Genomics-assisted mapping in Cicer-Ascochyta pathosystem to unravel the quantitative resistance genes

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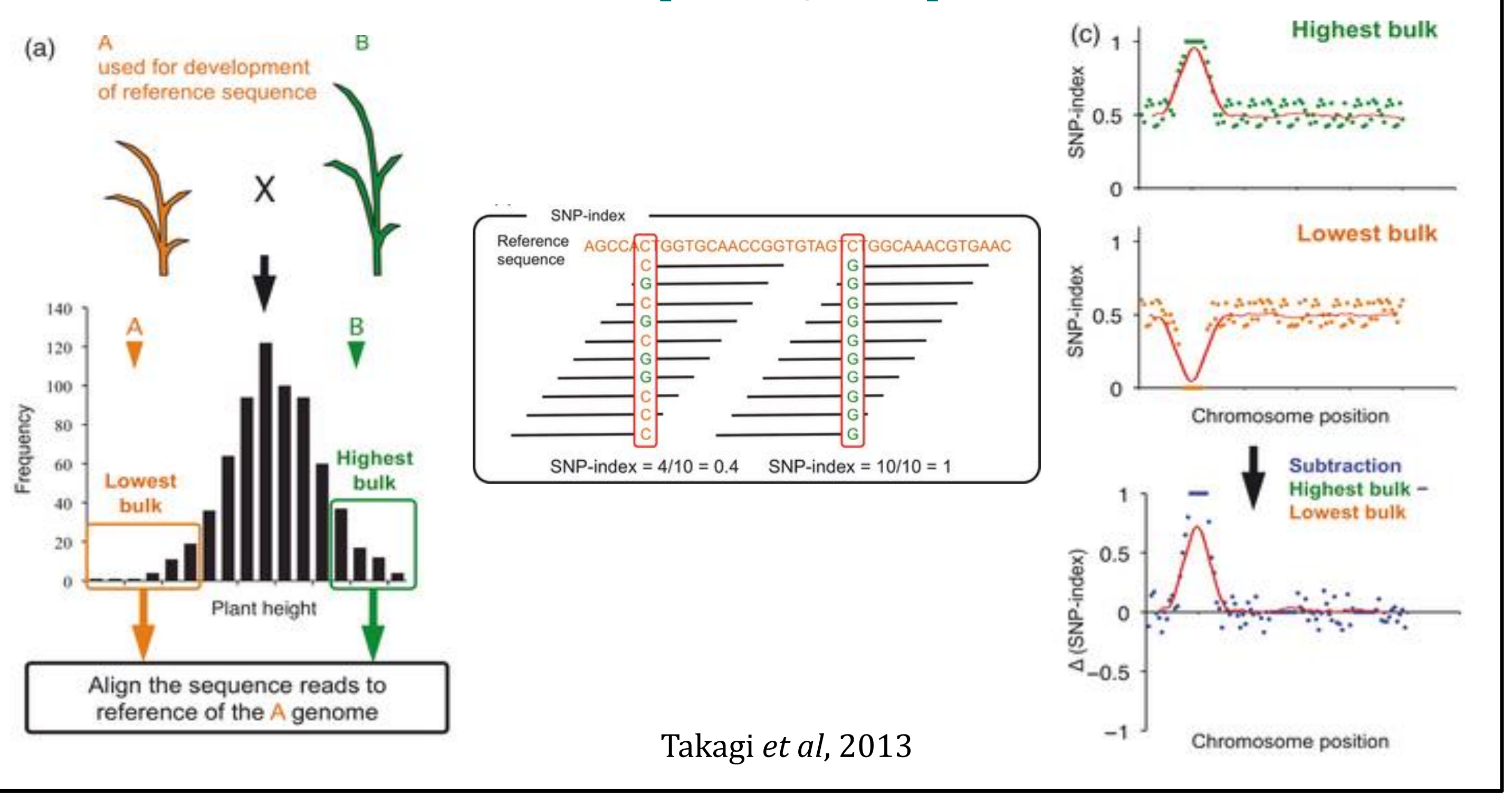
INTRODUCTION

- Chickpea (*Cicer arietinum*), a legume crop that is valued for its rich protein content, is affected by many diseases of which Ascochyta blight (AB) caused by the fungus *Ascochyta rabiei is a* major one.
- Genetic studies suggest that resistance to AB is quantitative in nature.
- Here we present a genome-wide robust approach to map the QTLs responsible for *Ascochyta* resistance by using mQTL-seq, a technique that combines Bulk - Segregant Analysis with Next Generation Sequencing.
- Three QTLs have been identified in AB resistance, two of which are major and the third one is novel minor QTL.
- To translate the obtained genetic information and polymorphic markers from our AB resistance study, we intend to introgress multiple fungal resistance loci (for AB and Fusarium Wilt resistant) in few mega varieties of chickpea.

Principle of QTLseq

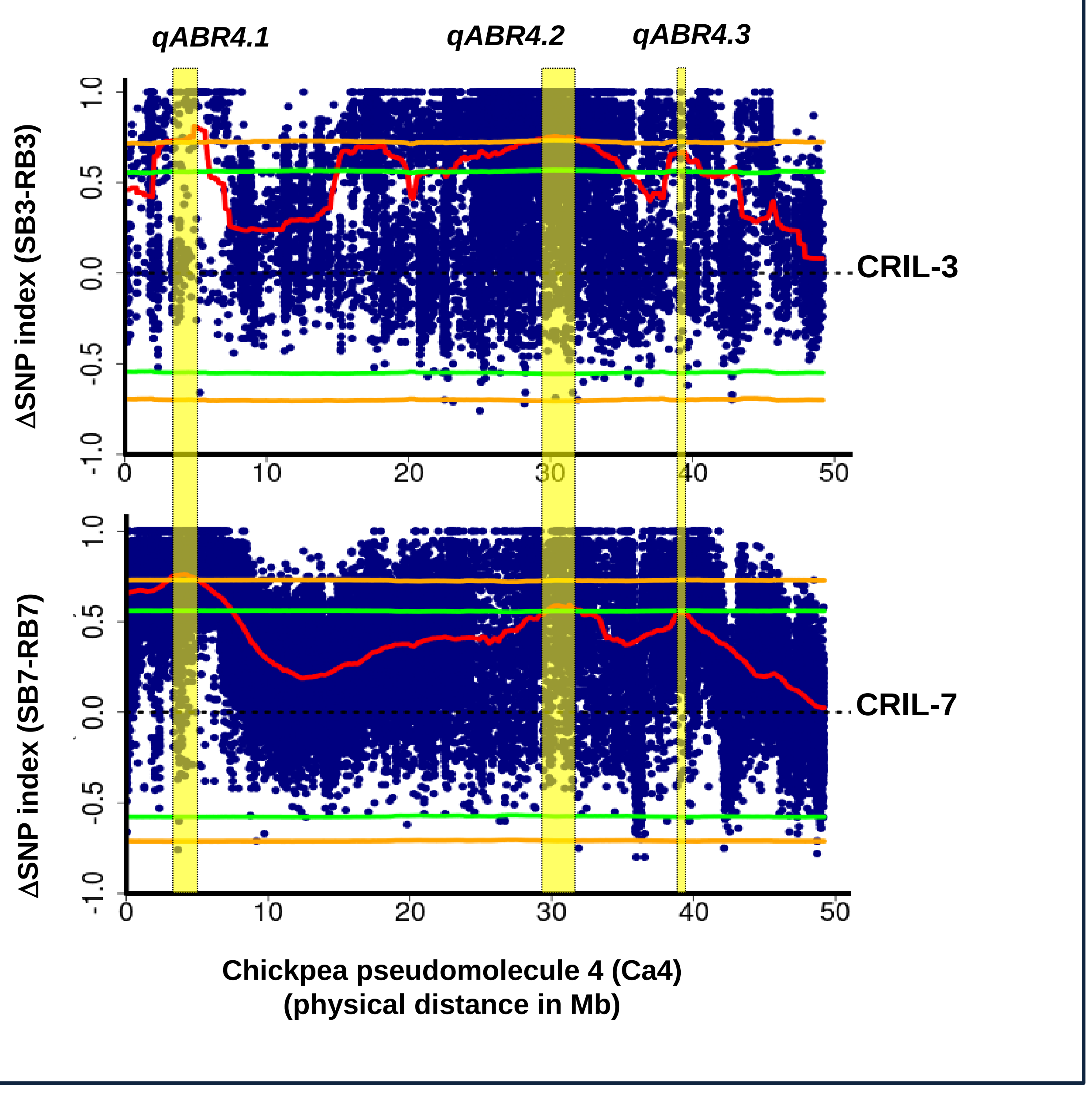


Takagi *et al*, 2013

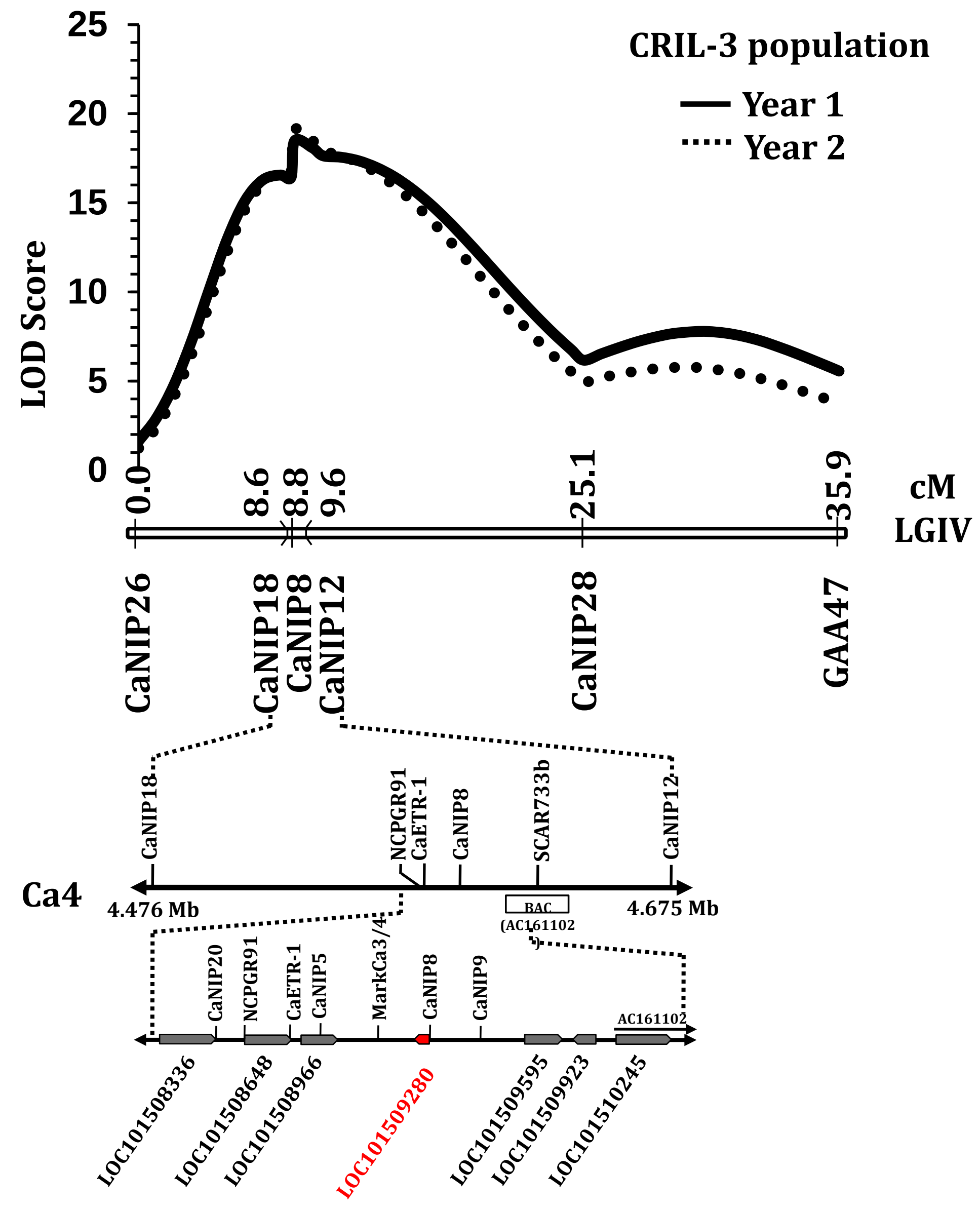
POPULATIONS USED FOR QTL MAPPING

Intra-specific cross	Inter-specific cross
FLIP 84-92C x PI 359075	FLIP 84-92C x PI599072
(*C. arietinum*) (*C. arietinum*)	(*C. arietinum*) (*C. reticulatum*)
R S	R S
250 RILs	217 RILs

AB RESISTANCE ASSOCIATED GENOMIC REGIONS OF CHICKPEA



FINE MAPPING OF *qABR4.1* REGION IN CRIL -3 POPULATION



POLYMORPHISM IN CaAHL18 PROMOTER

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FLIP84-92C AATTATAACTAACTTTCACACACTTATATATATATA------TCTAGGTTTTTGAGATTTCTTT
PI359075   AATTATAACTAACTTTCACACACTTATATATATATATATATATATCTAGG------------TTT
           ***********************************      ******            ***
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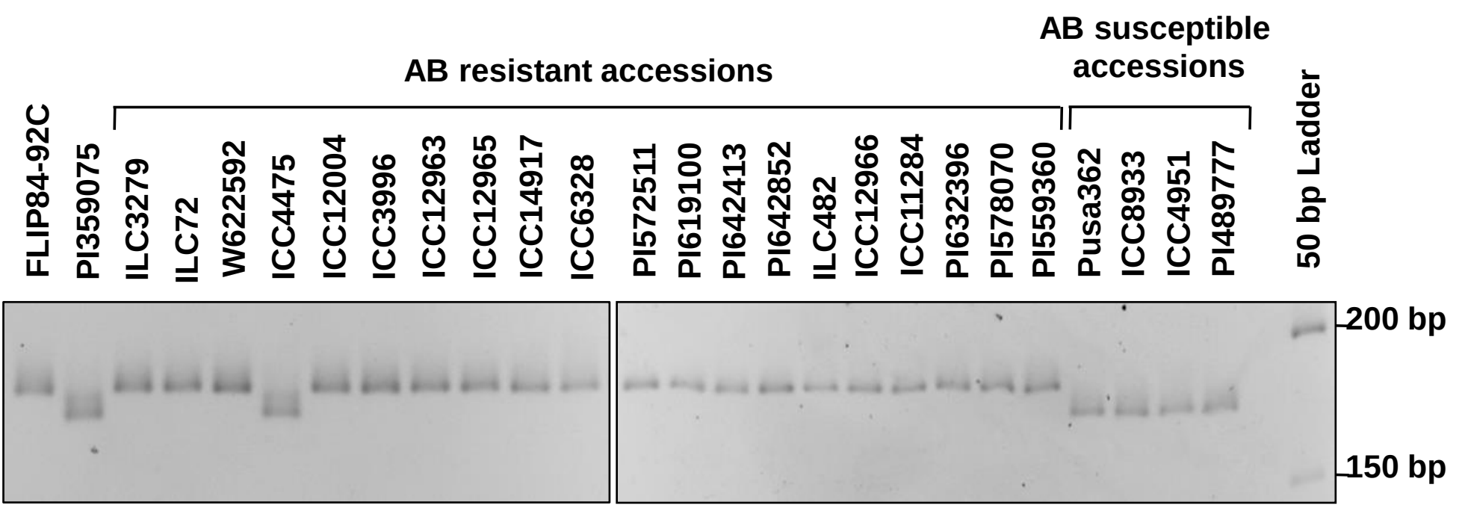
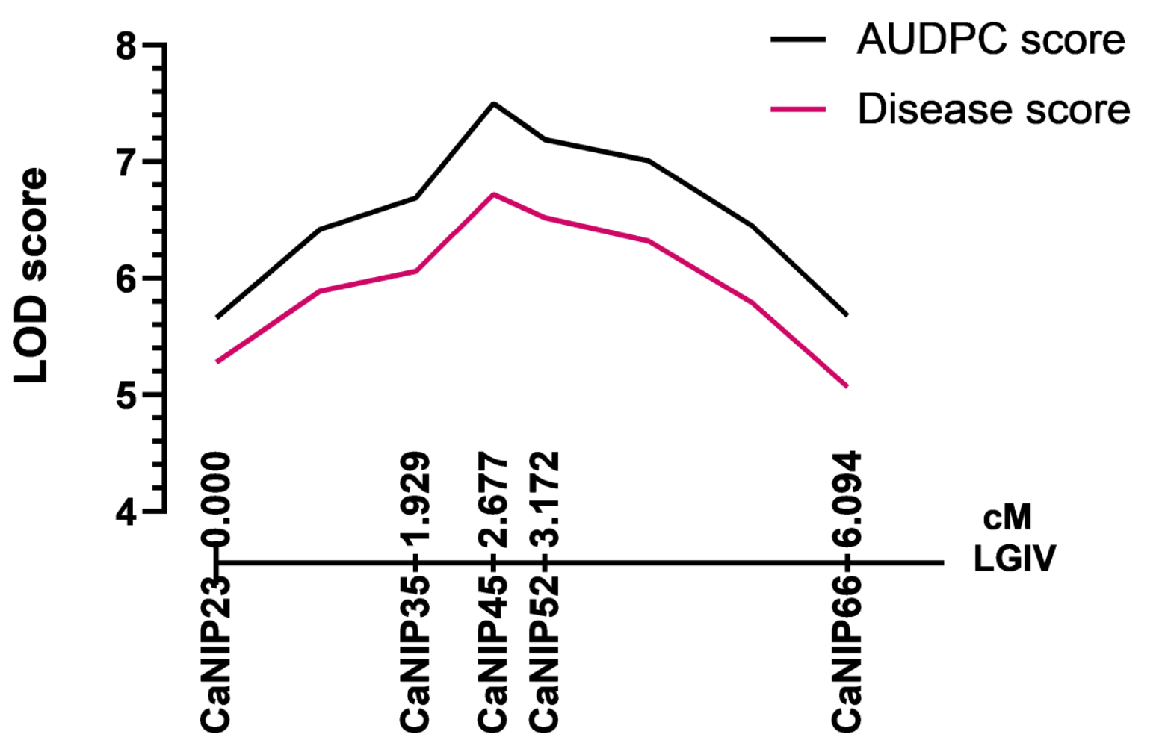
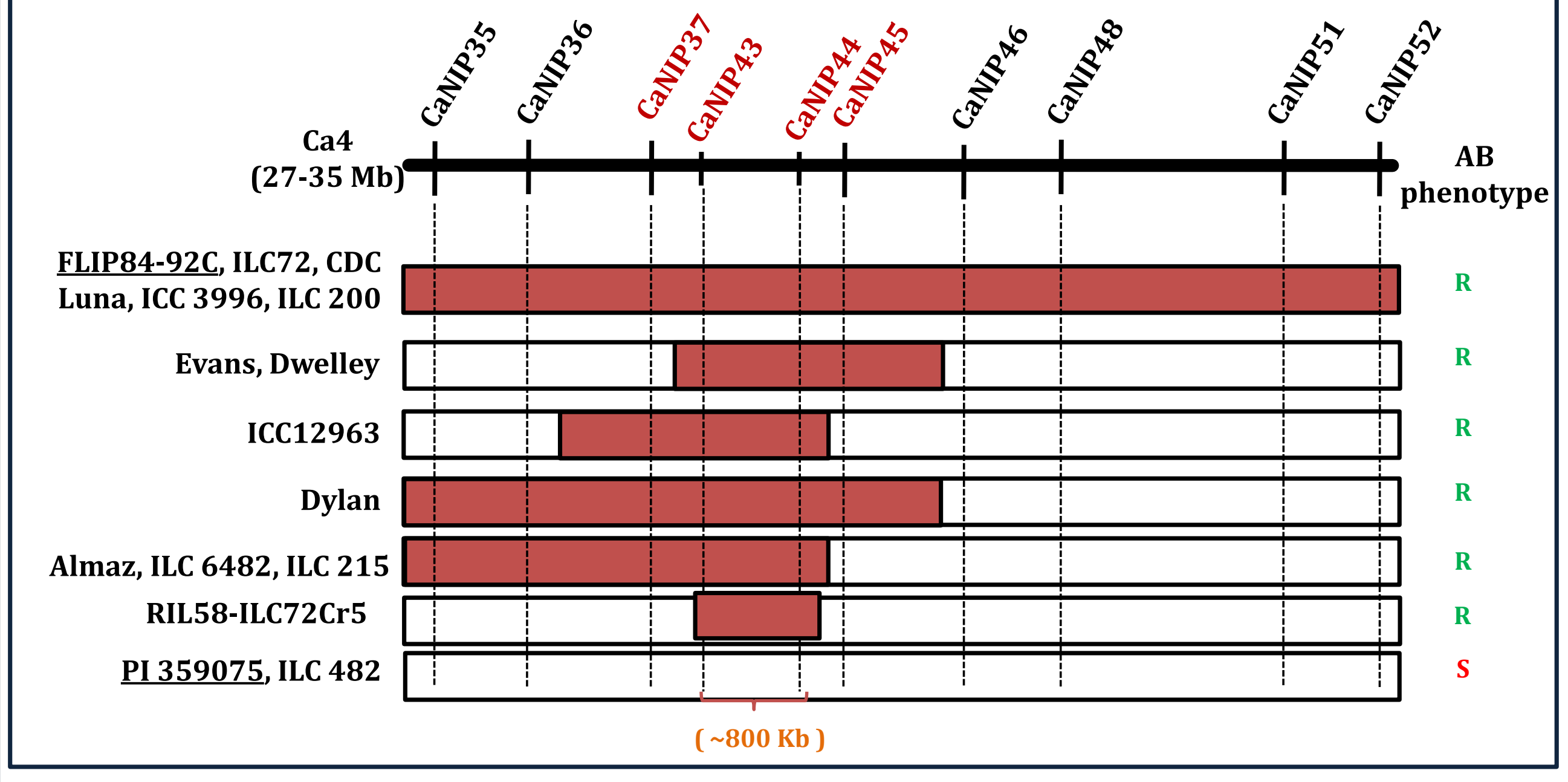


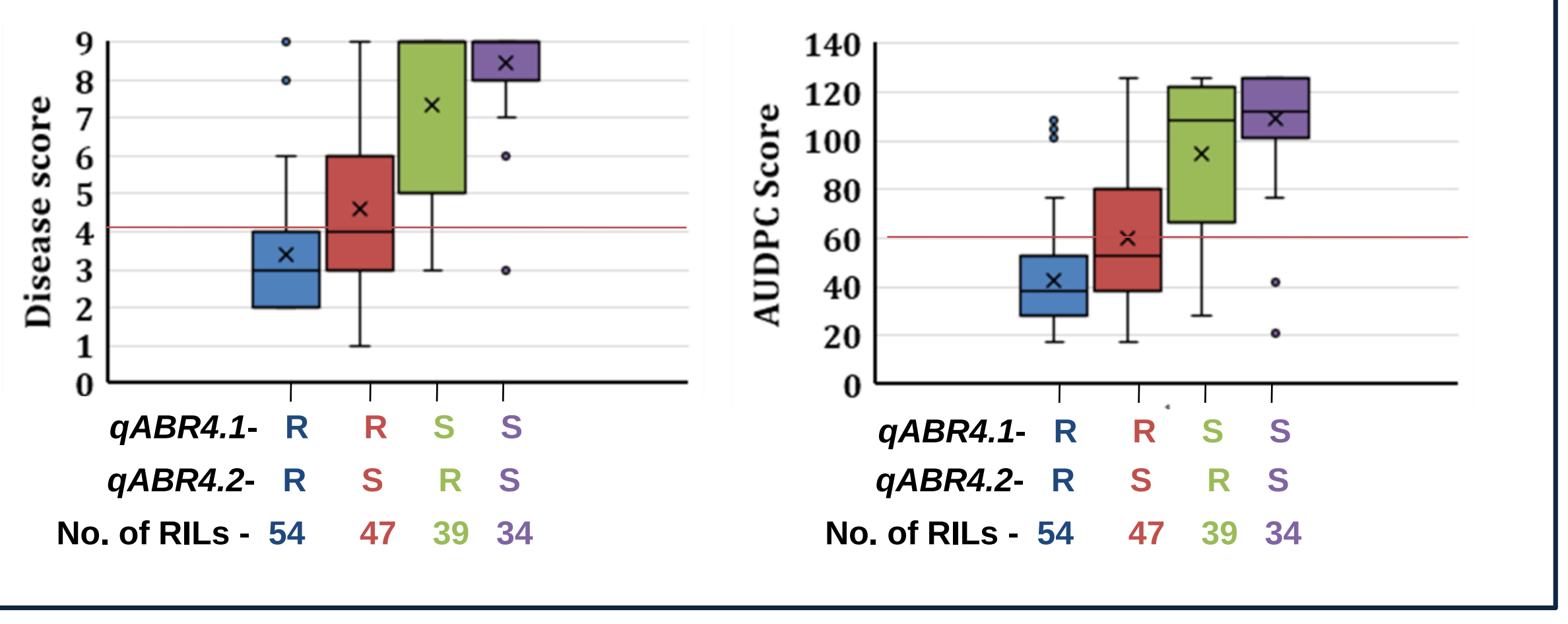
FINE MAPPING OF *qABR4.2* REGION



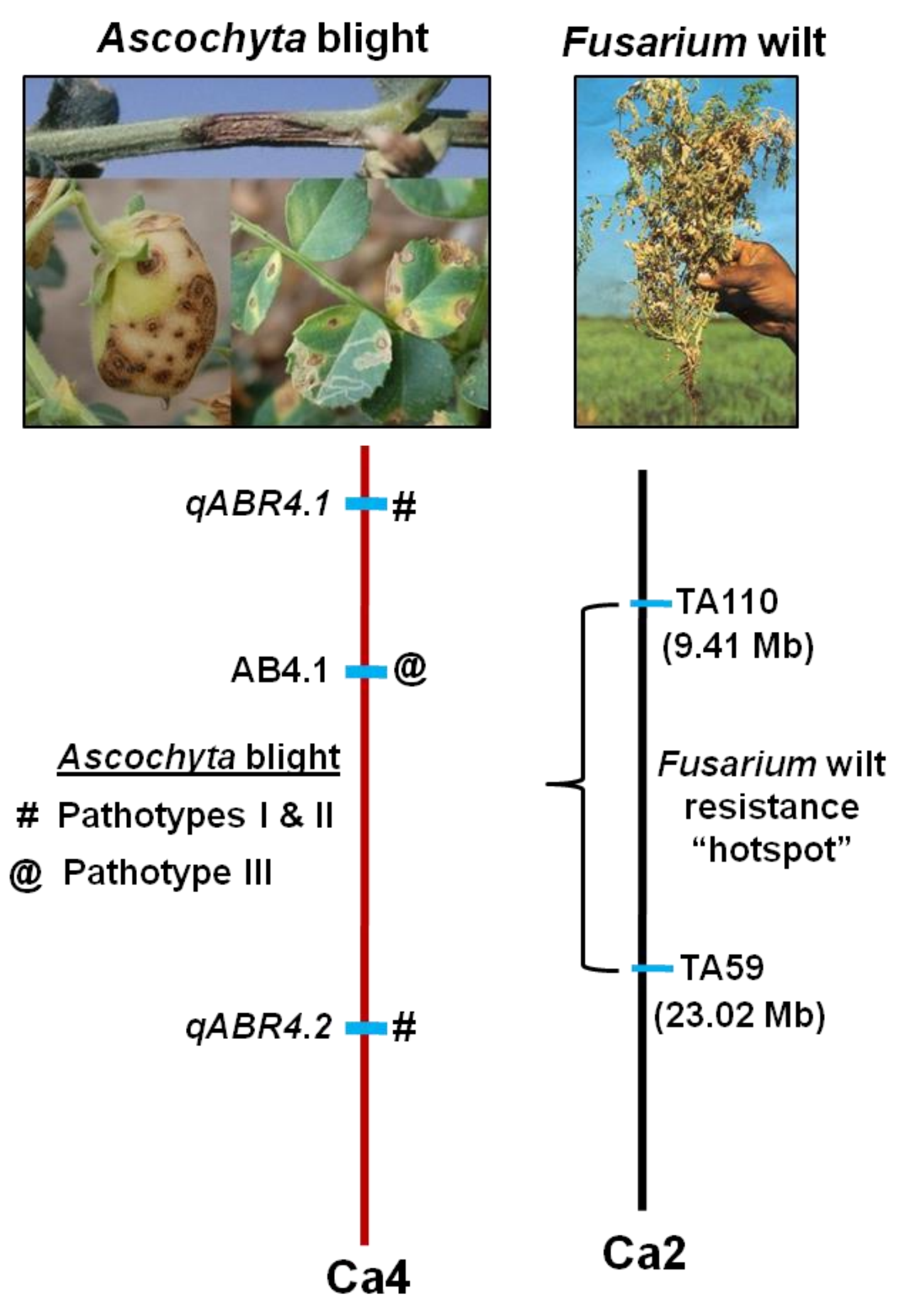


COMBINATORIAL EFFECT OF QTLs ON ASCOCHYTA BLIGHT PHENOTYPE

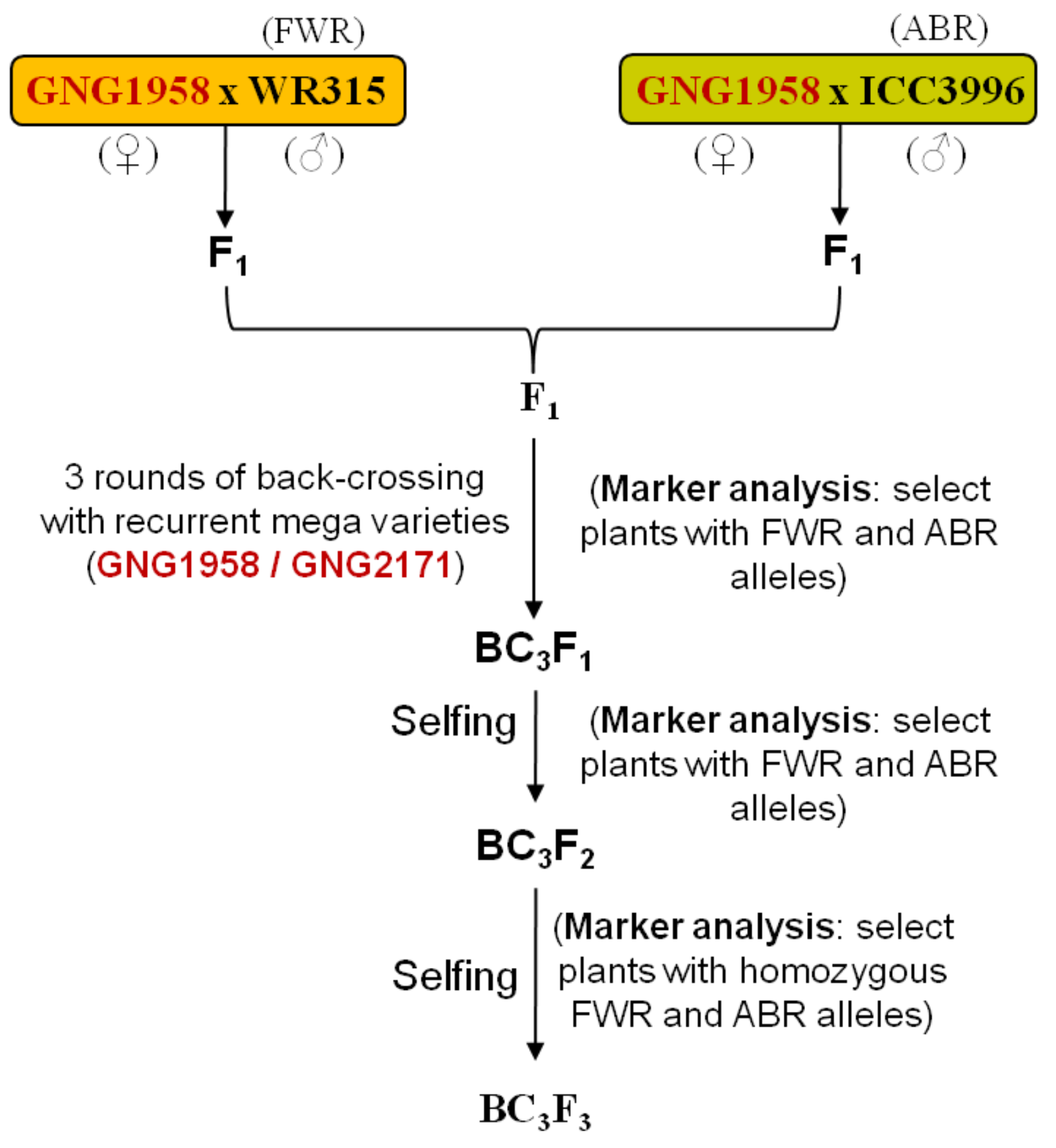
qABR4.1: CaNIP8 marker
qABR4.2 : CaNIP37 marker



MARKER - ASSISTED BREEDING FOR ASCOCHYTA BLIGHT AND FUSARIUM WILT RESISTANCE IN CHICKPEA VARITIES



Ascochyta blight
\# Pathotypes I & II
@ Pathotype III


(FWR) GNG1958 x WR315 (♀) (♂) → F_1

(ABR) GNG1958 x ICC3996 (♀) (♂) → F_1

F_1

3 rounds of back-crossing with recurrent mega varieties (GNG1958 / GNG2171) (**Marker analysis**: select plants with FWR and ABR alleles)

BC_3F_1

Selfing (**Marker analysis**: select plants with FWR and ABR alleles)

BC_3F_2

Selfing (**Marker analysis**: select plants with homozygous FWR and ABR alleles)

BC_3F_3

Chickpea mega varieties resistant to Fusarium wilt and Ascochyta blight fungal diseases.

RESULTS

- Multiple QTL-seq analysis using two populations that share one parent revealed that three QTLs responsible for AB resistance were present on chromosome IV of chickpea.
- A differentially expressed candidate gene *CaAHL18* was identified under *qABR4.1* region and co-dominant CaNIP8 marker was developed.
- So far, *qABR4.2* region was narrowed down to ~800 kb and CaNIP37 marker was developed for further breeding purpose.
- Combinatorial effect of *qABR4.1* and *qABR4.2* shows resistance against Ascohyta blight.

WAY FORWARD

- Association mapping in different resistant and susceptible accessions to discern the gene(s) under these two QTLs.
- Breeding for AB and FW resistance in Indian chickpea varieties.

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