A *Brassica carinata* pan-genome platform for Brassica crop improvement

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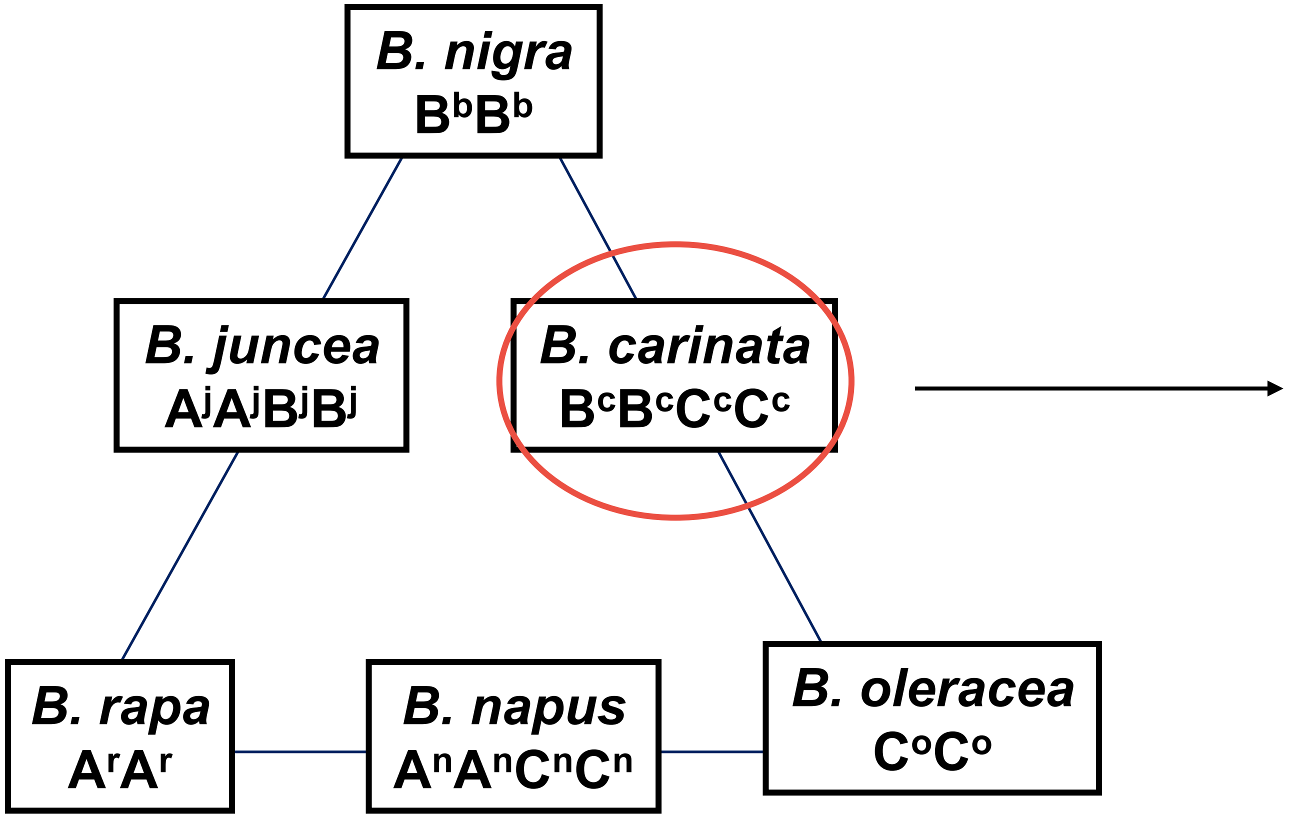
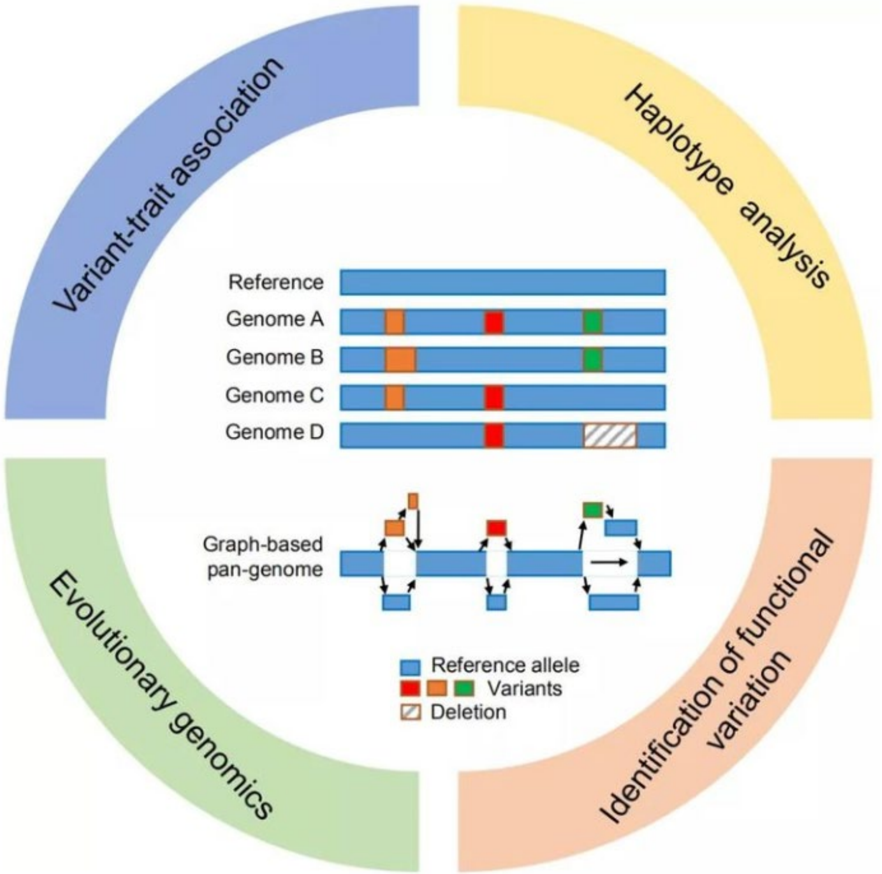
Brassica carinata is an important agricultural crop

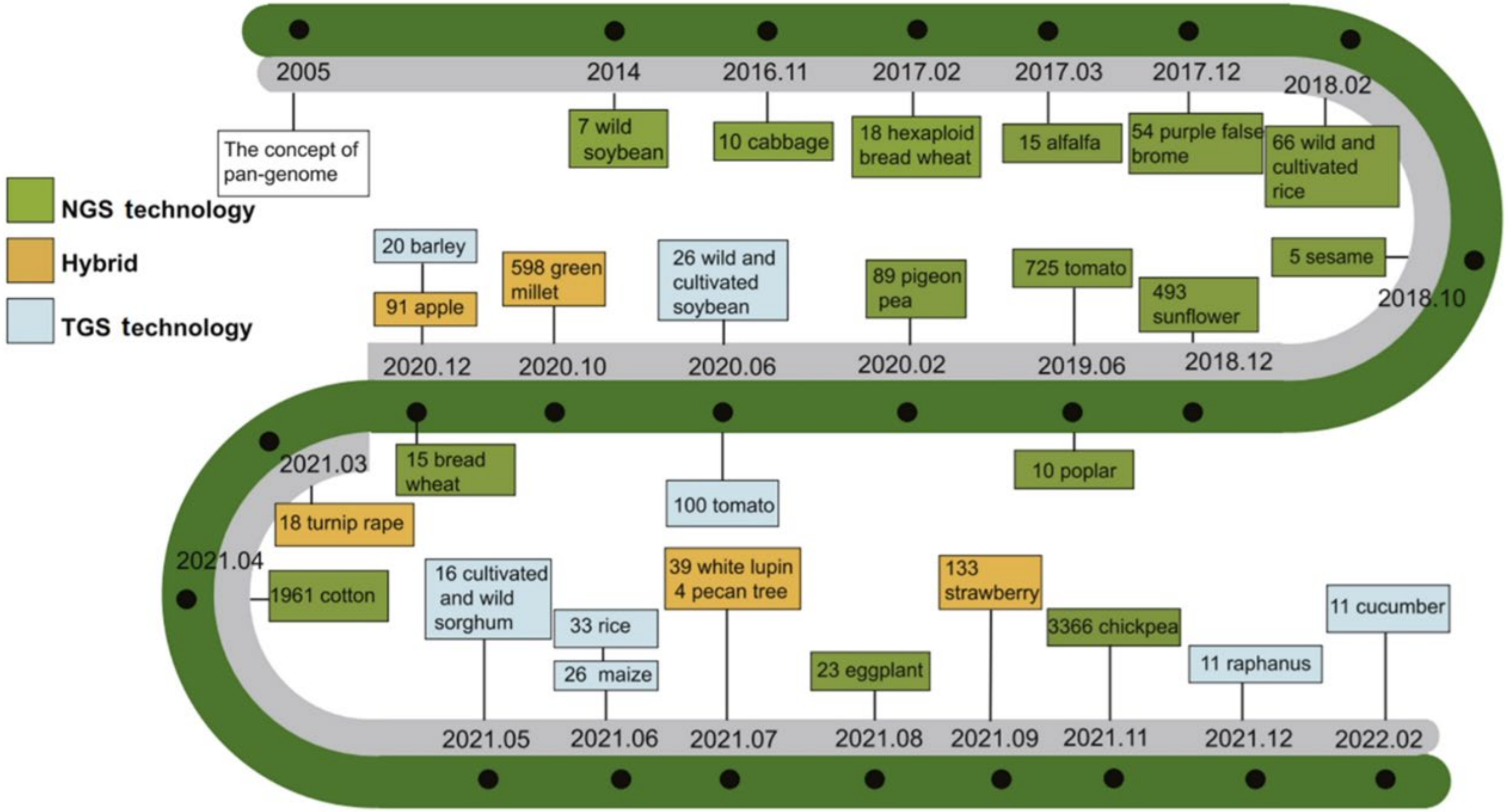


***Brassica* U's triangle**

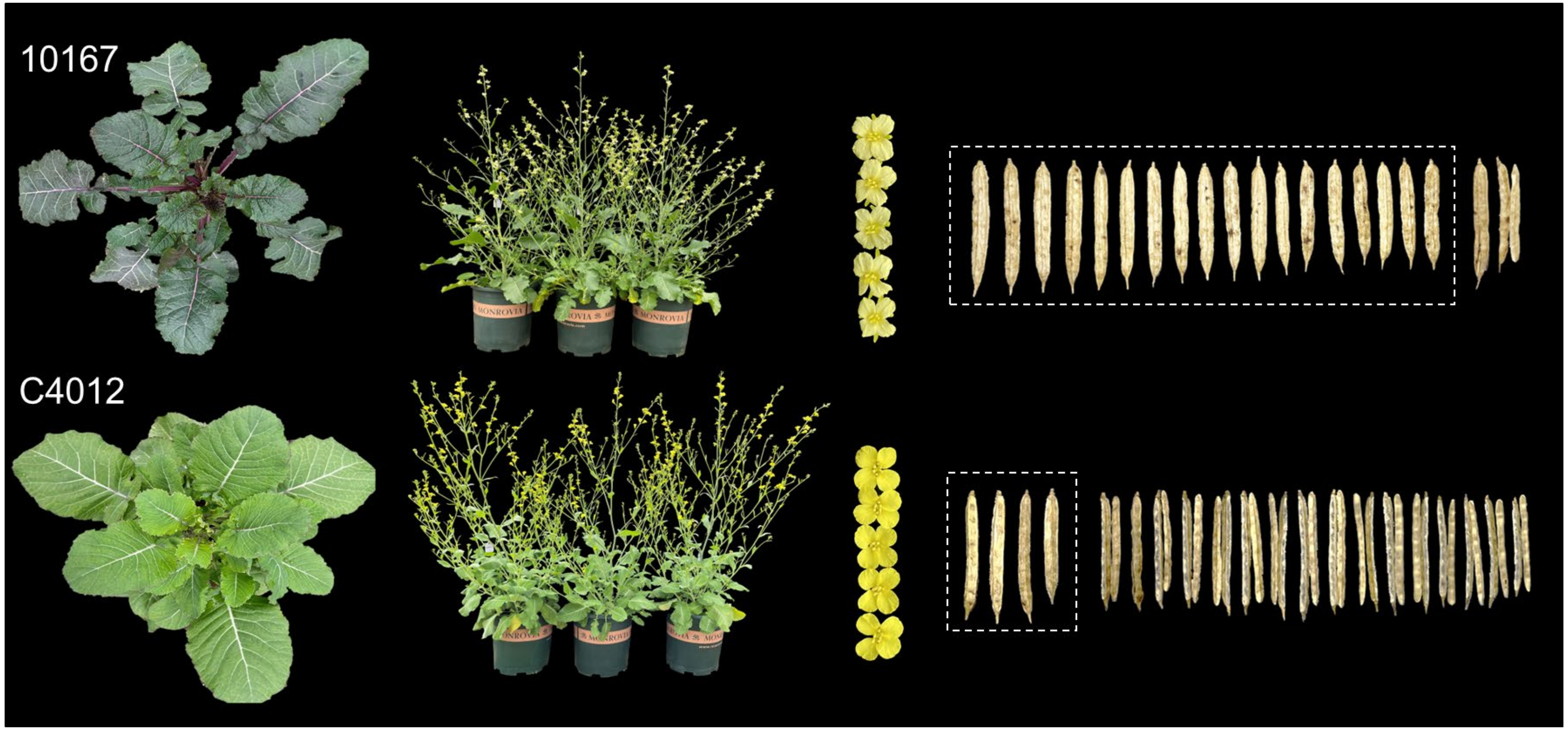
- high glucosinolate
- high erucic acid
- pod shatter resistance
- disease resistance
- drought tolerance
- salt tolerance

No available pan-genome for *B. carinata*





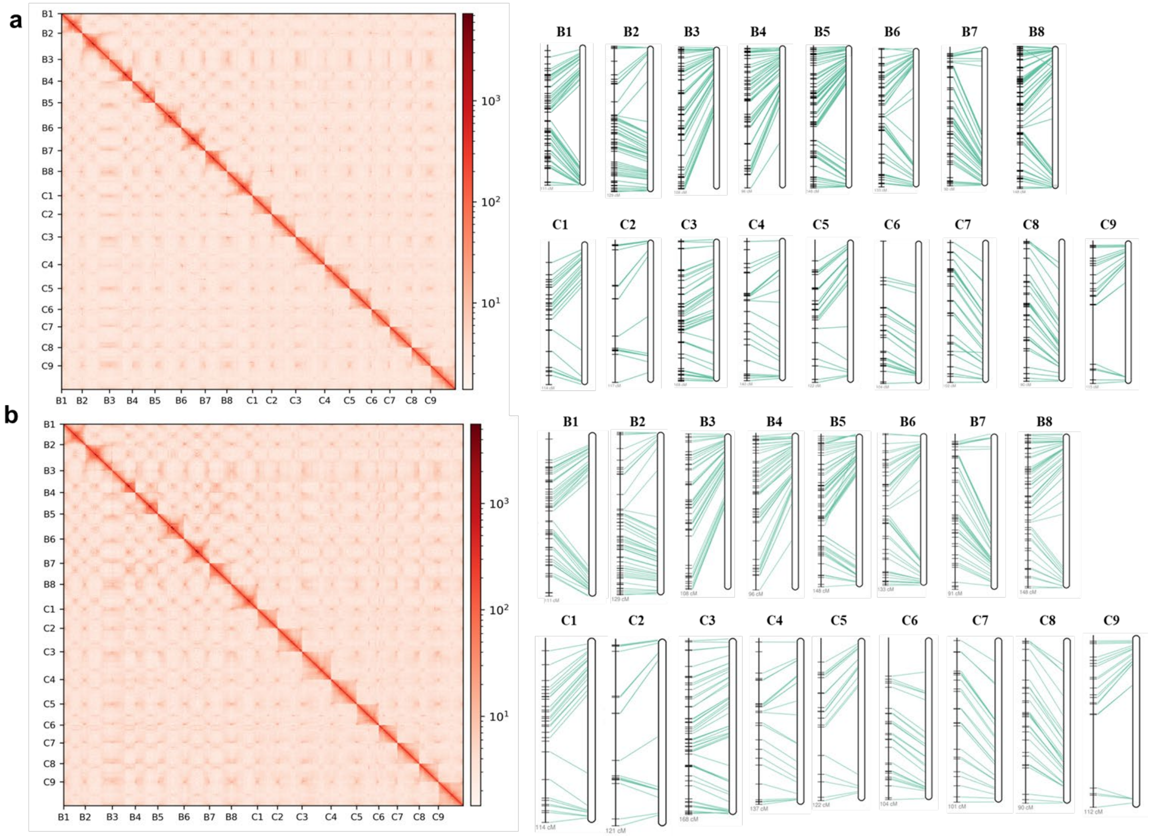
The assembly of two *B. carinata* genomes



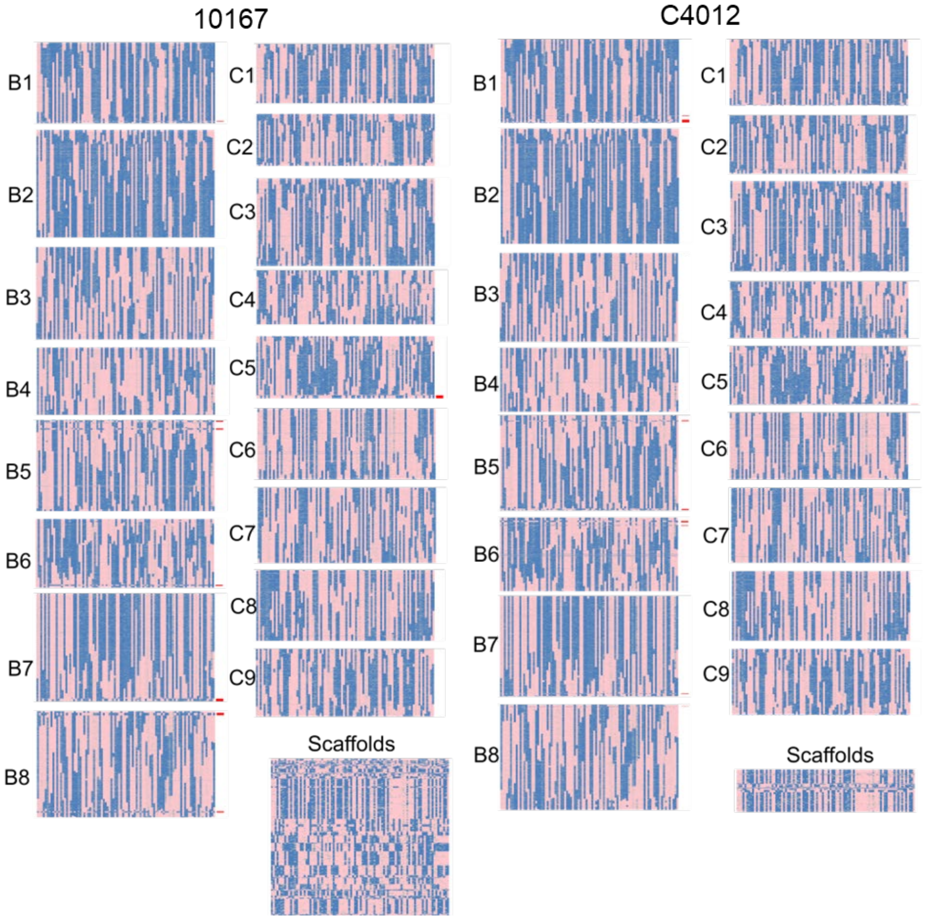
- **10167 (pod shatter-resistant accession):** 50× Illumina + 83× ONT + 121× Hi-C
- **C4012 (shatter-susceptible accession):** 45× Illumina + 75× ONT + 115× Hi-C

The assembly of two *B. carinata* genomes

96.2% and 96.8% contigs of 10167 and C4012 were anchored to 17 pseudochromosomes by **Hi-C**, **linkage mapping** and **GOGGs**.

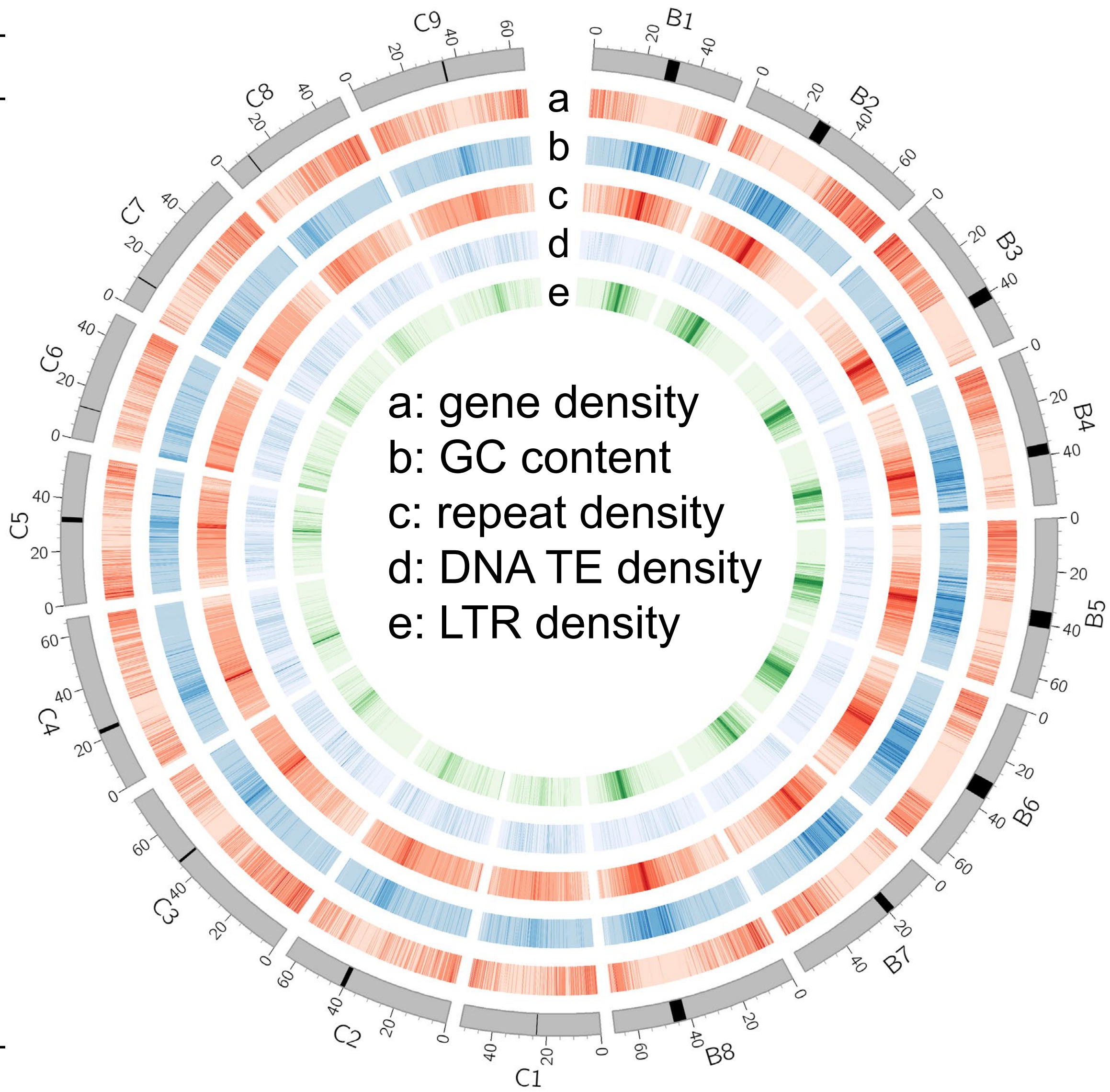


(a-b) The Hi-C map and collinearity with genetic map of 10167 and C4012.



The assembly of two *B. carinata* genomes

Parameters	10167	C4012
Estimated genome size (Mb)	1,156	1,131
Final Genome size (Mb)	**1,071**	**1,074**
Contig number	375	391
Longest contig (Mb)	70.5	45.8
Contig N50 (Mb)	**26.7**	**24.3**
Scaffold number	268	531
Scaffold N50 (Mb)	62.4	64.1
Longest Scaffold (Mb)	74.9	75.4
Anchored to chromosome (%)	96.2	96.8
GC (%)	37.4	37.4
LAI	**15. 5**	**16**
Mapping rate of short reads (%)	99.3	99.4
BUSCO (%)	**99.7**	**99.6**
Number of protein-coding genes	102,334	103,866
Repeat proportion (%)	59.1	58.5



The genomic features of C4012

The construction of *B. carinata* pan-genome

(1) Firstly using *de novo* strategy

Source	Order added	Sub genome	Number	No. At	% At
B. carinata C4012	1	B	46,808	28,726	61.37
B. carinata C4012	1	C	55,593	29,924	53.83
B. carinata 10167	2	B	2,353	717	30.47
B. carinata 10167	2	C	2,350	675	28.72
B. carinata zd1	3	B	2,050	588	28.68
B. carinata zd1	3	C	2,498	716	28.66
B. carinata Gomenzer	4	B	3,077	620	20.15
B. carinata Gomenzer	4	C	2,496	410	16.43
BcaPan		B	54,288	30,651	56.46
		C	62,937	31,725	50.41
		BBCC	117,225	62,376	53.21

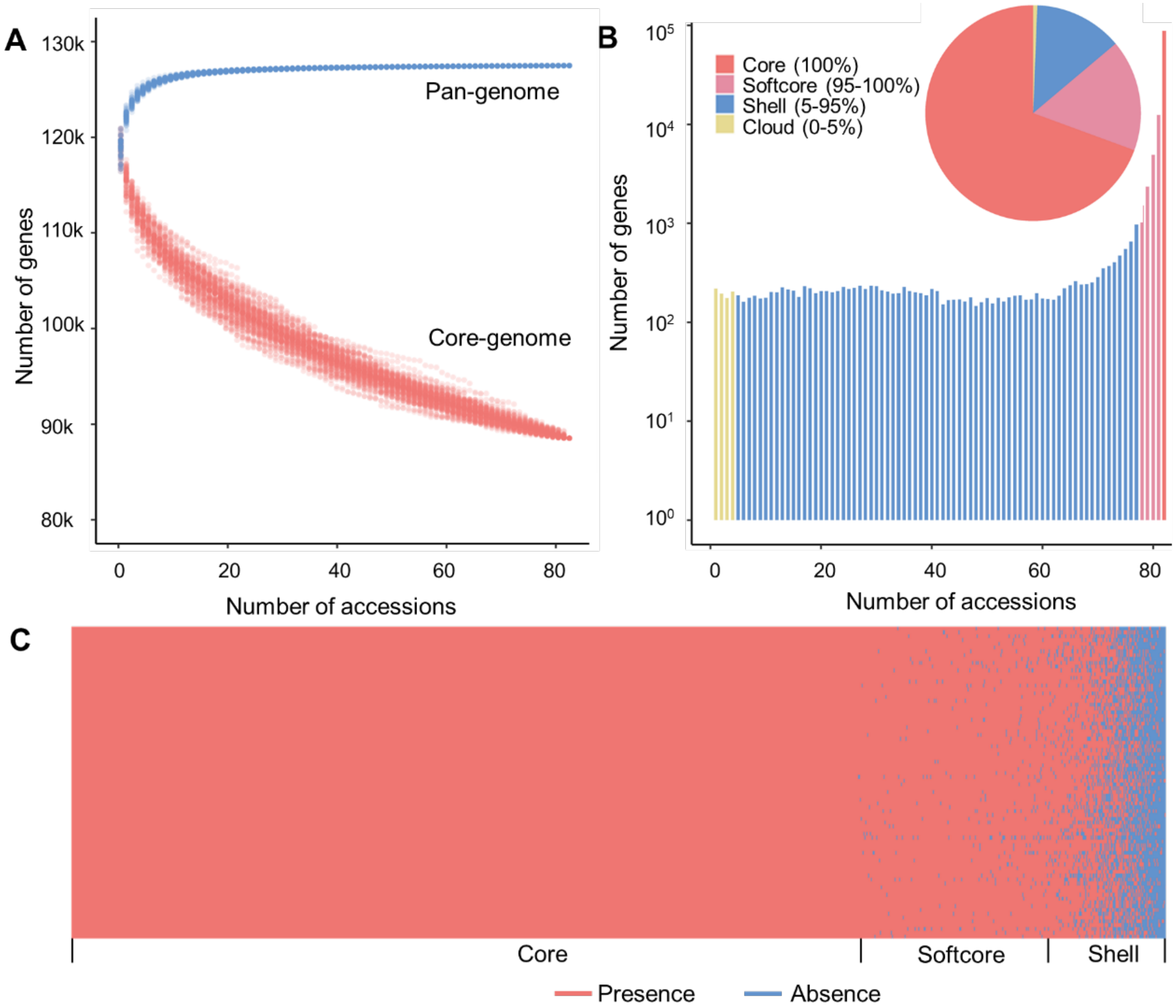
◆ 117,225 gene models in the initial pan-genome

◆ 14,824 (12.65%) gene models were added to the reference genome

The construction of *B. carinata* pan-genome

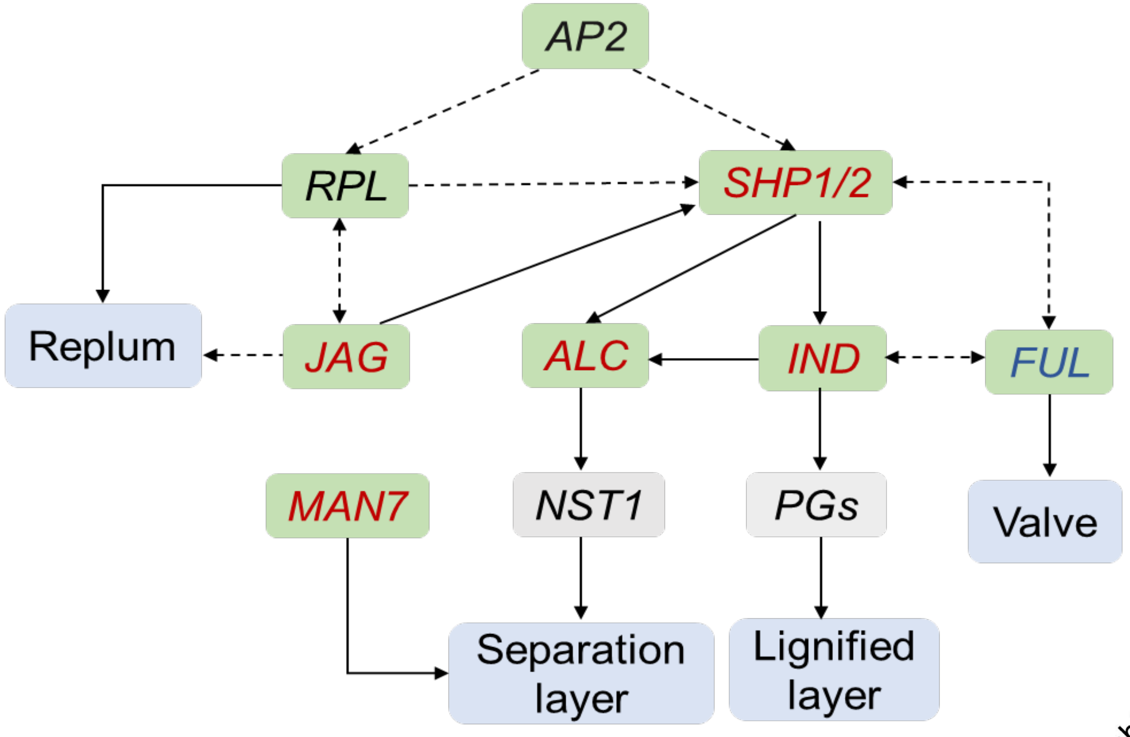
(2) Then using map to pan

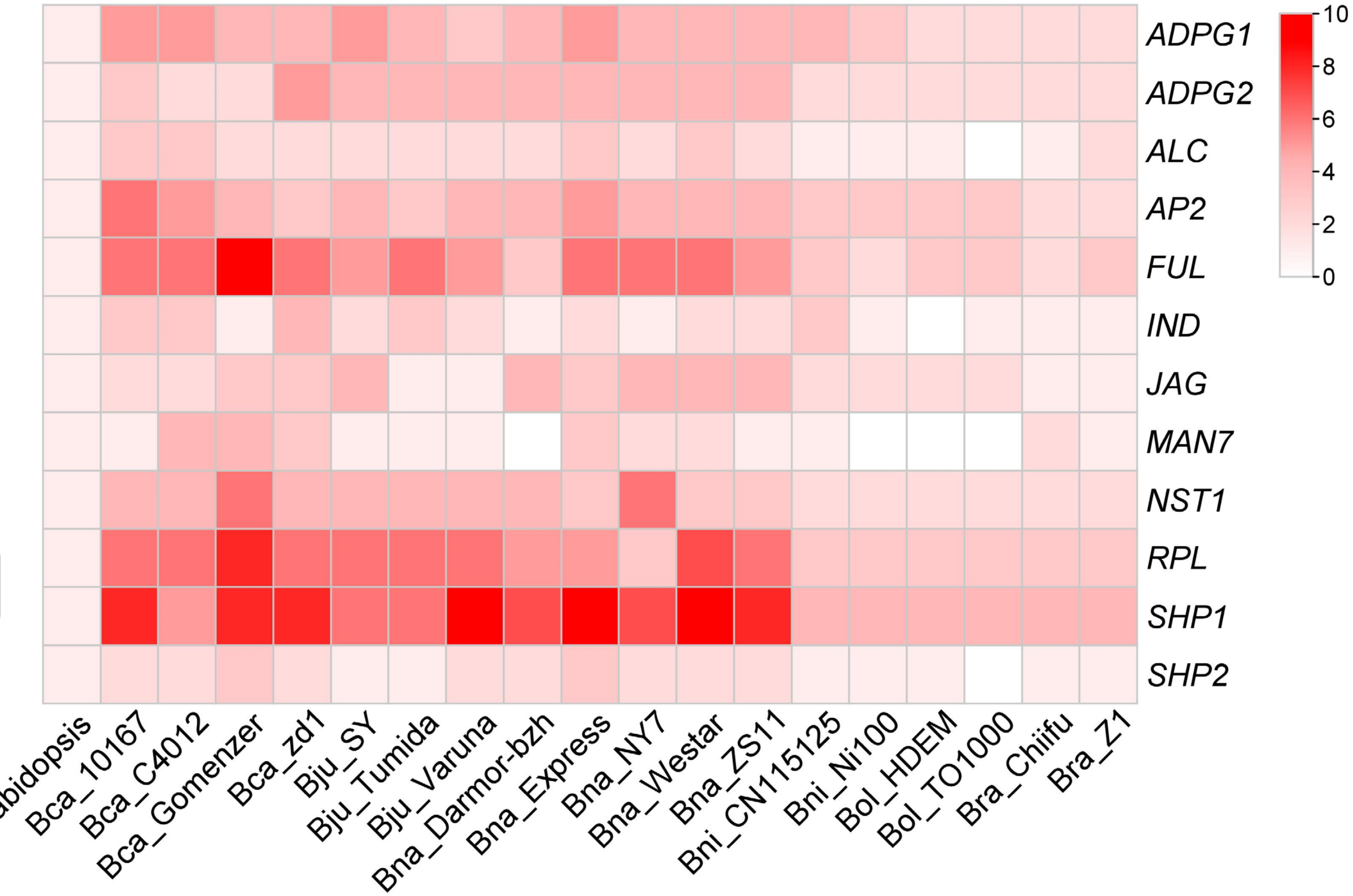
- ➢ The final pan-genome size of the *B. carinata* was ~ **2.52 Gb with 127,421 gene models.**
- ➢ 88,307 (69.42%) core genes were shared by all accessions, and 21,262 softcore, 16,852 shell and 792 cloud genes.



The genomic basis of PSR for *B. carinata*

B. carinata is reported to possess higher levels of **pod shatter resistance (PSR)** than other *Brassica* species.

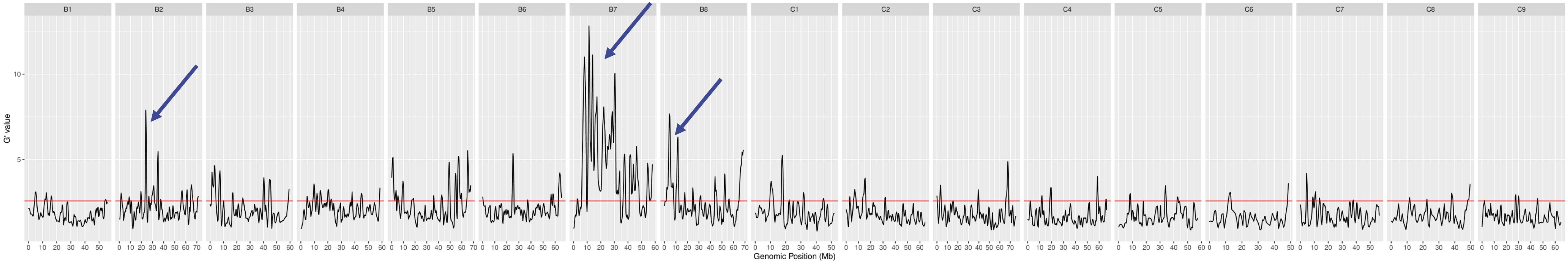


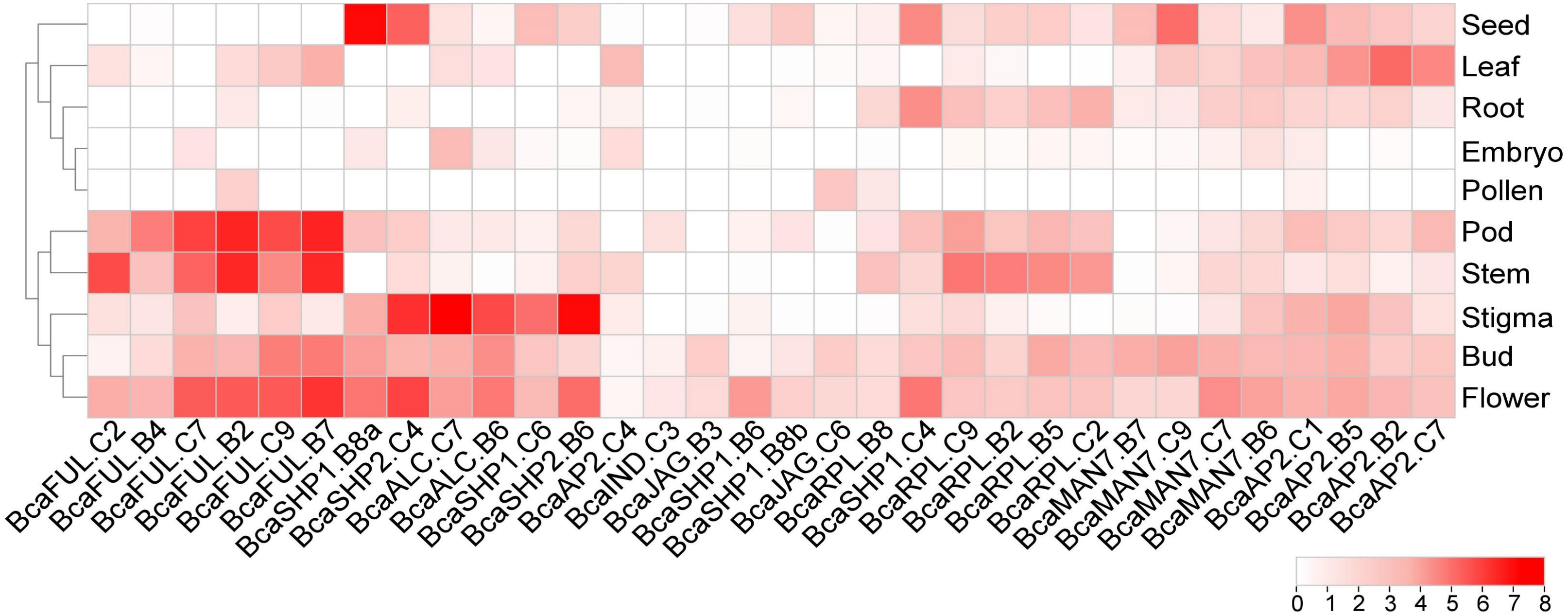


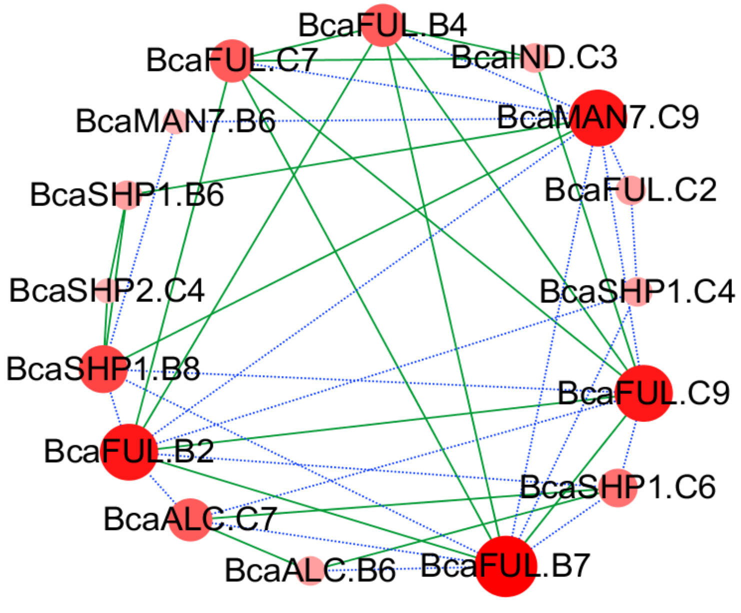
(Raman et al., 2014; Raman *et al.*, 2017)

The genomic basis of PSR for *B. carinata*

BcaFUL.B7 **was the hub gene of PSR**

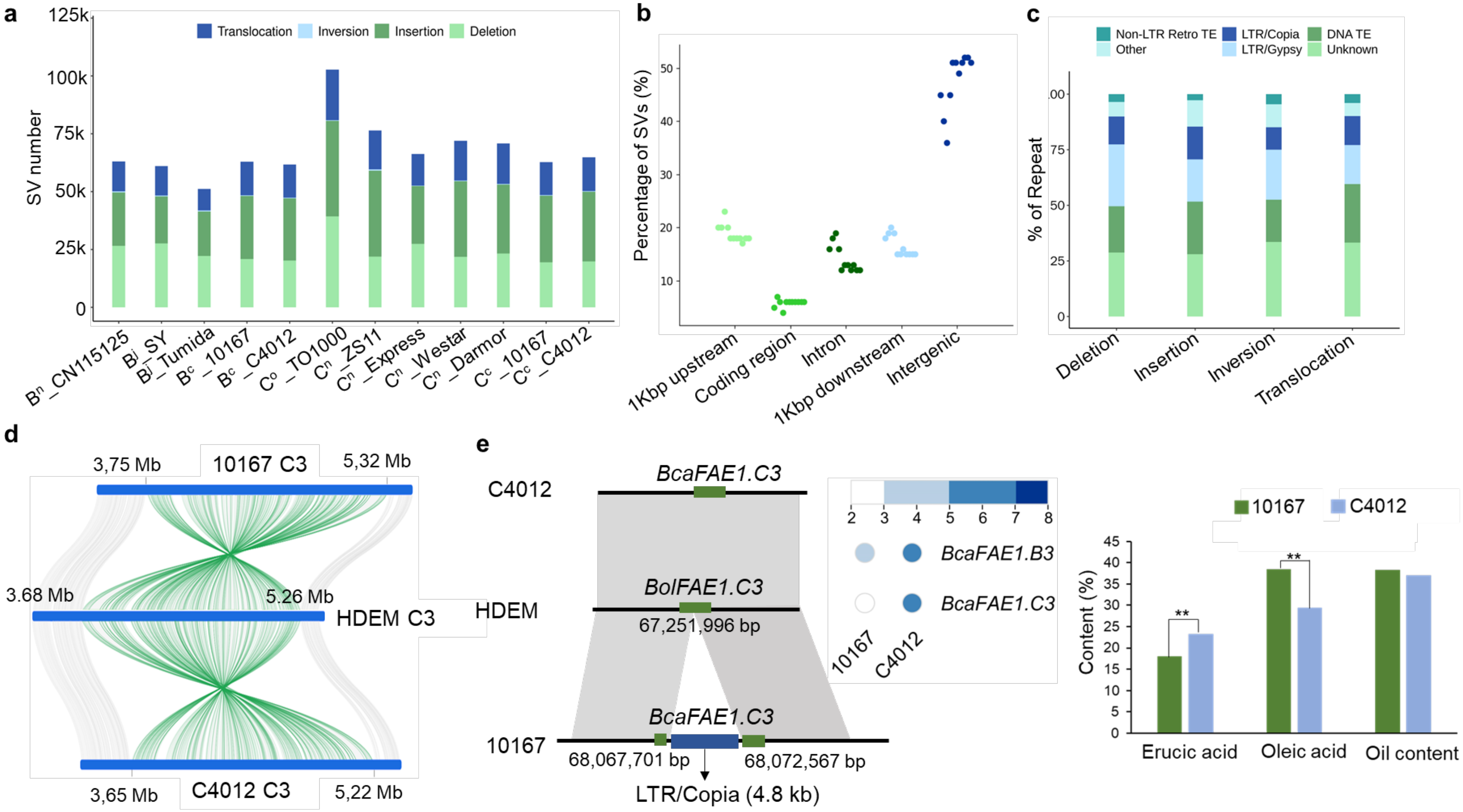






The species specificity of *B. carinata*

- 5,342 SNPs and 9,078 Indels unique to B^c compared to B^j and B^n.
- 4,209 SNPs and 3,981 Indels unique to C^c compared to C^o and C^n.
- Eight large inversions (>1 Mb) unique to *B. carinata.*



Summary

- Two high-quality *B. carinata* reference genomes were assembled with a total size at ~1.07 Gb and **contig N50 length at ~24 Mb**.
- The first *B. carinata* pan-genome **comprising 127,421 gene** models was constructed using 86 accessions.
- **One hub gene *BcaFUL.B7*** ssociated with PSR was detected by co-expression and QTL-seq.
- Species-specific genomic variations for *B. carinata* were identified.

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