

Figure S1. Images of the seedling and mature rhizome of the sequenced individual and its mitotic metaphase chromosomes. (a) Images of the whole seedling and its mature rhizome. (b) The chromosome number in mitotic metaphase was 22, indicating that the sequenced individual was diploid.

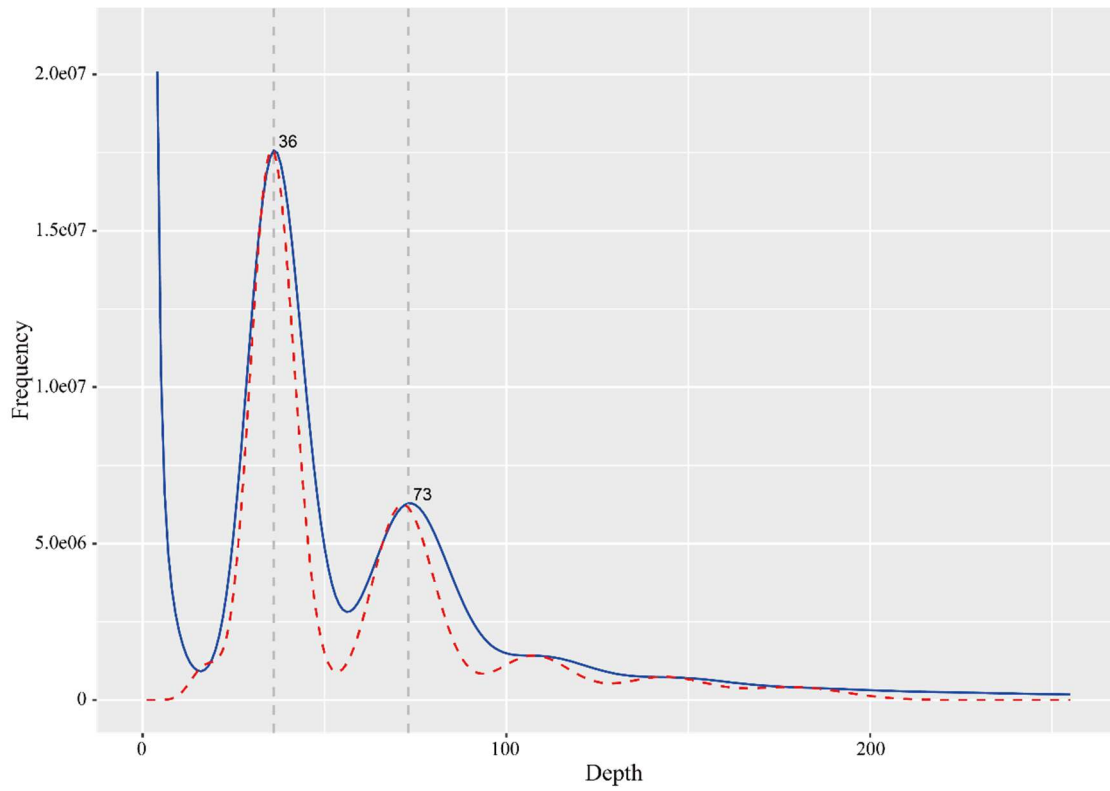


Figure S2. The 17-mer distribution of Illumina short-read data. A K -mer refers to an artificial sequence division of K nucleotides. Genomic characteristics (genome size and repeat structure) can be estimated based on K -mer frequencies.

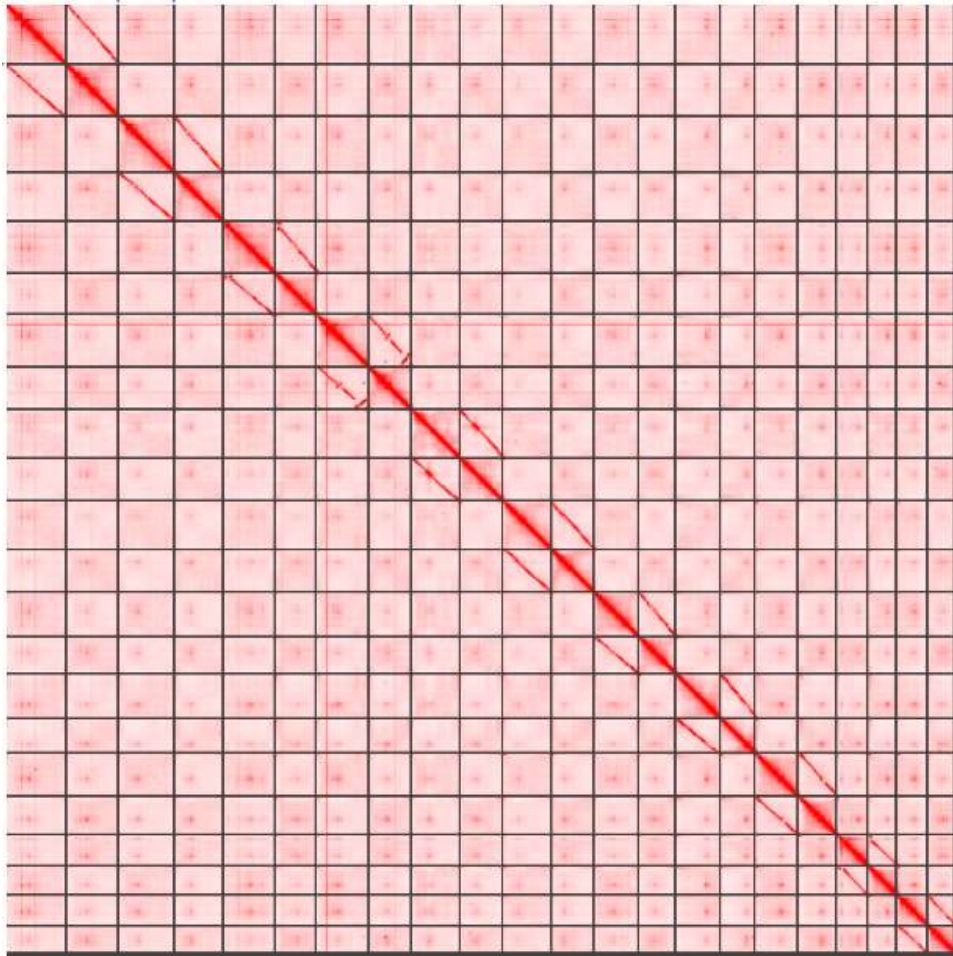


Figure S3. Hi-C linkage density heat map of assemble contigs.

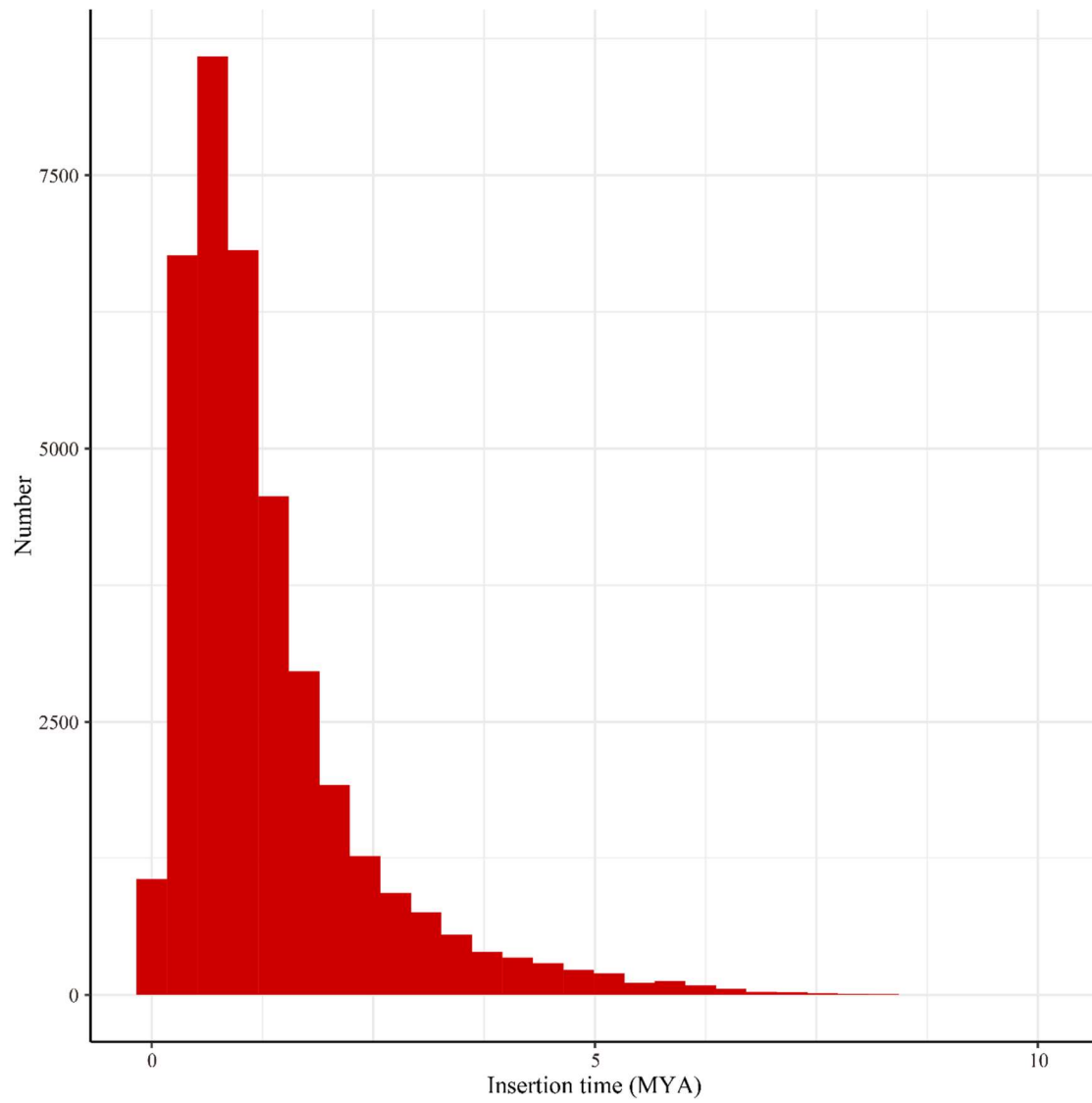


Figure S4. Insertion time of long terminal repeat retrotransposons (LTR-RTs) in the ginger genome.

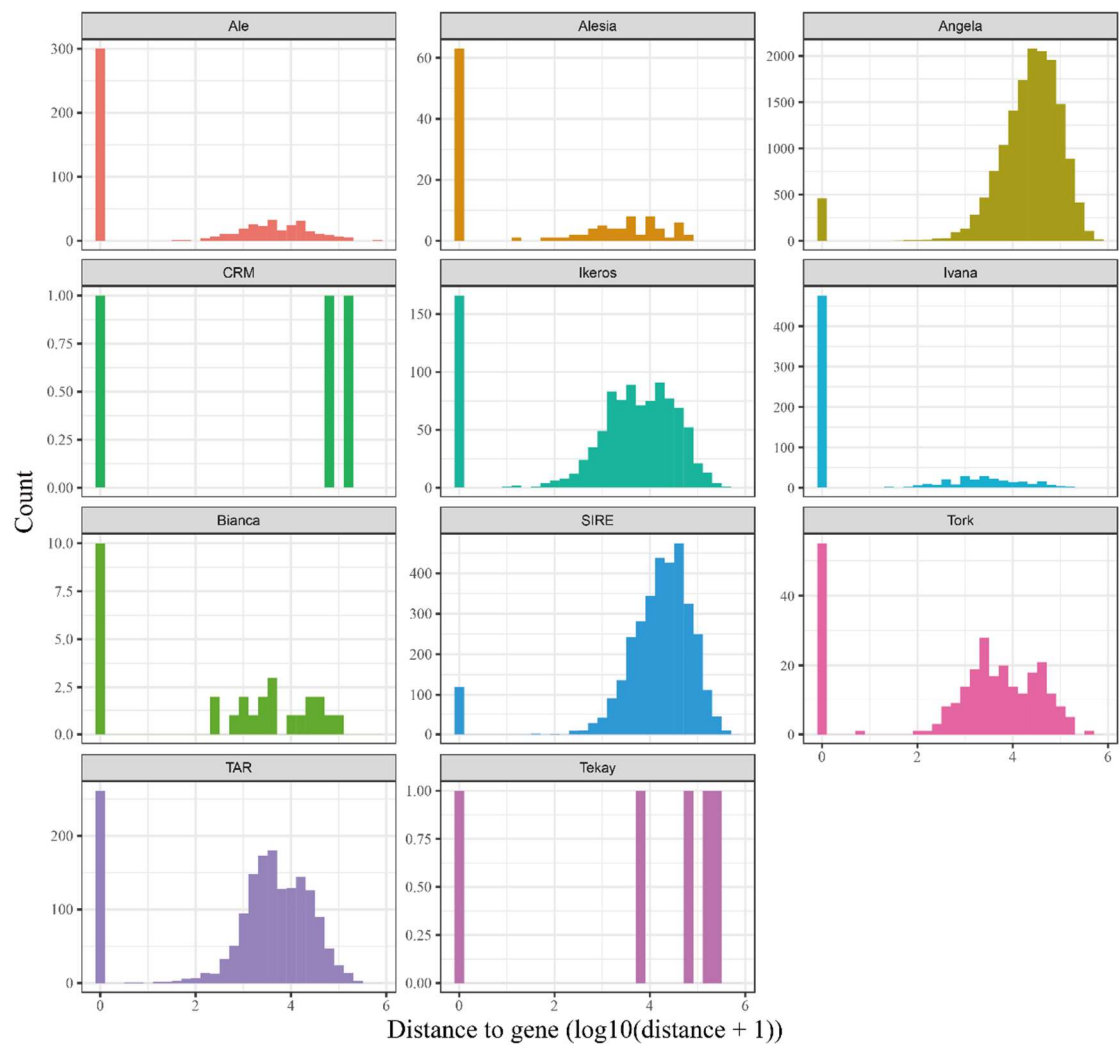


Figure S5. Proliferation history of different subfamilies of the *Copia* class of long terminal repeat retrotransposons (LTR-RTs) in the ginger genome.

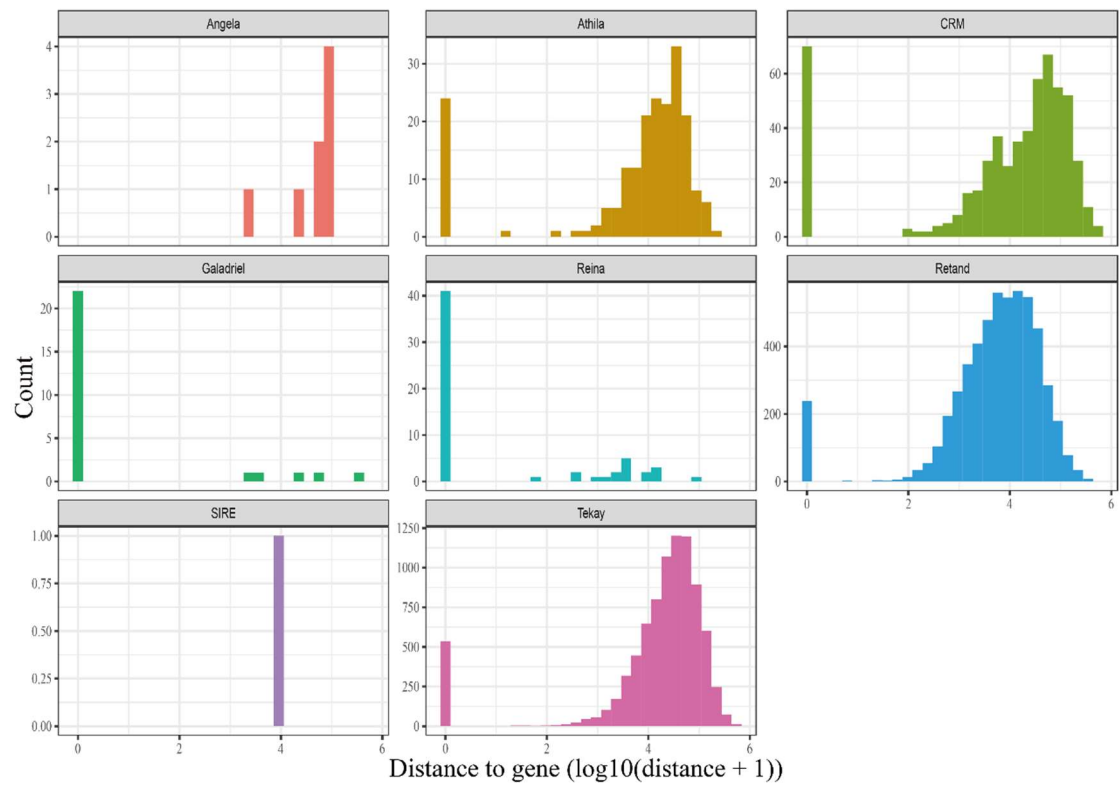


Figure S6. Proliferation history of different subfamilies of the *Gypsy* class of long terminal repeat retrotransposons (LTR-RTs) in the ginger genome.

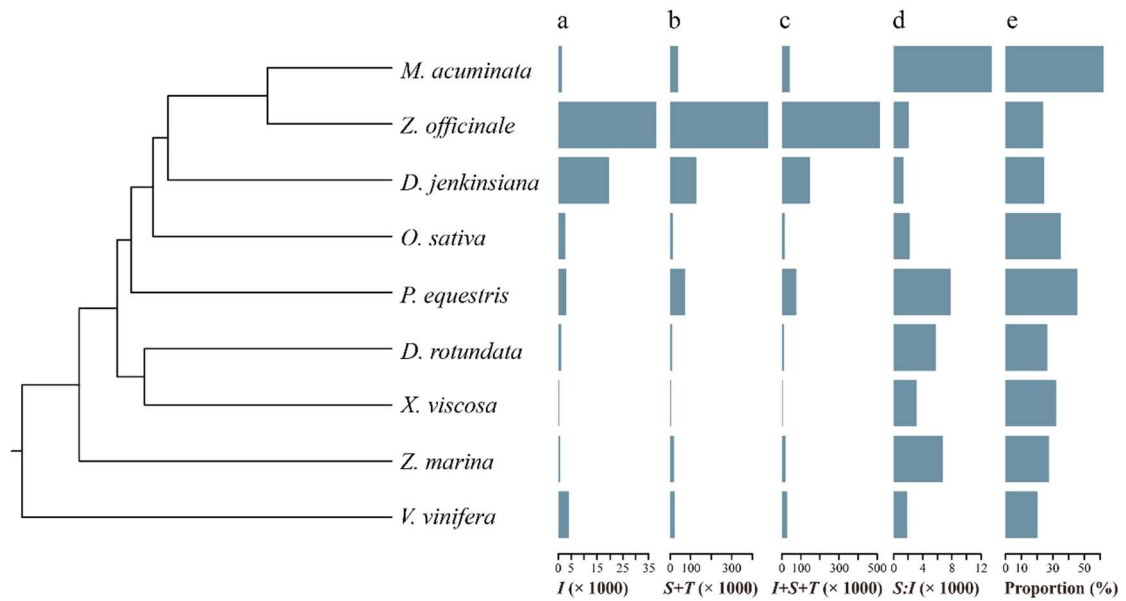


Figure S7. Birth and death of long terminal repeat-retrotransposons (LTR-RTs) in the genome of ginger. (a) Total numbers of LTR-RTs in the genome; (b) comparison of $S + T$ values among plant species; S , number of solo-LTRs; T , number of truncated LTR-RTs. (c) Total numbers of intact LTR-RTs and traces of LTR-RT deaths; I , number of intact LTR-RTs. (d) ratios of solo-LTRs to intact LTR-RTs ($S:I$). (e) The proportions of LTR-RTs found in the clusters with high removal rates (filtered $S:I \geq 3$).

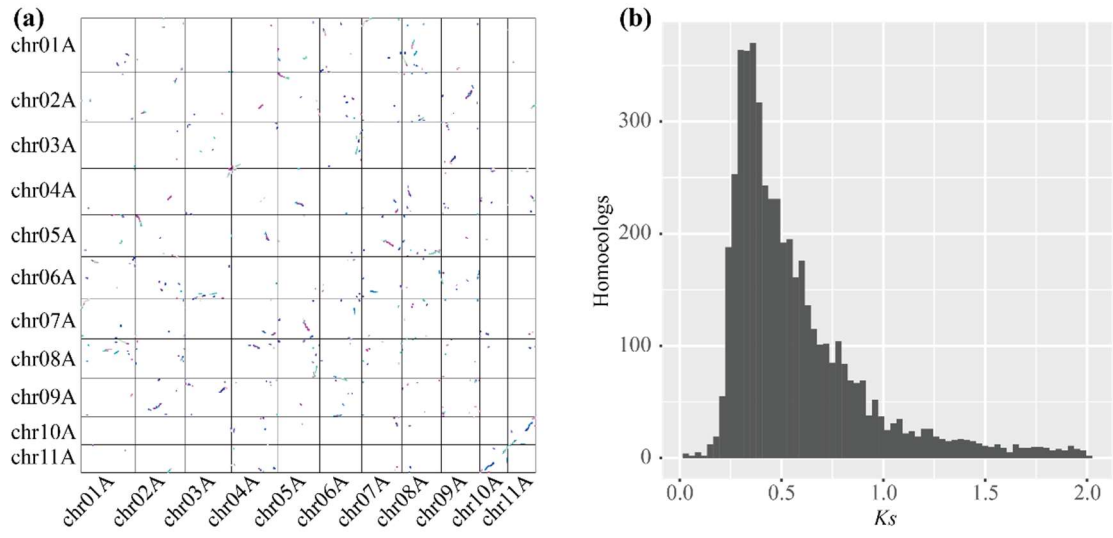


Figure S8. Gene collinearity and K_s distribution of ginger haplotype chromosome

A.

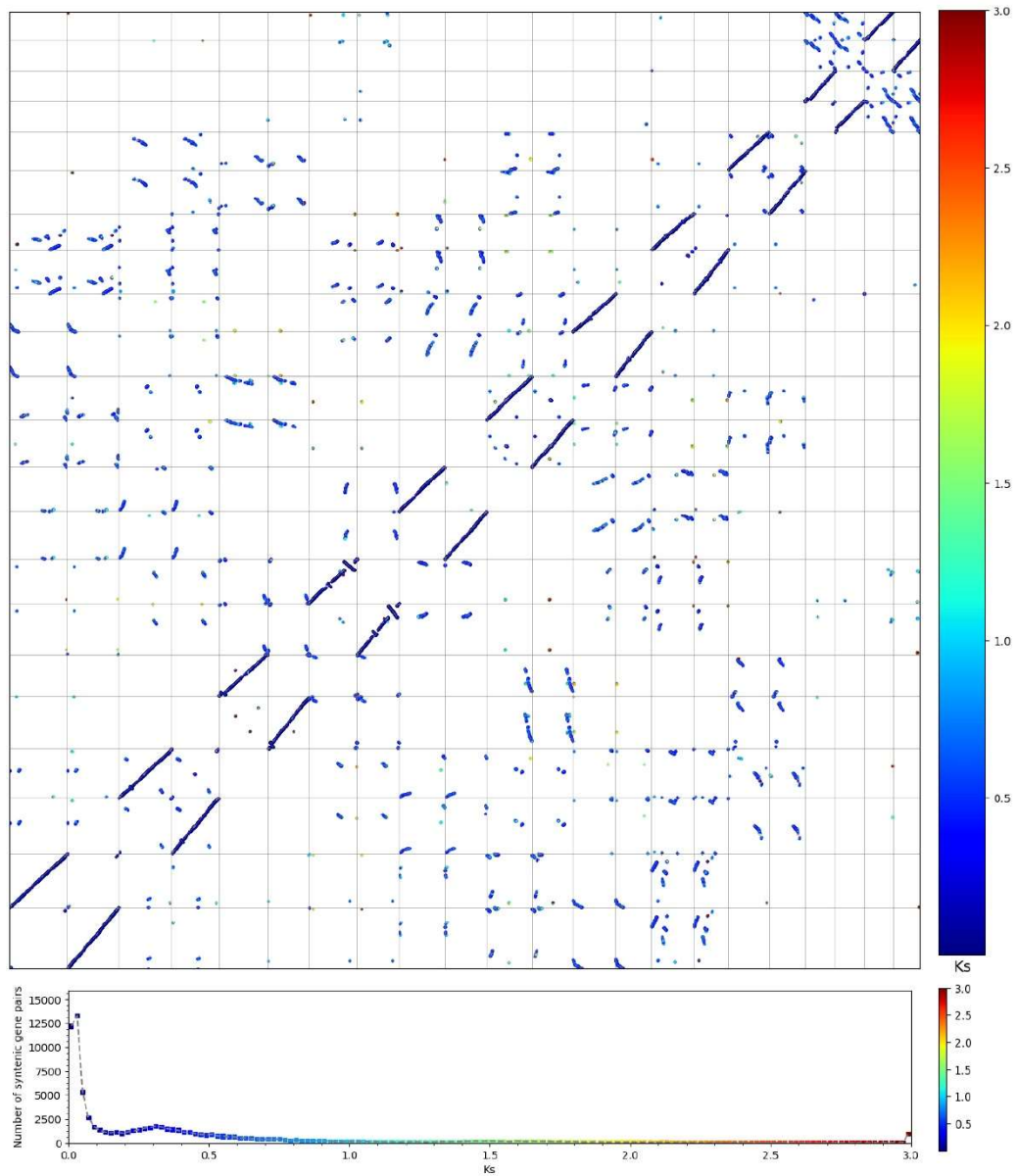


Figure S9. Gene collinearity and K_s distribution in ginger.

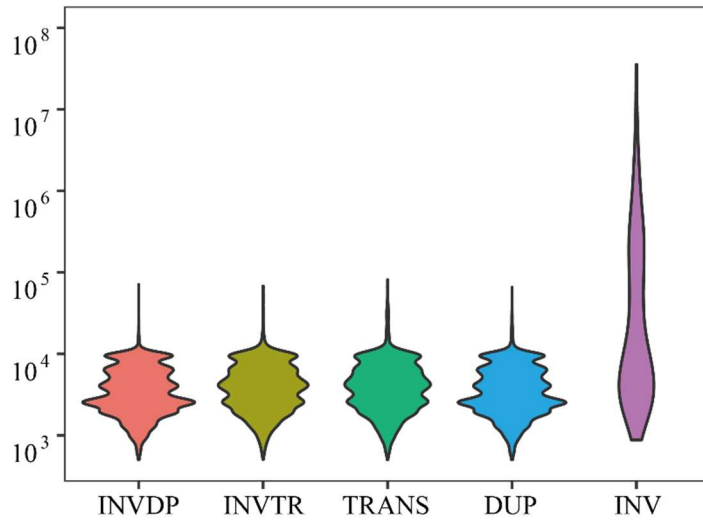


Figure S10. Statistics of structural variation between allelic chromosome pairs.

Size distributions of different types of structural variation in the ginger genome. INVDP: inverted duplications, INVTR: inverted translocations, TRANS: translocations, DUP: duplications, INV, inversions.

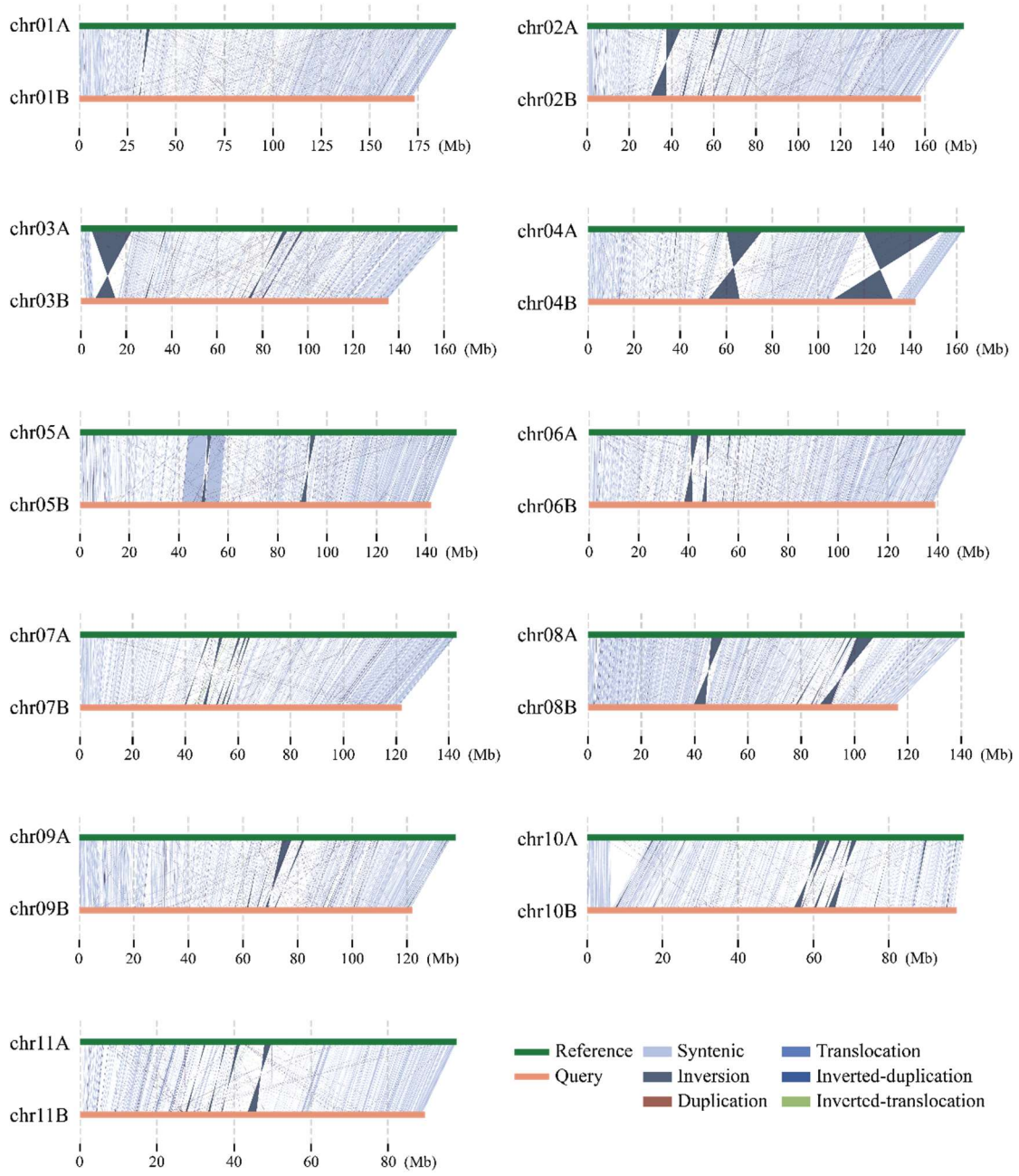


Figure S11. Visualization of structural variation between allelic chromosome pairs.

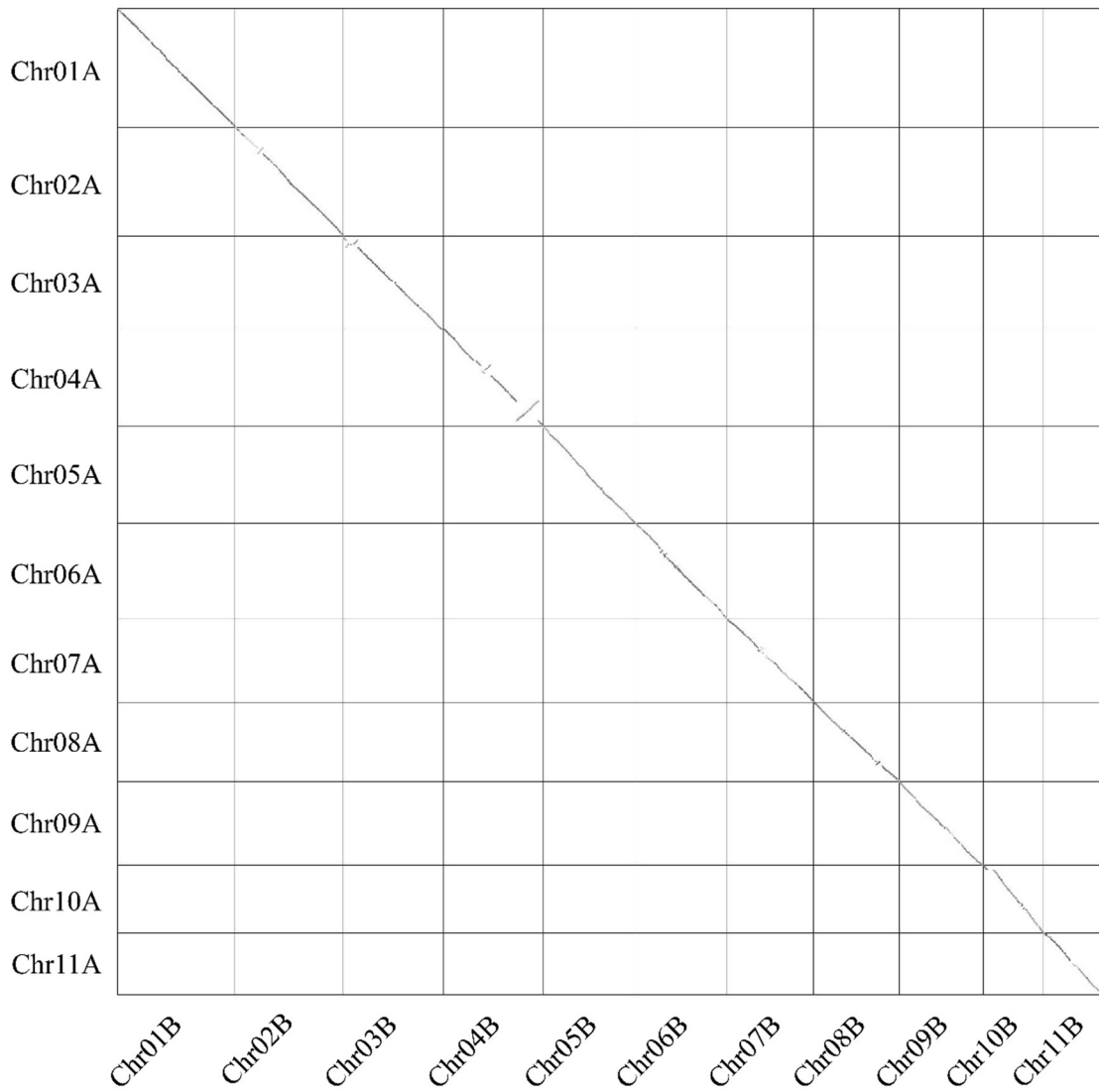


Figure S12. Dot plots of identified alleles along allelic chromosome pairs in the ginger genome.

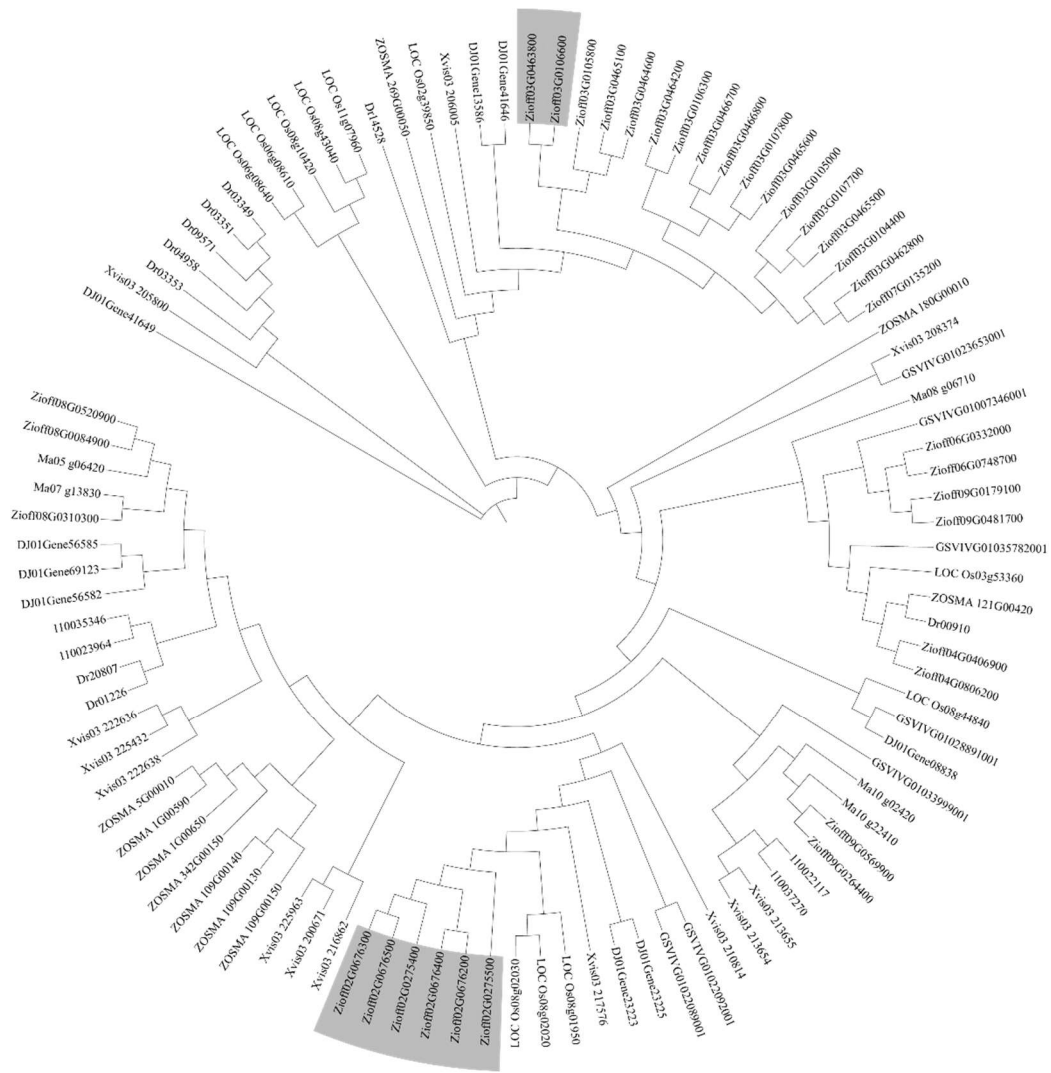


Figure S13. Phylogenetic analysis of shikimate O-hydroxycinnamoyltransferase enzyme (EC: 2.3.1.133) genes using the full sequences of 9 species (*M. acuminata*, *D. jenkinsiana*, *O. sativa*, *X. viscosa*, *P. questris*, *D. rotundata*, *Z. marina*, *V. vinifera* and ginger). The genes with a gray background are responsible for key steps in ginger.

Table S1. DNA-seq and RNA-seq data.

Accession	Title	Raw Reads(M)	Raw Bases(G)	Raw Q20(G)	Raw Q30(G)	Clean Reads(M)	Clean Bases(G)	Clean Q20(G)	Clean Q30(G)	Average Length(bp)
SRR12340663	WGS of Zingiber officinale (ONT)									
SRR12340665	WGS of Zingiber officinale (ONT)									
SRR12340664	WGS of Zingiber officinale (ONT)									
SRR12340661	WGS of Zingiber officinale (ONT)									
SRR12340662	WGS of Zingiber officinale (ONT)									
SRR12329118	WGS of Zingiber officinale (Illumina PCR-free)	306.86	46.336	45.216(97.58%)	43.707(94.33%)	301.375(98.21%)	45.362(97.90%)	44.520(98.15%)	43.707(95.18%)	150.5
SRR12329118	WGS of Zingiber officinale (Illumina PCR-free)	324.16	48.948	47.806(97.67%)	46.264(94.52%)	318.587(98.28%)	47.948(97.96%)	47.089(98.21%)	46.264(95.33%)	150.5
SRR12329118	WGS of Zingiber officinale (Illumina PCR-free)	329.74	49.791	48.681(97.77%)	47.159(94.71%)	324.458(98.40%)	48.838(98.09%)	47.992(98.27%)	47.159(95.47%)	150.5
SRR12329107	Hi-C sequencing of Zingiber officinale	1,881.83	282.274	271.845(96.3%)	255.806(90.6%)	NA	NA	NA	NA	150.0
SRR12329096	RNA-Seq of Zingiber officinale rhizome	47.74	7.161	6.927(96.73%)	6.562(91.63%)	47.162(98.78%)	7.056(98.53%)	6.859(97.20%)	6.562(92.21%)	149.6
SRR12329093	RNA-Seq of Zingiber officinale rhizome	52.97	7.945	7.728(97.27%)	7.371(92.77%)	52.440(99.00%)	7.849(98.79%)	7.664(97.65%)	7.371(93.24%)	149.7
SRR12329092	RNA-Seq of Zingiber officinale rhizome	42.61	6.391	6.158(96.36%)	5.805(90.83%)	42.033(98.65%)	6.290(98.42%)	6.092(96.84%)	5.805(91.44%)	149.6
SRR12329091	RNA-Seq of Zingiber officinale bud	51.86	7.779	7.521(96.68%)	7.112(91.43%)	51.280(98.88%)	7.674(98.65%)	7.451(97.10%)	7.112(91.94%)	149.7
SRR12329090	RNA-Seq of Zingiber officinale bud	59.49	8.924	8.514(95.41%)	7.893(88.45%)	58.818(98.87%)	8.804(98.66%)	8.435(95.80%)	7.893(88.93%)	149.7
SRR12329089	RNA-Seq of Zingiber officinale bud	50.96	7.644	7.410(96.93%)	7.035(92.03%)	50.417(98.93%)	7.545(98.70%)	7.344(97.33%)	7.035(92.53%)	149.7
SRR12329088	RNA-Seq of Zingiber officinale leaf	54.66	8.199	7.941(96.85%)	7.520(91.72%)	54.111(99.00%)	8.101(98.80%)	7.874(97.19%)	7.520(92.15%)	149.7
SRR12329117	RNA-Seq of Zingiber officinale leaf	53.60	8.040	7.765(96.58%)	7.332(91.20%)	52.983(98.85%)	7.929(98.62%)	7.689(96.97%)	7.332(91.70%)	149.6
SRR12329116	RNA-Seq of Zingiber officinale leaf	45.82	6.873	6.625(96.39%)	6.241(90.80%)	45.274(98.81%)	6.775(98.58%)	6.559(96.81%)	6.241(91.33%)	149.7
SRR12329115	RNA-Seq of Zingiber officinale tip of laterally growing rhizome	48.593	7.289	7.079(97.1%)	6.753(92.6%)	47.185(97.1%)	7.034(96.5%)	6.895(98.0%)	6.607(93.9%)	149.1
SRR12329114	RNA-Seq of Zingiber officinale tip of laterally growing rhizome	49.062	7.359	7.141(97.0%)	6.803(92.4%)	47.618(97.1%)	7.099(96.5%)	6.954(97.9%)	6.654(93.7%)	149.1
SRR12329113	RNA-Seq of Zingiber officinale tip of laterally growing rhizome	49.849	7.477	7.275(97.3%)	6.948(92.9%)	48.591(97.5%)	7.251(97.0%)	7.112(98.1%)	6.819(94.0%)	149.2
SRR12329112	RNA-Seq of Zingiber officinale tip of laterally growing rhizome	50.399	7.56	7.359(97.3%)	7.030(93.0%)	49.189(97.6%)	7.345(97.2%)	7.204(98.1%)	6.908(94.1%)	149.3
SRR12329111	RNA-Seq of Zingiber officinale tip of laterally growing rhizome	42.961	6.444	6.273(97.3%)	6.000(93.1%)	41.854(97.4%)	6.242(96.9%)	6.127(98.2%)	5.884(94.3%)	149.1
SRR12329110	RNA-Seq of Zingiber officinale tip of upward growing rhizome	53.077	7.962	7.737(97.2%)	7.390(92.8%)	51.603(97.2%)	7.693(96.6%)	7.545(98.1%)	7.238(94.1%)	149.1
SRR12329109	RNA-Seq of Zingiber officinale tip of upward growing rhizome	44.74	6.711	6.527(97.3%)	6.235(92.9%)	43.561(97.4%)	6.498(96.8%)	6.374(98.1%)	6.114(94.1%)	149.2
SRR12329108	RNA-Seq of Zingiber officinale tip of upward growing rhizome	48.008	7.201	6.992(97.1%)	6.673(92.7%)	46.575(97.0%)	6.943(96.4%)	6.807(98.0%)	6.526(94.0%)	149.1
SRR12329106	RNA-Seq of Zingiber officinale tip of upward growing rhizome	47.778	7.167	6.985(97.5%)	6.689(93.3%)	46.628(97.6%)	6.955(97.0%)	6.833(98.2%)	6.568(94.4%)	149.2
SRR12329105	RNA-Seq of Zingiber officinale rhizome heart	45.481	6.822	6.641(97.3%)	6.347(93.0%)	44.304(97.4%)	6.615(97.0%)	6.490(98.1%)	6.227(94.1%)	149.3
SRR12329104	RNA-Seq of Zingiber officinale rhizome heart	45.878	6.882	6.694(97.3%)	6.393(92.9%)	44.670(97.4%)	6.669(96.9%)	6.540(98.1%)	6.270(94.0%)	149.3
SRR12329103	RNA-Seq of Zingiber officinale rhizome heart	48.342	7.251	7.052(97.2%)	6.726(92.8%)	47.101(97.4%)	7.032(97.0%)	6.891(98.0%)	6.600(93.9%)	149.3
SRR12329102	RNA-Seq of Zingiber officinale rhizome heart	44.466	6.67	6.489(97.3%)	6.193(92.8%)	43.361(97.5%)	6.474(97.1%)	6.347(98.0%)	6.081(93.9%)	149.3
SRR12329101	RNA-Seq of Zingiber officinale rhizome heart	48.993	7.349	7.158(97.4%)	6.853(93.2%)	47.710(97.4%)	7.118(96.9%)	6.989(98.2%)	6.717(94.4%)	149.2
SRR12329100	RNA-Seq of Zingiber officinale rhizome heart	50.475	7.571	7.381(97.5%)	7.061(93.3%)	49.322(97.7%)	7.364(97.3%)	7.229(98.2%)	6.940(94.2%)	149.3
SRR12329099	RNA-Seq of Zingiber officinale rhizome skin	47.151	7.073	6.875(97.2%)	6.557(92.7%)	45.882(97.3%)	6.850(96.8%)	6.712(98.0%)	6.428(93.8%)	149.3
SRR12329098	RNA-Seq of Zingiber officinale rhizome skin	41.998	6.3	6.133(97.3%)	5.857(93.0%)	40.976(97.6%)	6.119(97.1%)	6.000(98.1%)	5.752(94.0%)	149.3
SRR12329097	RNA-Seq of Zingiber officinale rhizome skin	47.131	7.07	6.884(97.4%)	6.583(93.1%)	45.982(97.6%)	6.864(97.1%)	6.735(98.1%)	6.465(94.2%)	149.3
SRR12329095	RNA-Seq of Zingiber officinale rhizome skin	50.375	7.556	7.364(97.5%)	7.046(93.2%)	49.134(97.5%)	7.338(97.1%)	7.203(98.2%)	6.918(94.3%)	149.3
SRR12329094	RNA-Seq of Zingiber officinale rhizome skin	45.729	6.859	6.661(97.1%)	6.343(92.5%)	44.509(97.3%)	6.645(96.9%)	6.506(97.9%)	6.222(93.6%)	149.3

See Table S2

Table S2. Statistics of the ONT datasets.

Raw data	Read length
Base number (bp)	332,729,122,028
Reads number	25,644,829
Max. length (bp)	1,105,994
Mean length (bp)	12,974
Median length (bp)	11,014
N10 (bp)	46,316
L10	581,733
N50 (bp)	22,814
L50	4,932,400
N90 (bp)	11,478
L90	12,652,826

Table S3. Statistics of assemblies with different methods.

Number	Assembly method	Assembled genome size	Assembled contig number	N50 length	L50 number	Maximum contig length
v0.1	SMARTDENOV0 (-K 19)	3.07Gb	4,315	1.27Mb	740	7.8Mb
v0.2	WTDBG2	3.0Gb	90,418	59Kb	13,765	1.1Mb
v0.3	Corrected by CANU + SMARTDENOV0 (-K 19)	2.79Gb	1,185	5.57Mb	136	48.6Mb
v0.4	Corrected by CANU + WTDBG2	3.09Gb	25,047	373Kb	1,870	4.2Mb

Table S4. Statistics of preliminary assemblies.

Assembly feature	Number/Size
Genome size (bp)	3,085,088,269
GC content	39.18%
Contig number	1,185
Max. length (bp)	49,920,313
Min. length (bp)	47,335
Mean length (bp)	2,603,450
Median length (bp)	1,213,495
N10 (bp)	21,378,024
L10	11
N50 (bp)	5,743,545
L50	136
N90 (bp)	1,213,495
L90	593
Complete BUSCOs (C)	1,309
Complete and single-copy BUSCOs (S)	307
Complete and duplicated BUSCOs (D)	1,002
Fragmented BUSCOs (F)	20
Missing BUSCOs (M)	111
Total BUSCO groups searched	1,440

Table S5. Chromosome length in the final ginger genome assembly.

Pseudochromosomes	Length (bp)
chr01A	194,392,478
chr01B	171,592,823
chr02A	178,304,392
chr02B	156,697,907
chr03A	165,904,803
chr03B	134,210,104
chr04A	163,535,463
chr04B	141,013,095
chr05A	152,382,109
chr05B	140,800,694
chr06A	151,157,472
chr06B	137,712,093
chr07A	142,854,748
chr07B	120,890,498
chr08A	141,269,392
chr08B	115,052,570
chr09A	137,703,343
chr09B	120,735,021
chr10A	99,747,443
chr10B	97,102,896
chr11A	97,714,083
chr11B	88,687,397

Table S6. Summary of BUSCO evaluation results for the final ginger genome assembly.

Type	Number	Percentage (%)
Complete BUSCOs	1296	90
Complete and single-copy BUSCOs (S)	240	16.7
Complete and duplicated BUSCOs (D)	1056	73.3
Missing BUSCOs (M)	144	10
Total BUSCO groups searched	1,440	100.0

Table S7. Summary of RNAs in the ginger genome annotation.

Types	Copy Numbers
mRNA	73,006
rRNA/28S	29
rRNA/18S	30
rRNA/5S	657
tRNA	3,514
ncRNA	1,687
Total	78,923

Table S8. Functional annotation of the predicted ginger genes.

	Number	Percent
Swiss Prot	48,672	66.70%
TrEMBL	69,067	94.60%
NR	68,905	94.40%
Pfam	59,476	81.50%
eggNOG	67,166	92.00%
GO	61,621	84.40%
KO	30,394	41.60%
Unannotated	3,513	4.80%
TIGRFAM	6,180	8.47%
PANTHER	67,705	92.74%
Gene3D	48,328	66.20%
PRINTS	9,451	12.95%
SignalP_EUK	6,344	8.69%
ProSitePatterns	13,326	18.25%
Coils	11,016	15.09%
Pfam	57,510	78.77%
SUPERFAMILY	45,783	62.71%
SignalP_GRAM_POSITIVE	5,538	7.59%
SFLD	504	0.69%
MobiDBLite	31,188	42.72%
GO	46,160	63.23%
ProSiteProfiles	26,998	36.98%
TMHMM	16,794	23.00%
ProDom	906	1.24%
SMART	21,711	29.74%
CDD	22,373	30.65%
SignalP_GRAM_NEGATIVE	2,775	3.80%
Phobius	26,786	36.69%
PIRSF	3,492	4.78%
Hamap	1,785	2.45%
IPR	62,184	85.18%
KEGG	5,546	7.60%
Reactome	8,270	11.33%
MetaCyc	3,845	5.27%
Unannotated	1,428	1.96%
Gene	73,006	100%

Table S9. Repetitive DNA sequences in the ginger genome.

order	superfamily	number	length (bp)	percent (%)	mean length (bp)
LTR		1,627,077	1,753,525,166	56.57	1,077.71
	Cassandra	3,137	1,317,944	0.04	420.13
	Caulimovirus	8,389	7,097,116	0.23	846.00
	Copia	904,292	1,043,376,072	33.66	1,153.80
	ERV1	1,197	444,639	0.01	371.46
	Gypsy	648,621	672,218,774	21.69	1,036.38
	Pao	1,793	372,196	0.01	207.58
LINE		86,544	39,917,629	1.29	461.24
	CRE	2,966	435,561	0.01	146.85
	L1	31,720	14,871,316	0.48	468.83
	L1-Tx1	13,896	5,368,226	0.17	386.31
	L2	6,123	820,972	0.03	134.08
	R1	456	133,755	0.00	293.32
	RTE-BovB	31,383	18,287,799	0.59	582.73
SINE		70,011	18,086,180	0.58	258.33
	Alu	47,112	15,040,322	0.49	319.25
	U	677	224,444	0.01	331.53
	tRNA	6,882	637,513	0.02	92.63
	tRNA-RTE	15,340	2,183,901	0.07	142.37
DNA		284,869	133,393,022	4.30	468.26
	CMC-EnSpm	133,658	61,327,257	1.98	458.84
	MULE-MuDR	3,114	2,257,049	0.07	724.81
	MuLE-MuDR	27,853	8,669,086	0.28	311.24
	PIF-Harbinger	19,787	8,351,163	0.27	422.05
	hAT-Ac	85,596	43,736,681	1.41	510.97
	hAT-Tag1	3,821	2,653,211	0.09	694.38
	hAT-Tip100	11,040	6,398,575	0.21	579.58
RC		29,364	29,447,298	0.95	1,002.84
	Helitron	29,364	29,447,298	0.95	1,002.84
Unknown		1,126,054	442,875,183	14.29	393.30
Satellite		476	104,843	0.00	220.26
Simple_repeat		459,115	109,356,625	3.53	238.19
Low_complexity		63,087	3,853,012	0.12	61.07
snRNA		3,601	706,898	0.02	196.31
total		3,750,198	2,531,265,856	81.66	674.97

Table S10. Summary of structural variations between allelic chromosome pairs.

Chromosomes	Duplications		Inversions		Translocations		Inverted-duplications		Inverted-translocations		Sum		Length of chromosomes	Percent (%)
	Number	Size (bp)	Number	Size (bp)	Number	Size (bp)	Number	Size (bp)	Number	Size (bp)	Number	Size (bp)		
chr01A	2,511	10,290,852	36	2,540,185	893	4,250,256	2,439	9,923,945	922	4,204,899	6,801	31,210,137	194,392,478	16.06
chr01B		10,334,318		1,386,682		4,237,827		9,909,828		4,214,615		30,083,270		
chr02A	1,986	8,507,240	25	11,506,170	779	3,553,906	2,023	8,368,921	690	3,076,053	5,503	35,012,290	178,304,392	19.64
chr02B		8,530,951		11,706,643		3,581,159		8,360,271		3,100,336		35,279,360		
chr03A	1,921	8,202,670	20	22,791,430	675	3,368,664	1,844	7,757,752	597	2,759,575	5,057	44,880,091	165,904,803	27.05
chr03B		8,193,012		13,716,559		3,394,227		7,751,523		2,784,085		35,839,406		
chr04A	1,346	5,904,433	22	53,035,895	375	2,004,576	1,292	5,768,948	345	1,609,712	3,380	68,323,564	163,535,463	41.78
chr04B		5,897,228		43,594,914		1,982,423		5,731,755		1,609,099		58,815,419		
chr05A	1,668	7,097,610	24	6,039,724	506	2,520,409	1,654	7,039,077	483	2,240,285	4,335	24,937,105	152,382,109	16.36
chr05B		7,084,820		5,490,860		2,490,985		7,062,392		2,231,090		24,360,147		
chr06A	1,654	7,476,468	25	7,211,434	609	2,971,859	1,581	6,884,735	565	2,740,236	4,434	27,284,732	151,157,472	18.05
chr06B		7,483,560		6,945,035		2,960,855		6,851,338		2,733,664		26,974,452		
chr07A	1,467	6,185,046	34	5,192,278	557	2,729,525	1,410	5,689,243	569	2,836,728	4,037	22,632,820	142,854,748	15.84
chr07B		6,183,947		4,843,172		2,717,555		5,697,348		2,830,856		22,272,878		
chr08A	1,410	6,415,696	23	13,553,604	499	2,486,571	1,301	5,414,410	447	2,105,777	3,680	29,976,058	141,269,392	21.22
chr08B		6,453,927		10,918,334		2,484,600		5,413,203		2,104,417		27,374,481		
chr09A	1,476	6,508,143	28	6,478,783	593	2,904,052	1,383	5,840,896	576	2,569,978	4,056	24,301,852	137,703,343	17.65
chr09B		6,502,882		4,514,446		2,892,873		5,867,065		2,587,716		22,364,982		
chr10A	1,090	4,158,078	20	7,074,862	459	2,034,551	1,050	4,104,997	442	1,956,577	3,061	19,329,065	99,747,443	19.38
chr10B		4,145,463		6,282,969		2,044,557		4,092,349		1,961,363		18,526,701		
chr11A	916	3,950,128	24	3,941,195	422	2,036,005	810	3,345,574	386	1,853,854	2,558	15,126,756	97,714,083	15.48
chr11B		3,998,659		4,176,645		2,027,601		3,385,969		1,844,711		15,433,585		
sum	17,445	149,505,131	281	252,941,819	6,367	61,675,036	16,787	140,261,539	6,022	55,955,626	46,902	660,339,151	3,049,460,824	21.65

Table S11. Summary of structural variations in the ginger genome.

	Size (bp)	Number	Minimum size (bp)	Maximum size (bp)	Median size (bp)
Duplications	149,505,131	17,445	504	70,145	3,301
Inversions	252,941,819	281	882	35,629,541	9,770
Translocations	61,675,036	6,367	504	81,390	3,921
Inverted-duplications	140,261,539	16,787	504	71,131	3,244
Inverted-translocations	55,955,626	6,022	510	68,050	3,882

Table S12. Summary of differences in allelic gene expression in the ginger genome.

	Leaf		Rhizome		Bud		Tip of laterally growing rhizome		Tip of upward growing rhizome		Rhizome heart		Rhizome skin	
	Number	Ratio (%)	Number	Ratio (%)	Number	Ratio (%)	Number	Ratio (%)	Number	Ratio (%)	Number	Ratio (%)	Number	Ratio (%)
Balanced allele-difference to regular allele-difference	161	5.86	595	21.64	430	15.64	281	10.22	569	20.70	394	14.33	290	10.55
Balanced allele-difference to highest allele-difference	1	0.04	14	0.51	6	0.22	1	0.04	6	0.22	0	0.00	2	0.07
Regular allele-difference to balanced allele-difference	10	0.36	245	8.71	168	5.97	75	2.67	110	3.91	26	0.92	172	6.11
Regular allele-difference to highest allele-difference	210	7.47	570	20.26	354	12.58	243	8.64	511	18.17	274	9.74	292	10.38
(+) Regular allele-difference to (-) regular allele-difference	1	0.04	11	0.39	5	0.18	2	0.07	11	0.39	1	0.04	2	0.07
(-) Regular allele-difference to (+) regular allele-difference	1	0.04	11	0.39	4	0.14	1	0.04	6	0.21	1	0.04	6	0.21
Highest allele-difference to balanced allele-difference	0	0.00	2	0.09	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Highest allele-difference to regular allele-difference	55	2.61	95	4.50	111	5.26	82	3.89	61	2.89	56	2.66	109	5.17
(+) Highest allele-difference to (-) highest allele-difference	1	0.05	4	0.19	2	0.09	1	0.05	2	0.09	1	0.05	4	0.19
(-) Highest allele-difference to (+) highest allele-difference	1	0.05	3	0.14	4	0.19	3	0.14	1	0.05	1	0.05	5	0.24

Table S13. GO enrichment of stably expressed alleles in the ginger genome.

ID	Description	Categories	pvalue	p.adjust	qvalue
GO:0016607	nuclear speck	cellular component	1.24E-09	3.24E-06	2.68E-06
GO:0019346	transsulfuration	biological process	3.43E-09	4.47E-06	3.71E-06
GO:0006378	mRNA polyadenylation	biological process	6.11E-09	5.31E-06	4.40E-06
GO:0000285	1-phosphatidylinositol-3-phosphate 5-kinase activity	molecular function	1.93E-08	1.26E-05	1.04E-05
GO:0006406	mRNA export from nucleus	biological process	5.34E-08	2.78E-05	2.31E-05
GO:0044257	cellular protein catabolic process	biological process	1.32E-07	5.72E-05	4.74E-05
GO:2000028	regulation of photoperiodism flowering	biological process	4.29E-07	1.52E-04	1.26E-04
GO:0030488	tRNA methylation	biological process	5.05E-07	1.52E-04	1.26E-04
GO:0036002	pre-mRNA binding	molecular function	5.24E-07	1.52E-04	1.26E-04
GO:0003743	translation initiation factor activity	molecular function	7.39E-07	1.93E-04	1.60E-04
GO:0000381	regulation of alternative mRNA splicing via spliceosome	biological process	9.32E-07	2.09E-04	1.73E-04
GO:0007507	heart development	biological process	9.63E-07	2.09E-04	1.73E-04
GO:0000049	tRNA binding	molecular function	2.01E-06	0.0004025	3.34E-04
GO:0000445	THO complex part of transcription export complex	cellular component	3.57E-06	0.0006201	0.00051397
GO:0032786	positive regulation of DNA-templated transcription elongation	biological process	3.57E-06	0.0006201	0.00051397
GO:0006626	protein targeting to mitochondrion	biological process	4.69E-06	0.00076456	0.00063371
GO:0048255	mRNA stabilization	biological process	5.04E-06	0.00077203	0.0006399
GO:0000502	proteasome complex	cellular component	5.73E-06	0.00083013	0.00068806
GO:0046655	folic acid metabolic process	biological process	6.46E-06	0.00088607	0.00073442
GO:0043248	proteasome assembly	biological process	7.45E-06	0.00097044	0.00080436
GO:0031072	heat shock protein binding	molecular function	8.19E-06	0.00101695	0.00084291
GO:2000185	regulation of phosphate transmembrane transport	biological process	1.08E-05	0.00127967	0.00106066
GO:0008094	DNA-dependent ATPase activity	molecular function	1.13E-05	0.0012848	0.00106492
GO:0048638	regulation of developmental growth	biological process	1.59E-05	0.00156146	0.00129423
GO:0003690	double-stranded DNA binding	molecular function	1.63E-05	0.00156146	0.00129423
GO:0046854	phosphatidylinositol phosphorylation	biological process	1.65E-05	0.00156146	0.00129423
GO:0016307	phosphatidylinositol phosphate kinase activity	molecular function	1.73E-05	0.00156146	0.00129423
GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	biological process	1.74E-05	0.00156146	0.00129423

Table S14. GO enrichment of dynamically expressed alleles in the ginger genome.

ID	Description	Categories	pvalue	p.adjust	qvalue
GO:0010333	terpene synthase activity	molecular function	4.45E-52	7.94E-49	6.74E-49
GO:0016114	terpenoid biosynthetic process	biological process	9.24E-44	8.25E-41	7.00E-41
GO:0016758	transferase activity transferring hexosyl groups	molecular function	6.04E-23	3.59E-20	3.05E-20
GO:0003690	double-stranded DNA binding	molecular function	4.79E-21	2.14E-18	1.81E-18
GO:0008194	UDP-glycosyltransferase activity	molecular function	7.31E-19	2.61E-16	2.22E-16
GO:0010334	sesquiterpene synthase activity	molecular function	2.38E-17	7.08E-15	6.01E-15
GO:0035251	UDP-glucosyltransferase activity	molecular function	2.92E-17	7.45E-15	6.33E-15
GO:0033383	geranyl diphosphate metabolic process	biological process	5.94E-14	1.18E-11	9.99E-12
GO:0080043	quercetin 3-O-glucosyltransferase activity	molecular function	7.59E-13	1.23E-10	1.04E-10
GO:0080044	quercetin 7-O-glucosyltransferase activity	molecular function	7.59E-13	1.23E-10	1.04E-10
GO:0045339	farnesyl diphosphate catabolic process	biological process	5.11E-12	7.59E-10	6.45E-10
GO:0102703	camphene synthase activity	molecular function	5.57E-12	7.64E-10	6.49E-10
GO:0043693	monoterpene biosynthetic process	biological process	1.35E-11	1.62E-09	1.38E-09
GO:0050552	(4S)-limonene synthase activity	molecular function	1.37E-11	1.62E-09	1.38E-09
GO:0071398	cellular response to fatty acid	biological process	6.71E-11	7.48E-09	6.35E-09
GO:0050551	myrcene synthase activity	molecular function	2.39E-10	2.51E-08	2.13E-08
GO:0051762	sesquiterpene biosynthetic process	biological process	3.53E-10	3.50E-08	2.97E-08
GO:0009815	1-aminocyclopropane-1-carboxylate oxidase activity	molecular function	4.61E-10	4.33E-08	3.68E-08
GO:0050004	isoflavone 7-O-glucosyltransferase activity	molecular function	7.35E-10	6.56E-08	5.57E-08
GO:0050057	linamarin synthase activity	molecular function	7.98E-10	6.78E-08	5.76E-08
GO:1900994	(-)-secologanin biosynthetic process	biological process	9.96E-10	8.07E-08	6.85E-08
GO:0009718	anthocyanin-containing compound biosynthetic process	biological process	5.01E-09	3.89E-07	3.30E-07
GO:0009992	cellular water homeostasis	biological process	6.51E-09	4.84E-07	4.11E-07
GO:0060416	response to growth hormone	biological process	9.97E-09	7.11E-07	6.04E-07
GO:0009311	oligosa cellular componentaride metabolic process	biological process	1.40E-08	9.64E-07	8.18E-07
GO:0102701	tricyclene synthase activity	molecular function	1.52E-08	1.00E-06	8.50E-07
GO:1901943	(+)-epi-alpha-bisabolol biosynthetic process	biological process	1.68E-08	1.07E-06	9.07E-07
GO:0009693	ethylene biosynthetic process	biological process	6.63E-08	4.08E-06	3.46E-06

Table S15. Allelic gene coexpression in the ginger genome.

the number of modules	Category (count)			Category (%)		
	same	similar	divergent	same	similar	divergent
36	9,876	4,267	5,956	49.14%	21.23%	29.63%

Table S16. GO enrichment of divergent expression alleles in the ginger genome.

ID	Description	Categories	pvalue	p.adjust	qvalue
GO:0010333	terpene synthase activity	molecular function	3.13E-21	1.17E-17	1.09E-17
GO:0008194	UDP-glycosyltransferase activity	molecular function	1.88E-18	3.53E-15	3.28E-15
GO:0009636	response to toxic substance	biological process	3.56E-18	4.46E-15	4.15E-15
GO:0016758	transferase activity transferring hexosyl groups	molecular function	1.38E-16	1.29E-13	1.20E-13
GO:0003690	double-stranded DNA binding	molecular function	2.62E-16	1.66E-13	1.54E-13
GO:0016114	terpenoid biosynthetic process	biological process	2.14E-15	1.15E-12	1.06E-12
GO:0080043	quercetin 3-O-glucosyltransferase activity	molecular function	5.73E-15	2.39E-12	2.22E-12
GO:0080044	quercetin 7-O-glucosyltransferase activity	molecular function	5.73E-15	2.39E-12	2.22E-12
GO:0009820	alkaloid metabolic process	biological process	2.52E-14	9.46E-12	8.79E-12
GO:0080156	mitochondrial mRNA modification	biological process	1.55E-12	5.29E-10	4.92E-10
GO:0031425	chloroplast RNA processing	biological process	1.83E-12	5.73E-10	5.33E-10
GO:0035251	UDP-glycosyltransferase activity	molecular function	5.09E-12	1.47E-09	1.37E-09
GO:0050004	isoflavone 7-O-glucosyltransferase activity	molecular function	1.31E-11	3.51E-09	3.26E-09
GO:0016135	saponin biosynthetic process	biological process	1.61E-10	4.04E-08	3.75E-08
GO:0004364	glutathione transferase activity	molecular function	1.65E-09	3.88E-07	3.60E-07
GO:0010334	sesquiterpene synthase activity	molecular function	3.45E-09	7.62E-07	7.08E-07
GO:0009807	lignan biosynthetic process	biological process	3.73E-09	7.79E-07	7.23E-07
GO:1902382	11-oxo-beta-amyrin catabolic process	biological process	6.25E-09	1.17E-06	1.09E-06
GO:1902386	glycyrrhetinate biosynthetic process	biological process	6.25E-09	1.17E-06	1.09E-06
GO:0006749	glutathione metabolic process	biological process	1.59E-08	2.85E-06	2.65E-06
GO:0043693	monoterpene biosynthetic process	biological process	1.88E-08	3.21E-06	2.99E-06
GO:0010413	glucuronoxylan metabolic process	biological process	2.20E-08	3.60E-06	3.34E-06
GO:0050736	O-malonyltransferase activity	molecular function	2.96E-08	4.63E-06	4.30E-06
GO:0034007	S-linalool synthase activity	molecular function	5.73E-08	8.62E-06	8.00E-06
GO:0050057	linamarin synthase activity	molecular function	7.70E-08	1.11E-05	1.03E-05
GO:0051762	sesquiterpene biosynthetic process	biological process	2.12E-07	2.94E-05	2.74E-05
GO:2001141	regulation of RNA biosynthetic process	biological process	6.23E-07	8.36E-05	7.76E-05
GO:0048527	lateral root development	biological process	7.60E-07	9.10E-05	8.45E-05

Table S17. Important transcription factor genes involved in 6-gingerol biosynthesis in ginger.

Genes	Gene families	Homoeologous gene in <i>Arabidopsis thaliana</i>	E-value	Description
Zioff02G0663800	ERF	AT1G53910.1	4.00E-42	related to AP2 12
Zioff03G0112100	ERF	AT1G53910.1	4.00E-44	related to AP2 12
Zioff01G0655000	bHLH	AT1G59640.1	4.00E-62	BIG PETAL P
Zioff02G0231600	HD-ZIP	AT3G01470.1	5.00E-50	homeobox 1
Zioff02G0634100	HD-ZIP	AT3G01470.1	1.00E-52	homeobox 1
Zioff11G0166700	HD-ZIP	AT3G01470.1	2.00E-56	homeobox 1
Zioff05G0128800	GATA	AT3G60530.1	1.00E-56	GATA transcription factor 4
Zioff05G0501300	GATA	AT3G60530.1	9.00E-56	GATA transcription factor 4
Zioff01G0512700	WRKY	AT4G18170.1	4.00E-43	WRKY DNA-binding protein 28
Zioff02G0636100	bZIP	AT5G10030.1	1.00E-158	TGACG motif-binding factor 4
Zioff01G0795400	ERF	AT5G18450.1	2.00E-39	ERF family protein
Zioff05G0491000	BBR-BPC	AT5G42520.1	1.00E-113	basic pentacysteine 6
Zioff09G0391700	Trihelix	AT1G76890.2	3.00E-61	Trihelix family protein