

Figure S1 K-mer based genome size estimates. K = 17, 21, 31, 51 and 71 count histograms of Illumina paired-end sequence data for tetraploid *Trapa natans*. These plots were used to estimate genome size (total k-mer number)/(peak depth). K = 17: a total of 50,029,871,544 17-mers were detected with a peak depth of 54 and an estimated genome size of 926.48 Mb; K = 21: a total of 51,476,584,112 21-mers were detected with a peak depth of 52 and an estimated genome size of 989.93 Mb; K = 31: a total of 50,607,610,875 31-mers were detected with a peak depth of 47 and an estimated genome size of 1076.76 Mb; K = 51: a total of 43,270,633,852 51-mers were detected with a peak depth of 38 and an estimated genome size of 1138.70 Mb; K = 71: a total of 34,807,248,461 71-mers were detected with a peak depth of 30 and an estimated genome size of 1160.24 Mb.

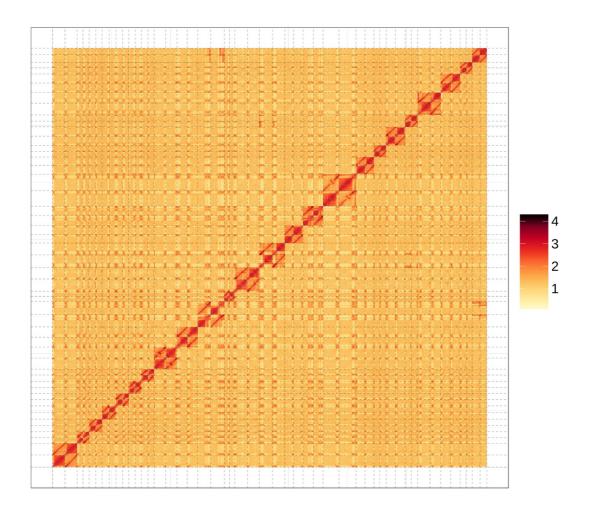


Figure S2 Genome-wide analysis of chromatin interactions in the tetraploid *Trapa natans* genome based on Hi-C data.

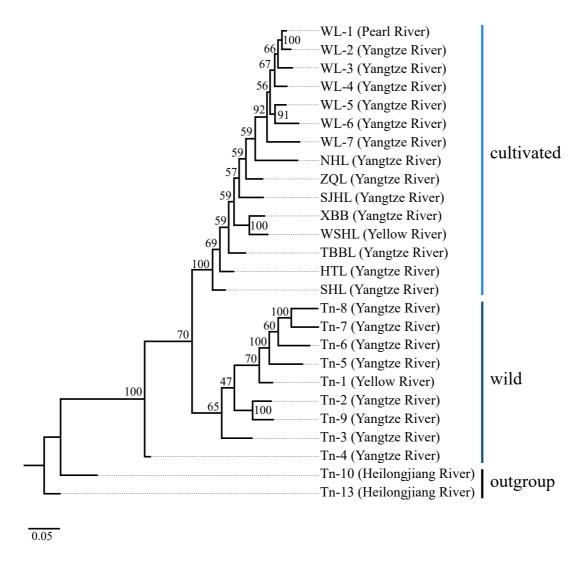


Figure S3 Phylogenetic relationships of diploid *Trapa natans* (2x, AA) from the PYY region inferred from maximum likelihood (ML) analysis based on SNP data.

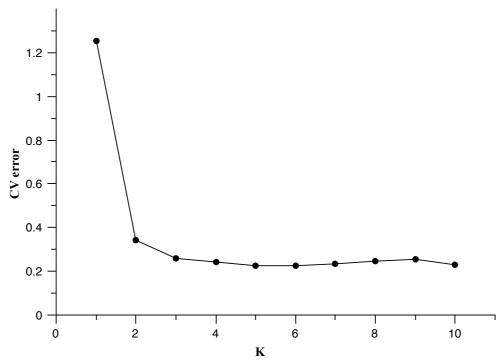


Figure S4 Plot of ADMIXTURE cross-validation error across values of K.

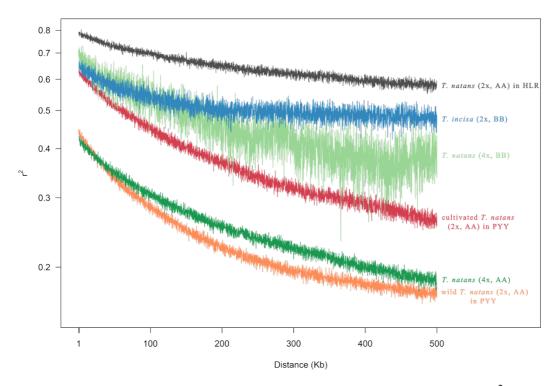


Figure S5 LD decay determined by correlation of allele frequencies (r^2) against distance (kb) in six Trapa populations. Note that the A and B subgenomes of tetraploid T. natans individuals were treated separately (4x, AA vs. BB). PYY, Pearl-Yangtze-Yellow River region; HLR, Heilongjiang River region.

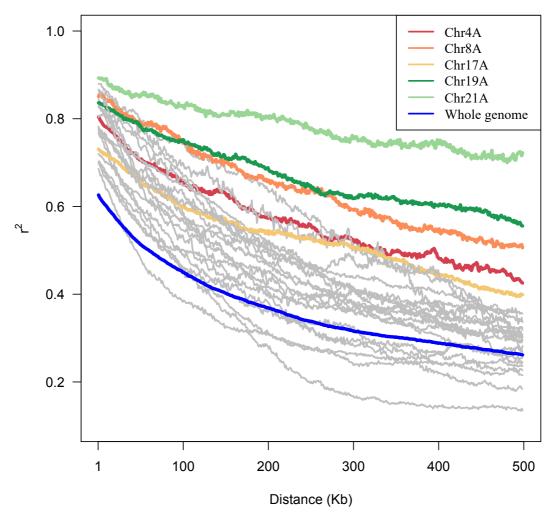


Figure S6 LD decay distances in cultivars of *Trapa natans* for each of the 24 chromosomes.

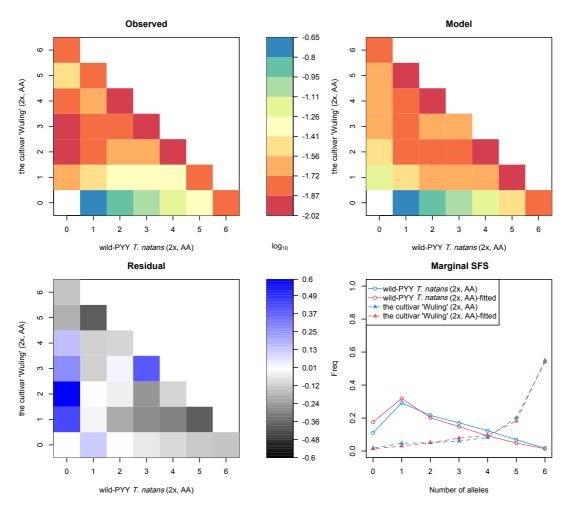


Figure S7 The goodness-of-fit of the best scenario summarized by the observed 2D-SFS, modeled 2D-SFS, residuals between the model and the data, and marginal SFS.

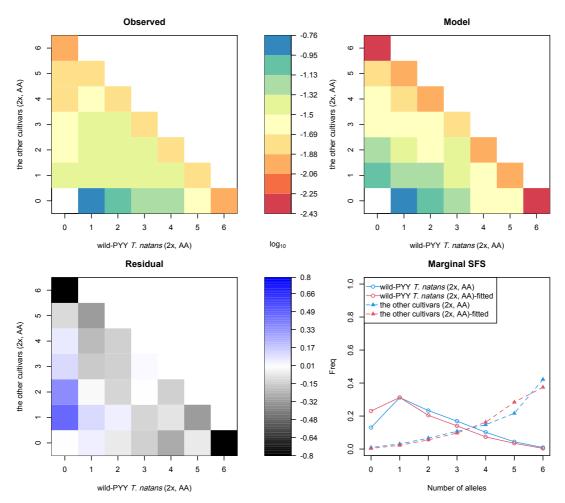


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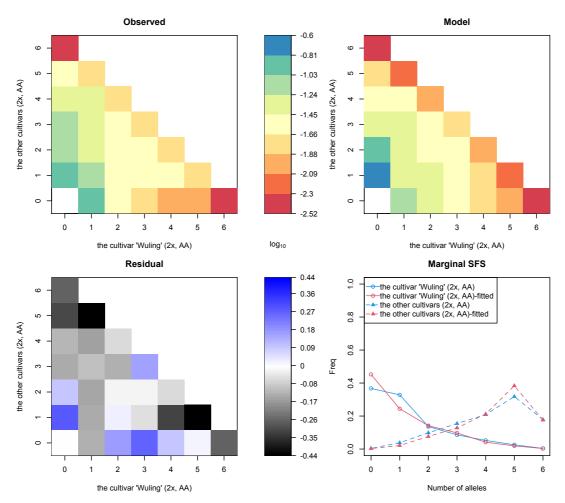


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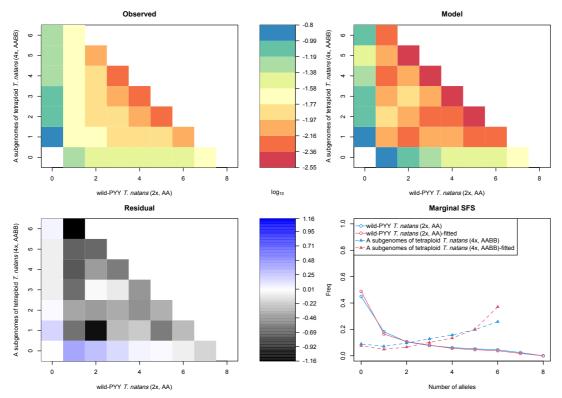


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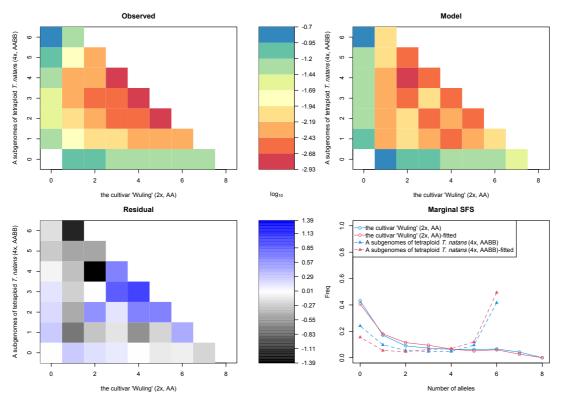


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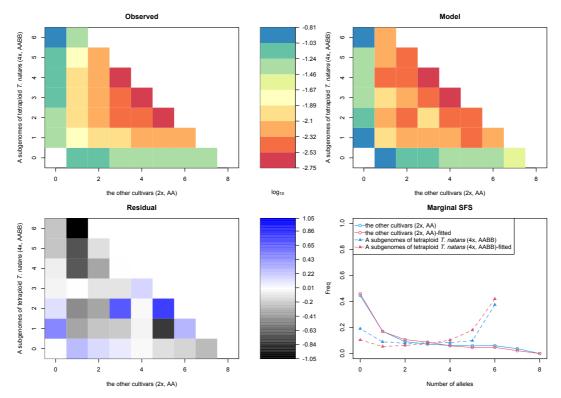


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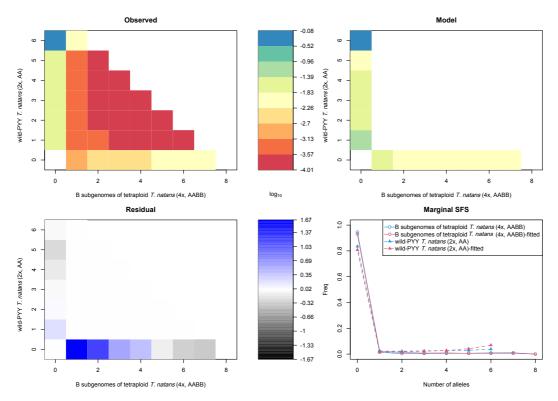


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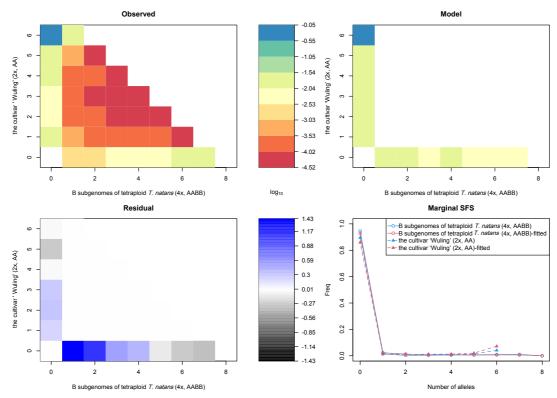


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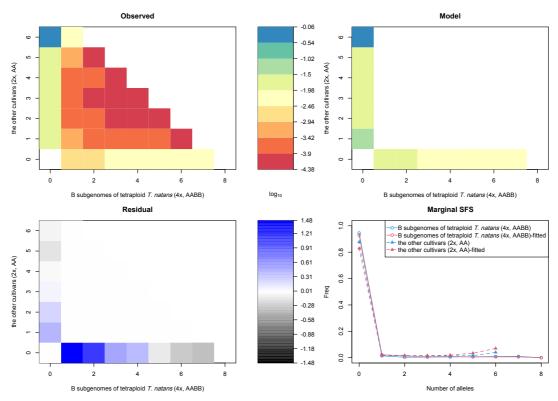


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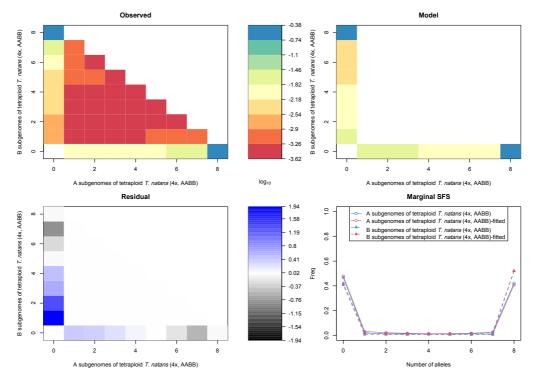


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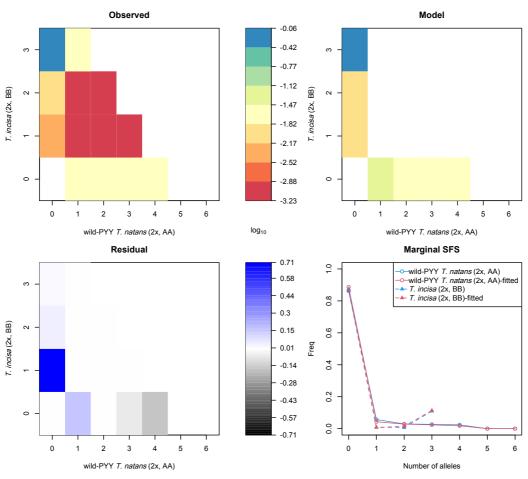


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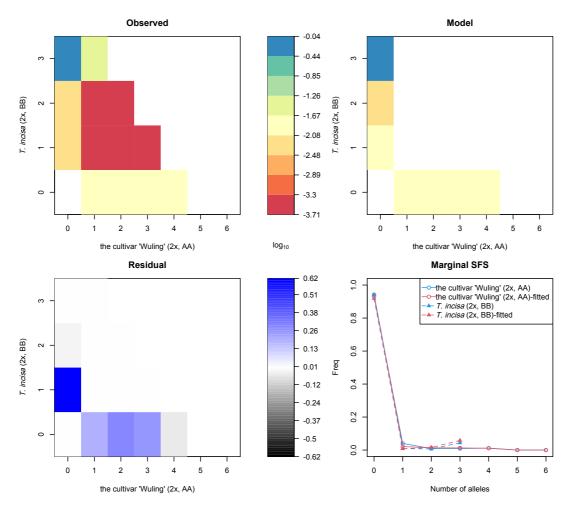


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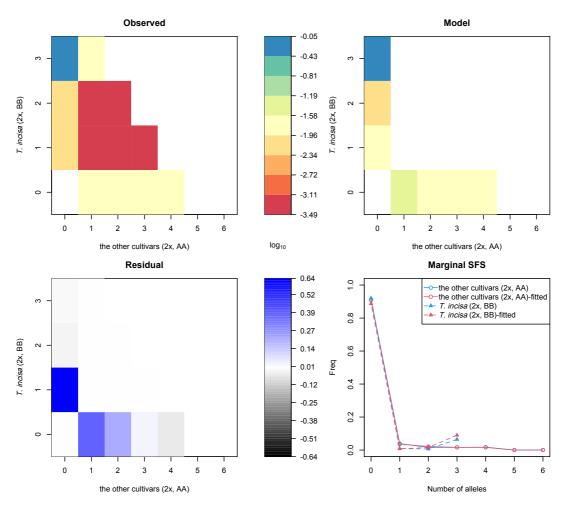


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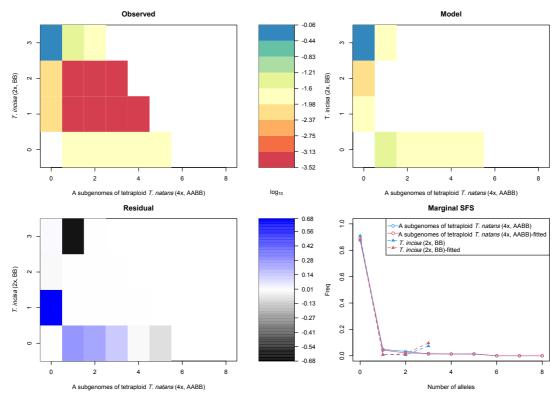


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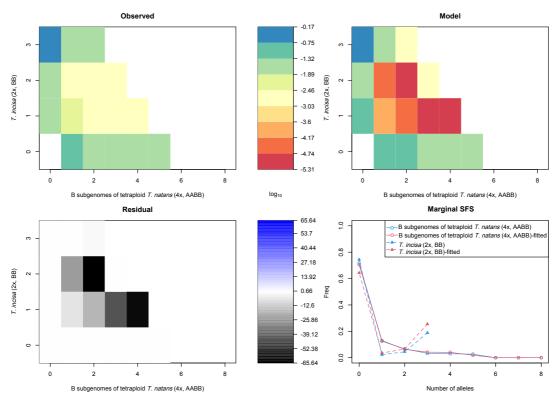


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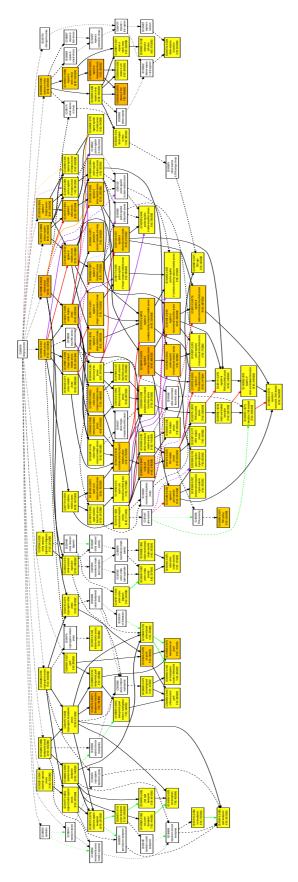


Figure S8 Significantly enriched biological process GO categories of 205 candidate genes under positive selection.

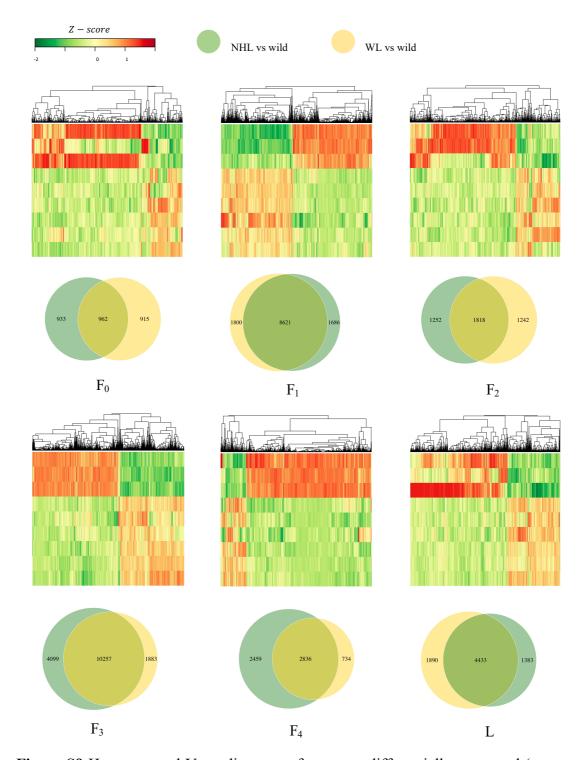
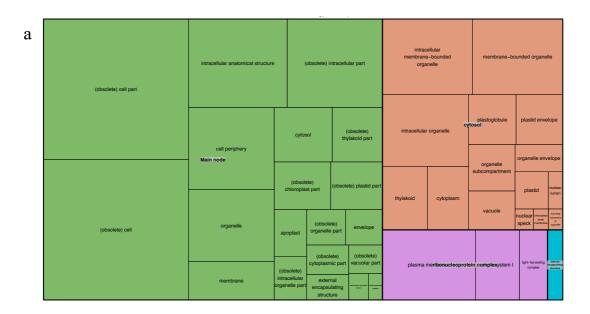


Figure S9 Heatmaps and Venn diagrams of common differentially expressed (up- or downregulated) genes (DEGs) shared by the two cultivar—wild comparisons (i.e. 'Wuling' vs. wild and 'Nanhuling' vs. wild). F_0 : flower bud, F_1 : fertilized flower, F_2 : fruit before sepal abscission, F_3 : fruit after sepal abscission, F_4 : juvenile fruit, L: leaf.



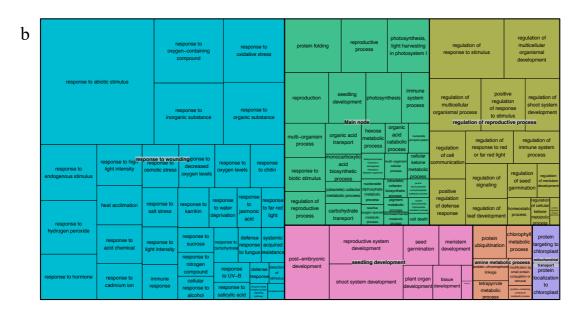
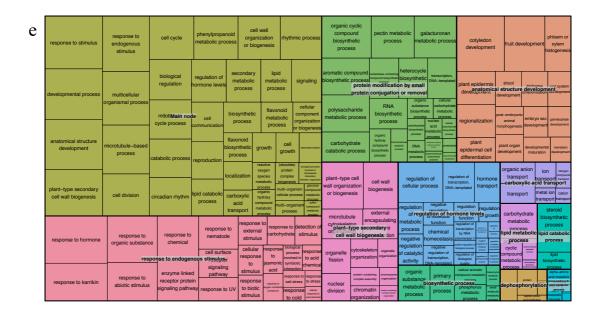


Figure S10 Significantly enriched GO categories under biological process of differentially expressed (up- or downregulated) genes (DEGs) shared by the two cultivar–wild comparisons (i.e. 'Wuling' vs. wild and 'Nanhuling' vs. wild). a, c, e, g, i, upregulated genes at developmental stages, F_0 (flower bud), F_1 (fertilized flower), F_2 (fruit before sepal abscission), F_3 (fruit after sepal abscission) and F_4 (juvenile fruit), and in leaf tissues, respectively. b, d, g, h, k, downregulated genes at F_0 , F_1 , F_2 , F_3 and F_4 stages and in leaf tissues, respectively.

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biosynthetic process	regulation of	response to jasmonic acid	amino acid import	regulation of meristem structural organization	water transport	pyrimidi nucleos biosynth	ide H etic met		symmetr ell division	ric res	defense sponse by callose eposition	meristem maintenance	root system development	phloem or x histogene			
flavonoid biosynthetic cytokinesis by cell process plate formation		photorespiration	mitotic recombination	histone H3-K9 modification	response to sucrose	regulation of defen response bacteriu	on pyri se ribonu to bios		ulation of D doreduplicat	INA C	callose calization			plant	_		
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response to water deprivation	seed germination	response to jasmonic acid	meristem development	regulation of tetrapyrrole metabolic process	regulation of flower development	isopreno cataboli t process	c catal	oolic	response to gravity	sucro biosynt proce	thetic	response to onosaccharide	flavonoid biosyntheti process	c seedling	
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response to cadmium ion			pathway	starch catabolic process	of response to water deprivation	homeostasis	microsporogenesis	regulation of globeretic acid mediated signaling	regulation of response to osmotic stress	animal of organ	response to salt stress	anatomical structure trans rrangement *	drug membrane developm	anatomical boundary	
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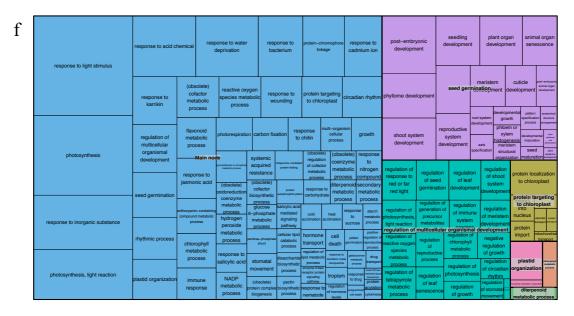
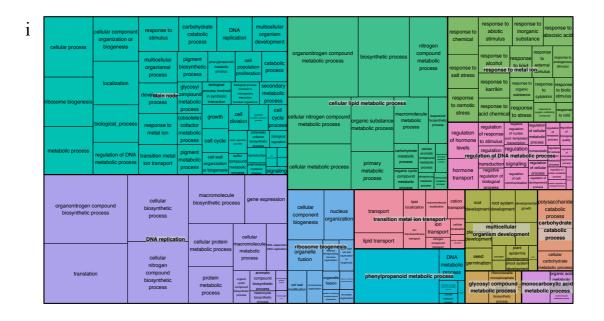


Figure S10 (continued)

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			plant-type cell wall biogenesis	seedling development	flavonoid metabolic process	positive regulation of multi-organism process	cytokinesis by cell plate formation	response to	fluid trans		system ogenesis	water transport	isocitrate metabolic process	terpene metabolic
	meristem development meristem maintenance	root system development	regulation of	plant epidermal cell	response to karrikin	regulation of anion transmembrane transport	cellular zinc ion homeostasis	zinc ion translation		chloroplast plant- RNA cell v processing loose		of stom	atal anthocyanir	process gibberellin metabolic process
		cellular response to acid chemical	meristem development	differentiation regulation of	seed coat development	stomatal complex patterning	cell wall assembly	asymmetric cell division	mRNA transcription	syncytium formation	response transitio metal	n regulat of lea developr	response to	diterpenoid metabolic process
		response to UV-B	cell cycle G1/S phase transition	abscisic acid-activated signaling pathway	Main node		regulation of meristem structural organization	regulation of auxin mediated signaling pathway	regulation of phenylpropanoic metabolic process	regulation of secondary metabolic process		or photoper		
			maintenance of cell number	regulation of response to alcohol	cell wall modification	process	regulation of root development	terpene metabolic process	regulation of carbohydrate biosynthetic	regulation of phosphorelay signal transduction system		nitrate ribor	rimidine sucleoside xylem synthetic developmen	chlorophyll catabolic process
	plant epidermis development				involved in multidimensional cell growth	biosynthetic process	photorespiration	jasmonic acid mediated signaling	mitotic recombination	response to disaccharide	regulation of multi-organisms process	netabolic bio	rimidine icleoside isynthetic process	pigment catabolic
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	gametophyte development	anatomical structure	RNA secondary	post-embryonic	pigment	regulation of	methylation	shoot system development histone	homeostasis	starch metabolic process	dehiscence 9	pollen regula ermination of go silen	ne previropism process	tetrapyrrole catabolic process
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response to salicylic acid	vegetative to reproductive phase transition of meristem	salicylic acid mediated signaling pathway	seed germination	entrainment of or prosprioretay		lay deadenytation	deadenylation-independent muclear-transcribed miTNA catabolic miTNA catabolic mitoria muclear-transcribed miTNA deadenylation-independent deady		cellul respor to dsR	nse anio	gulation of on channel activity	regulation of leaf development	meristem
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	response to karrikin	nonphotochemical quenching	metabolic process	regulation of phosphorelay signal	chloroplast RNA processing	response to freezing	regulation of flavonoid biosynthetic process	mitotic	xanthoph metabol proces:	lic acid media	auxir		animal organ
regulation of response	stomatal movement	response to sucrose	response to	transduction Main node system galactolipid	protein localization to chloroplast	regulation of photosynthesis, light reaction	regulation of defense response to bacterium RNA		nicrotubule '	glucose of i	meristem a	scisic diterpenoi process process	ic
to red or far red light		regulation of		biosynthetic process	alternative mRNA splicing, via spliceosome	regulation of abscisic acid-activated signaling	secondary structure unwinding	DNA endoreduplication pyrimidine	regulation of secondary metabolic process	cell wall fe	velopment, terochronic	cytokines by cell plate formation	epidermal differentia
regulation of shoot system development	regulation of flower development	stomatal movement	cyclopentenone	plastid localization	negative regulation of leaf	regulation of response	gravity	nucleoside biosynthetic process	process	omeostasisloc	alization pro	abolic membrani invaginatio	xylem developm
		regulation of tetrapyrrole metabolic process	response to nematode	cellular defense	senescence positive regulation of flavonoid	to alcohol regulation of phenylpropanoid	H3-K9 methylation	regulation of cytoknin-activated signaling pathway	positive regulation of multi-organism process (6	gulation of a		tabolic of sanation for egentative phase coess reproductive phase cellular response metabolic response respons	stomatal a lineage to progression an
response to jasmonic acid	seedling development	anthocyanin-containing compound metabolic	systemic acquired		biosynthetic process response to	metabolic process positive	innate immune response-activating signal transduction photorespiration	regulation of shoot system morphogenesis pectin	export across plasma membrane di	regulation res	offense regulation of sponse invested signaling pathway regulation	process species jasmoni tentinator acid tionaga a population process of cell wall comprose to cell wall compro	fat-solu vitami

Figure S10 (continued)



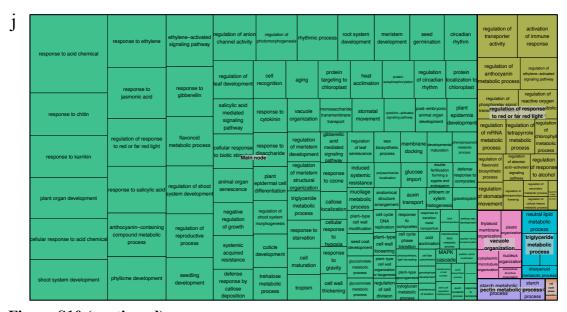
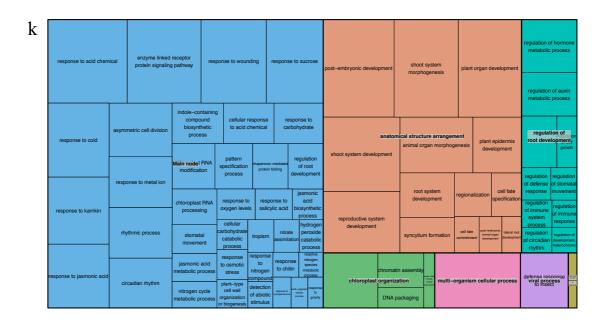


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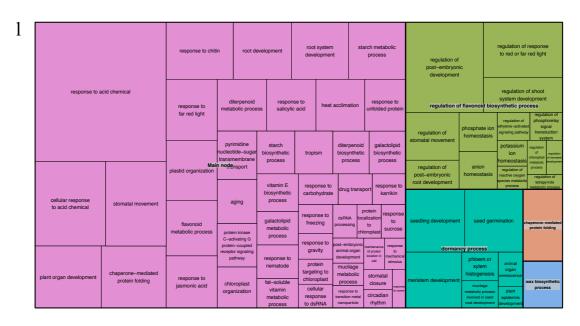
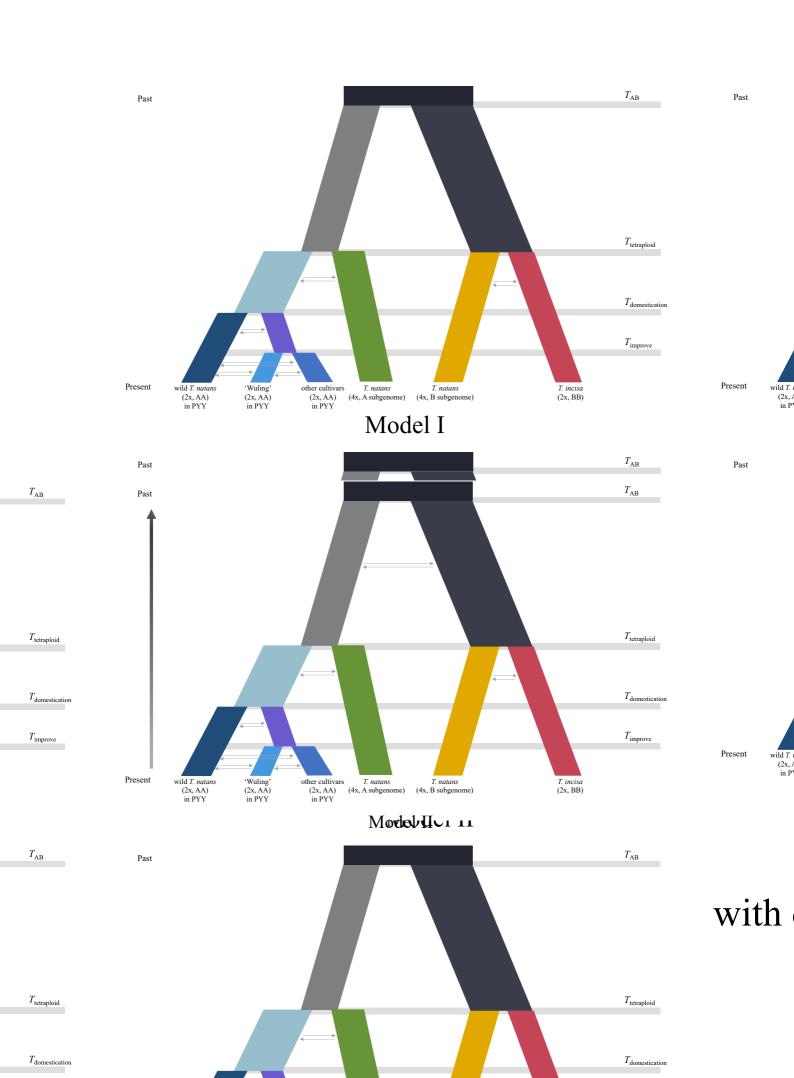
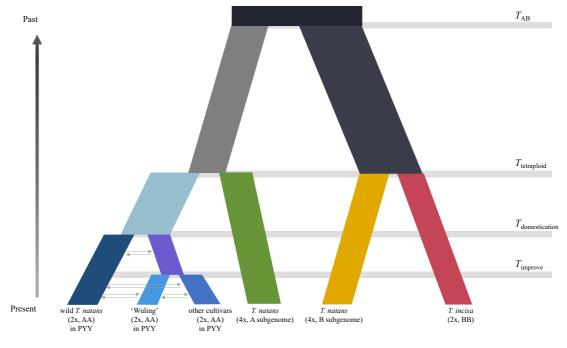


Figure S10 (continued)





Model III

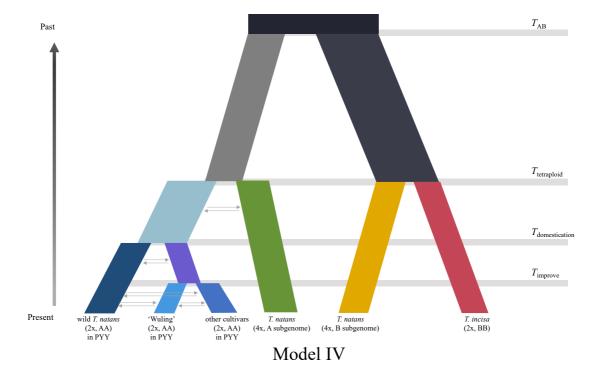


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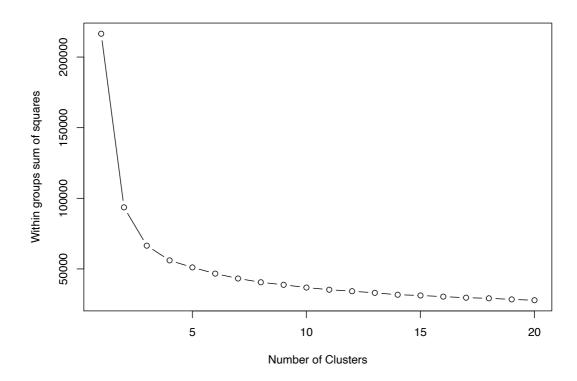


Figure S12 The relationship between the sum of squared error (SSE) and the number of clusters. The number of clusters was set from 1 to 20.