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Supplemental information

Differences in pseudogene evolution contributed to the contrasting flavors of turnip and Chiifu, two *Brassica rapa* subspecies

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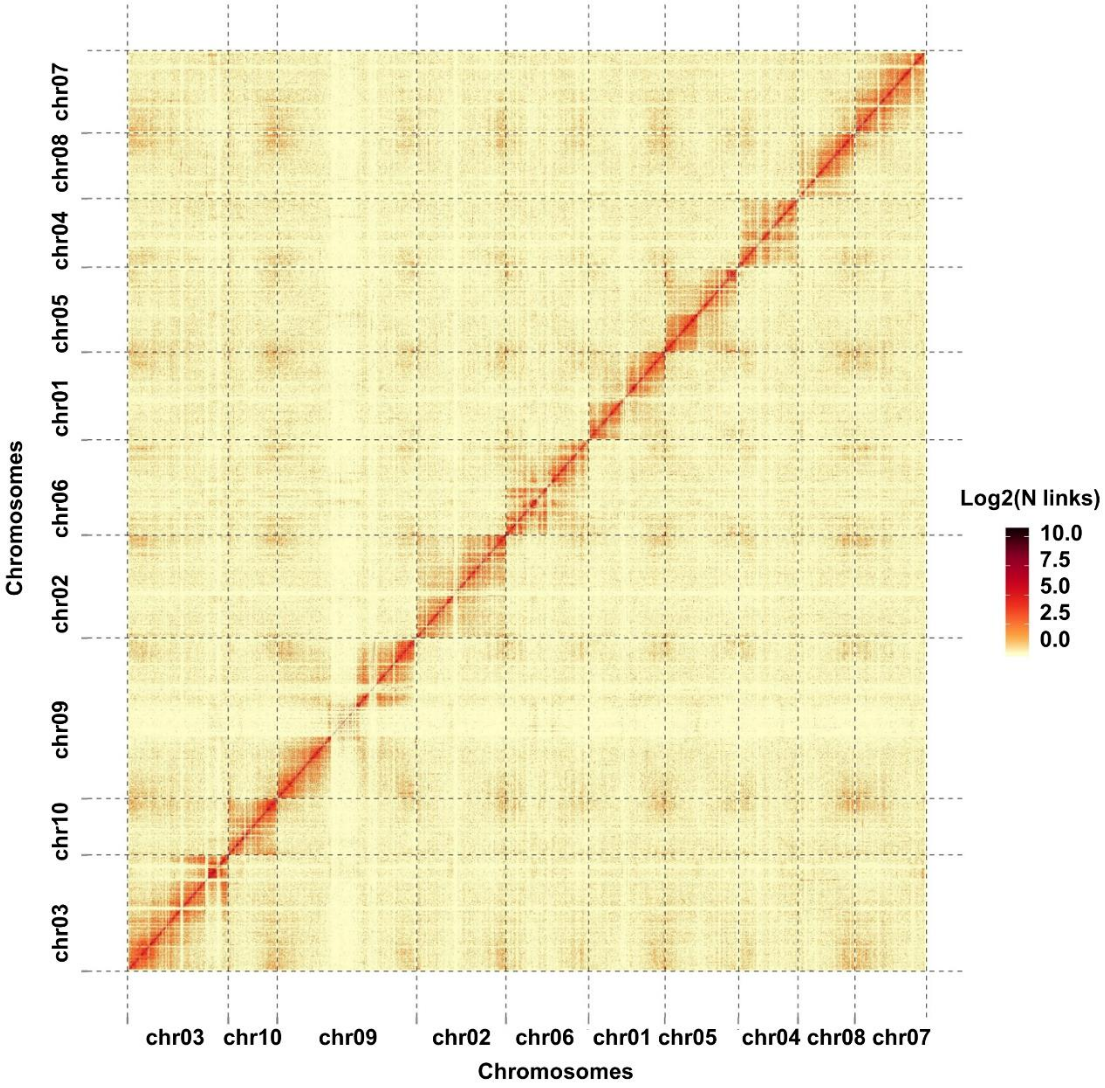
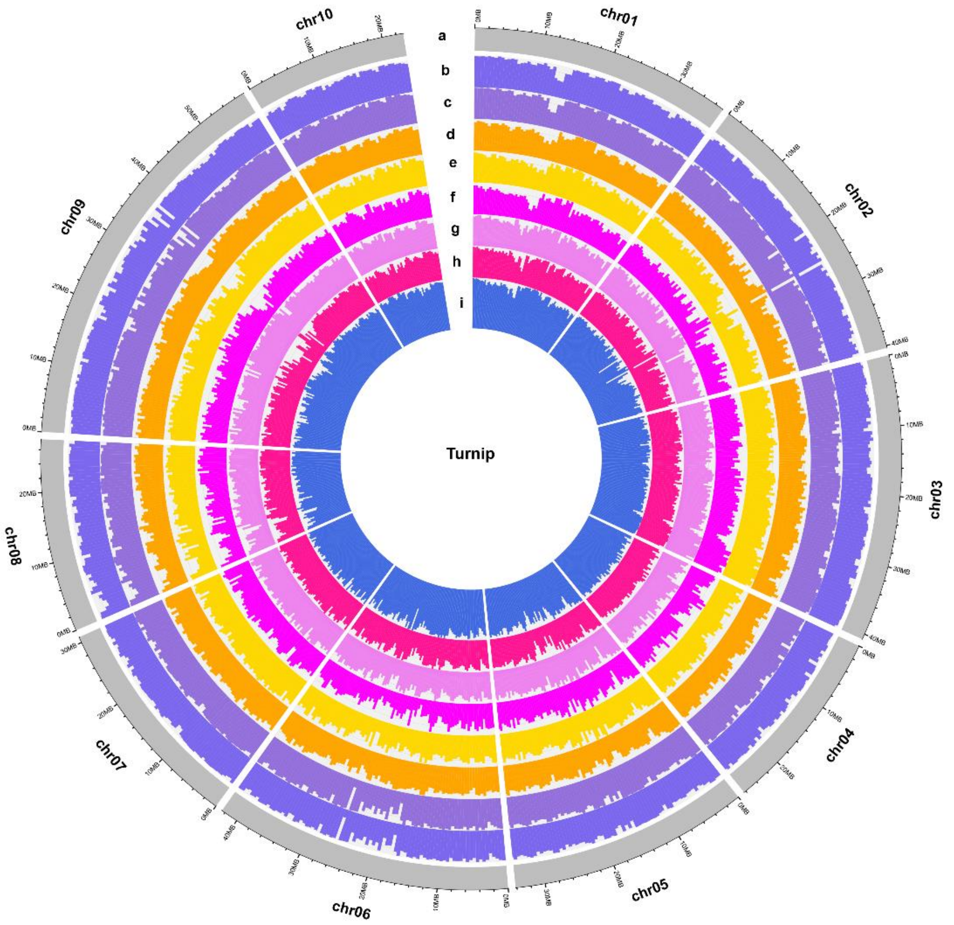
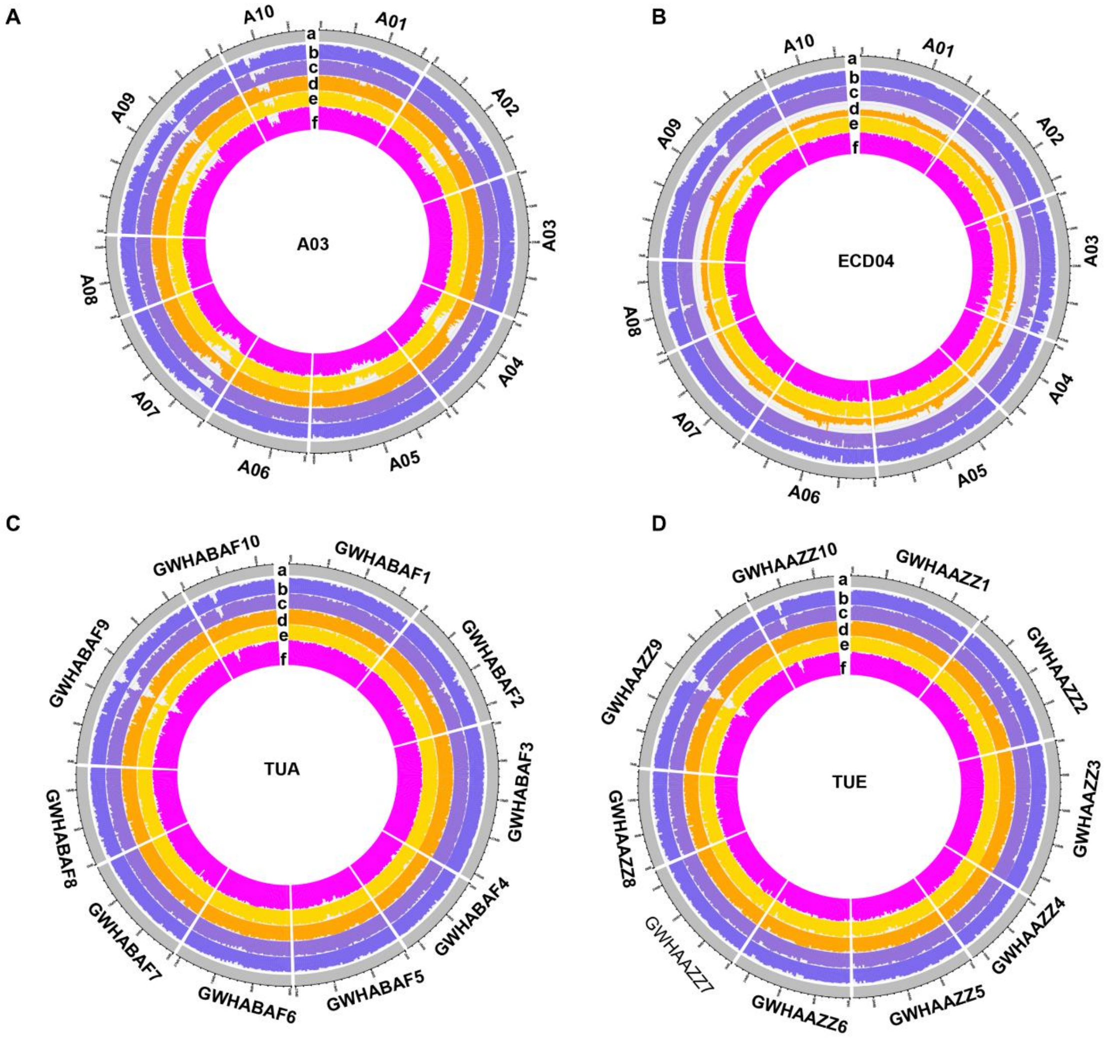
Supplemental Figures



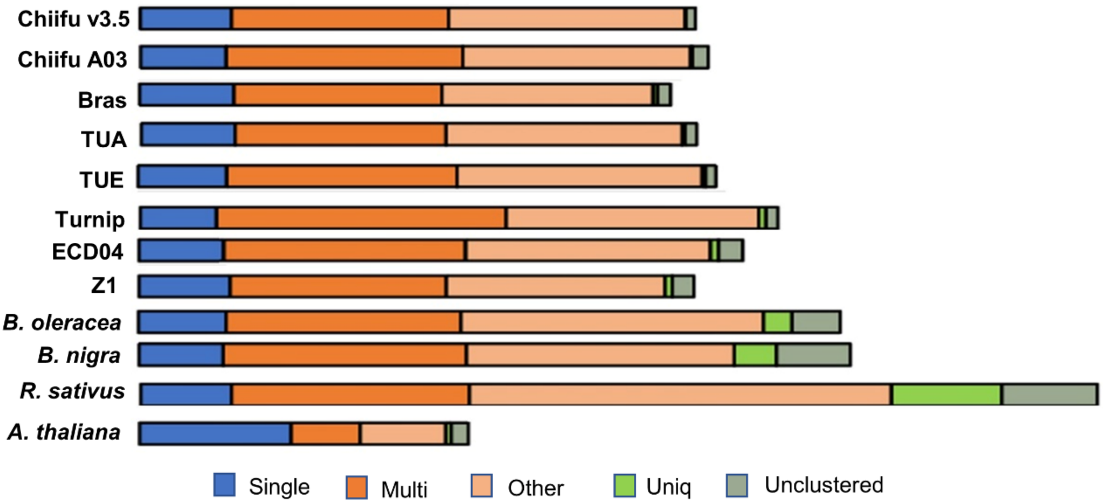
Supplemental Figure 1. Hi-C-assisted assembly of turnip pseudomolecules. The heat map presents the Hi-C chromosomal interactions (100 kb resolution). chr01–chr10, 10 turnip chromosomes. The x- and y-axes present the order of the positions of scaffolds on the corresponding pseudochromosomes.



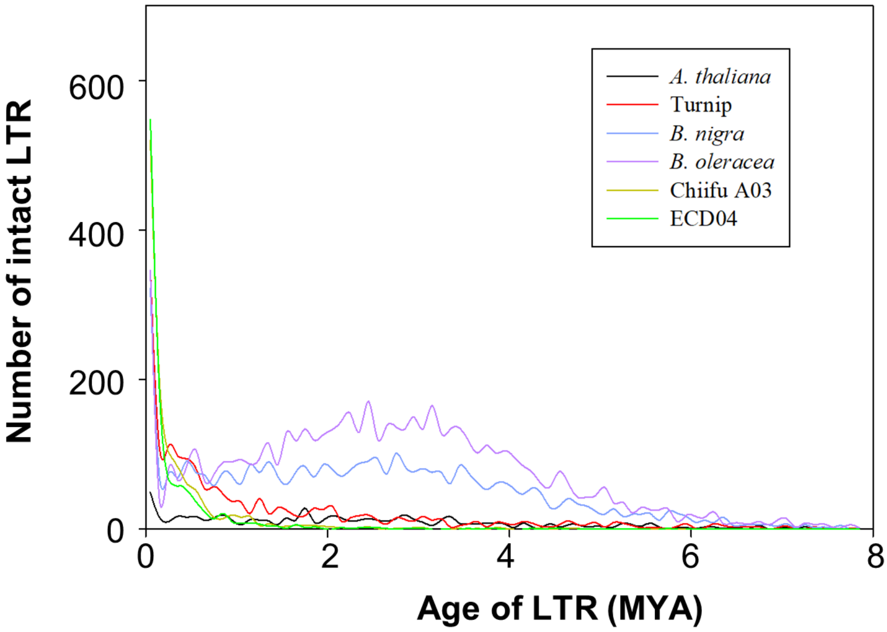
Supplemental Figure 2. Turnip, ECD04, TUA, and TUE Illumina paired-end reads (NGS) and 48A resequencing reads (48Areseq 1–3) from a turnip population were mapped to turnip chromosomes. a, chr1–chr10, circular representation of the pseudomolecules of turnip; b–f, turnip-DO1 NGS, turnip-DO2 NGS, ECD04 NGS, TUA NGS, and TUE NGS reads mapped to turnip chromosomes; g–i, 48A resequencing reads (48Areseq 1–3) from a turnip population mapped to turnip chromosomes.



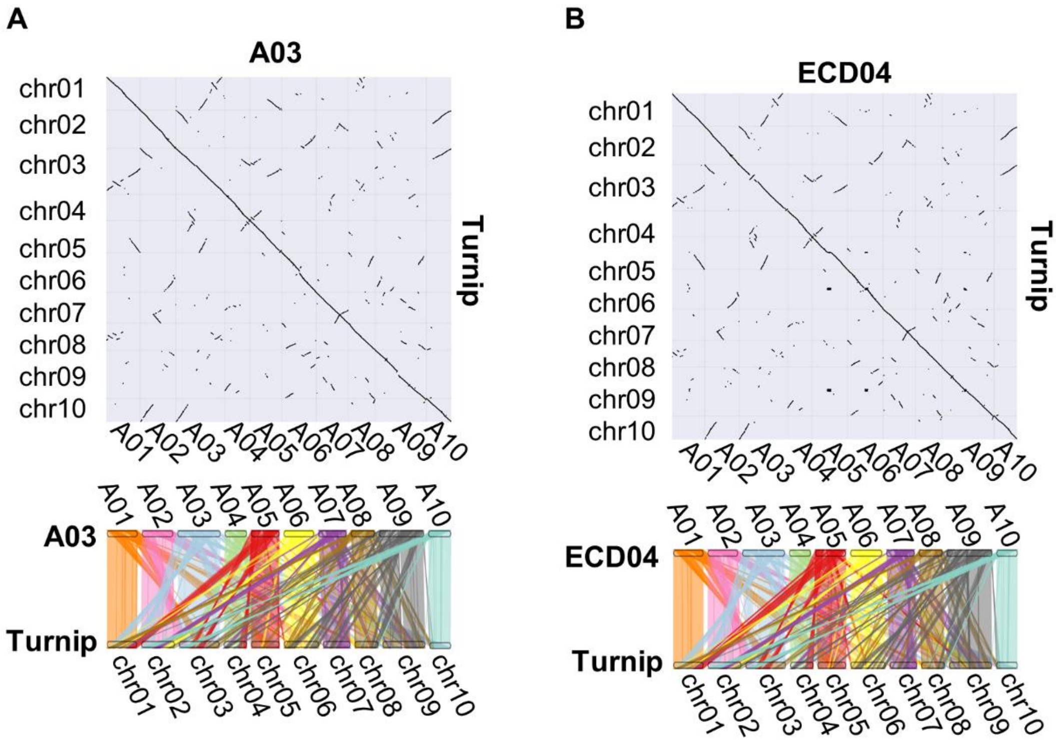
Supplemental Figure 3. Turnip Illumina paired-end reads (NGS) and 48A resequencing reads (48Areseq 1–3) from a turnip population were mapped to A03, ECD04, TUA, and TUE chromosomes (A–D). a, circular representation of the pseudomolecules of A03, ECD04, TUA, and TUE; b–c, turnip-DO1 NGS and turnip-DO2 NGS reads; d–f, 48A resequencing reads (48Areseq 1–3) from a turnip population mapped to turnip chromosomes.



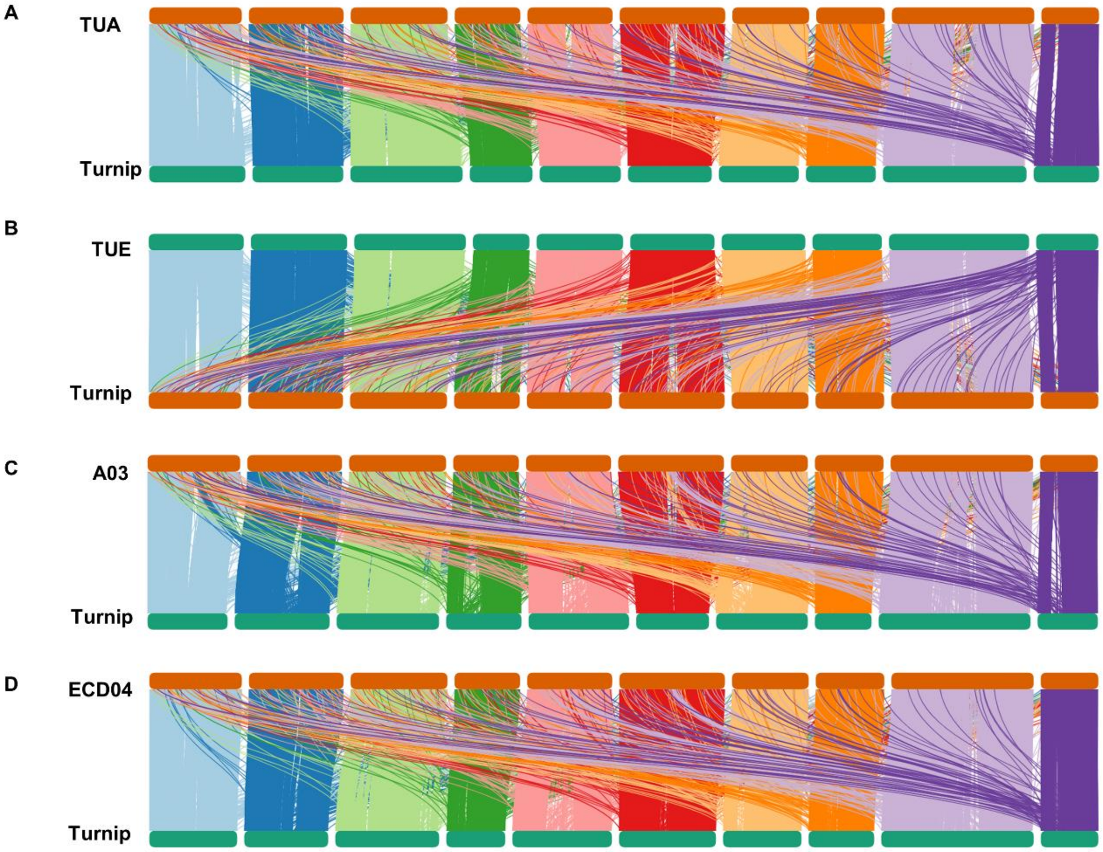
Supplemental Figure 4. Comparison of the number of gene families in the turnip genome and in the genomes of other diploid *Brassica* species and *A. thaliana*.



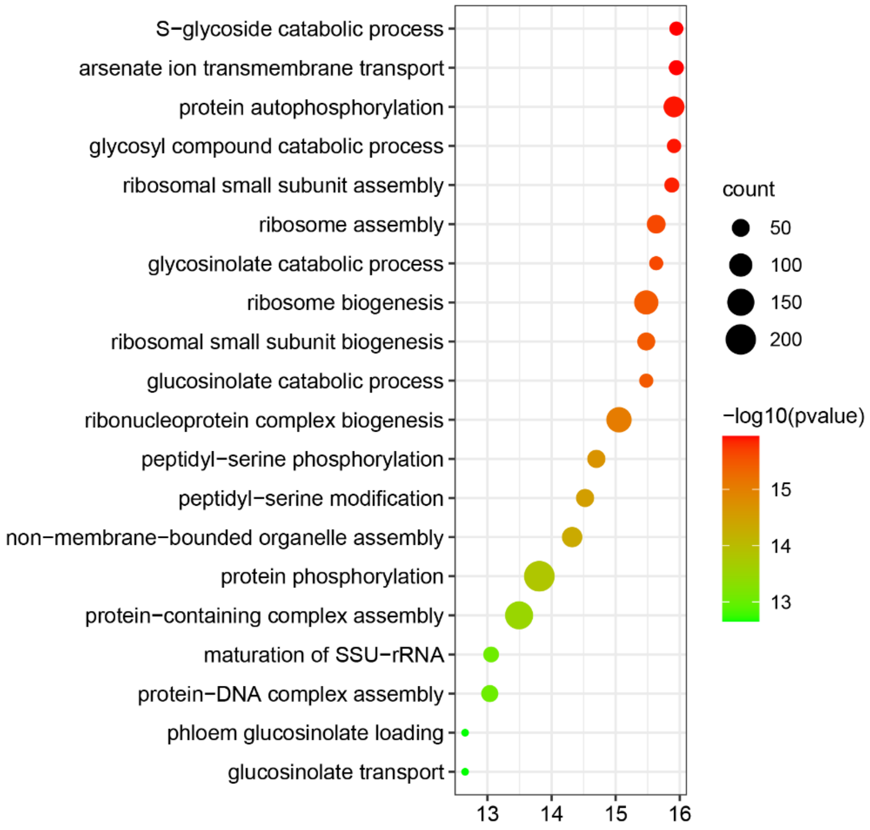
Supplemental Figure 5. Distribution of the LTR retrotransposon insertion times.



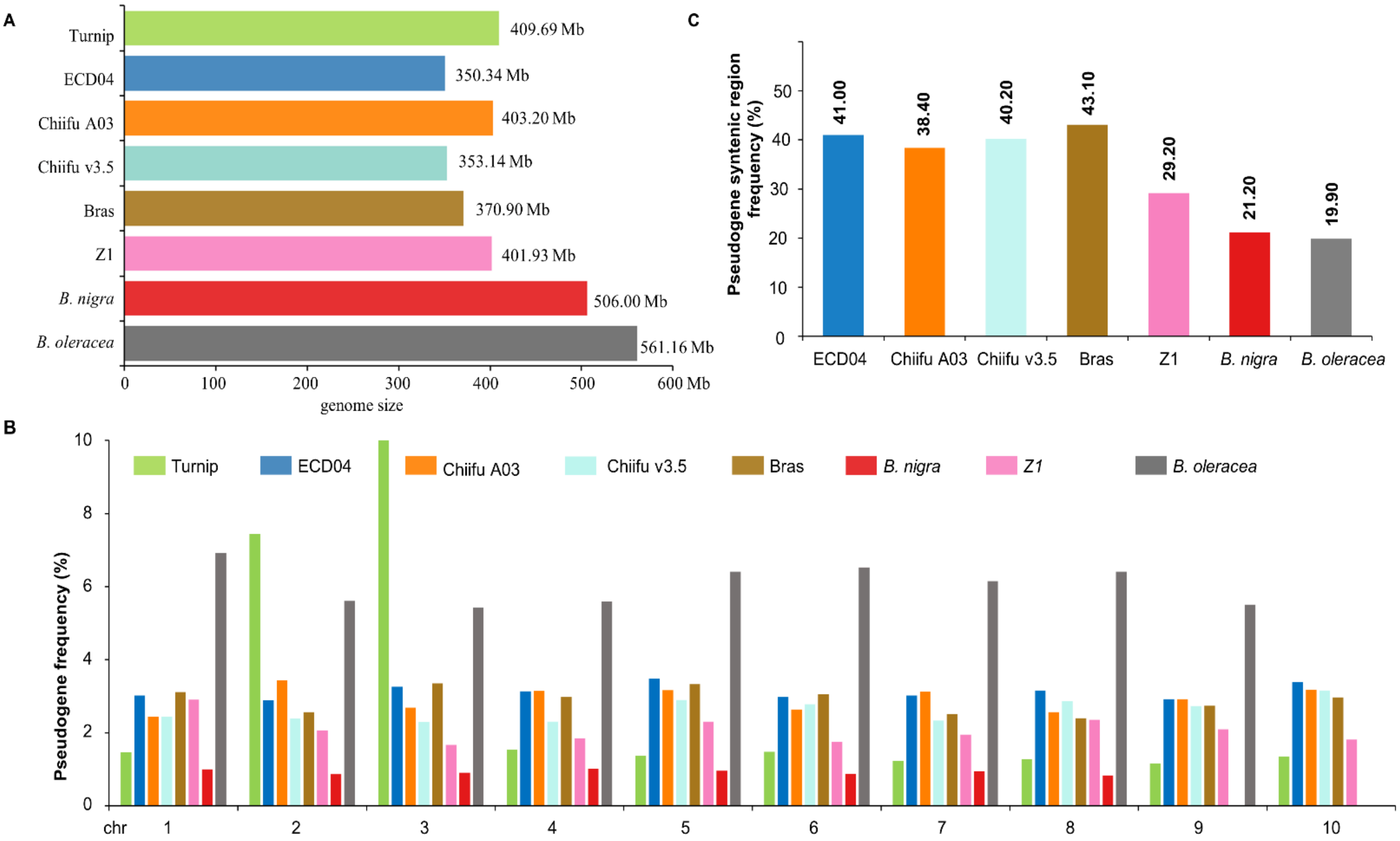
Supplemental Figure 6. Dot plot for the segmental collinearity between the turnip and Chiifu A03 genomes (A) and between the turnip and ECD04 genomes (B). Chiifu A03 and ECD04 chromosomes are presented in different colors, whereas orthologous chromosomal segments in turnip are presented in the same color. Conserved collinear blocks of gene models are presented for the 10 turnip chromosomes and the ECD04 and Chiifu A03 genomes.



Supplemental Figure 7. Sequence collinearity between the turnip genome and the TUA, TUE, Chiifu A03, and ECD04 genomes as determined by MUMmer.



Supplemental Figure 8. Results of the GO enrichment analysis of the most significantly expanded gene families in Chiifu A03. The enrichment factor, which indicates the degree of enrichment, was calculated as the ratio between the number of genes in the expanded families and all of the annotated genes in the pathway. The 15 most significantly enriched pathways are shown.

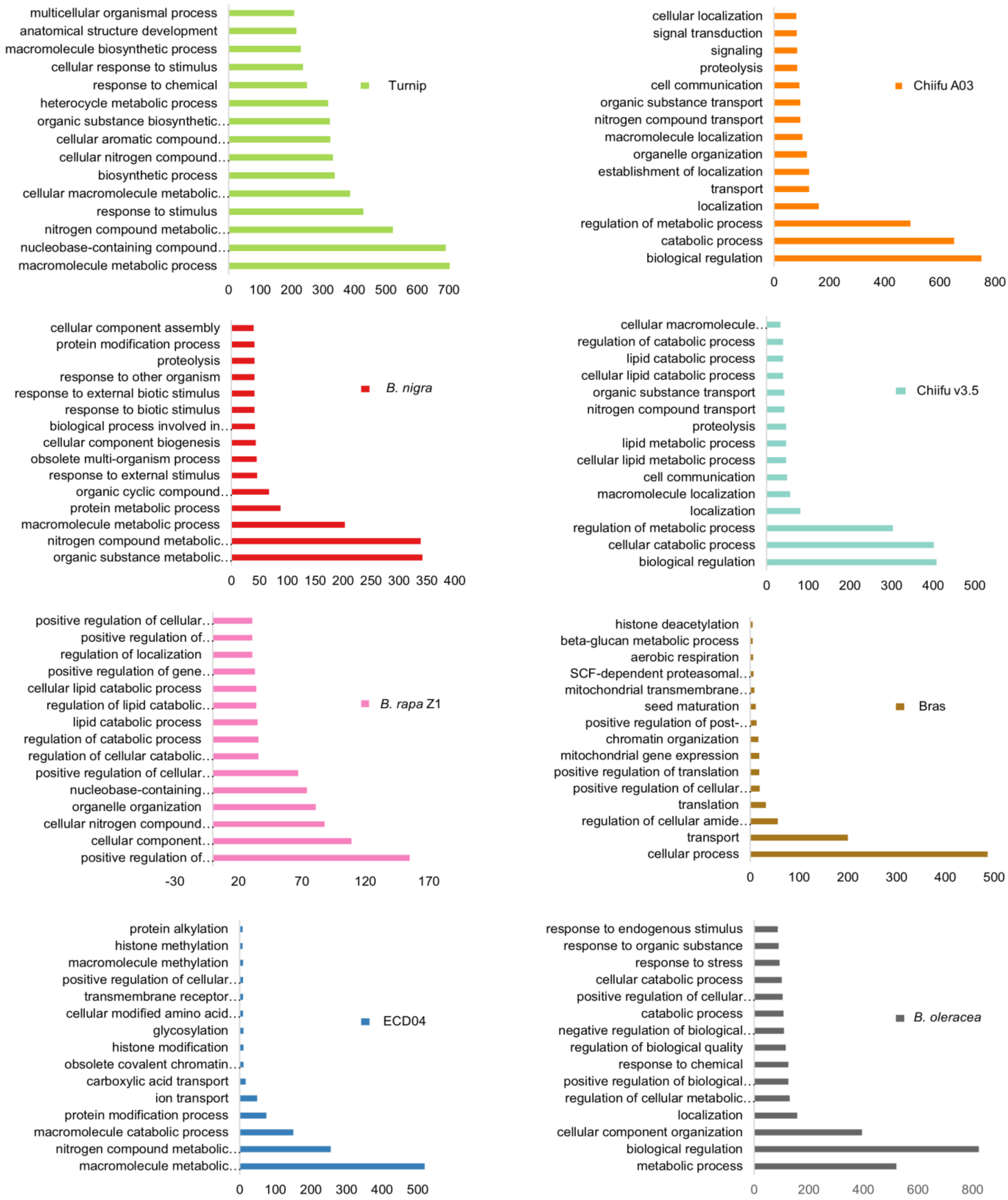


Supplemental Figure 9. Comparison of the pseudogenes in *Brassica* species/subspecies.

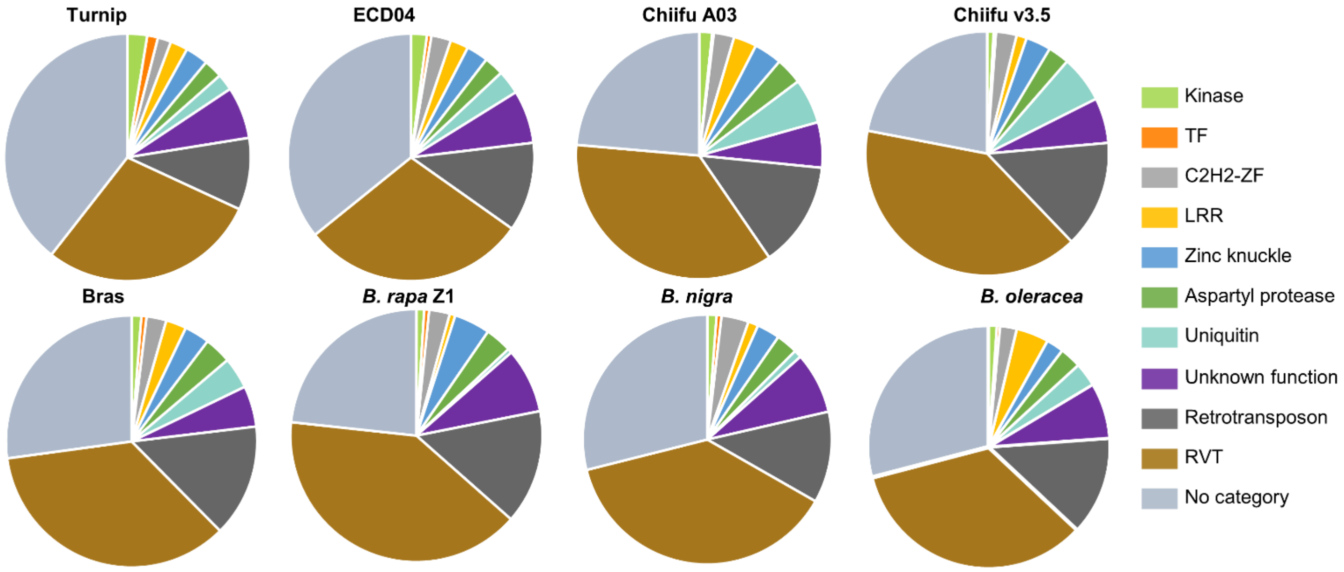
(A) Comparison of the genome sizes of *Brassica* species/subspecies, including turnip, ECD04, Chiifu A03, Chiifu v3.5, *B. rapa_chinensis* (Bras), *B. rapa* Z1, *B. nigra*, and *B. oleracea*

(B) Comparison of the pseudogene frequency (%) for each chromosome in *Brassica* species/subspecies. The y-axis presents the ratio of the pseudogene length to the chromosome length in *Brassica* species/subspecies. The x-axis presents the corresponding chromosome numbers.

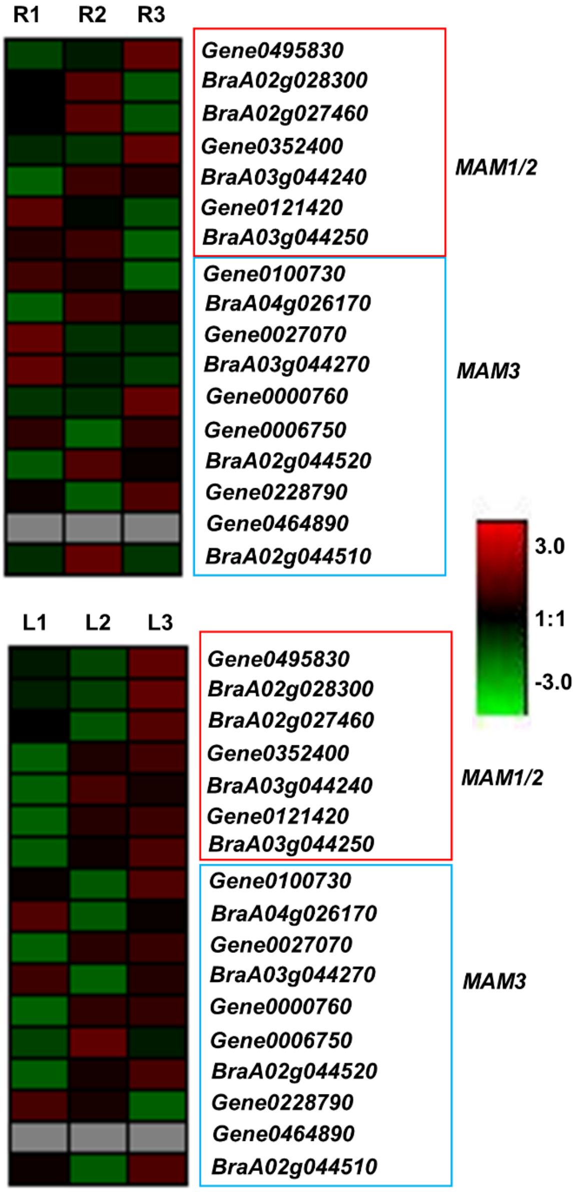
(C) Synteny (%) between turnip and other species/subspecies.



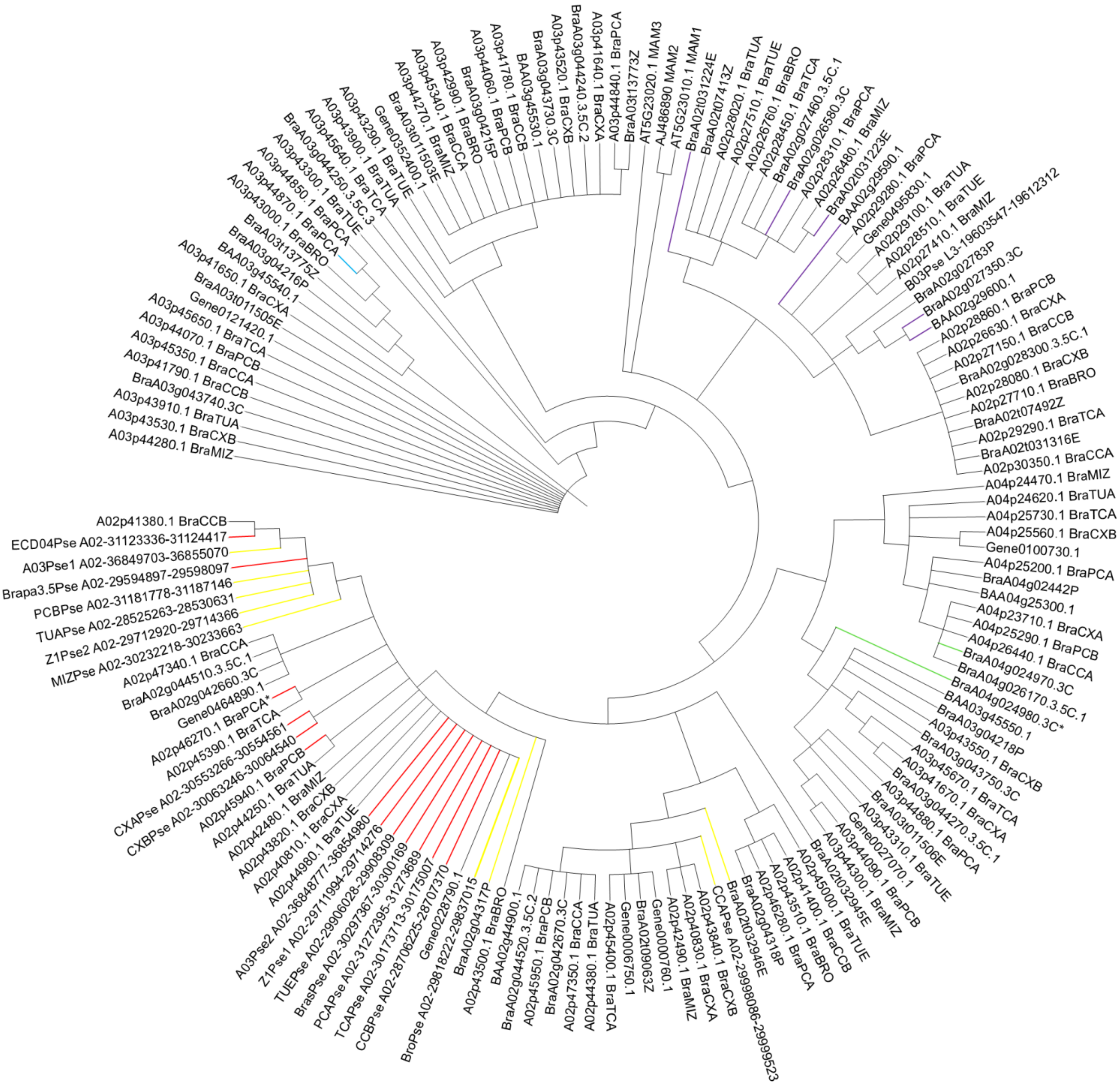
Supplemental Figure 10. Gene Ontology (GO)-based functional annotation of pseudogenes in *Brassica* species/subspecies. The GO enrichment analysis of the pseudogenes in *Brassica* species/subspecies was performed on the basis of the annotations of the closest functional paralogs.



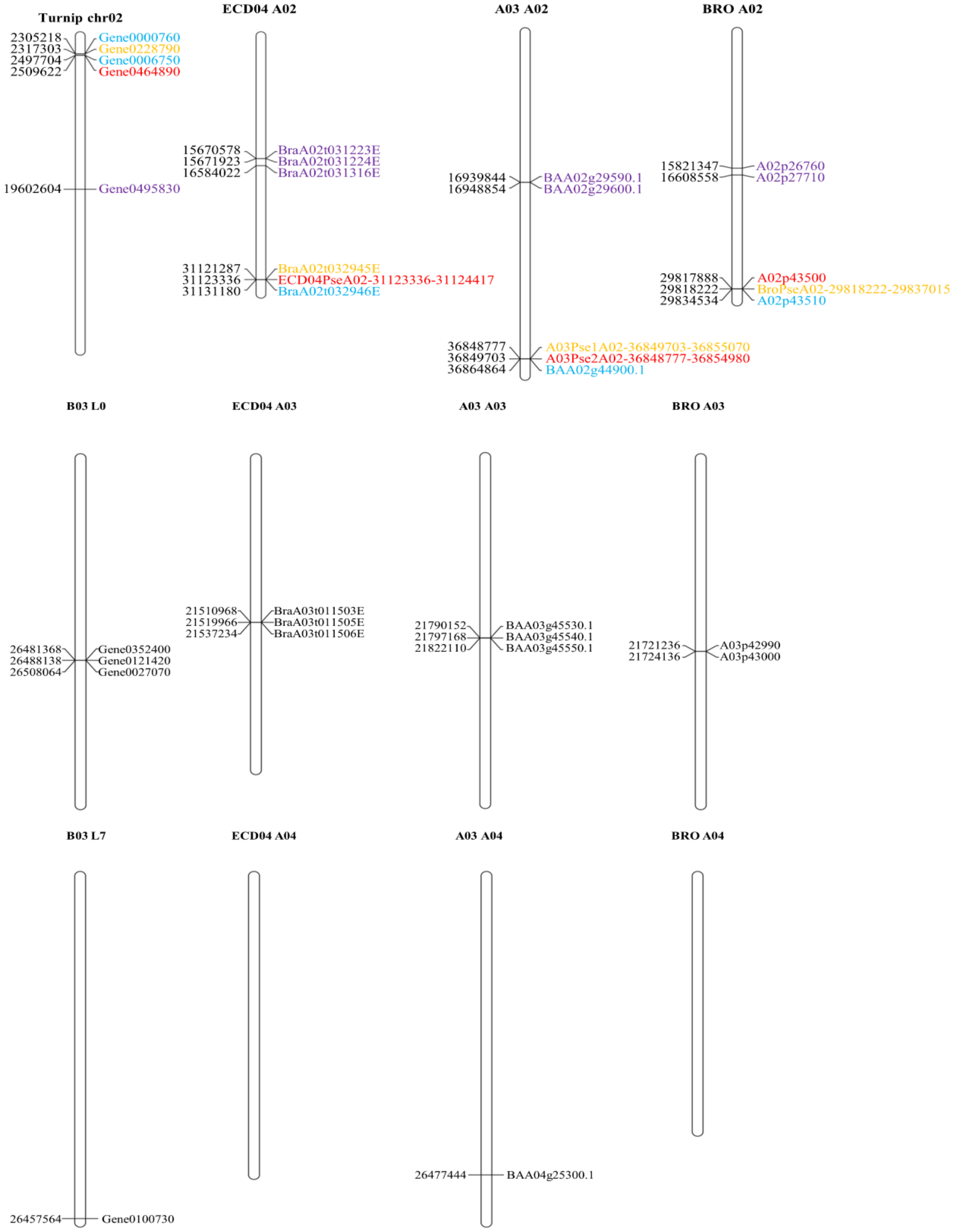
Supplemental Figure 11. Functional annotation of pseudogenes in *Brassica* species/subspecies according to Pfam domains.



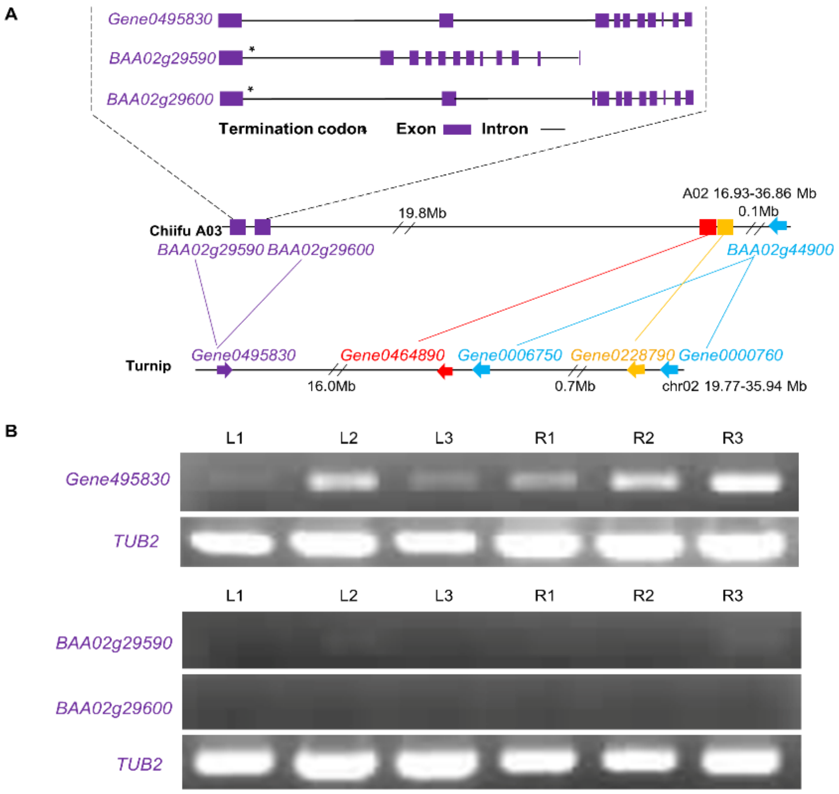
Supplemental Figure 12. Heat map of the quantitative real-time PCR (qRT-PCR) data for the turnip and Chiifu v3.5 *MAM* genes in different developmental stages. The qRT-PCR analysis was completed using three biological and technical replicates. R1, R2, and R3 represent the taproots collected at 10, 20, and 30 days after germination, respectively. L1, L2, and L3 represent the leaves collected at 10, 20, and 30 days after germination, respectively. Gene expression levels are presented in the colored bar. *TUB2* as reference (LOC103873913).



Supplemental Figure 13. Phylogenetic tree comprising *MAM* genes and pseudogenes. Neighbor-joining trees consisting of *MAM* genes were constructed by aligning coding sequences, with 1,000 bootstrap replicates. The *A. thaliana* genome includes only *MAM1* and *MAM3*. Colored lines represent pseudogenes, with numbers indicating the position of the pseudogene on the chromosome.



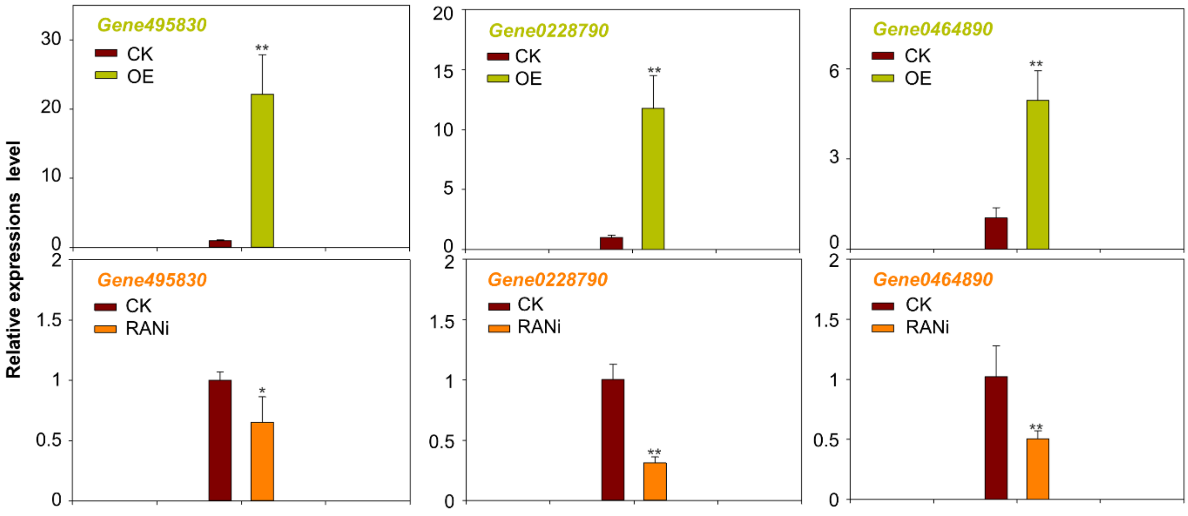
Supplemental Figure 14. Distribution of *MAM* genes on the turnip, ECD04, Chiifu A03, and BRO chromosomes. Turnip has the most *MAM* functional genes, which are distributed on chromosomes chr02, chr03, and chr04; the collinear chromosomes in other species/subspecies are A02, A03, and A04, respectively. Identical colors represent the same homologous regions on turnip chr02 and ECD04, Chiifu A03, and BRO A02 chromosomes.



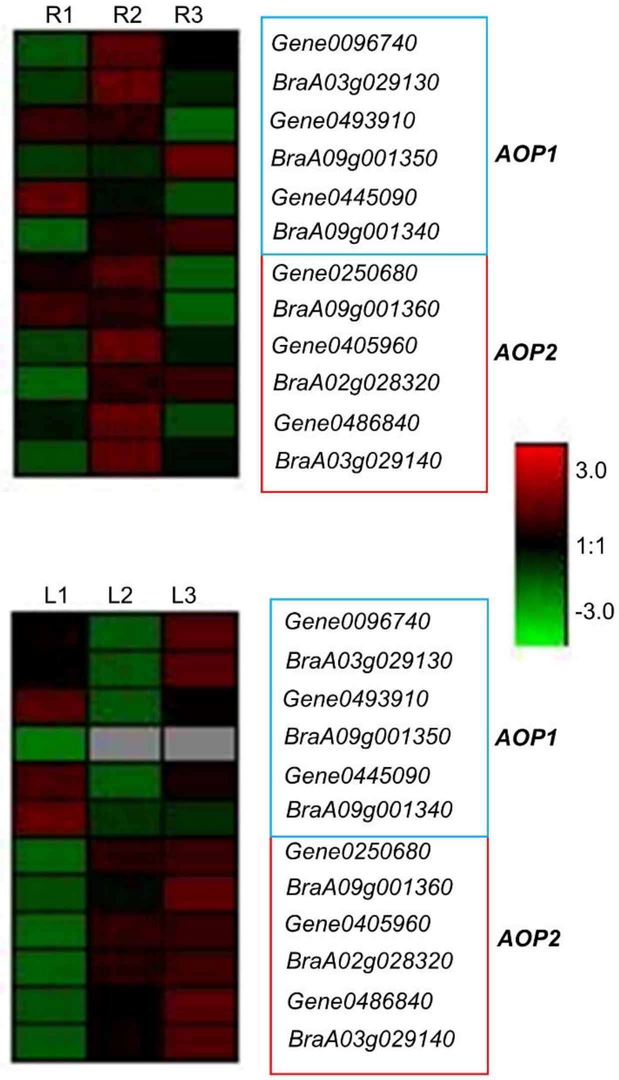
Supplemental Figure 15. Identification of pseudogenes.

(A) Analysis of the synteny among *MAM* genes in turnip and Chiifu A03. Turnip chromosome chr02 with *MAM* genes and the collinear chromosome A02 in Chiifu A03 are presented. Identical colors represent the same homologous region. Lines indicate genes with colinearity. Arrows indicate the gene orientation on the chromosome. Boxes represent pseudogenes in Chiifu A03. Specifically, dashed box represents *MAM* (*Gene0495830*) in turnip converted into pseudogenes (*BAA02g29590* and *BAA02g29600*) due to codon termination (asterisks) in Chiifu A03. Syntenic regions in both genomes, with one turnip genome containing two functional gene (*Gene0464890* and *Gene0228790*) and others containing homologous sequence in Chiifu A03 genome with clear markers indicative of a pseudogene, are presented.

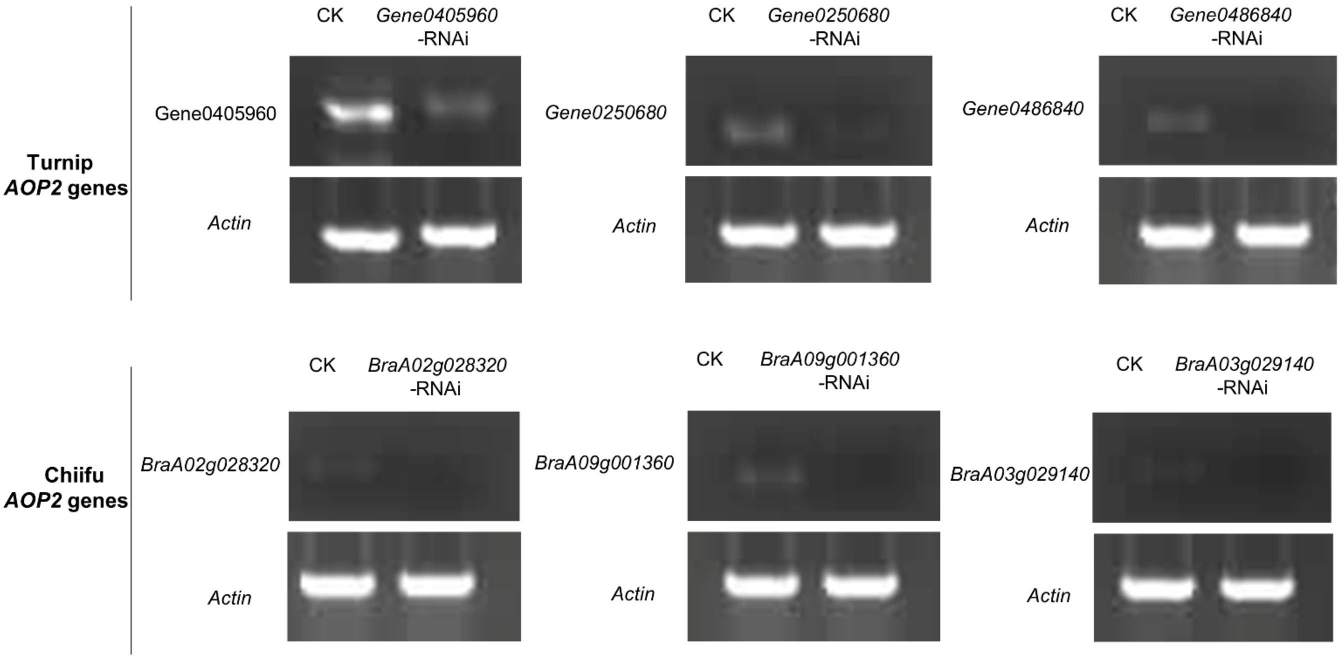
(B) Validation of pseudogenes. The expression levels of pseudogenes *BAA02g29590* and *BAA02g29600* in Chiifu at different developmental stages (L1–L3 in leaves and R1–R3 in taproots) were compared with the expression levels of the functional gene *Gene0495830* in turnip via semi-quantitative PCR (RT-PCR). L1, L2, and L3 and R1, R2, and R3 represent the leaf samples and taproot samples collected at 10, 20, and 30 days after germination, respectively. *ACT* as reference.



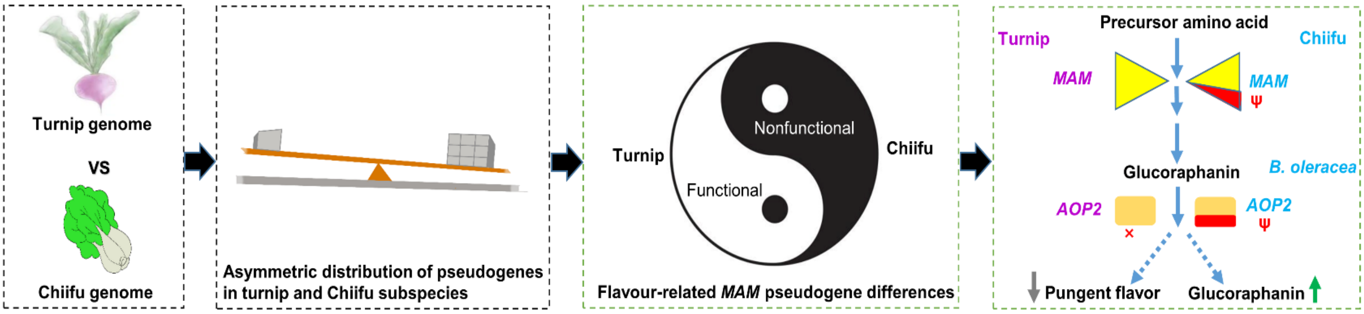
Supplemental Figure 16. Overexpression (OE) of three turnip *MAM* functional genes in Chiifu hairy roots (top) and silencing of these genes in turnip hairy roots via RNAi (bottom). Non-transgenic roots served as the control (CK). The analysis was completed using three biological and technical replicates. Error bars indicate the standard deviation. The *MAM* genes with significant differences in expression between the transgenic and CK samples are indicated by asterisks (*, $P < 0.05$; **, $P < 0.01$). *TUB2* as reference (LOC103873913).



Supplemental Figure 17. Heat map of the quantitative real-time PCR (qRT-PCR) data for the turnip and Chiifu v3.5 *AOP* gene expression levels at different developmental stages. The qRT-PCR analysis was completed using three biological and technical replicates. R1, R2, and R3 represent the taproot samples collected at 10, 20, and 30 days after germination, respectively. L1, L2, and L3 represent the leaf samples collected at 10, 20, and 30 days after germination, respectively. Gene expression levels are presented in the colored bar. *TUB2* as reference (LOC103873913).



Supplemental Figure 18. Results of the RT-PCR analysis of *AOP2* genes in turnip and Chiifu v3.5. *AOP2*-RNAi and control samples were analyzed. *Actin* as reference.



Supplemental Figure 19. Article flowchart. The pseudogenetic differences in turnip and Chiifu genomes resulted in the differential evolution of the flavor-related GSL metabolic pathway. Pseudogenes were distributed asymmetrically on the chromosomes in these two subspecies. The *MAM* gene family expanded in turnip but converted into pseudogenes in Chiifu. There are three functional *AOP2* genes both in turnip and *B. rapa*. Although *B. oleracea* also contains three *AOP2* genes, only one is functional; the other two genes are mutated. These differences explain the diversity in the flavors of turnip and Chiifu. In turnip, the accumulation of anticancer substances may be enhanced and the pungency may be decreased by the RNAi-based silencing of the flavor- and anticancer-associated *AOP2* gene in the GSL pathway. Pseudogenes are indicated by “ψ”.

Supplemental tables

Supplemental Table 1. Estimation of the turnip genome size according to a k-mer analysis.

K-mer	K-mer number	K-mer depth	Genome size (Mb)
19	45,695,255,046	14	446.09

Supplemental Table 2. Sequencing data for the turnip genome assembly.

Sequencing libraries	Illumina reads	Pacbio reads	Hi-C reads
Insert size (bp)	270	20 000	270
Clean data (Gb)	59.4	44.93	26.79
Mean read length (bp)	-	8,595	-
Sequence coverage (×)	50	110	65.5

Supplemental Table 3. Reads mapped to the turnip genome assembly.

Library	Total reads	Mapped reads	Mapped (%)
270 bp	226,529,887	219,034,986	96.69

Supplemental Table 4. BUSCO results for the turnip genome assembly.

Complete BUSCOs	Complete and single-copy BUSCOs	Complete and duplicated BUSCOs	Fragmented BUSCOs	Missing BUSCOs
1,568 (97.20%)	1065 (66.00%)	503 (31.20%)	7 (0.40%)	39 (2.40%)

Supplemental Table 5. Hi-C sequencing data statistics.

Read Pairs Number	Base Number	GC Content（%）	% ≥Q30
89,707,160	26,796,366,884	40.46	92.39

Supplemental Table 6. Evaluation of the coverage on the basis of mapped clean reads.

Mapping Type	**Number**	**Ratio（%）**
Total Read Pairs	89,707,160	100
Mapped Reads	153,017,543	85.28
Unique Mapped Read Pairs	19,744,769	22.01

Supplemental Table 7. Chromosome length data statistics.

Group	**Sequence Length (bp)**
chr01	37215573
chr02	38061388
chr03	38969619
chr04	26283953
chr05	34184301
chr06	42502065
chr07	30802089
chr08	27475427
chr09	57405788
Chr10	23028969

Supplemental Table 8. Summary of the transposable elements in the turnip, ECD04, and Chiifu A03 genomes.

Species	class	Subclass	Copy Number	Length (bp)	% Genome
A03	classI	LTR/Copia	22050	20087298	5.56
		LTR/Gypsy	35435	37614783	10.41
		LTR/unkonwn	31179	13195197	3.65
	classII	CACTA	10046	5289144	1.46
		Mutator	51177	31478394	8.71
		PIF_Harbinger	9328	3677627	1.02
		Tc1_Mariner	3624	1009162	0.28
		hAT	13346	4372430	1.21
	classIII	helitron	127160	49668898	13.74
	others	-	48403	15461914	4.27
	total	-	351748	181854847	50.31
Turnip	classI	LTR/Copia	18379	14963893	4.21
		LTR/Gypsy	32017	30291604	8.51
		LTR/unkonwn	26760	15674789	4.41
	classII	CACTA	11923	6775596	1.90
		Mutator	22949	12410888	3.49
		PIF_Harbinger	11872	4237219	1.19
		Tc1_Mariner	5058	1308878	0.37
		hAT	13454	4530589	1.27
	classIII	helitron	110792	48125049	13.53
	others	-	31951	13248625	3.72
	total	-	285155	151567130	42.60
ECD04	classI	LTR/Copia	24172	21758690	6.27
		LTR/Gypsy	46055	35901048	10.35
		LTR/unkonwn	22666	14390627	4.15
	classII	CACTA	10731	5942413	1.71
		Mutator	32738	23415477	6.75
		PIF_Harbinger	9486	3689151	1.06
		Tc1_Mariner	3556	1109901	0.32
		hAT	15925	4825756	1.39
	classIII	helitron	99347	37286850	10.75
	others	-	32786	14347884	4.15
	total	-	297462	162667797	46.90

Supplemental Table 9. Functional annotations of turnip genes.

database	Annotated number	Percentage (%)
eggNOG	51069	89.86
GO	25322	44.56
KEGG_ko	23848	41.96
PFAM	34724	61.10
Swiss-Prot	38236	67.28
NR	56018	98.57
All_Annotated	56832	

Supplemental Table 10. miRNA data statistics.

Types	Number
miRNA	326
rRNA	2010
tRNA	1174

Supplemental Table 11. Statistics of the turnip Illumina paired-end reads (NGS) and turnip 48A resequencing reads mapped on the new turnip chromosomes.

NGS/resequencing reads	Data sources	Average sequencing depth	Mapping rate (%)	Coverage (%)
Turnip NGS-D01	This study	70.21	96.79	94.78
Turnip NGS-D02		54.82	96.50	94.61
ECD04 NGS	NCBI project: PRJNA672906	58.31	97.30	86.94
TUA NGS	GSA number: CRA003187 (Yang et al., 2019)	23.44	96.47	84.50
TUE NGS		76.42	96.63	86.41
B48Areseq-1		27.81	96.87	92.23
B48Areseq-2		21.44	97.41	90.27
B48Areseq-3		25.11	97.42	90.28

Supplemental Table 12. Statistics of the turnip Illumina paired-end reads (NGS) and turnip 48A resequencing reads mapped on A03 chromosomes.

NGS/resequencing reads	Accession number	Average sequencing depth	Mapping rate (%)	Coverage (%)
Turnip NGS-D01	This study	68.27	97.27	93.50
Turnip NGS-D02		53.33	97.06	93.08
B48Areseq-1	(Yang et al., 2019)	26.84	97.42	91.73
B48Areseq-2		20.65	98.31	89.29
B48Areseq-3		23.52	98.56	89.19

Supplemental Table 13. Statistics of the turnip Illumina paired-end reads (NGS) and turnip 48A resequencing reads mapped on ECD04 chromosomes.

NGS/resequencing reads	Accession number	Average sequencing depth	Mapping rate (%)	Coverage (%)
Turnip NGS-D01	This study	88.17	97.00	93.41
Turnip NGS-D02		69.33	96.78	93.16
B48Areseq-1	(Yang et al., 2019)	34.83	97.24	92.76
B48Areseq-2		27.50	98.12	91.87
B48Areseq-3		32.59	98.42	91.90

Supplemental Table 14. Statistics of the turnip Illumina paired-end reads (NGS) and turnip 48A resequencing reads mapped on TUA chromosomes.

NGS/resequencing reads	Accession number	Average sequencing depth	Mapping rate (%)	Coverage (%)
Turnip NGS-D01	This study	64.99	97.25	94.77
Turnip NGS-D02		50.72	97.03	94.60
B48Areseq-1	(Yang et al., 2019)	25.72	97.41	94.40
B48Areseq-2		19.42	98.30	93.63
B48Areseq-3		22.21	98.56	93.11

Supplemental Table 15. Statistics of the turnip Illumina paired-end reads (NGS) and turnip 48A resequencing reads mapped on TUE chromosomes.

NGS/resequencing reads	Accession number	Average sequencing depth	Mapping rate (%)	Coverage (%)
Turnip NGS-D01	This study	67.49	96.76	94.64
Turnip NGS-D02		52.68	96.54	94.47
B48Areseq-1	(Yang et al., 2019)	26.55	96.34	93.95
B48Areseq-2		20.18	97.92	93.61
B48Areseq-3		23.14	98.19	93.10

Supplemental Table 16. Statistical analysis of the retained genes in three subgenomic blocks in Chiifu A03 and turnip.

A. thaliana	No. of A03 genes							No. of Turnip genes					
Block	No. of genes	LF	LF-R	MF1	MF1-R	MF2	MF2-R	LF	LF-R	MF1	MF1-R	MF2	MF2-R
A	1902	751	0.39	748	0.39	623	0.33	815	0.43	570	0.30	400	0.21
B	1539	582	0.38	442	0.29	428	0.28	643	0.42	477	0.31	412	0.27
C	1081	334	0.31	325	0.30	290	0.27	412	0.38	319	0.30	132	0.12
D	586	278	0.47	121	0.21	43	0.07	298	0.51	134	0.23	20	0.03
E	1610	1315	0.82	542	0.34	114	0.07	1351	0.84	562	0.35	67	0.04
F	2691	1365	0.51	985	0.37	833	0.31	1435	0.53	1012	0.38	903	0.34
G	186	19	0.10	19	0.10	15	0.08	16	0.09	14	0.08	0	0.00
H	557	251	0.45	190	0.34	79	0.14	239	0.43	185	0.33	84	0.15
I	811	331	0.41	228	0.28	91	0.11	381	0.47	109	0.13	100	0.12
J	1797	925	0.51	777	0.43	589	0.33	950	0.53	820	0.46	627	0.35
K	255	115	0.45	91	0.36	69	0.27	127	0.50	104	0.41	73	0.29
L	439	189	0.43	124	0.28	98	0.22	229	0.52	94	0.21	22	0.05
M	666	319	0.48	95	0.14	41	0.06	356	0.53	97	0.15	47	0.07
N	1240	690	0.56	468	0.38	335	0.27	692	0.56	402	0.32	324	0.26
O	518	254	0.49	162	0.31	74	0.14	261	0.50	188	0.36	70	0.14
P	357	133	0.37	88	0.25	44	0.12	135	0.38	97	0.27	55	0.15
Q	602	267	0.44	164	0.27	149	0.25	280	0.47	189	0.31	156	0.26
R	2060	1175	0.57	783	0.38	752	0.37	1166	0.57	761	0.37	745	0.36
S	731	268	0.37	103	0.14	45	0.06	331	0.45	101	0.14	38	0.05
T	415	108	0.26	97	0.23	60	0.14	123	0.30	109	0.26	84	0.20
U	2477	1445	0.58	877	0.35	657	0.27	1421	0.57	912	0.37	666	0.27
V	620	284	0.46	186	0.30	176	0.28	357	0.58	212	0.34	193	0.31
W	1180	547	0.46	432	0.37	397	0.34	536	0.45	503	0.43	394	0.33
X	734	290	0.40	249	0.34	205	0.28	360	0.49	240	0.33	236	0.32
Total	25054	12235		8296		6207		12914		8211		5848	

Note: The LF (least fractionated), MF1 (medium fractionated), and MF2 (most fractionated) subgenomes of Chiifu A03 and turnip were obtained on the basis of the homology with *A. thaliana* blocks. The retention rates were calculated as the proportion of the genes in each subgenomic block that had a corresponding gene in *A. thaliana* blocks. R, retention rate.

Supplemental Table 17. *MAM* genes and pseudogenes in *Brassica* genomes

Gene ID	Species	Chr	Start	End
AT5G23010.1	*A. thaliana*	Chr5	7702848	7707172
AJ486890	*A. thaliana*	Chr5		
AT5G23020.1	*A. thaliana*	Chr5	7718118	7721866
BAA02g29590.1	*Brassica rapa* Chiifu A03	A02	16939844	16941344
BAA02g29600.1	*Brassica rapa* Chiifu A03	A02	16948854	16949309
BAA02g44900.1	*Brassica rapa* Chiifu A03	A02	36864864	36869292
BAA03g45530.1	*Brassica rapa* Chiifu A03	A03	21790151	21792578
BAA03g45540.1	*Brassica rapa* Chiifu A03	A03	21797168	21802282
BAA03g45550.1	*Brassica rapa* Chiifu A03	A03	21822110	21824526
BAA04g25300.1	*Brassica rapa* Chiifu A03	A04	26477444	26480189
Gene0352400.1	Turnip B03	chr03	26481369	26483548
Gene0121420.1	Turnip B03	chr02	2497704	2501665
Gene0027070.1	Turnip B03	chr03	26508063	26510950
Gene0000760.1	Turnip B03	chr02	2305218	2309166
Gene0228790.1	Turnip B03	chr02	2317303	2318748
Gene0006750.1	Turnip B03	chr02	2497704	2501665
Gene0464890.1	Turnip B03	chr02	2509622	2512810
Gene0495830.1	Turnip B03	chr02	19602605	19612312
Gene0100730.1	Turnip B03	chr04	26457563	26460316
BraA02g027460.3.5C.1	*Brassica rapa* Chiifu v3.5	A02	15960475	15974715
BraA02g028300.3.5C.1	*Brassica rapa* Chiifu v3.5	A02	16660024	16669763
BraA02g044510.3.5C.1	*Brassica rapa* Chiifu v3.5	A02	29594897	29598097
BraA02g044520.3.5C.2	*Brassica rapa* Chiifu v3.5	A02	29607024	29611499
BraA03g044240.3.5C.2	*Brassica rapa* Chiifu v3.5	A03	22082460	22085246
BraA03g044250.3.5C.3	*Brassica rapa* Chiifu v3.5	A03	22088206	22094550
BraA03g044270.3.5C.1	*Brassica rapa* Chiifu v3.5	A03	22114597	22117013
BraA04g026170.3.5C.1	*Brassica rapa* Chiifu v3.5	A04	18013584	18016329
BraA02g026580.3C	*Brassica rapa* Chiifu v3.0	A02	15960475	15960927
BraA02g027350.3C	*Brassica rapa* Chiifu v3.0	A02	16669308	16669763
BraA02g042660.3C	*Brassica rapa* Chiifu v3.0	A02	29594897	29598097
BraA02g042670.3C	*Brassica rapa* Chiifu v3.0	A02	29607154	29611410
BraA03g043730.3C	*Brassica rapa* Chiifu v3.0	A03	22082638	22085062
BraA03g043740.3C	*Brassica rapa* Chiifu v3.0	A03	22089652	22094767
BraA03g043750.3C	*Brassica rapa* Chiifu v3.0	A03	22114597	22117013
BraA04g024970.3C	*Brassica rapa* Chiifu v3.0	A04	18013584	18015367
BraA04g024980.3C	*Brassica rapa* Chiifu v3.0	A04	18015386	18016329
BraA02g02783P	*Brassica rapa* chinensis	A02	17294254	17304661
BraA02g04317P	*Brassica rapa* chinensis	A02	30297471	30300018
BraA02g04318P	*Brassica rapa* chinensis	A02	30306808	30312436
BraA03g04215P	*Brassica rapa* chinensis	A03	21567279	21569915
BraA03g04216P	*Brassica rapa* chinensis	A03	21572747	21579487

BraA03g04218P	*Brassica rapa* chinensis	A03	21598090	21600506
BraA04g02442P	*Brassica rapa* chinensis	A04	18181429	18184173
A02p26760.1_BraBRO	*Brassica rapa* BraBRO	A02	15821348	15826813
A02p27710.1_BraBRO	*Brassica rapa* BraBRO	A02	16608558	16618326
A02p43500.1_BraBRO	*Brassica rapa* BraBRO	A02	29817889	29819947
A02p43510.1_BraBRO	*Brassica rapa* BraBRO	A02	29834535	29839175
A03p42990.1_BraBRO	*Brassica rapa* BraBRO	A03	21721237	21723414
A03p43000.1_BraBRO	*Brassica rapa* BraBRO	A03	21724136	21732233
A02p30350.1_BraCCA	*Brassica rapa* BraCCA	A02	17275036	17284774
A02p47340.1_BraCCA	*Brassica rapa* BraCCA	A02	29985801	29989001
A02p47350.1_BraCCA	*Brassica rapa* BraCCA	A02	29997052	30001319
A03p45340.1_BraCCA	*Brassica rapa* BraCCA	A03	21954602	21956781
A03p45350.1_BraCCA	*Brassica rapa* BraCCA	A03	21961371	21966485
A04p26440.1_BraCCA	*Brassica rapa* BraCCA	A04	17458545	17461290
A02p27150.1_BraCCB	*Brassica rapa* BraCCB	A02	16847321	16857387
A02p41380.1_BraCCB	*Brassica rapa* BraCCB	A02	28707728	28710330
A02p41400.1_BraCCB	*Brassica rapa* BraCCB	A02	28717453	28722350
A03p41780.1_BraCCB	*Brassica rapa* BraCCB	A03	21576924	21579457
A03p41790.1_BraCCB	*Brassica rapa* BraCCB	A03	21582421	21589194
A02p26630.1_BraCXA	*Brassica rapa* BraCXA	A02	17062135	17071869
A02p40810.1_BraCXA	*Brassica rapa* BraCXA	A02	30553370	30555638
A02p40830.1_BraCXA	*Brassica rapa* BraCXA	A02	30566276	30570419
A03p41640.1_BraCXA	*Brassica rapa* BraCXA	A03	21664986	21667166
A03p41650.1_BraCXA	*Brassica rapa* BraCXA	A03	21671755	21676870
A03p41670.1_BraCXA	*Brassica rapa* BraCXA	A03	21695528	21699269
A04p23710.1_BraCXA	*Brassica rapa* BraCXA	A04	18315795	18318540
A02p28080.1_BraCXB	*Brassica rapa* BraCXB	A02	16976779	16986521
A02p43820.1_BraCXB	*Brassica rapa* BraCXB	A02	30063350	30065376
A02p43840.1_BraCXB	*Brassica rapa* BraCXB	A02	30076254	30080397
A03p43520.1_BraCXB	*Brassica rapa* BraCXB	A03	21584467	21587185
A03p43530.1_BraCXB	*Brassica rapa* BraCXB	A03	21591499	21596614
A03p43550.1_BraCXB	*Brassica rapa* BraCXB	A03	21615269	21617685
A04p25560.1_BraCXB	*Brassica rapa* BraCXB	A04	19089372	19092125
BraA03t011503E	Turnip ECD04	A03	21510967	21514685
BraA03t011505E	Turnip ECD04	A03	21519966	21525728
BraA03t011506E	Turnip ECD04	A03	21537234	21548661
BraA02t031223E	Turnip ECD04	A02	15670577	15671029
BraA02t031224E	Turnip ECD04	A02	15671924	15676050
BraA02t031316E	Turnip ECD04	A02	16584022	16594081
BraA02t032945E	Turnip ECD04	A02	31121287	31124919
BraA02t032946E	Turnip ECD04	A02	31131180	31136203
A02p26480.1_BraMIZ	*Brassica rapa* BraMIZ	A02	16362670	16366821
A02p27410.1_BraMIZ	*Brassica rapa* BraMIZ	A02	17153545	17163010
A02p42480.1_BraMIZ	*Brassica rapa* BraMIZ	A02	30231396	30232788

A02p42490.1_BraMIZ	*Brassica rapa* BraMIZ	A02	30241605	30245752
A03p44270.1_BraMIZ	*Brassica rapa* BraMIZ	A03	22804269	22806447
A03p44280.1_BraMIZ	*Brassica rapa* BraMIZ	A03	22811037	22816151
A03p44300.1_BraMIZ	*Brassica rapa* BraMIZ	A03	22834805	22837587
A04p24470.1_BraMIZ	*Brassica rapa* BraMIZ	A04	18680083	18682849
A02p28310.1_BraPCA	*Brassica rapa* BraPCA	A02	16472482	16486716
A02p29280.1_BraPCA	*Brassica rapa* BraPCA	A02	17220043	17229747
A02p46270.1_BraPCA	*Brassica rapa* BraPCA	A02	31272988	31275046
A02p46280.1_BraPCA	*Brassica rapa* BraPCA	A02	31282613	31287255
A03p44840.1_BraPCA	*Brassica rapa* BraPCA	A03	22000930	22005178
A03p44850.1_BraPCA	*Brassica rapa* BraPCA	A03	22006059	22010189
A03p44870.1_BraPCA	*Brassica rapa* BraPCA	A03	22017369	22018235
A03p44880.1_BraPCA	*Brassica rapa* BraPCA	A03	22030064	22032846
A04p25200.1_BraPCA	*Brassica rapa* BraPCA	A04	17231544	17234288
A02p28860.1_BraPCB	*Brassica rapa* BraPCB	A02	17379174	17388890
A02p45940.1_BraPCB	*Brassica rapa* BraPCB	A02	31180956	31182349
A02p45950.1_BraPCB	*Brassica rapa* BraPCB	A02	31196946	31201358
A03p44060.1_BraPCB	*Brassica rapa* BraPCB	A03	21740960	21743139
A03p44070.1_BraPCB	*Brassica rapa* BraPCB	A03	21747729	21752842
A03p44090.1_BraPCB	*Brassica rapa* BraPCB	A03	21771499	21774281
A04p25290.1_BraPCB	*Brassica rapa* BraPCB	A04	17060073	17062817
A02p28450.1_BraTCA	*Brassica rapa* BraTCA	A02	16458631	16472817
A02p29290.1_BraTCA	*Brassica rapa* BraTCA	A02	17182970	17192709
A02p45390.1_BraTCA	*Brassica rapa* BraTCA	A02	30174306	30182525
A02p45400.1_BraTCA	*Brassica rapa* BraTCA	A02	30185826	30189771
A03p45640.1_BraTCA	*Brassica rapa* BraTCA	A03	22258279	22260297
A03p45650.1_BraTCA	*Brassica rapa* BraTCA	A03	22265046	22270159
A03p45670.1_BraTCA	*Brassica rapa* BraTCA	A03	22288814	22291886
A04p25730.1_BraTCA	*Brassica rapa* BraTCA	A04	18645836	18648694
A02p28020.1_BraTUA	*Brassica rapa* BraTUA	A02	16413113	16414673
A02p29100.1_BraTUA	*Brassica rapa* BraTUA	A02	17355496	17364891
A02p44250.1_BraTUA	*Brassica rapa* BraTUA	A02	28524441	28525834
A02p44380.1_BraTUA	*Brassica rapa* BraTUA	A02	28583045	28587450
A03p43900.1_BraTUA	*Brassica rapa* BraTUA	A03	21650016	21652036
A03p43910.1_BraTUA	*Brassica rapa* BraTUA	A03	21655250	21661978
A04p24620.1_BraTUA	*Brassica rapa* BraTUA	A04	16803042	16807920
A02p27510.1_BraTUE	*Brassica rapa* BraTUE	A02	16044120	16049605
A02p28510.1_BraTUE	*Brassica rapa* BraTUE	A02	16897813	16907210
A02p44980.1_BraTUE	*Brassica rapa* BraTUE	A02	29906621	29909939
A02p45000.1_BraTUE	*Brassica rapa* BraTUE	A02	29918379	29923559
A03p43290.1_BraTUE	*Brassica rapa* BraTUE	A03	21400608	21402780
A03p43300.1_BraTUE	*Brassica rapa* BraTUE	A03	21408678	21414281
A03p43310.1_BraTUE	*Brassica rapa* BraTUE	A03	21430639	21433428
BraA02t07413Z	*Brassica rapa* BrapaZ1	A02	15881597	15884186

BraA02t07492Z	*Brassica rapa* BrapaZ1	A02	16577334	16587104
BraA02t09063Z	*Brassica rapa* BrapaZ1	A02	29723188	29727132
BraA03t13773Z	*Brassica rapa* BrapaZ1	A03	21573766	21576003
BraA03t13775Z	*Brassica rapa* BrapaZ1	A03	21579649	21584763
A03Pse1_A02-36849703-36855070	*Brassica rapa* A03	A02	36849703	36855070
A03Pse2_A02-36848777-36854980	*Brassica rapa* A03	A02	36848777	36854980
B03Pse_chr02-19603547-19612312	Turnip B03	chr02	19603547	19612312
Brapa3.5Pse_A02-29594897-29598097	*Brassica rapa* Chiifu v3.5	A02	29594897	29598097
BrasPse_A02-30297367-30300169	*Brassica rapa* chinensis	A02	30297367	30300169
Z1Pse1_A02-29711994-29714276	*Brassica rapa* BrapaZ1	A02	29711994	29714276
Z1Pse2_A02-29712920-29714366	*Brassica rapa* BrapaZ1	A02	29712920	29714366
CCAPse_A02-29998086-29999523	*Brassica rapa* BraCCA	A02	29998086	29999523
CCBPse_A02-28706225-28707370	*Brassica rapa* BraCCB	A02	28706225	28707370
CXAPse_A02-30553266-30554561	*Brassica rapa* BraCXA	A02	30553266	30554561
CXBPse_A02-30063246-30064540	*Brassica rapa* BraCXB	A02	30063246	30064540
ECD04Pse_A02-31123336-31124417	Turnip ECD04	A02	31123336	31124417
MIZPse_A02-30232218-30233663	*Brassica rapa* BraMIZ	A02	30232218	30233663
PCAPse_A02-31272395-31273689	*Brassica rapa* BraPCA	A02	31272395	31273689
PCBPse_A02-31181778-31187146	*Brassica rapa* BraPCA	A02	31181778	31187146
TCAPse_A02-30173713-30175007	*Brassica rapa* BraTCA	A02	30173713	30175007
TUAPse_A02-28525263-28530631	*Brassica rapa* BraTUA	A02	28525263	28530631
TUEPse_A02-29906028-29908309	*Brassica rapa* BraTUE	A02	29906028	29908309

Supplemental Table 18. ***AOP*** **genes in turnip**

	A. thaliana	Turnip
AOP1	AT4G03070.1	Gene0096740.1 Gene0493910.1 Gene0445090.1
AOP2	AT4G03060.1	Gene0250680.1 Gene0405960.1 Gene0486840.1

Supplemental Table 19. Primers used in this study

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
The primers for real-time quantitative PCR (qRT-PCR) analysis.		
Gene0495830	CTATCCGCACAAGAAGCCAAC	GACGGGCTGGAGGTCAATAC
Gene0352400	CCTTTCACTCTCCCGGTCTG	ACGGAGCGTCGTGTCAAATA
Gene0121420	ATGATCTCCATCTCCCCCACT	TAGCACCAGTCCCAGCCTTA
Gene0100730	CTTCTGGCATCTCCCGCAAT	GTACTTCGGCCATCGTTCCA
Gene0027070	ATGTCCCACAATGATCCCCAC	CGATTCAGGCGTAGAGAGGG
Gene0000760	CCCTTACTCCACCGCAGAAG	CACGGTTTTGGCGATGGTTT
Gene0006750	GGAGCATTTGTGATGGGTGG	CAAATGCCTGAATTTGAGATTT
Gene0228790	AAGTGGAAATGCACCACTTGA	TTACCGCCTTACCATCTTGCT
Gene0464890	TAAGGCGGCTTGGGAATCAG	ATGTTGATCCCCACCGTGTC
Gene0096740	GACAAAGTGTCAGTGGAGC	CATGAGGACGAGGTGGTGTATA
Gene0493910	CAAAGTGGGATGAAGTGAAG	CTCTGAGAACTTGTGCATCGTC
Gene0445090	AGTGGGATAAAGTGAAGGCTG	GCGTCGAGAACTTGTGCATCAT
Gene0250680	GAGGAGTGATGTCCGTAAAGC	CATCCAATTCTGCTAACTTCT
Gene0405960	GTCCGTAAAGCTCTTGAAGAC	CATTGACTTGAGGTTCTCATCA
Gene0486840	ACAAGAGTACCAGCGAAAGG	CGCCAGCACCAACATCCGCACC
BraA03g029130	GGGACAAAGTGAAGACTGATG	ACACCACCTCGTCCTCATGAAG
BraA09g001350	CTCTCTGAATCTCTTGAGCTCC	TGAGACGATGCACAAATTCGC
BraA09g001340	ATAAAGTGAAGGCTGATGTCC	GATGATGCACAAGTTCTCGACG
BraA09g001360	CGTAAAGCTCTTGAAGACTAC	GCTGATGCTGATGATATTGCT
BraA02g028320	TAAAGCAATCGGTTTTGGAAG	CCCGCTGCAACATTAGTATCA
BraA02g029140	AAGATGATTAGCGAGCCGG	CGCGTCGATTCCCATCTCTAG
BraA03g044240	CCTTTCACTCTCCCGGTCTG	ACGGAGCGTCGTGTCAAATA
BraA03g044250	ATGATCTCCATCTCCCCCACT	TAGCACCAGTCCCAGCCTTA
BraA03g044270	CTTCTGGCATCTCCCGCAAT	GTACTTCGGCCATCGTTCCA
BraA02g044520	CCCTTACTCCACCGCAGAAG	CACGGTTTTGGCGATGGTTT
BraA02g044510	AAAGTGGAAATGCACCACTTGA	TTACCGCCTTACCATCTTGCT

BraA02g027460	TCTCCAGGTGGAGCCCTTAC	CGCATATTACCGGGACGTATC
BraA02g028300	GCCGCAACTAGTAGTATTGAC	GAGTTGCCTAGCAATCTCTAC
BraA04g026170	ACATTCACATGAAATATAAG	ATGCCCACCGTGGTTGCACC
TUB2	AGGCGTGTGAGTGAGCAGTT	CATCTCGTCCATTCCTTCACCTGT
The primers for RT-PCR analysis.		
BAA02g29590	TACCGCCAACACAATCTCCG	GGCCCCAATGTCTTCTGGTG
BAA02g29600	ACCTATCCGCACAAGAAGCC	CAACGGTCTTGGCAATGCTT
Gene0495830	TACGTCCCGGTAATATGCGTC	GCTCCACGACATTTCAAAGC
Gene0405960	GCTGATGCCAATGCTAATAC	TGAATGGTTTGAAGACTCGT
Gene0250680	ACTGGTGATTGTGCTAATGT	TAAGCGTGAAGAGTAGAACG
Gene0486840	AACCCTAAAACCAGGAAGTG	CCCAAAGCTCTCAAATACCA
BraA02g028320	AGTATCAGCGAAACAATCCA	ACCTCCAAACCTTCAATCTC
BraA09g001360	AACACCTCAAGTCAACGAAT	CCTCCAAACCTTCAATCTCA
BraA03g029140	CGTCTACGACTGATGAAGTA	CAGCGATAACAACGAAAGTG
Actin	CCTGGTCAGCTTAACTCCGAC	CATCTCGTCCATTCCTTCACCTGT