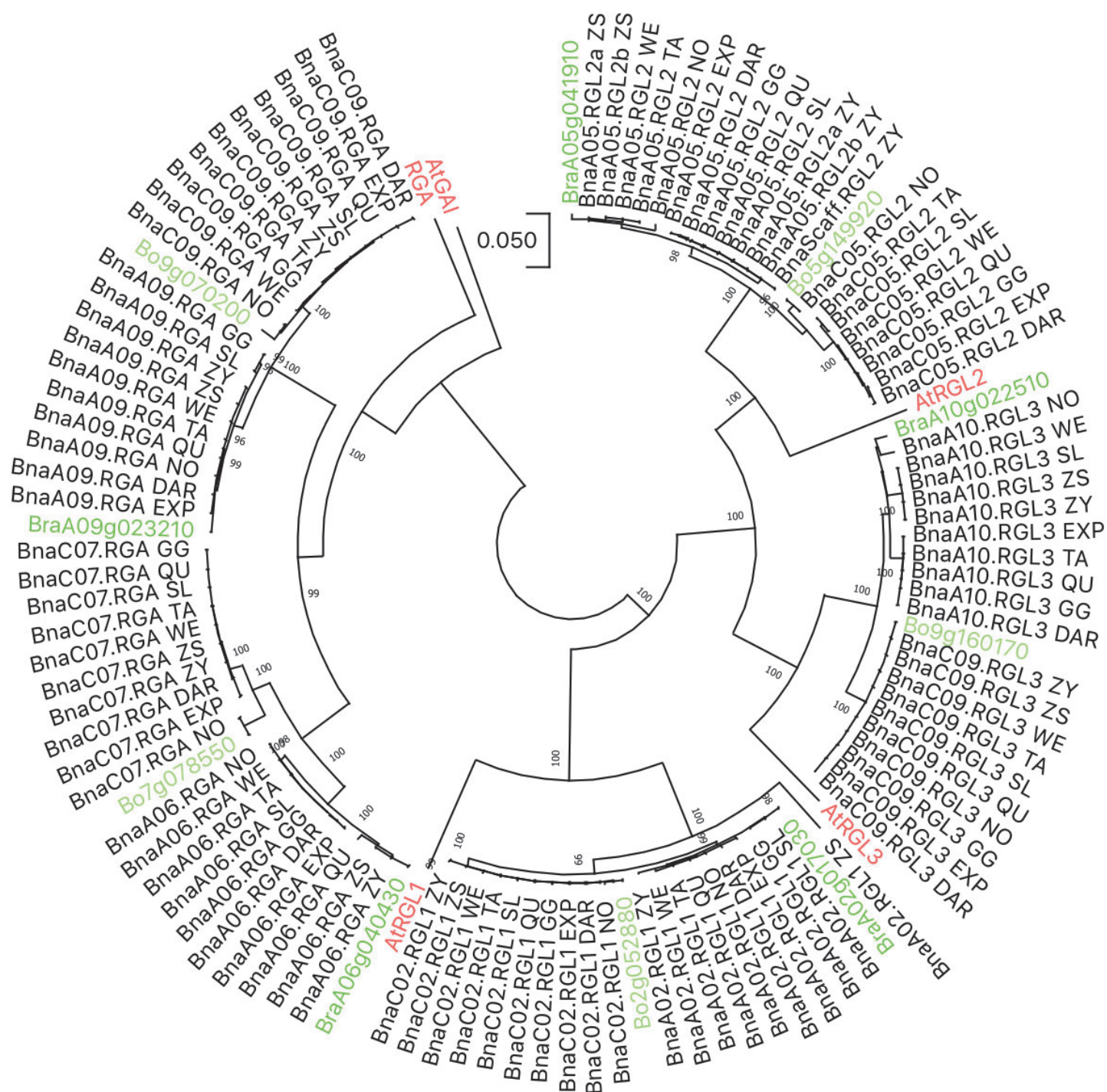
e

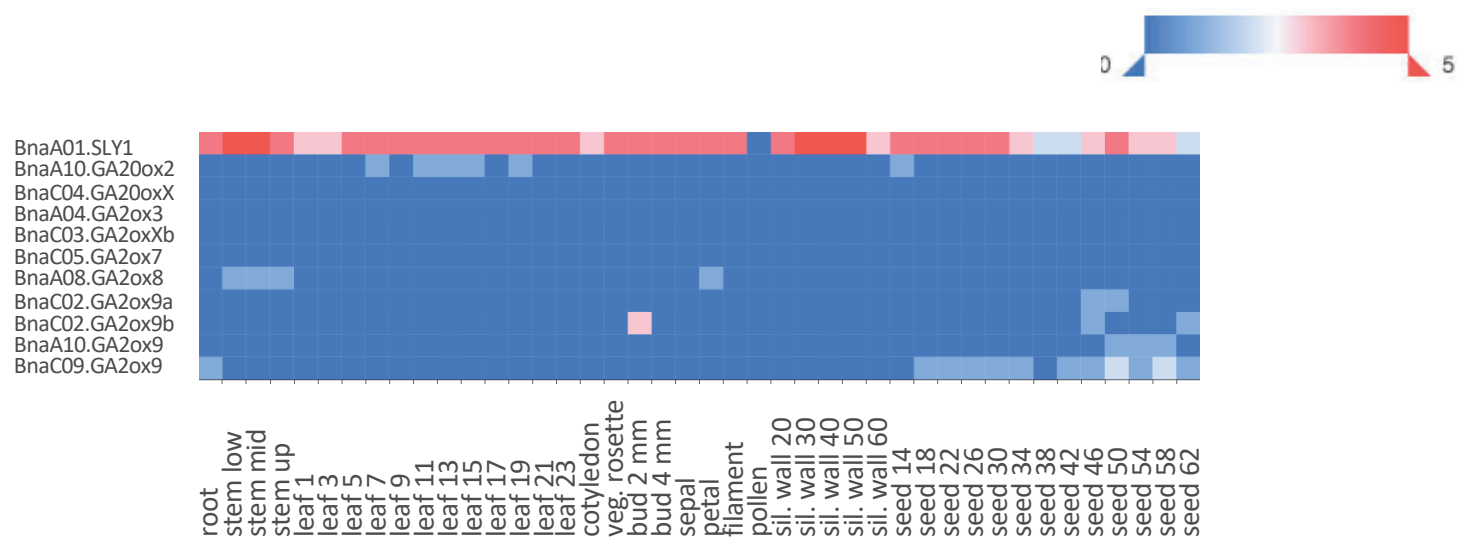


Supplemental Figure 11.1 continued

f

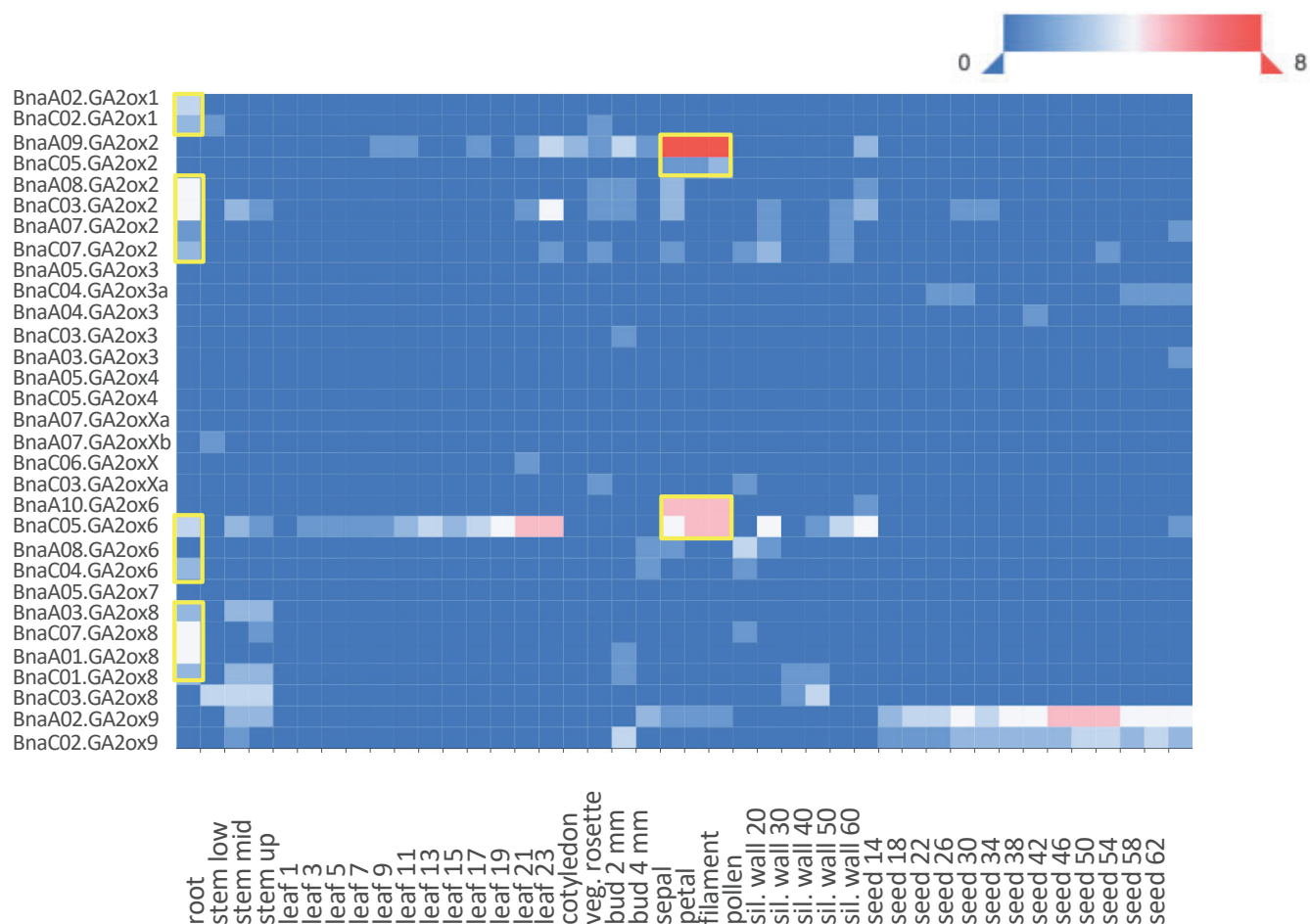






Supplemental Figure 11.2. Expression of truncated genes in ZS11

The heatmap shows the expression of six truncated genes in ZS11. An expressed gene, *BnaA01.SLY1*, is shown as a positive control. The samples indicated below are the same as Figure 11.2. The heatmaps were created at <http://yanglab.hzau.edu.cn/index/heatmap>.



Supplemental Figure 11.3. Developmental expression patterns of *BnaGA2ox*

Heatmaps represent expression of late GA biosynthesis and signaling genes in ZS11. Samples are same as Figure 11.2. The heatmap was created at <http://yanglab.hzau.edu.cn/index/heatmap>.

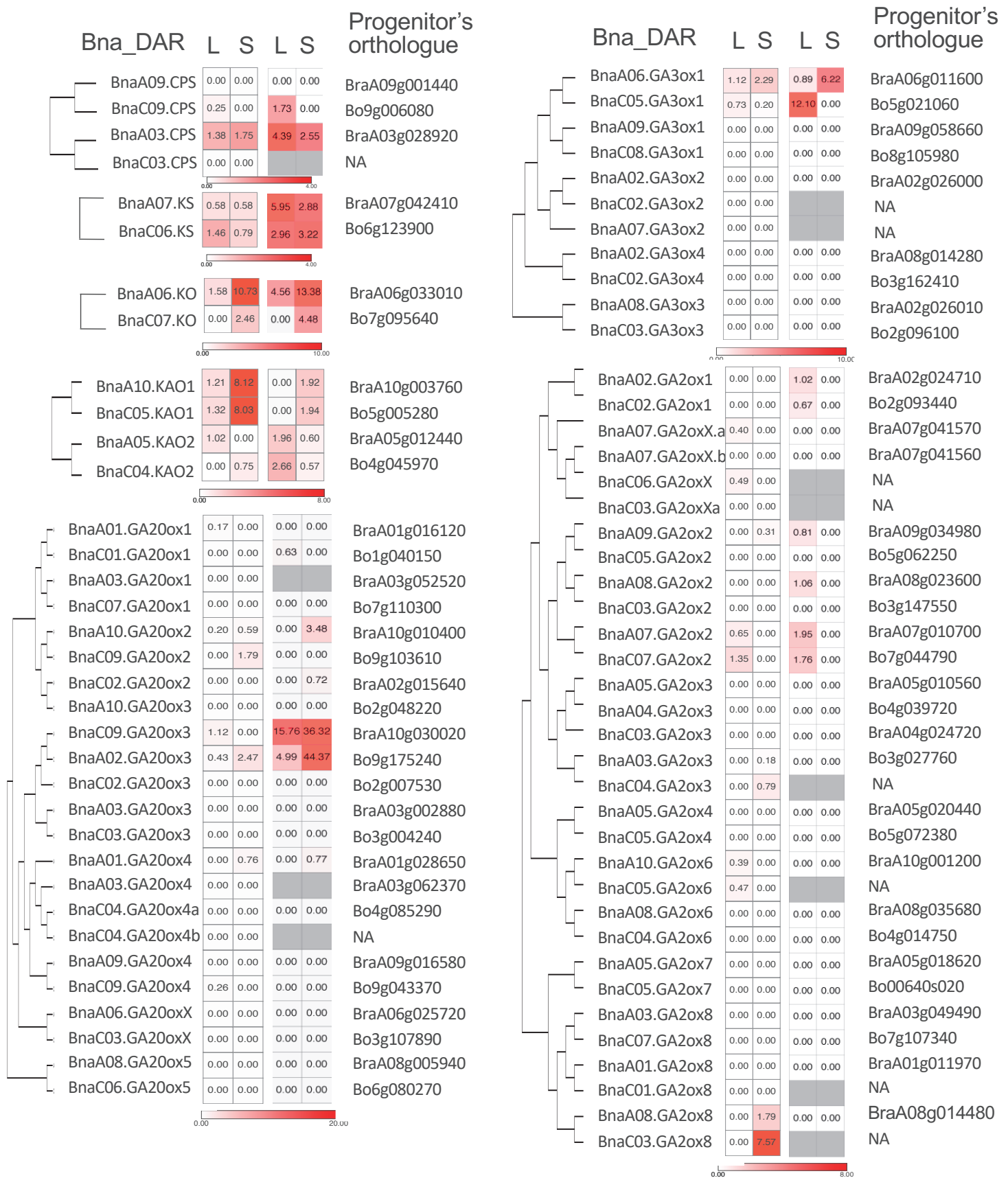
	Bra or Bol	DAR	EXP	GG	NO	QU	SL	TA	WE	ZS	ZY
BnaA05.GID1a											
BnaC05.GID1a											
BnaA07.GID1b											
BnaC06.GID1b											
BnaA04.GID1b											
BnaC04.GID1b											
BnaA09.GID1b											
BnaC08.GID1b											
BnaA06.GID1c											
BnaC07.GID1c											

BnaA01.SLY1											
BnaC01.SLY1											
BnaA02.SLY2											
BnaC02.SLY2											
BnaA06.SLY2											
BnaC07.SLY2											
BnaA09.SLY2											
BnaC09.SLY2											

BnaA05.RGL2											
BnaC05.RGL2											
BnaA10.RGL3											
BnaC09.RGL3											
BnaA02.RGL1											
BnaC02.RGL1											
BnaA09.RGA											
BnaC09.RGA											
BnaA06.RGA											
BnaC07.RGA											

Supplemental Figure 11.4. Gene gains and losses of GA signaling genes in *B. napus* accessions

Genes are shown by pale green cells. Truncated genes are yellow, and blue cells indicate corresponding genes were not found. Each line indicates progenitor, Darmor-*bzh* (DAR), Express617 (EXP), Gangan (GG), No2127 (NO), Quinta (QA), Tapidor (TA), Westar (WE), ZS11 (ZS), and Zhenyou7 (ZY), from left to right. Homeologous interactions are highlighted in red (gene gain-loss), orange (co-gene losses/truncations) or brown (homeologous exchange). Gene IDs are shown in Supplemental Table 11.1.



Supplemental Figure 11.5. Expression of orthologous genes encoding GA metabolism between resynthesized *B. napus* and its parents

Expression levels of GA signaling genes in leaf (L) and silique wall (S) in resynthesized *B. napus* and its parents were obtained from Zhang et al. (2015). Left two columns in the heatmap indicate the expression of genes in resynthesized *B. napus*. A simplified phylogenetic tree is shown to indicate homeologous genes. The right two columns in the heatmap indicate the expression of orthologous genes in *B. rapa* and *B. oleracea*. Grey columns indicate no orthologue was found in the progenitor genome.