Genomic insights into the origin, domestication and diversification of *Brassica juncea*

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Background

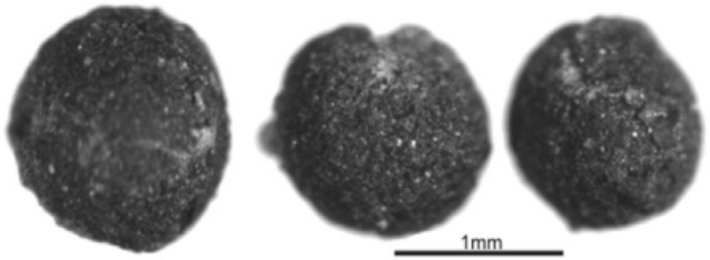
Four subspecies:

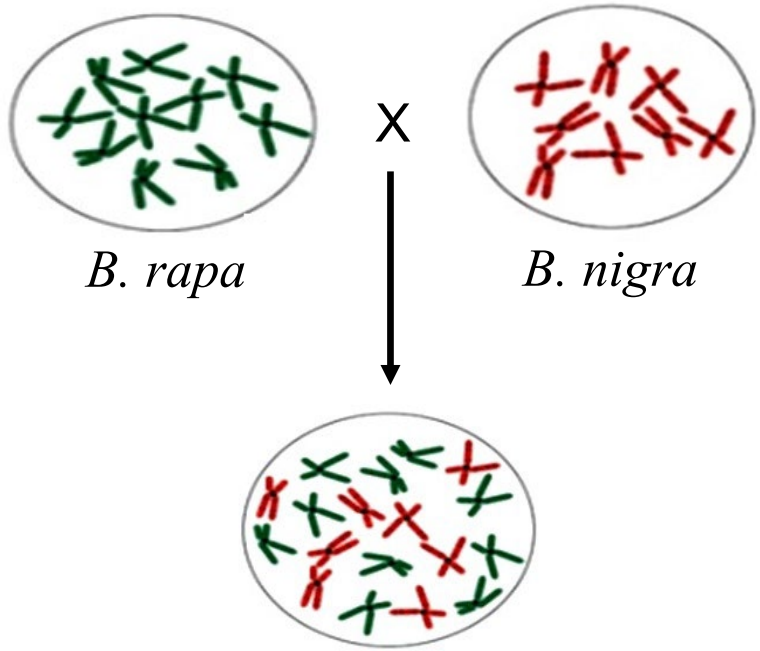
- *juncea* (seed mustard)
- *integrifolia* (leaf mustard)
- *napiformis* (root mustard)
- *tumida* (stem mustard)

Diverse *B. juncea species*

Background

Where is the origin center of *B. juncea*?





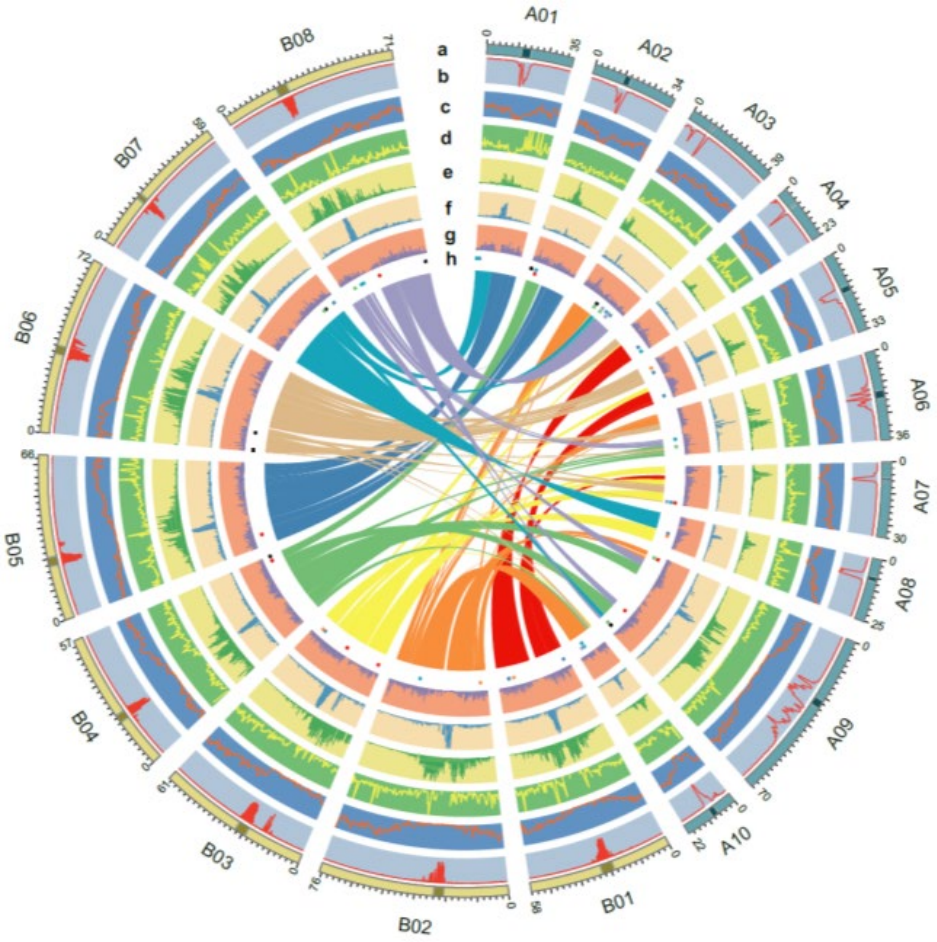
Assembly of *B. juncea* var. Sichuan Yellow (SY)

Assembly strategies

PacBio reads (~93×), Illumina reads (~130×),
BioNano data (~202x), Hi-C (~155x),
High-density linkage map (15,543 markers)

Table 1 | Summary statistics for the *Brassica juncea* var. Sichuan Yellow genome assembly

Genomic feature	SY
Estimated genome size (Mb)	1056.53
Total assembly size (bp)	933,496,244
Longest scaffold (bp)	76,001,744
Scaffold N50 (bp)	59,341,207
Contig N50 (bp)	1,926,153
Missing bases (%)	4.76
Sequences anchored to chromosome (%)	92.91
Annotated protein-coding genes (*n*)	82,723
TE proportion (%)	50.36



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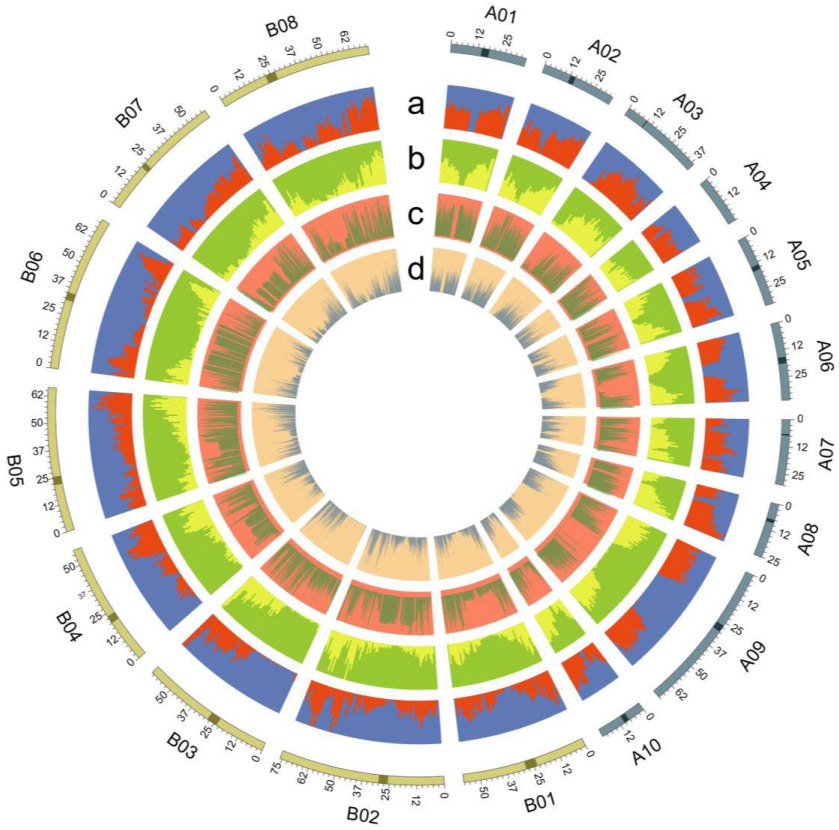
Re-sequencing of *B. juncea*

- 480 accessions representing the four subspecies from 38 countries
- average depth 15×
- 4,529,618 SNPs and 967,266 InDels



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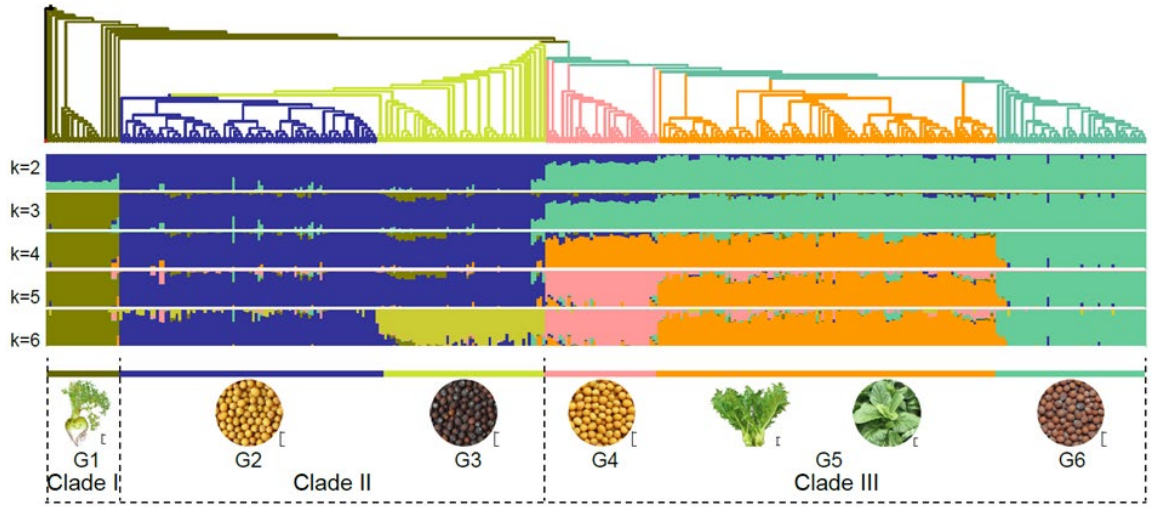
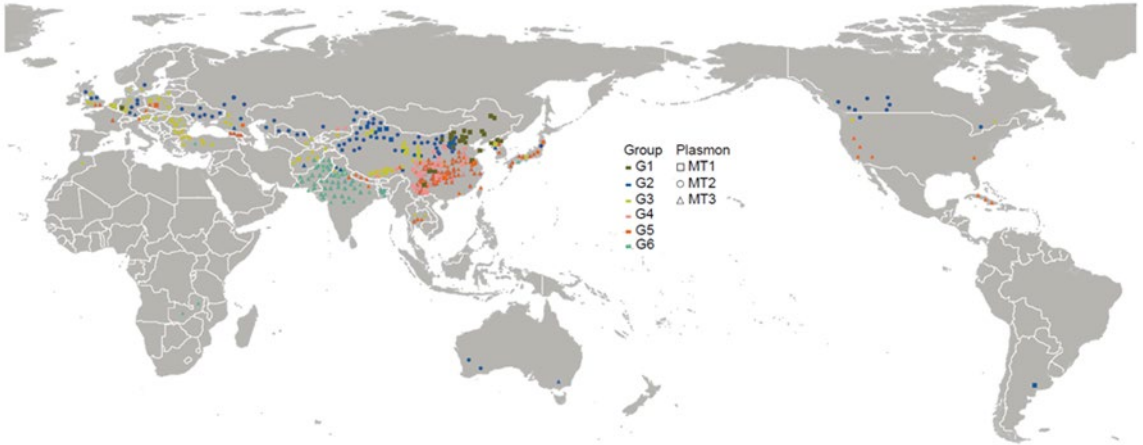
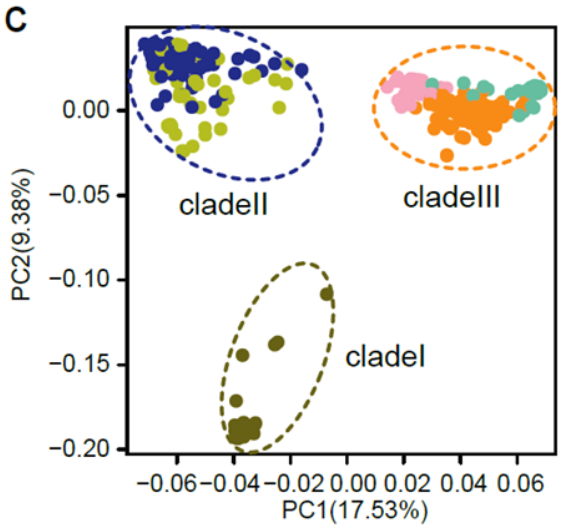
Genetic structure of the *B. juncea* population

- Six genetic groups in *B. juncea* population







- G1, root mustard
- G2, yellow-seeded mustard
- G3, seed mustard
- G4, yellow-seeded mustard
- G5, leaf and stem mustard
- G6, seed mustard

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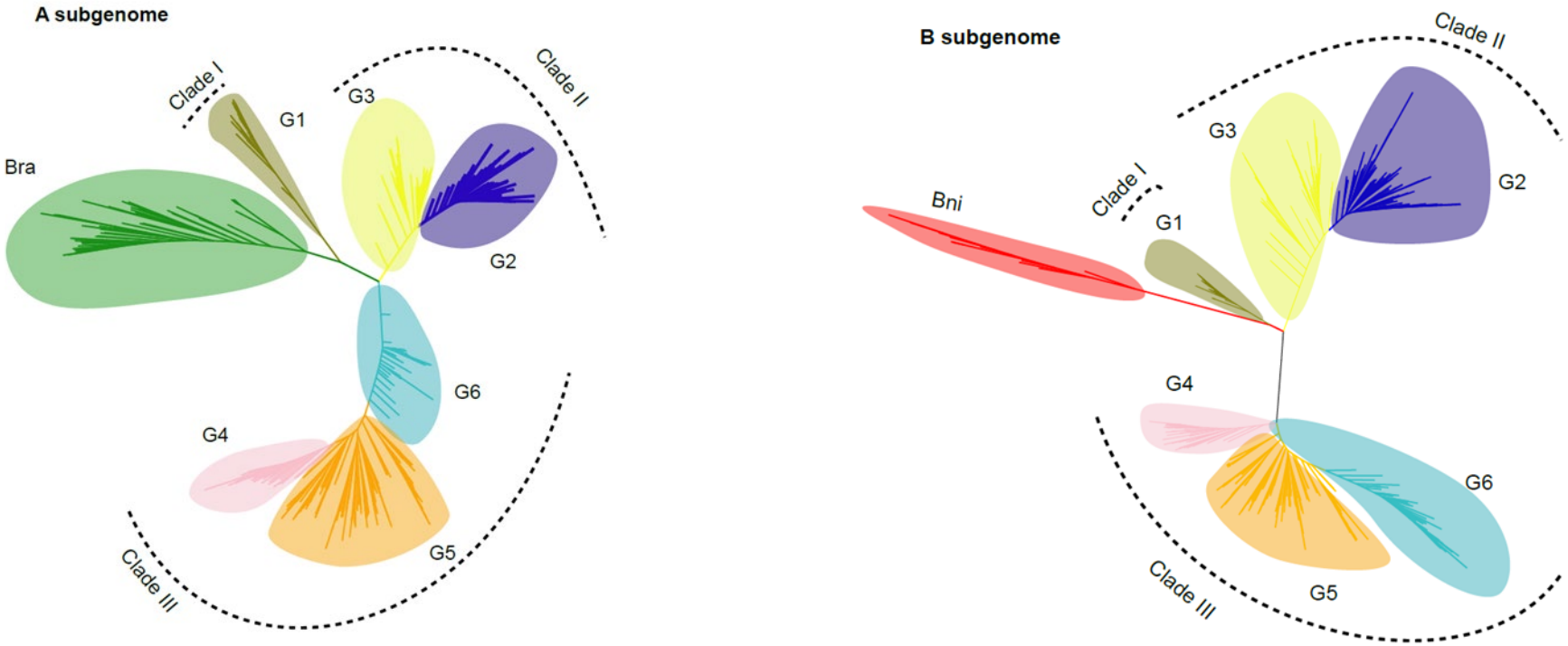
Monophyletic origin of *B. juncea*



The nuclear phylogenies supported that *B. juncea* originated monophyletically

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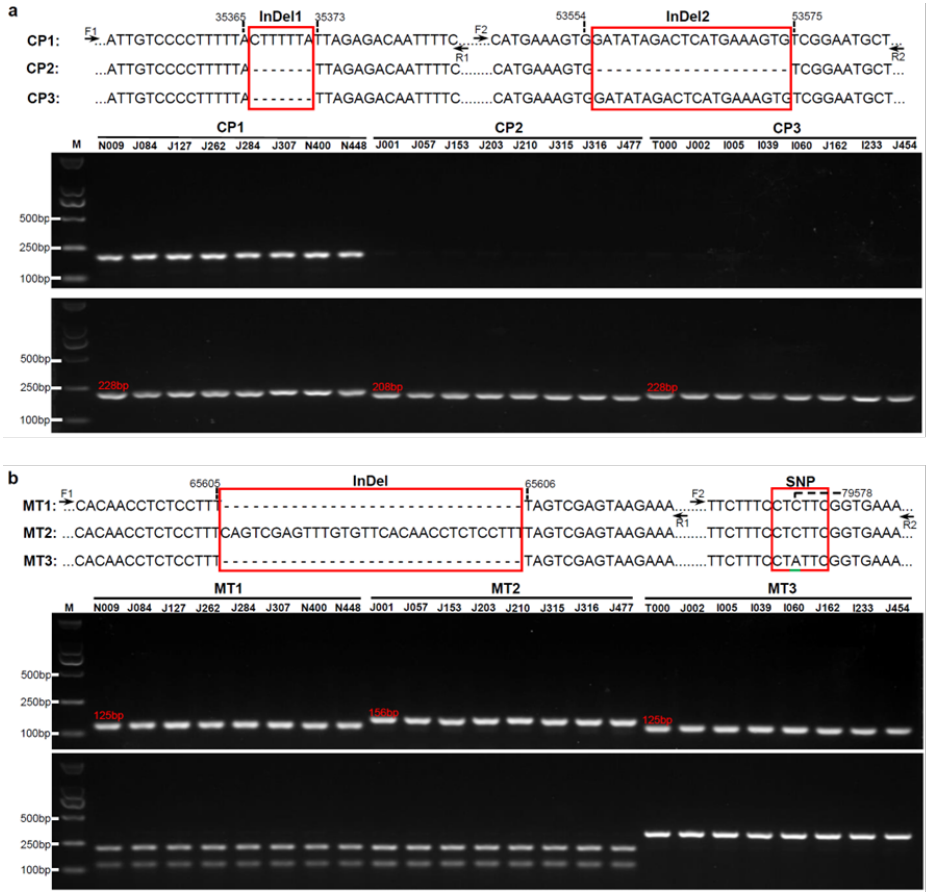
Monophyletic origin of *B. juncea*

- **Three plasmotypes I-III in *B. juncea* population**



Three types CPs 1–3

Plasmotypes I–III

Three types MTs 1–3

Clade I

G1: I, 100%

Clade II

G2: II, 91.3%(& I, 6.5%; III, 2.2%)

G3: II, 71.2% (& I, 20.3%; III, 8.5%)

Clade III

G4: II, 70% (& I, 15%; III, 15%)

G5: III, 94.2% (& I, 0.8%; Bra, 5%)

G6: III, 94.3% (& Bra, 5.7%)

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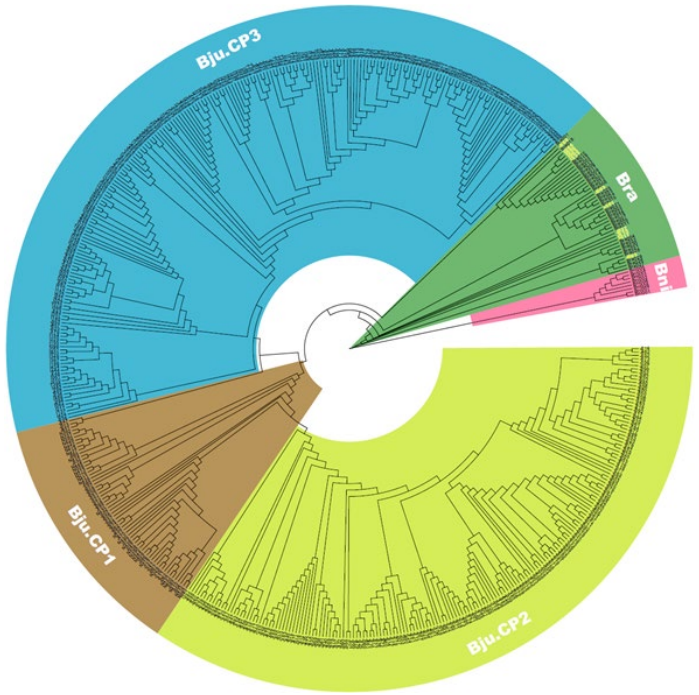
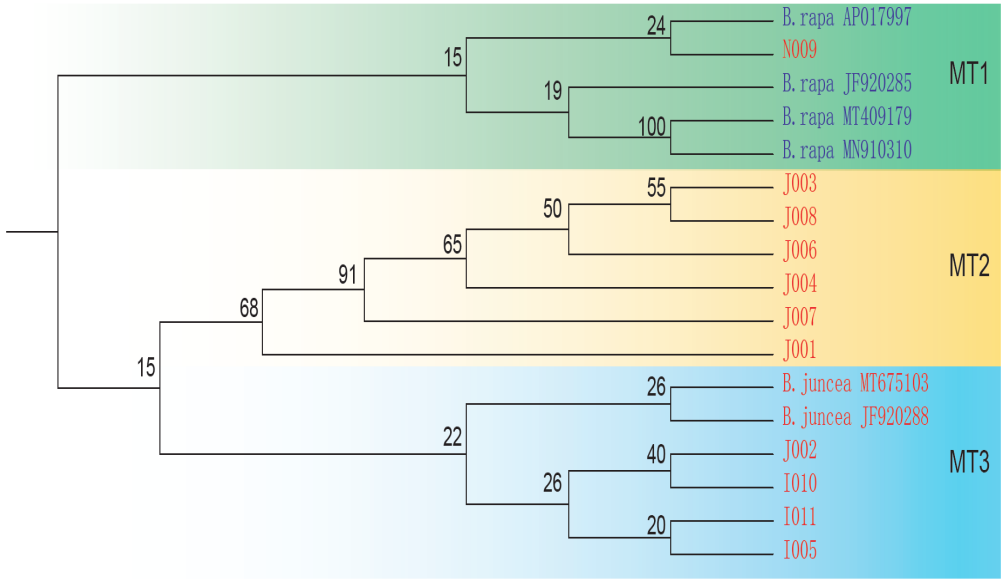
Monophyletic origin of *B. juncea*





The plasmotype I of *B. juncea* was descended from *B. rapa* and evolved into plasmotype II and III

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Origin and spread of *B. juncea*

***B. juncea* is most likely a single origin in West Asia, 8,000–14,000 years ago, followed by at least three independent domestication events**

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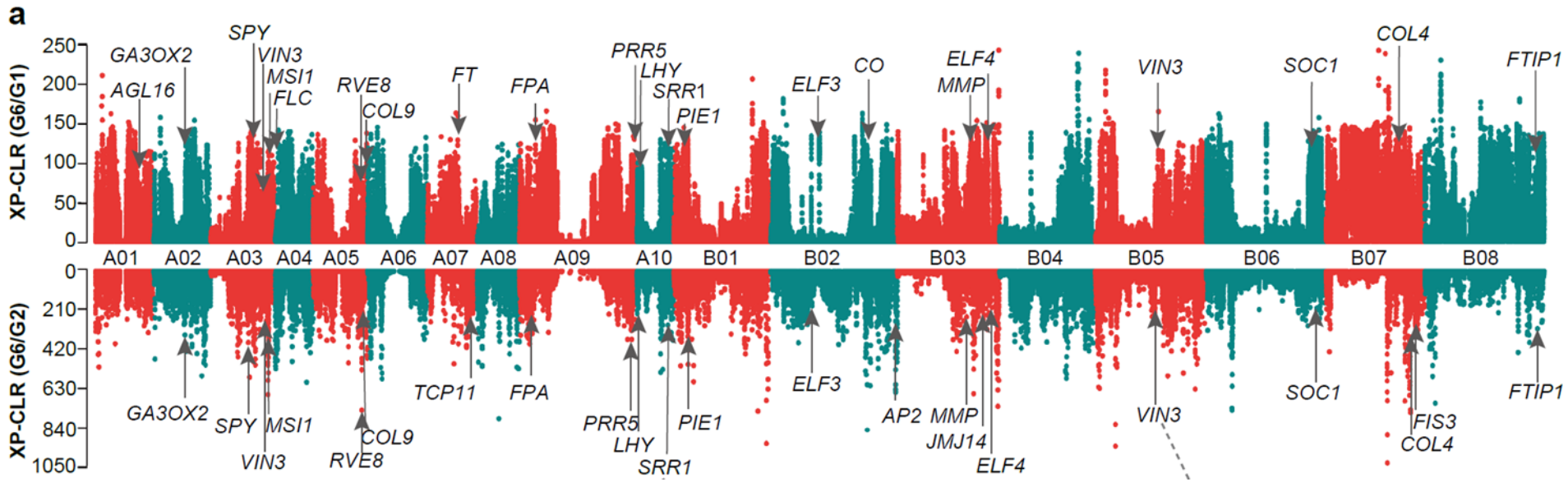
Ecogeographic adaptation of the flowering time



43 and 38 putative selective sweeps were identified in G6/G1 and G6/G2, respectively, containing 63 flowering time candidate genes

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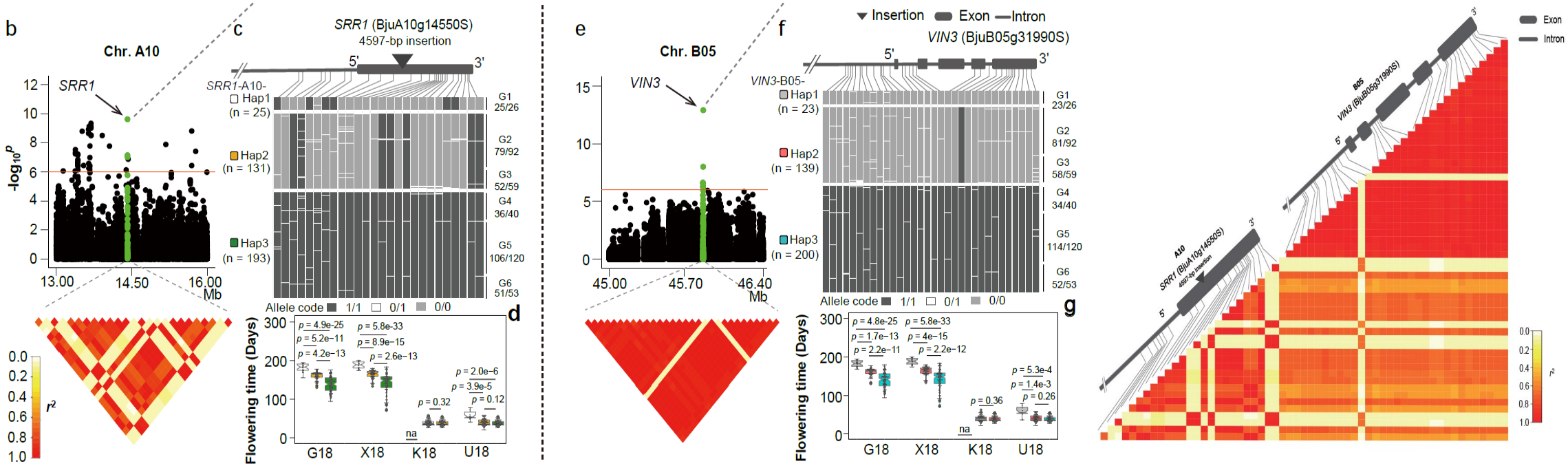
Ecogeographic adaptation of the flowering time



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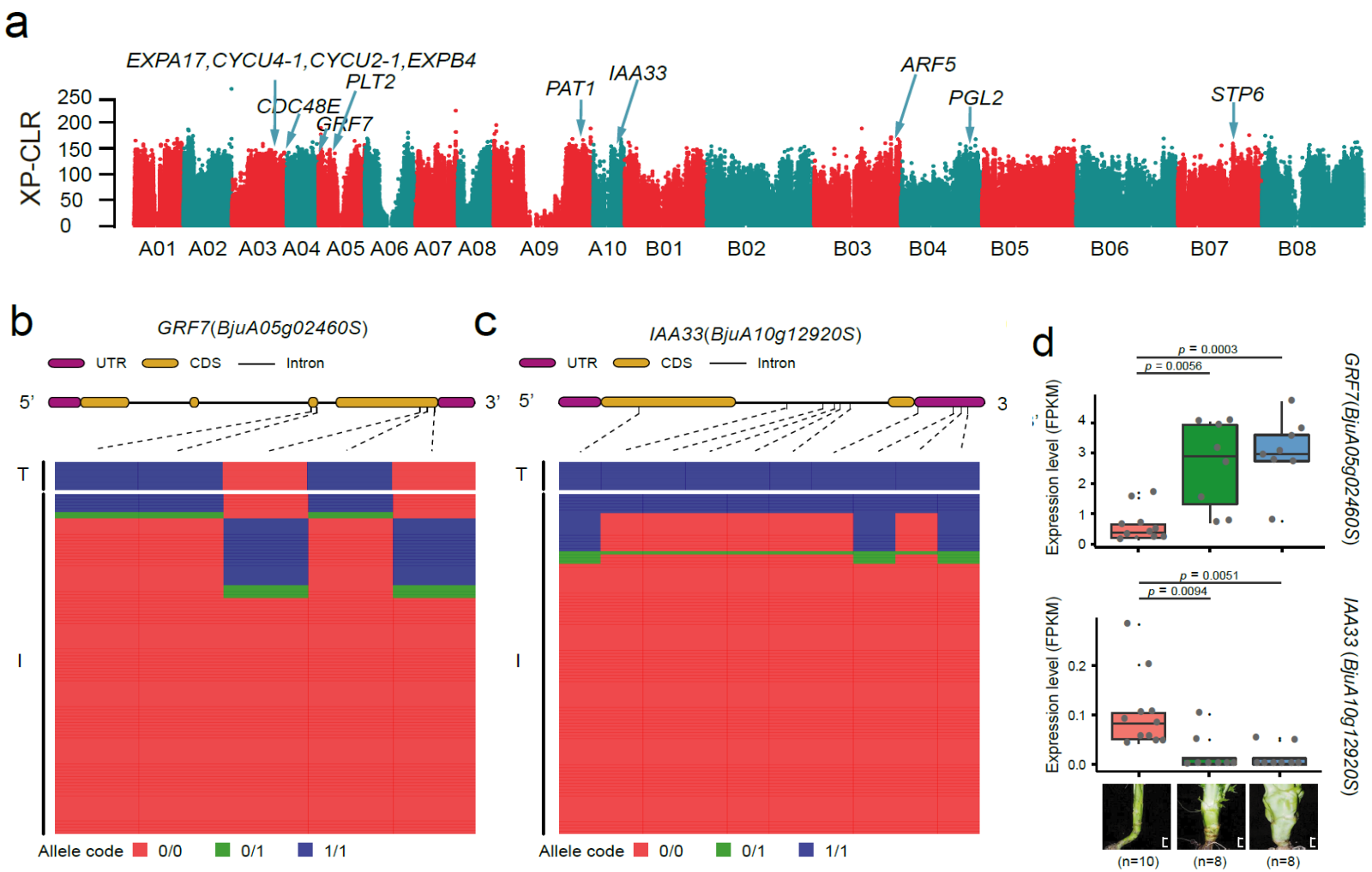
Morphological diversification of *B. juncea*

B. juncea var. tumida

Fuling 'zhacai'

Morphological diversification of *B. juncea*



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Summary

- **Chromosome-scale genome of the yellow-seeded *Brassica juncea***
- ***B. juncea* is most likely a single origin in West Asia, 8,000–14,000 years ago, followed by at least three independent domestication events**
- **Our results elucidate the domestication history and artificial selection of genes implicated in morphological diversification among diverse *B. juncea* species**

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