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Flowering for the Future

Whole-genome resequencing reveals *Brassica napus* origin and genetic loci involved in its improvement

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18 June, 2019
Berlin, Germany

Outline

- Backgrounds
- Identities of diploid progenitors of *B. napus*
- Improvement history of *B. napus*
- Key genes involved in improvement of *B. napus*
- Summary

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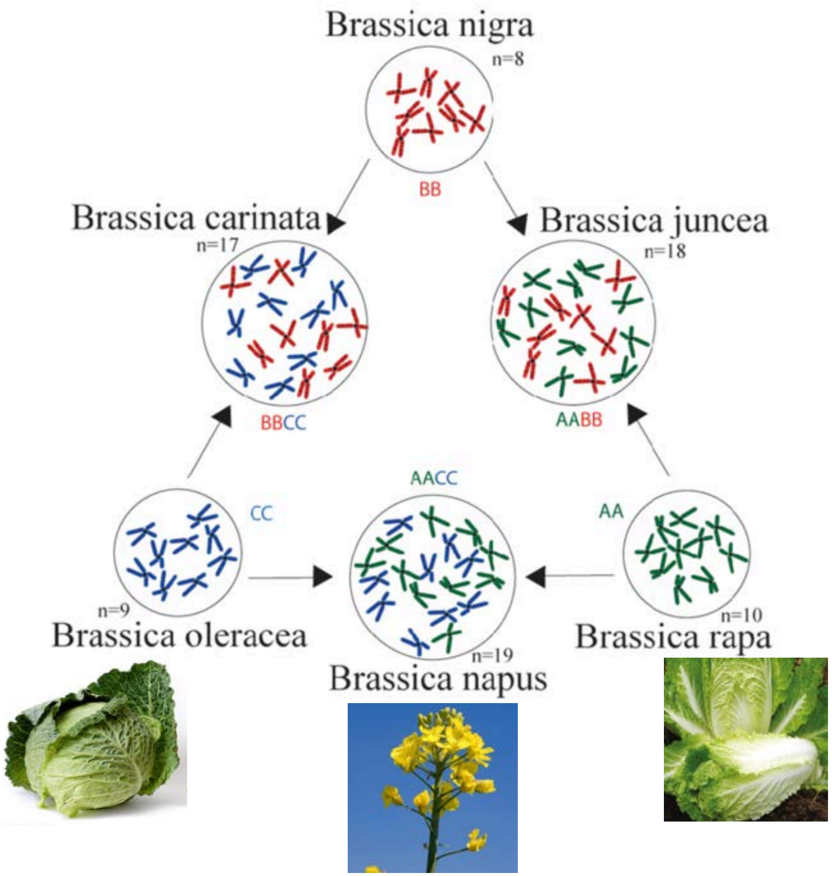
Backgrounds

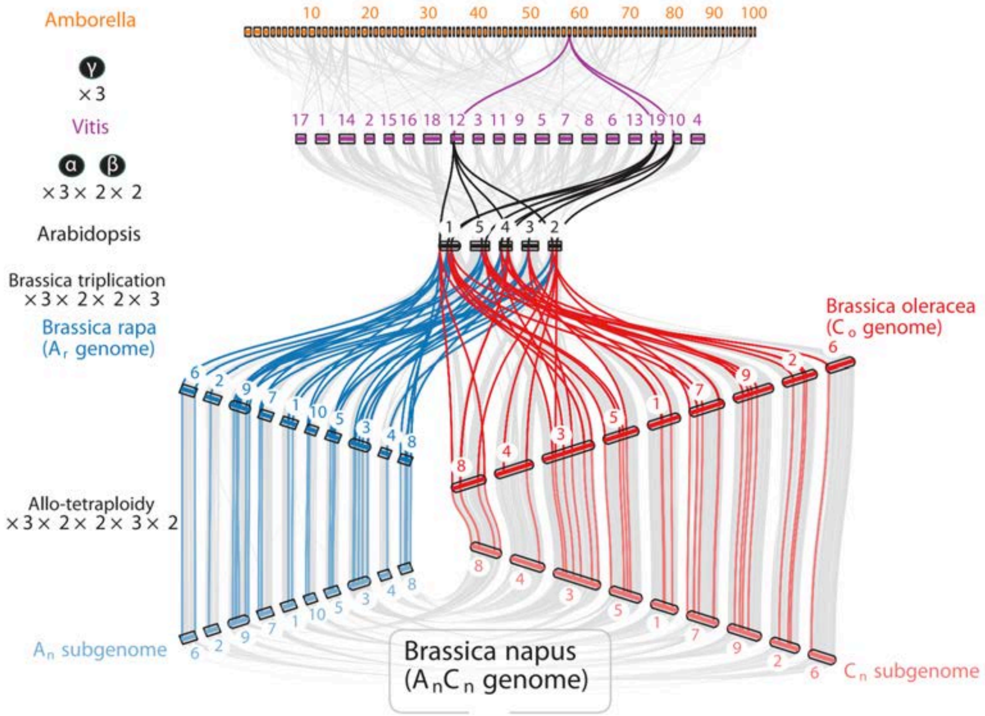
Traditional usage of *B. napus*

Backgrounds

Usage extension of *B. napus*

Backgrounds





Chalhoub et al (2014) Science

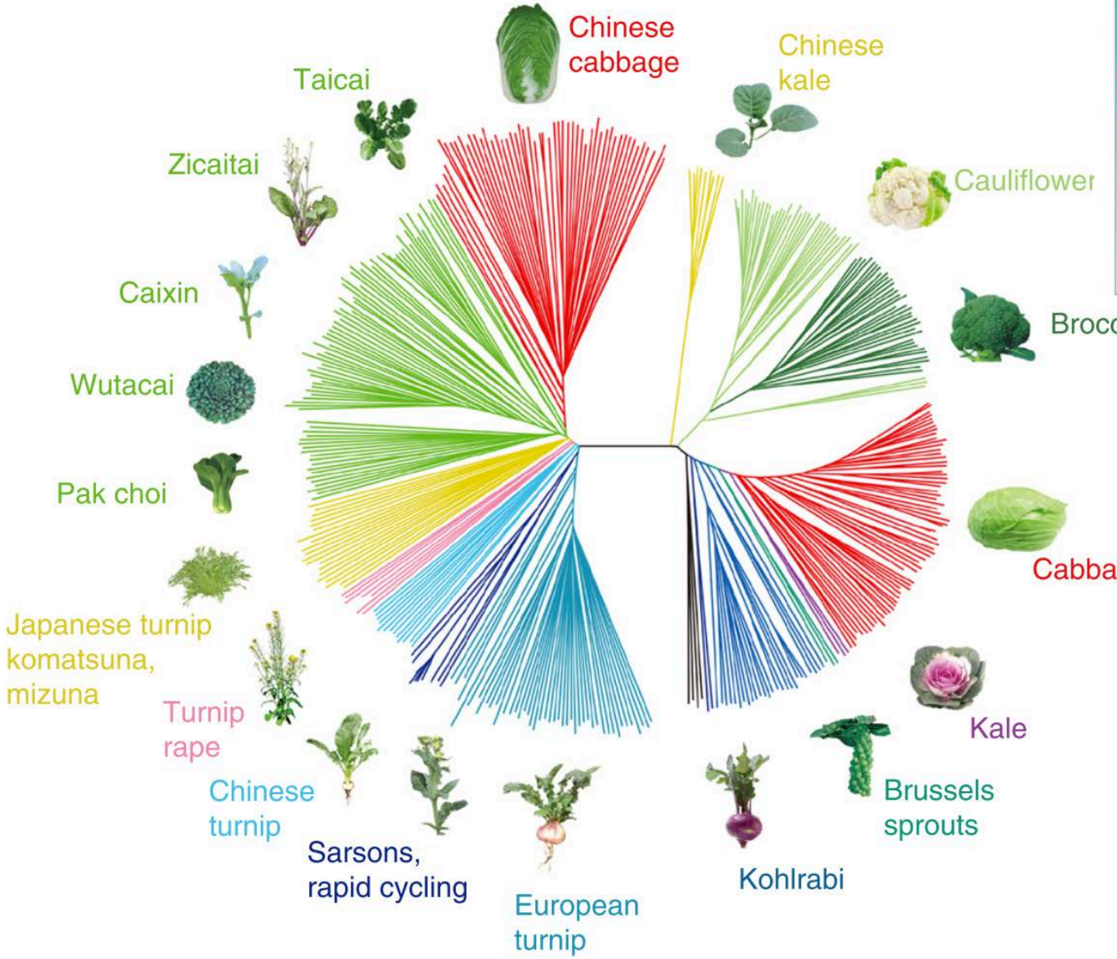
Backgrounds

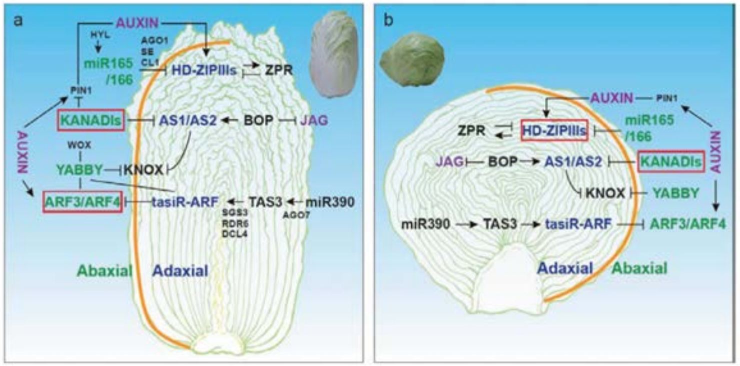
Brassica rapa

Brassica oleracea

Brassica napus

Backgrounds





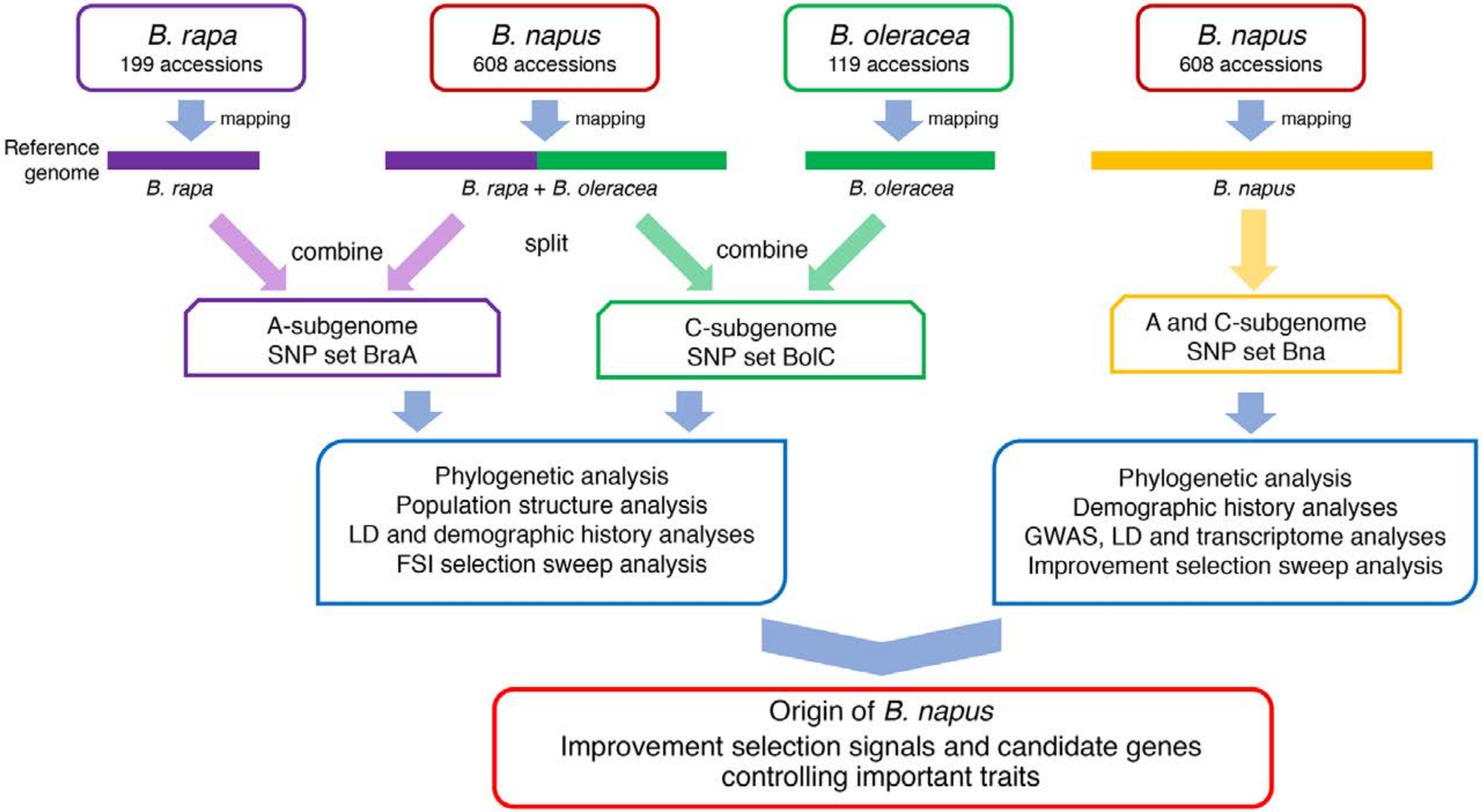

nature genetics

VOLUME 48 NUMBER 10 OCTOBER 2016
www.nature.com/naturegenetics

Brassica genome evolution
Vertebrate immunity without CD4+ T cells
Blood pressure regulation

Chen et al (2016) Nat. Genet.

Workflow for population genetic analysis



B. rapa
199 accessions

B. napus
608 accessions

B. oleracea
119 accessions

B. napus
608 accessions

mapping

Reference genome

B. rapa

B. rapa + *B. oleracea*

B. oleracea

B. napus

combine

split

combine

A-subgenome
SNP set BraA

C-subgenome
SNP set BolC

A and C-subgenome
SNP set Bna

Phylogenetic analysis
Population structure analysis
LD and demographic history analyses
FSI selection sweep analysis

Phylogenetic analysis
Demographic history analyses
GWAS, LD and transcriptome analyses
Improvement selection sweep analysis

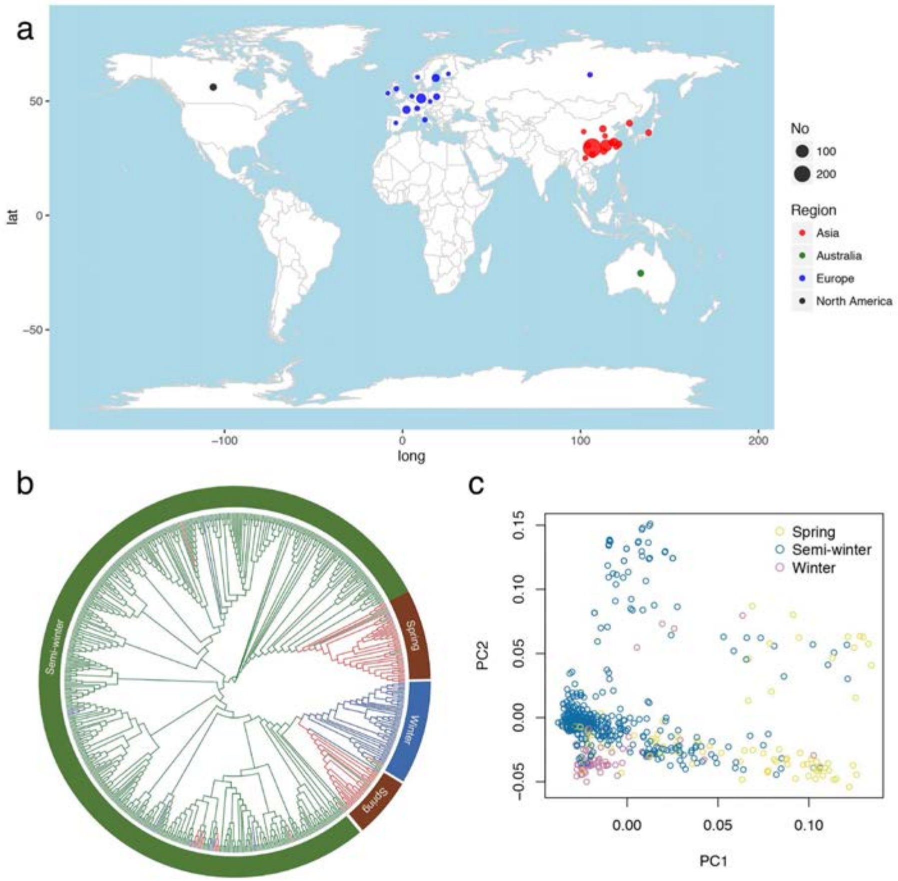
Origin of *B. napus*
Improvement selection signals and candidate genes controlling important traits

Lu et al (2019) Nat. Commun.

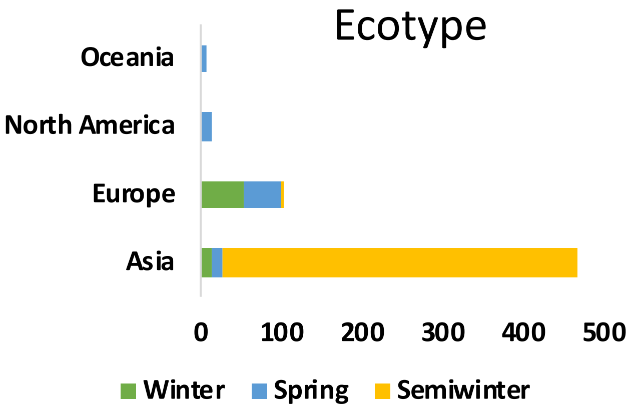
Identities of diploid progenitors of *B. napus*

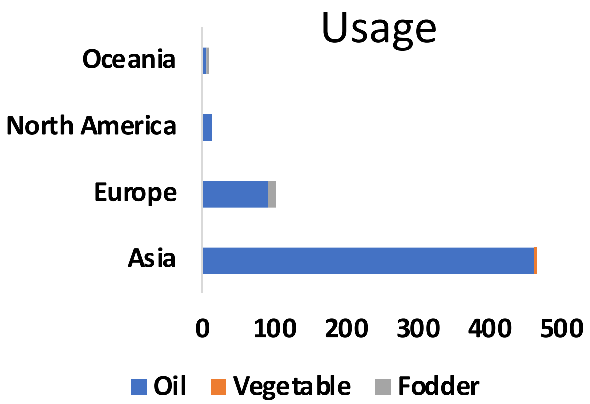
- Resequencing: 13.43 billion reads (**4.03 Tb**)
- RNA-seq 0.85 billion reads (**212.19** Gb).
- 5.29M SNPs in *B. napus*.
- 0.73M and 1.09M SNPs in A and C subgenomes.
- Majority of SNPs (95.1%) represent authentic SNPs.
- Biological replicated SNPs ranged from 93.5% to 96.4%.

Identities of diploid progenitors of *B. napus*

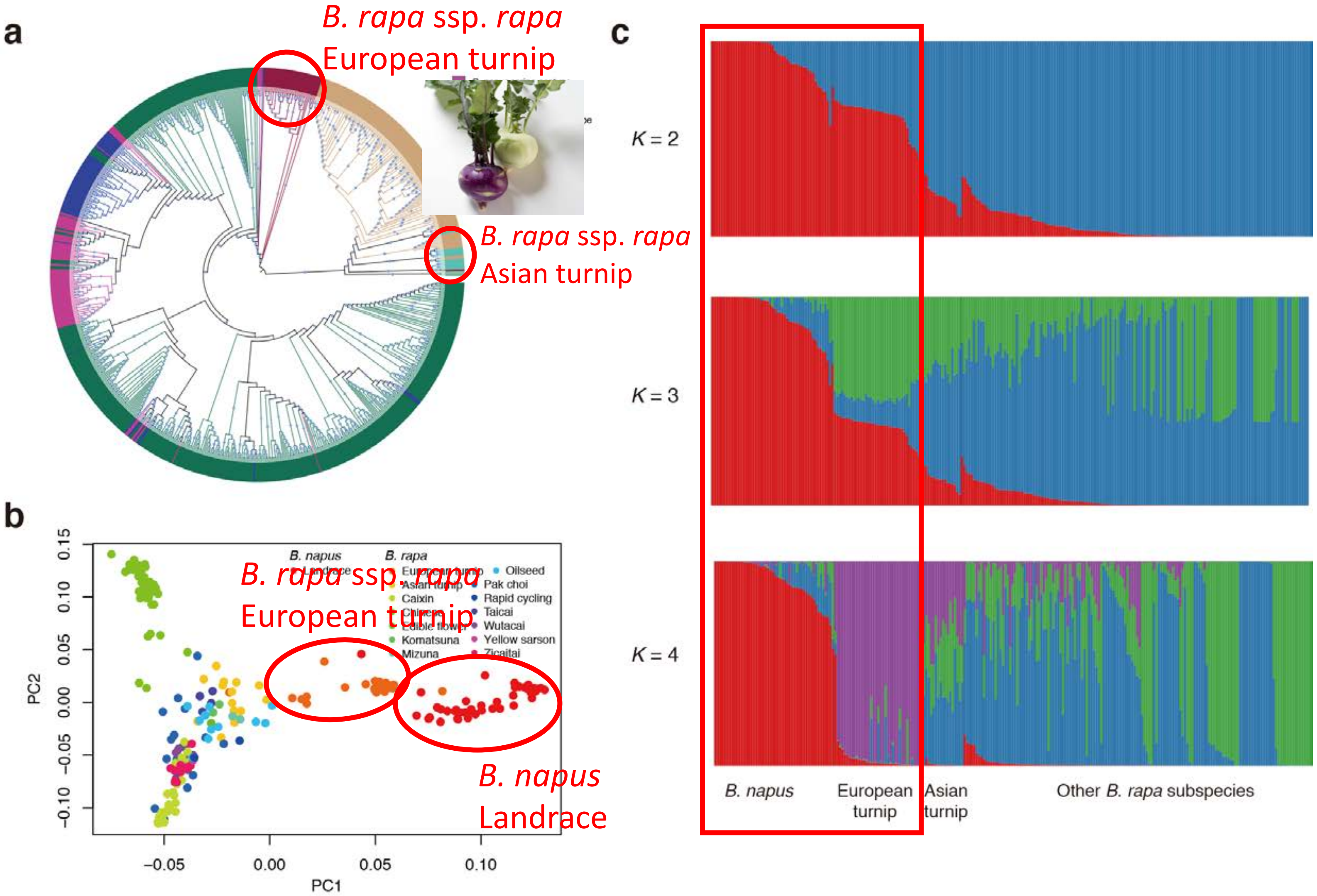


Geographic distribution and population structure of 588 *B. napus* accessions





Identities of diploid progenitors of *B. napus*



B. rapa ssp. *rapa*
European turnip

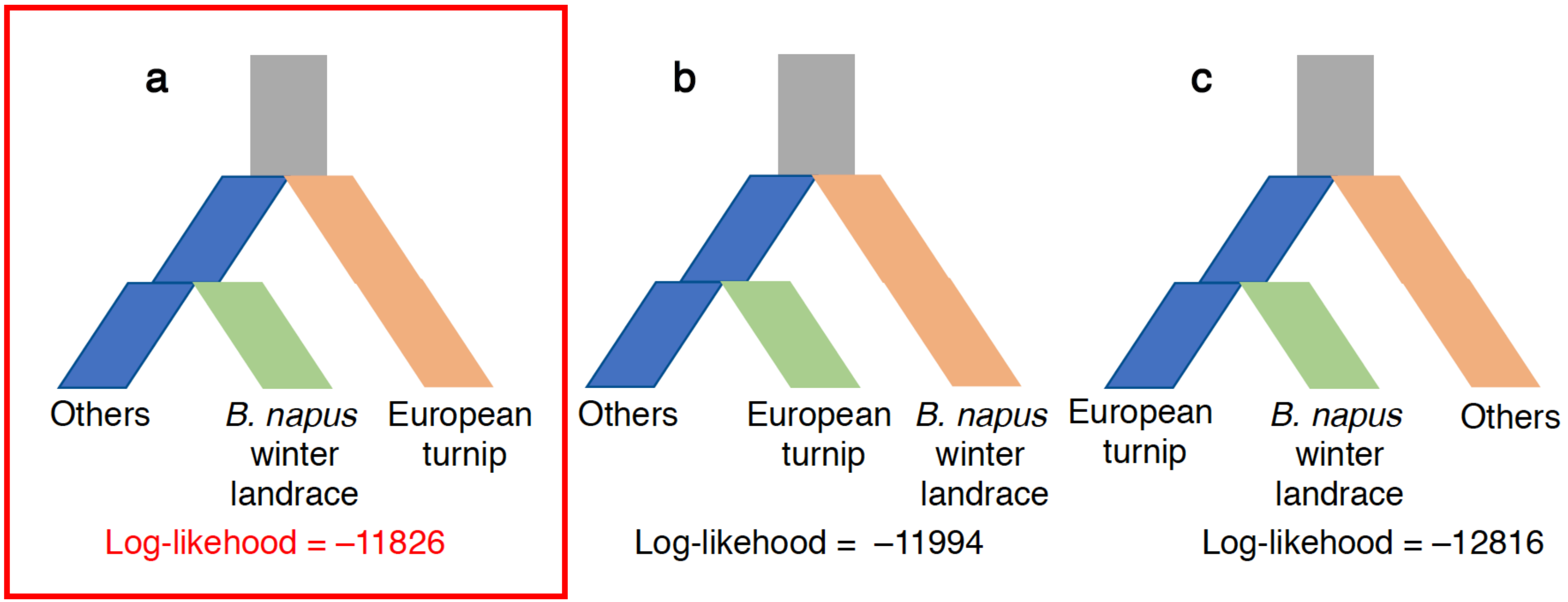
B. rapa ssp. *rapa*
Asian turnip

B. rapa ssp. *rapa*
European turnip

B. napus
Landrace

The A subgenome may evolve from the ancestor of European turnip.

Identities of diploid progenitors of *B. napus*

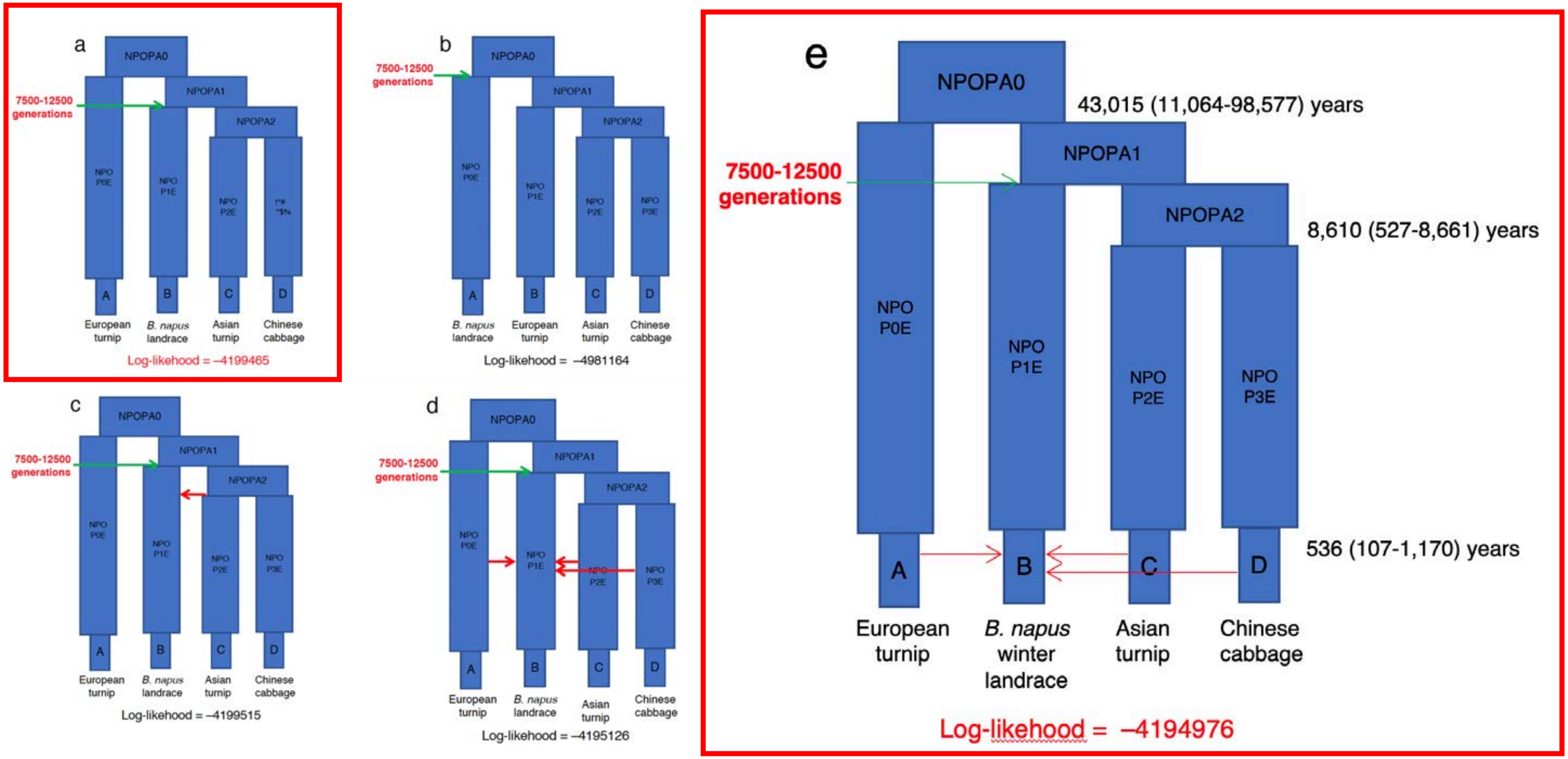


Log-likehood = –11826

Log-likehood = –11994

Log-likehood = –12816

Identities of diploid progenitors of *B. napus*



A gene flow event occurred ~107-1,170 years ago.

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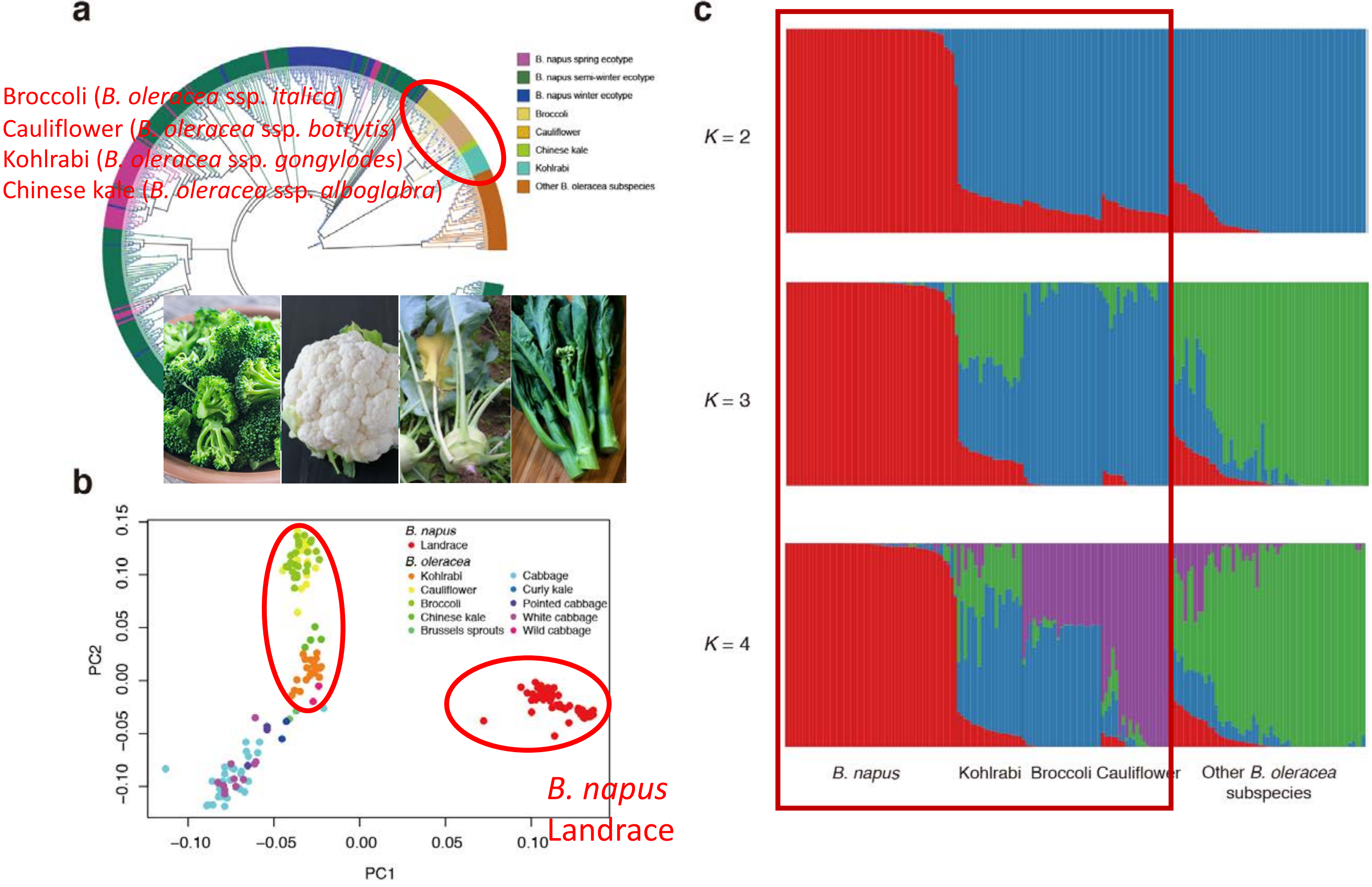
Identities of diploid progenitors of *B. napus*



Broccoli (*B. oleracea* ssp. *italica*)
Cauliflower (*B. oleracea* ssp. *botrytis*)
Kohlrabi (*B. oleracea* ssp. *gongylodes*)
Chinese kale (*B. oleracea* ssp. *alboglabra*)

B. napus Landrace

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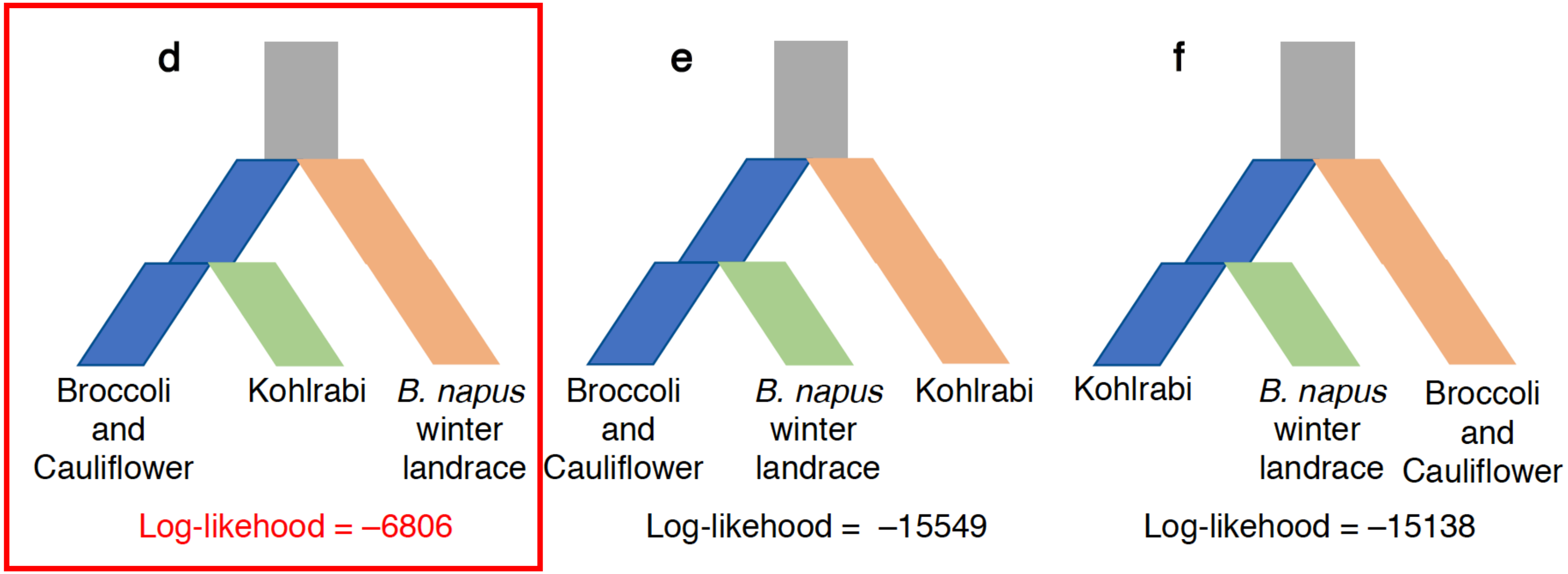
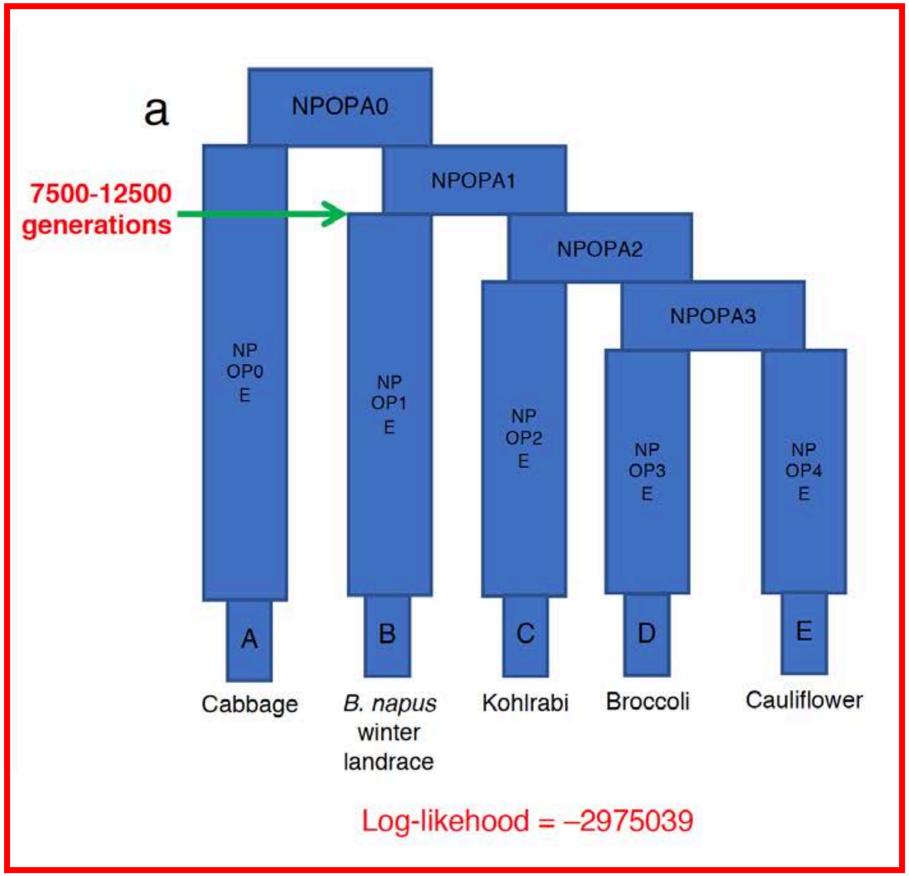
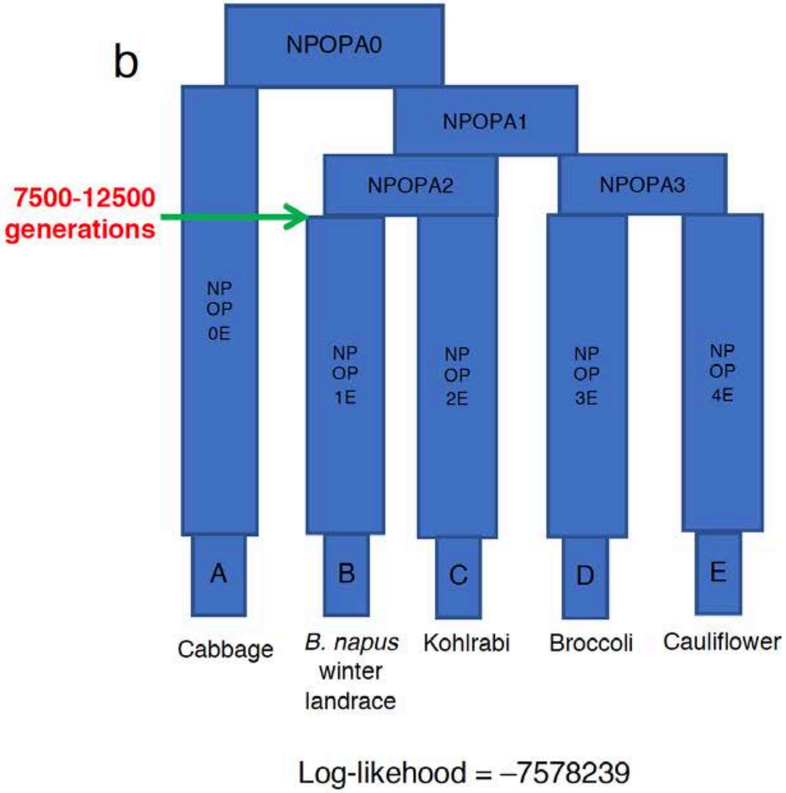
The C subgenome may evolve from the common ancestor of kohlrabi, cauliflower, broccoli, and Chinese kale.

Identities of diploid progenitors of *B. napus*



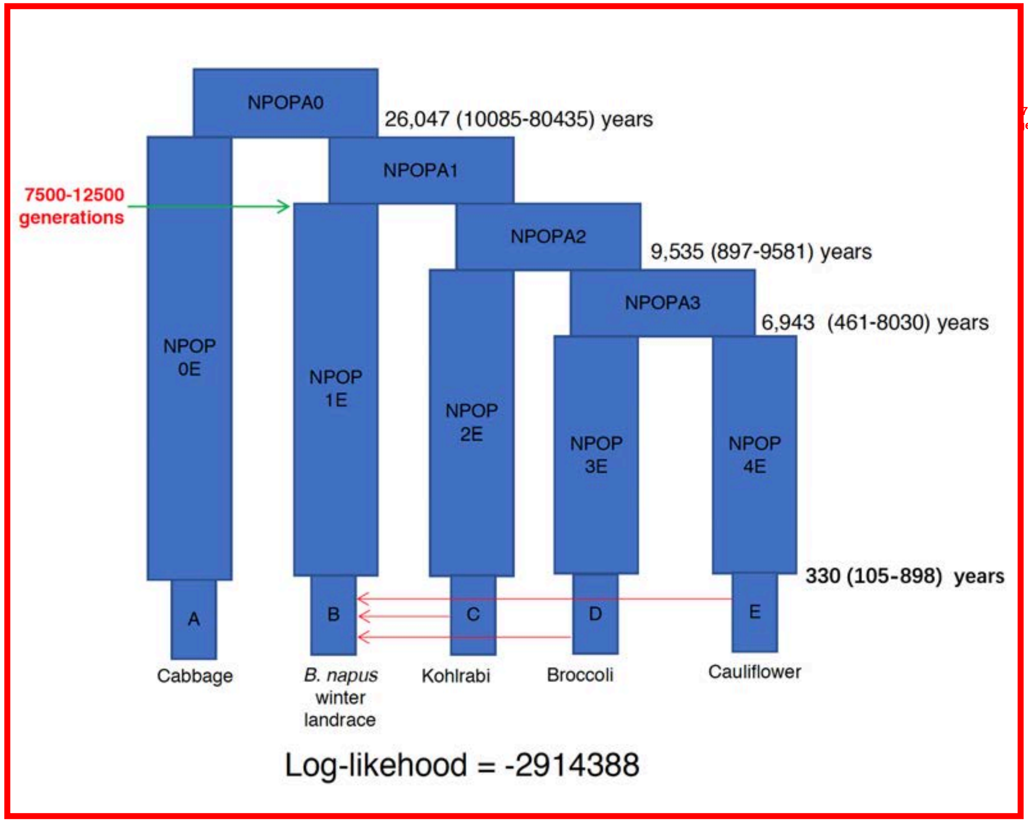
Identities of diploid progenitors of *B. napus*

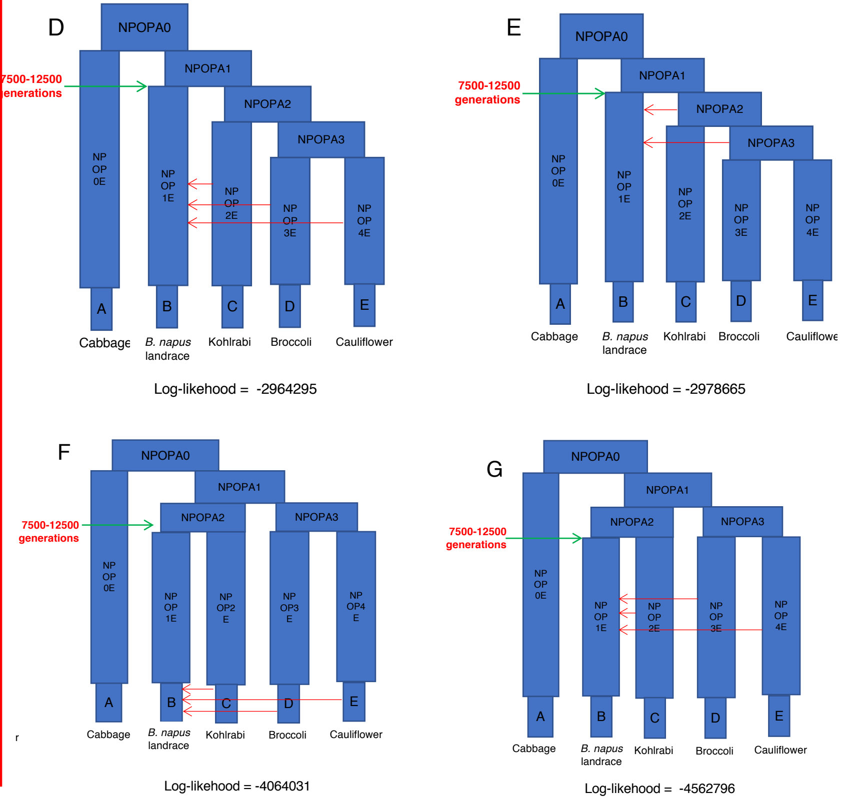




Model A suggests that the C subgenome of *B. napus* originated from the common ancestor of kohlrabi, cauliflower, and broccoli.

Identities of diploid progenitors of *B. napus*



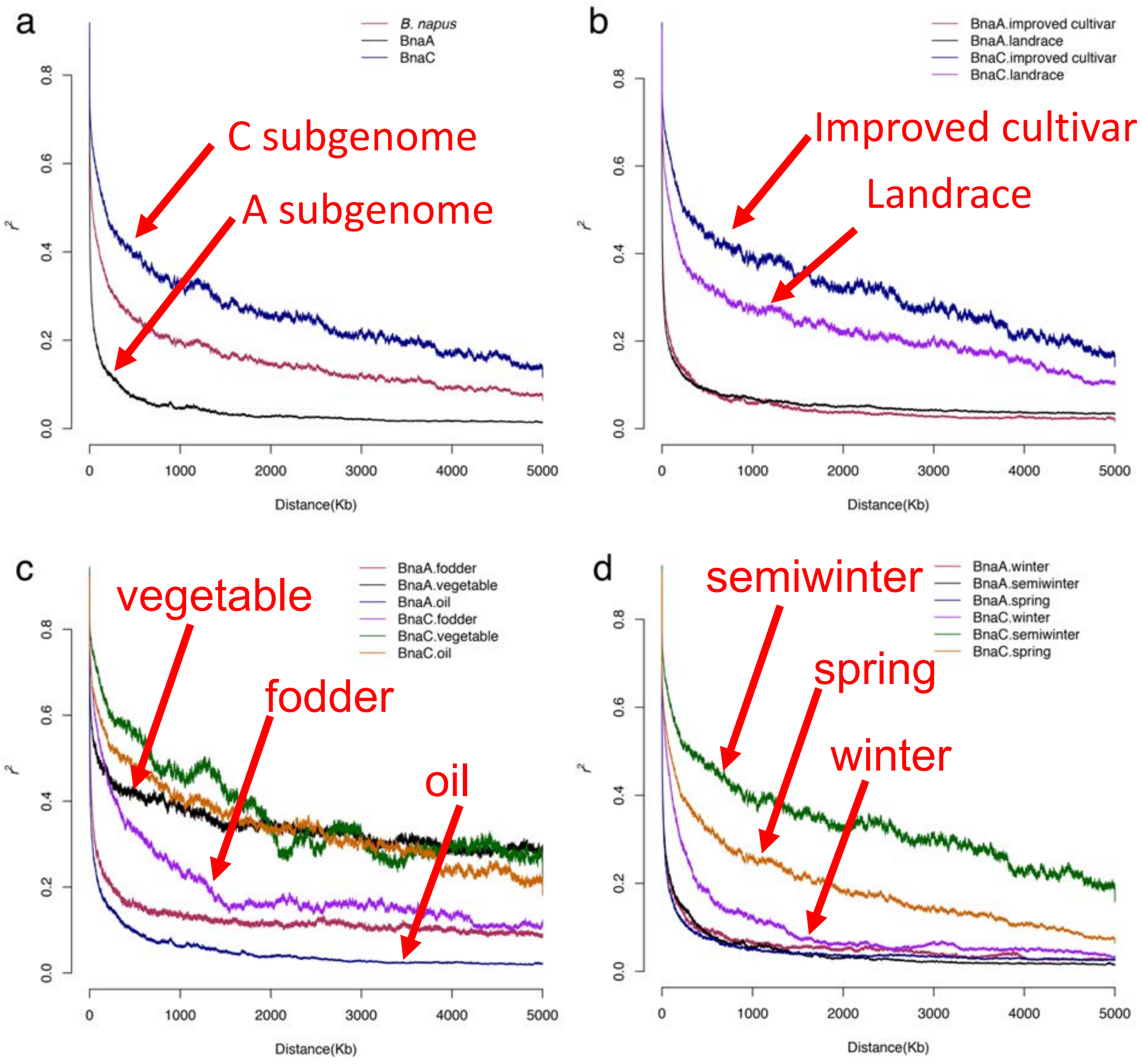


The ancestor of *B. napus* split from the common ancestor of four *B. oleracea* subspecies, with recent gene flow into *B. napus* approximately 105–898 years ago.

Improvement history of *B. napus*

Original type:

winter oilseed



C subgenome

A subgenome

Improved cultivar

Landrace

vegetable

fodder

oil

semiwinter

spring

winter

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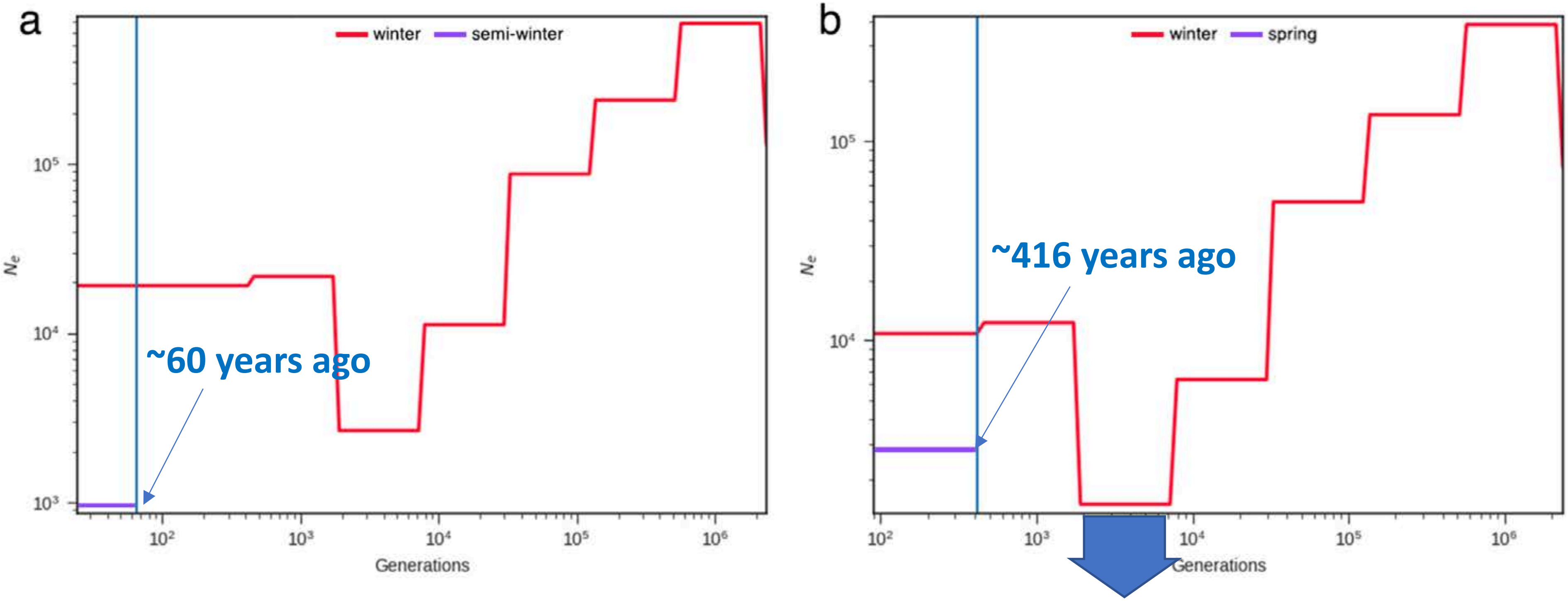
Improvement history of *B. napus*



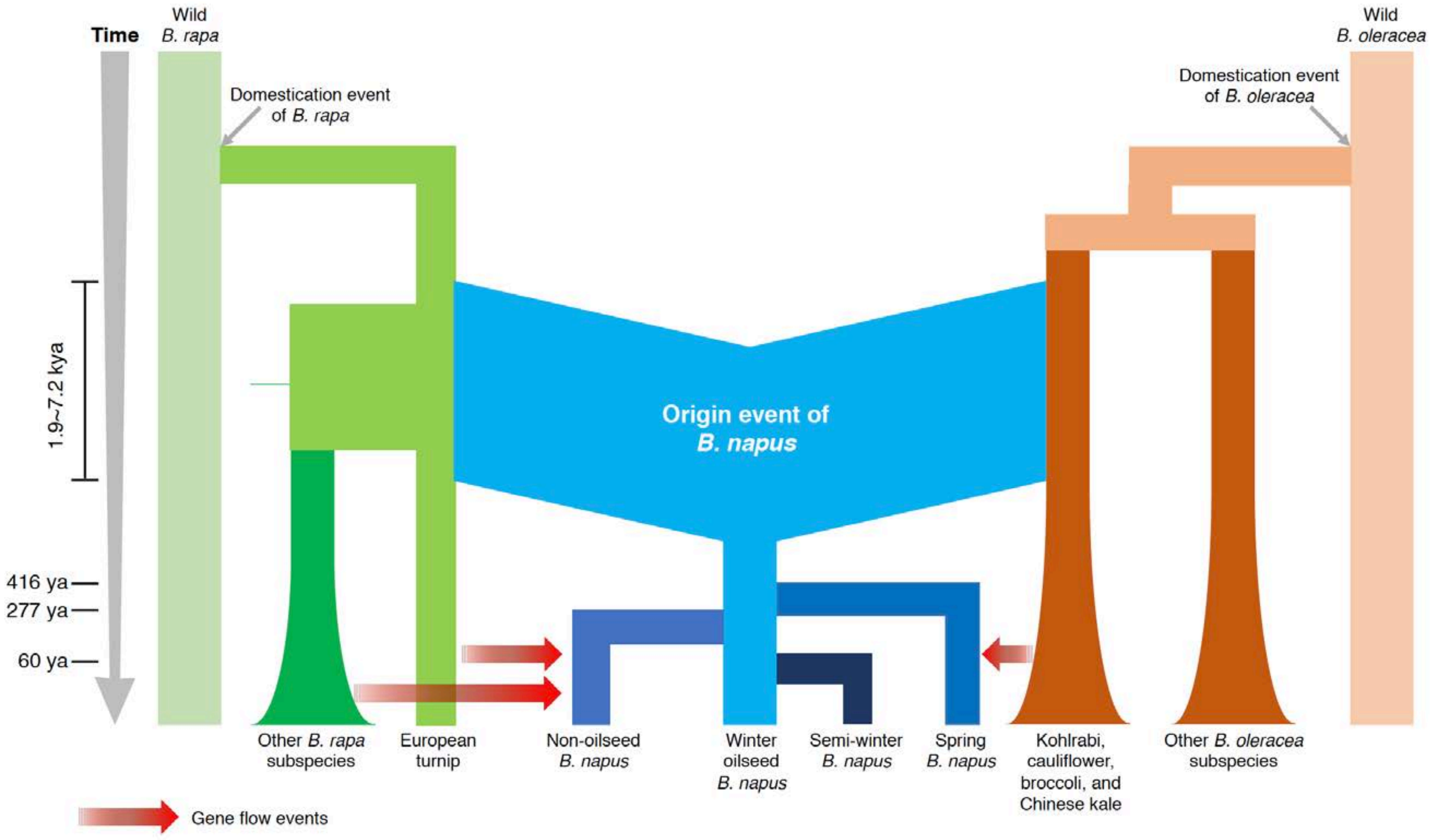
~60 years ago

~416 years ago

1912-7178 years ago

The winter and semi-winter ecotypes diverged ~60 years ago
The winter and spring *B. napus* diverged ~416 years ago
The oilseed and non-oilseed *B. napus* diverged ~277 years ago.

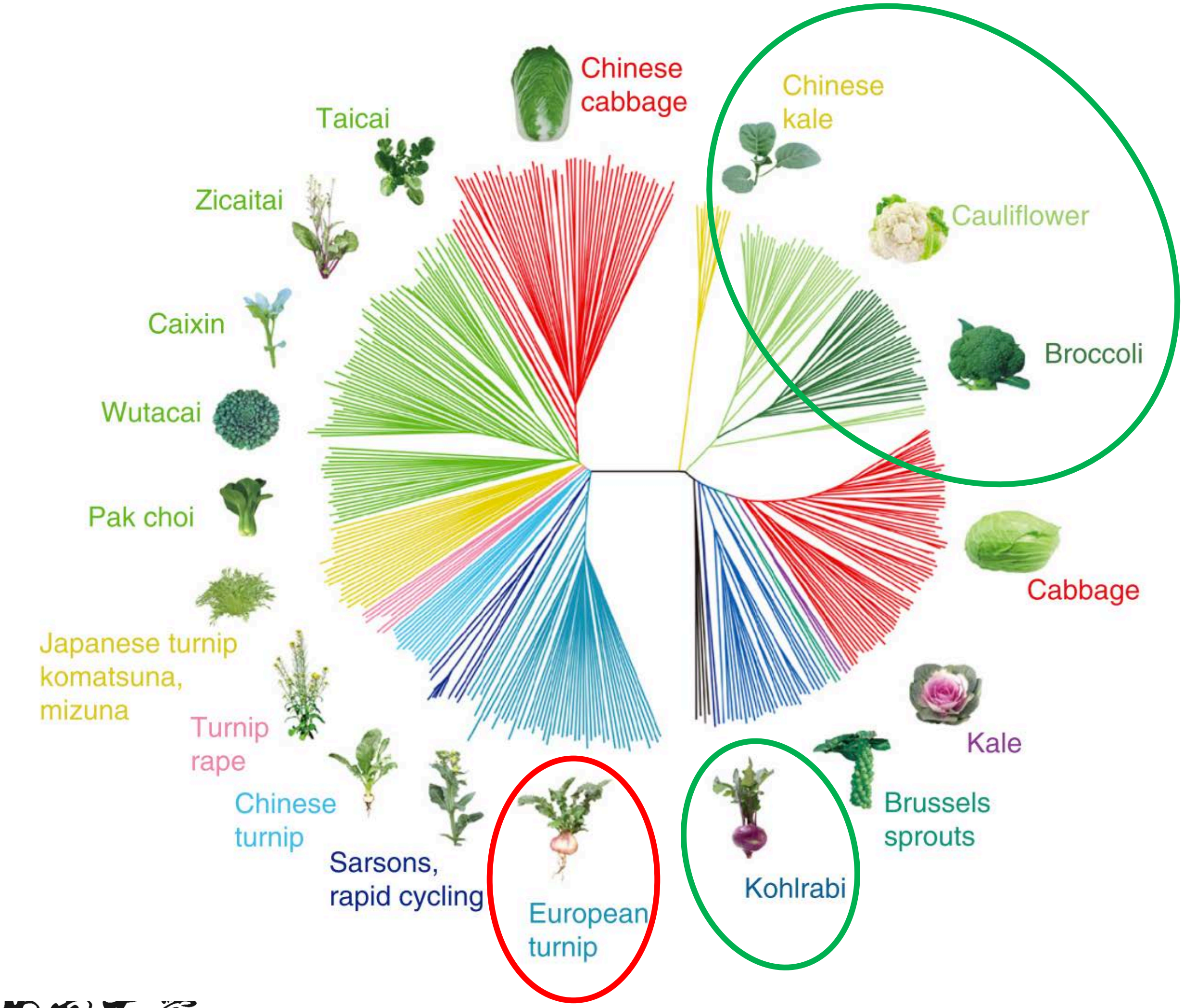
Improvement history of *B. napus*



Proposed model for origin and evolutionary history of *B. napus*

Lu et al, (2019) Nat. Commun.

Key genes involved in improvement of *B. napus*

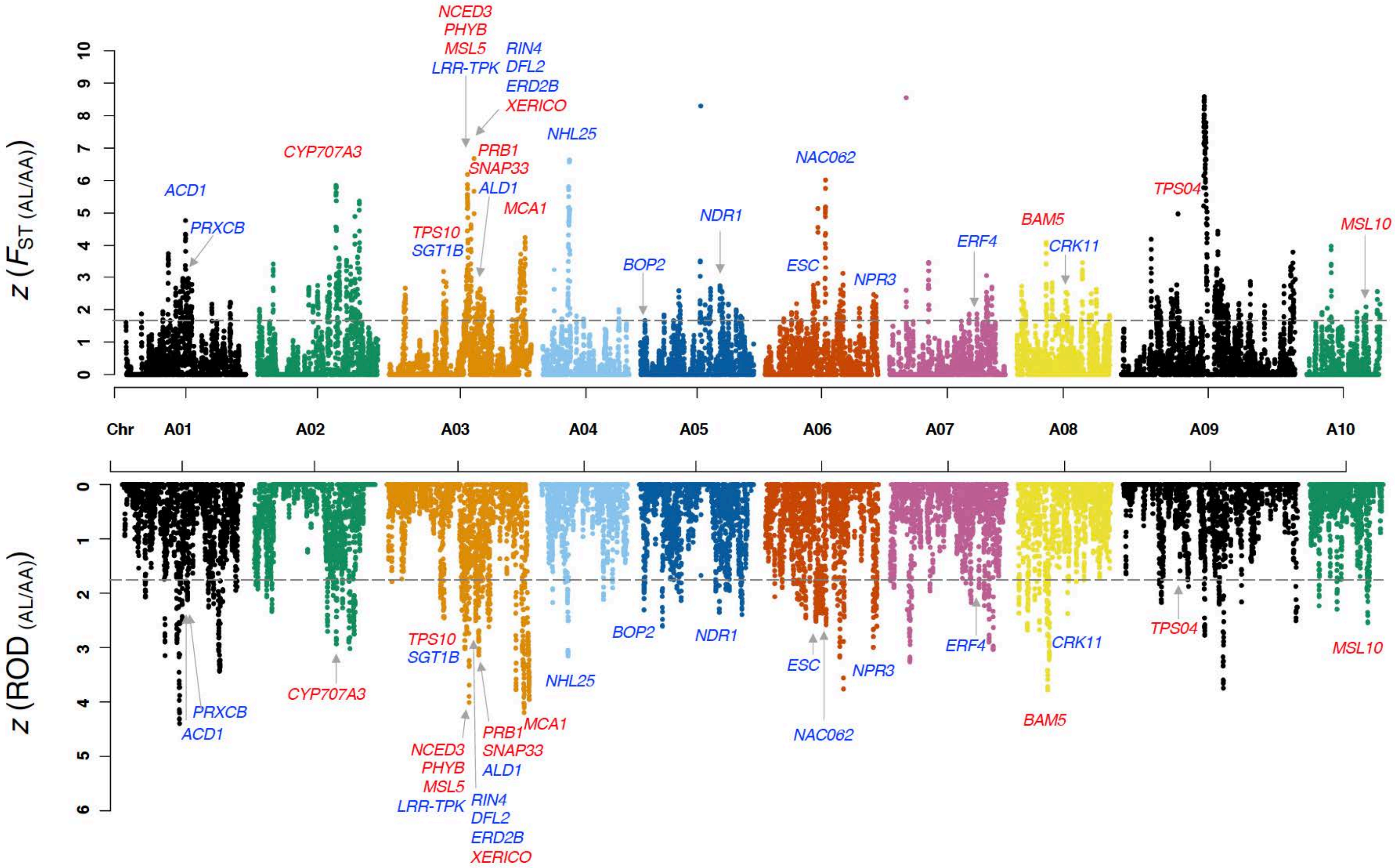


Pseudo-ancestral populations of wild *B. napus*

B. rapa
***n* = 33**

B. oleracea
***n* = 66**

Key genes involved in improvement of *B. napus*



Selection signatures in A subgenome of *B. napus* during first-stage of improvement

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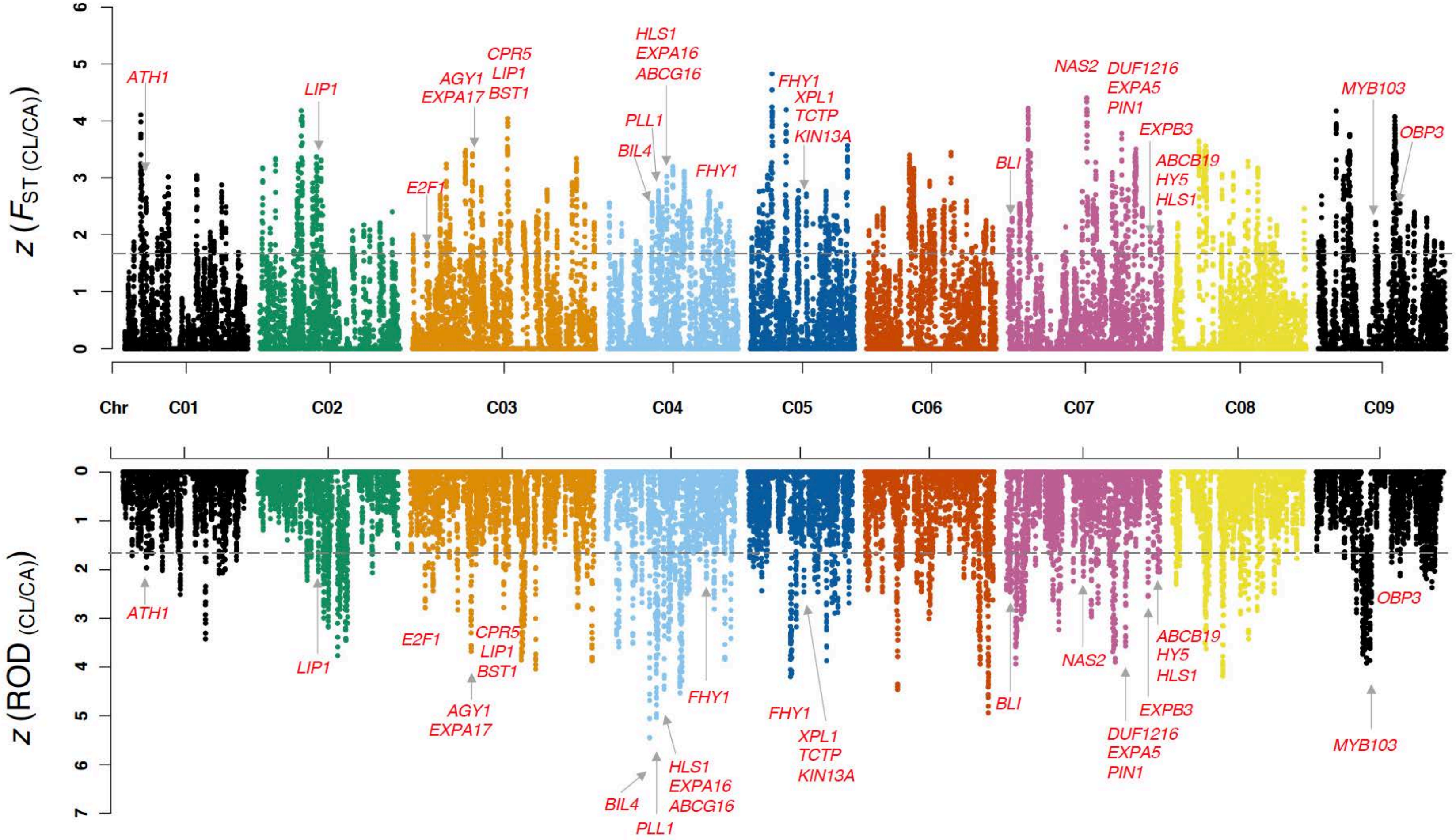
Key genes involved in improvement of *B. napus*



Selection signatures in C subgenome of *B. napus* during first-stage of improvement

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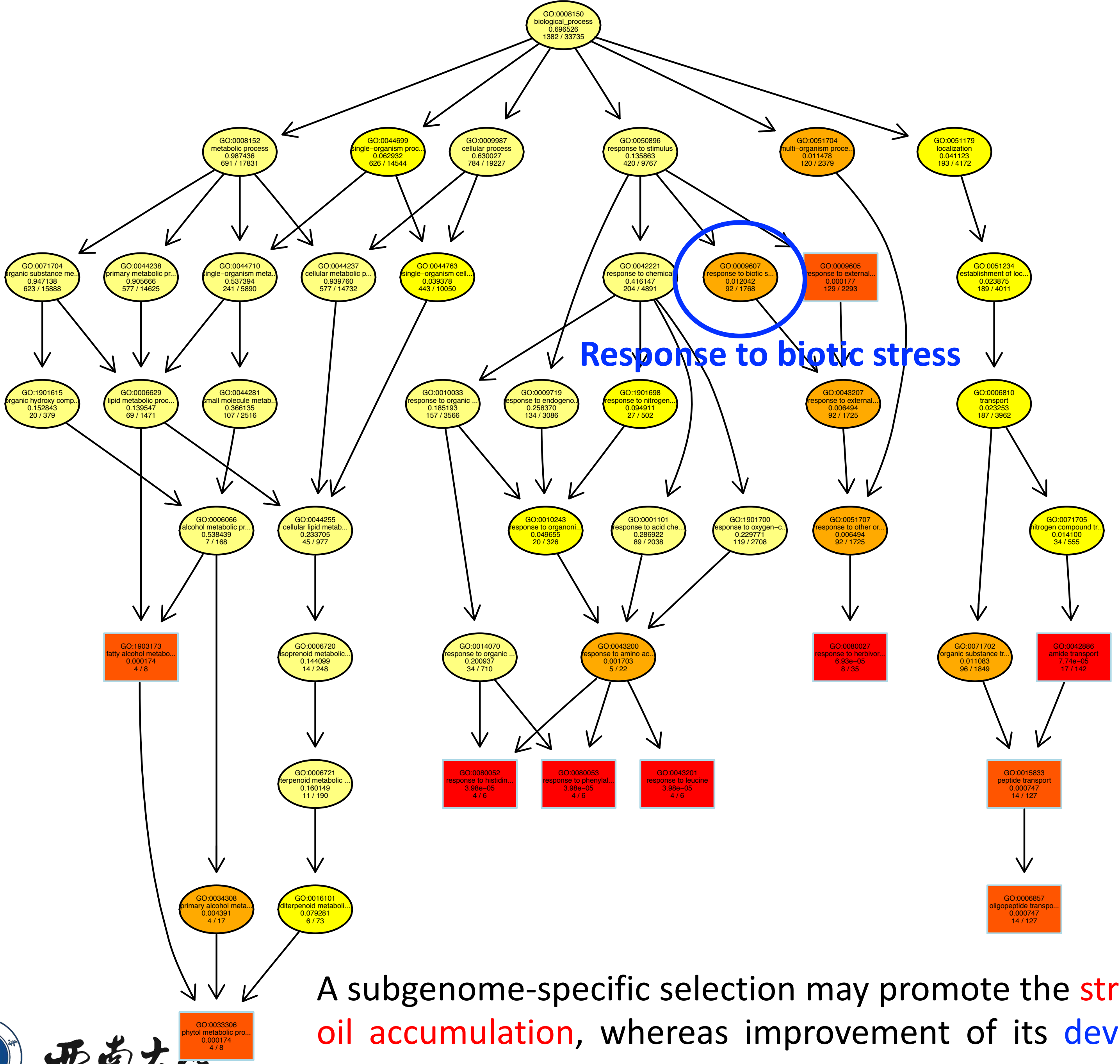
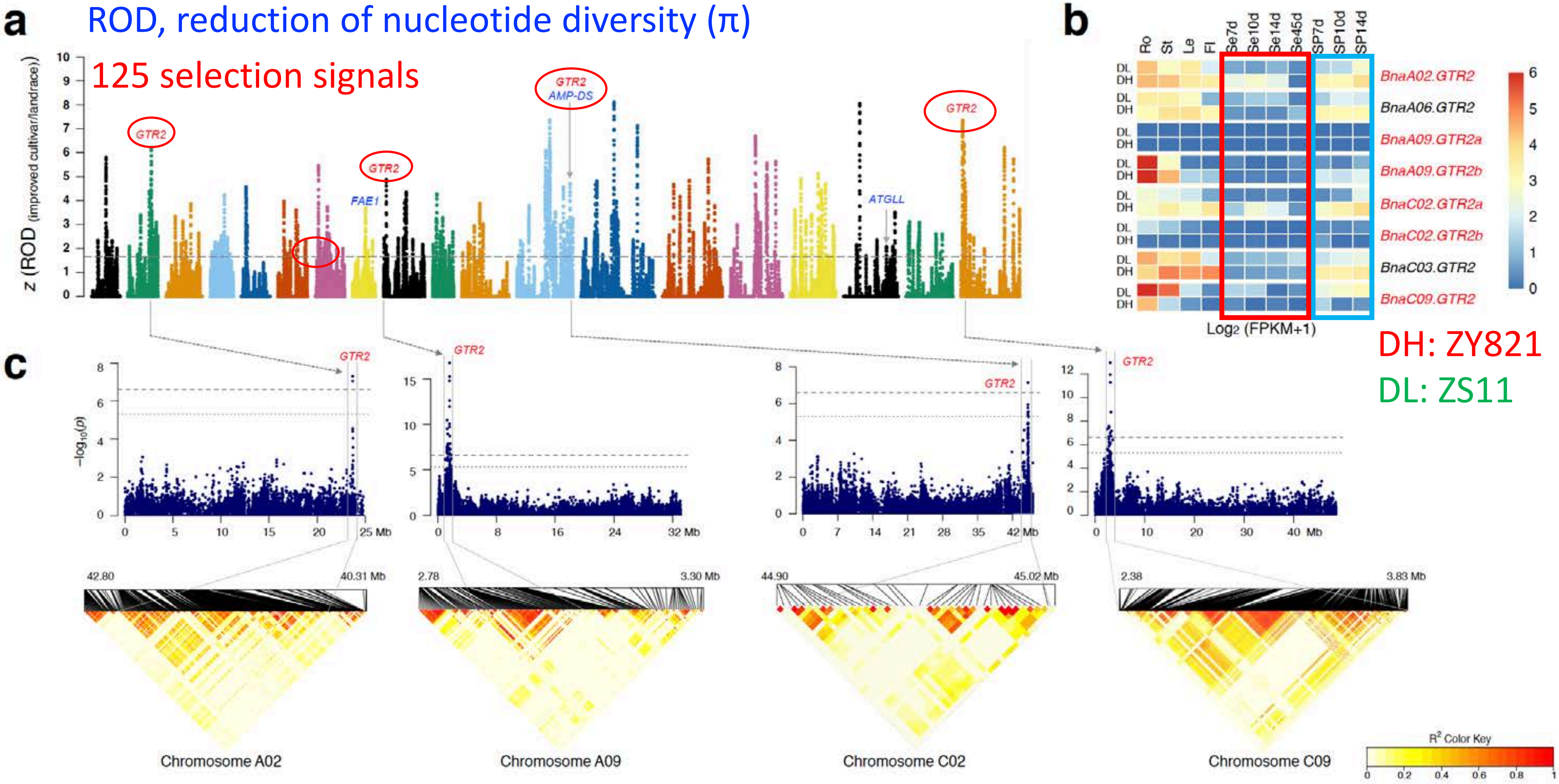


Response to biotic stress

A subgenome-specific selection may promote the stress tolerance and oil accumulation, whereas improvement of its developmental traits may have been due to asymmetrical selection in the C subgenomes.

Key genes involved in improvement of *B. napus*


ROD, reduction of nucleotide diversity (π)

125 selection signals

DH: ZY821

DL: ZS11

Three *GTR2* genes in the outlier and QTL overlapped regions are improvement targets for further elimination of seed glucosinolate.

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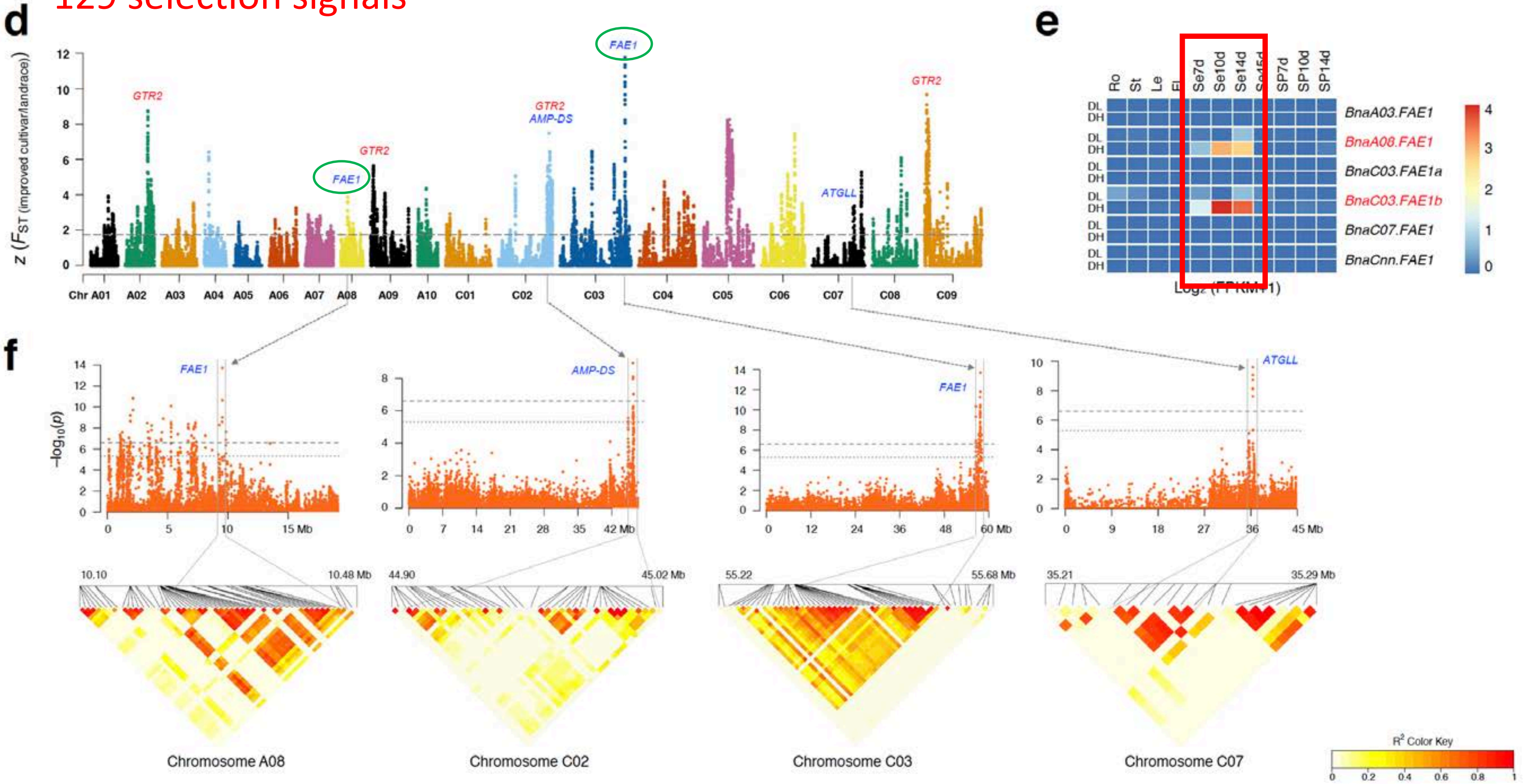
Key genes involved in improvement of *B. napus*



129 selection signals

Reduction of erucic acid content

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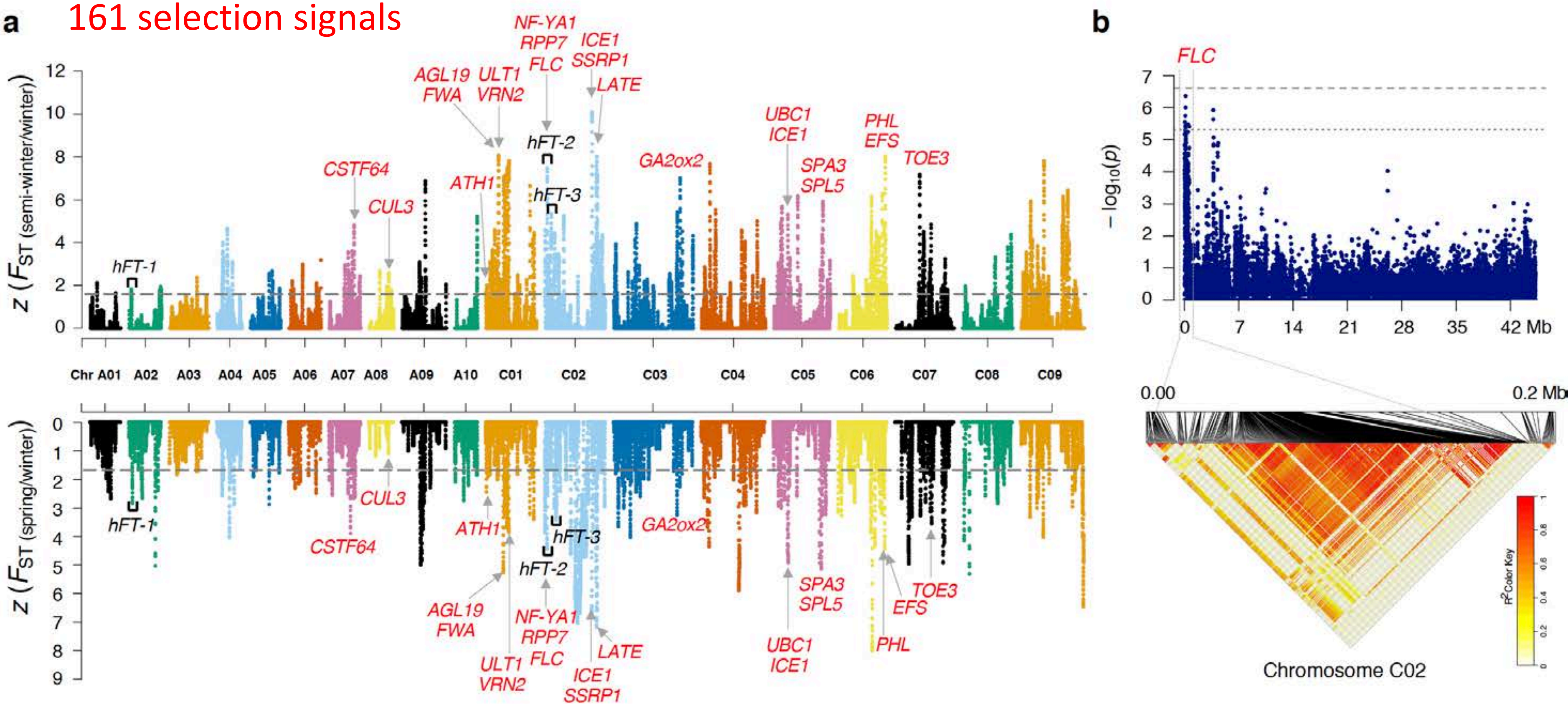
Two *FAE1* genes undergone strong selection in modern *B. napus* breeding. Parallel subgenomic selection may have contributed to improved seed quality.

Key genes involved in improvement of *B. napus*

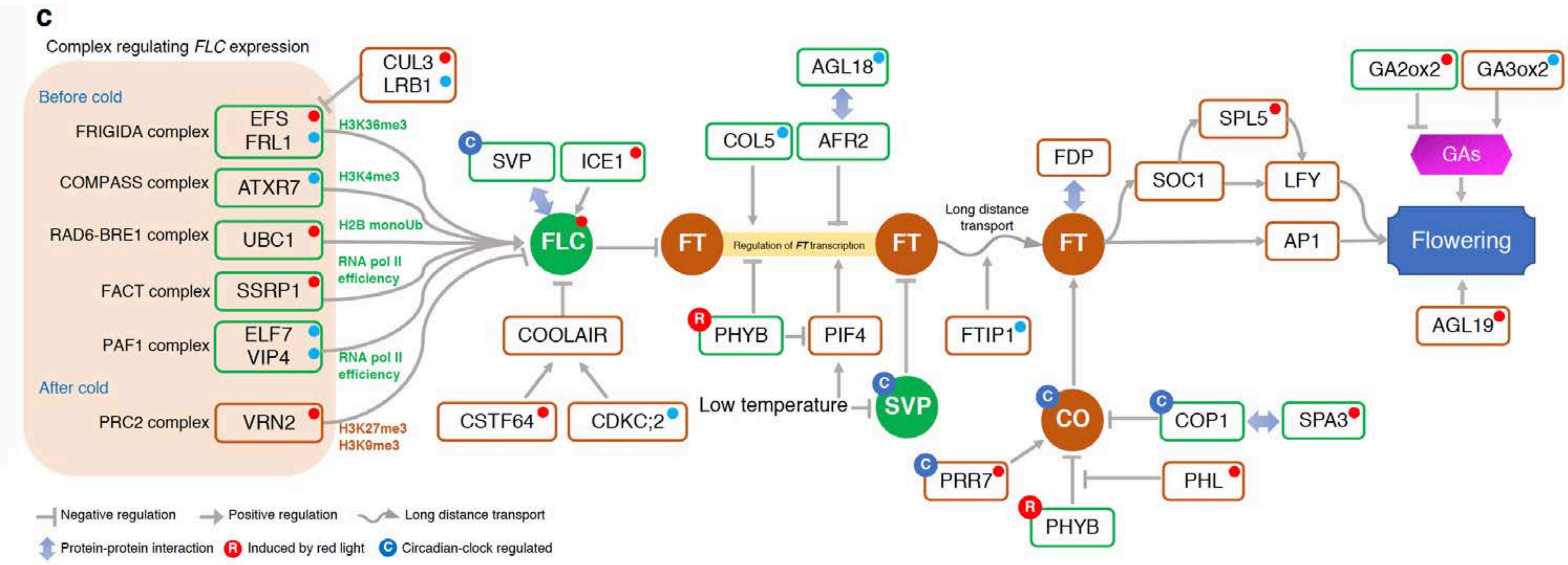
Ecotype improvement

161 selection signals



189 selection signals

Key genes involved in improvement of *B. napus*



Histone modifications involved in regulating *FLC* expression, are closely associated with flowering time in *B. napus*. These genes therefore represent promising regulatory targets in future *B. napus* breeding programs.

Summary

- Wild *B. napus* is evolved from hybridization between the ancestors of European turnip and four *B. oleracea* subspecies.
- Original wild *B. napus* is most likely winter oilseed.
- Parallel subgenomic pseudo-domestication benefited *B. napus* for adaptation to environmental variation. Parallel subgenomic improvement increase the seed quality.
- Asymmetrical selection involved in chromatin modification is associated with ecotype improvement.

Acknowledgements

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BIOMARKER TECHNOLOGIES

Dr. Xiaolong Li

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