Genetics Of Barley Grain Morphometric Traits:

Integration Of The Natural And Induced Variation

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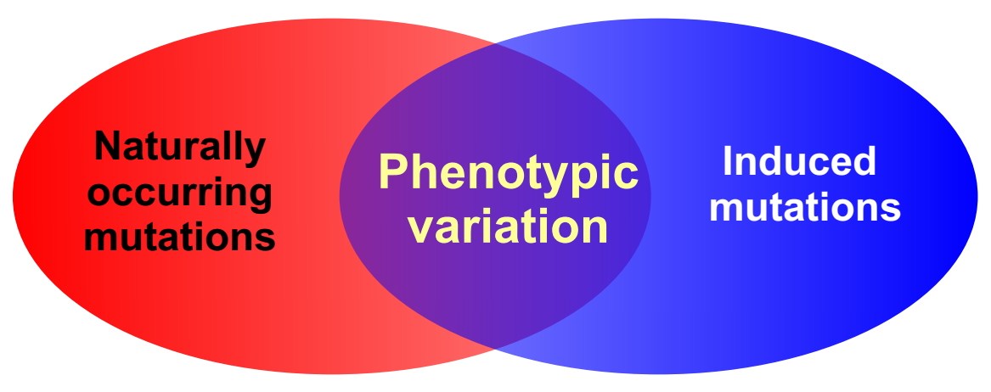
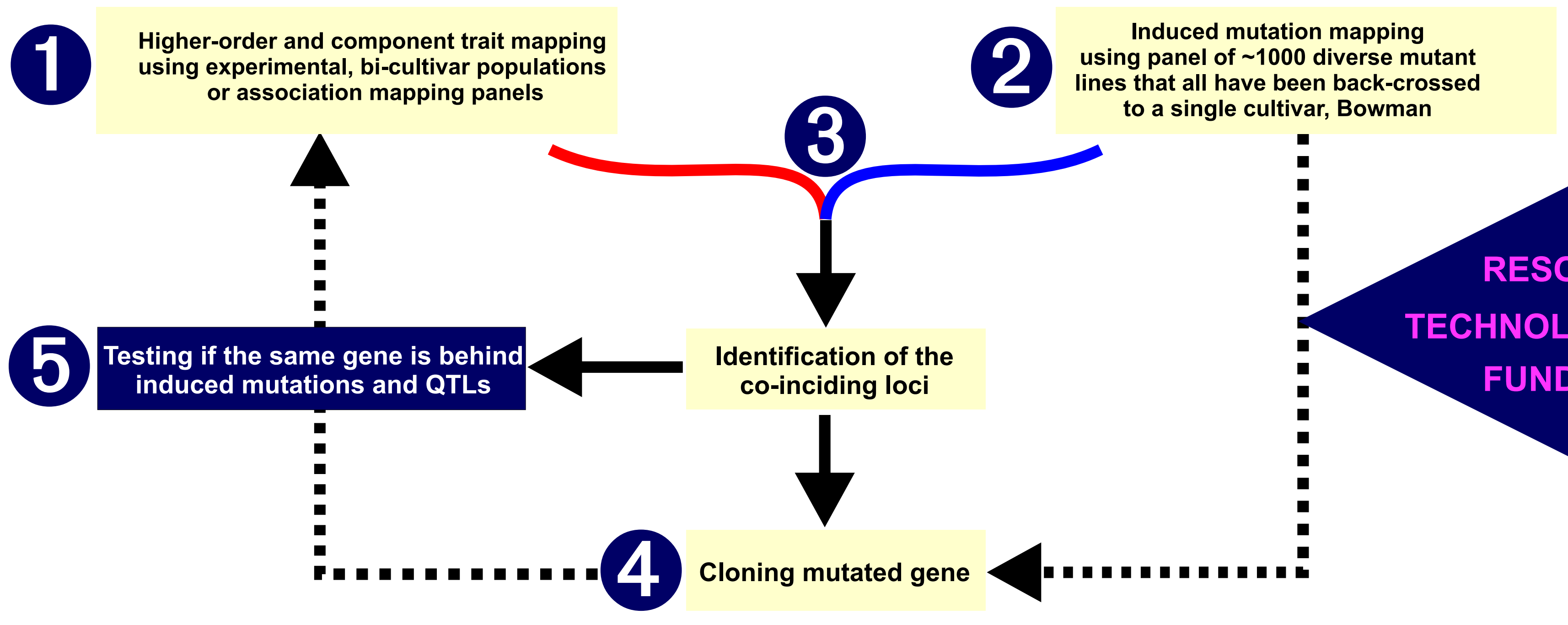
THE QUESTION

How many common genes?



EXPERIMENTAL SYSTEM



① Higher-order and component trait mapping using experimental, bi-cultivar populations or association mapping panels

② Induced mutation mapping using panel of ~1000 diverse mutant lines that all have been back-crossed to a single cultivar, Bowman

③ Identification of the co-inciding loci

④ Cloning mutated gene

⑤ Testing if the same gene is behind induced mutations and QTLs

RESOURCES

TECHNOLOGY

FUNDING

Induced mutant lines:
989 lines back-crossed to a single cv Bowman
Bi-parental cultivar based populations:
* Steptoe x Morex
* Golden Promise x Morex
* Barke x Morex
* Derkado x B83
Collection of diverse barley germplasm:
~3000 accessions

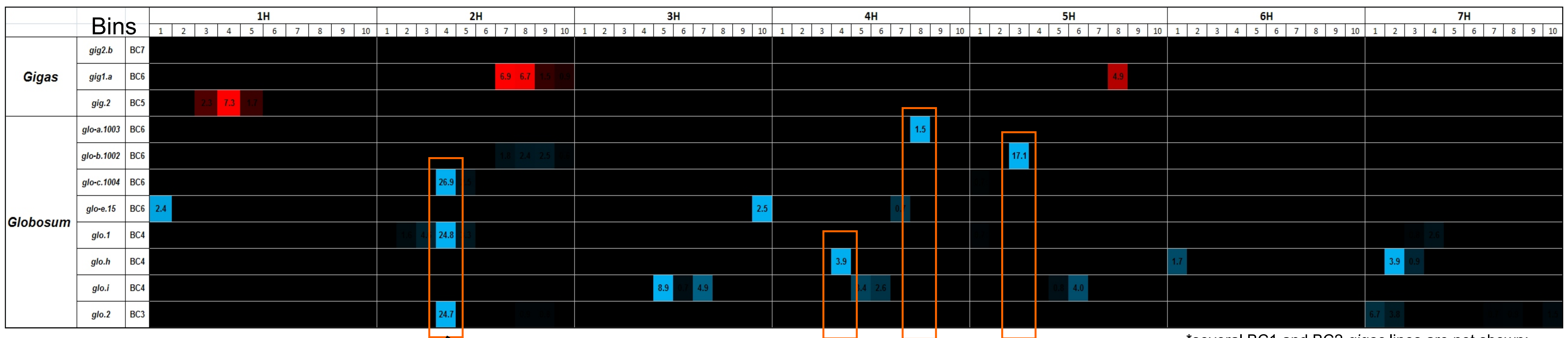
Gene- and SNP-based genotyping platform:
The Illumina **GoldenGate** Genotyping Assay based on the Illumina's **BeadArray** Technology. **Assays** 1,536 **loci per genotype.**

Genomics assisted dissection of barley morphology and development (BARCODE).
ERA-PG project, EU
Optimising wheat grain shape for improved processing quality.
Crop Science Initiative project. BBSRC, UK
Association Genetics of UK Elite Barley (AGOUEB).
LINK project. BBSRC, UK

TARGETS AND RESULTS

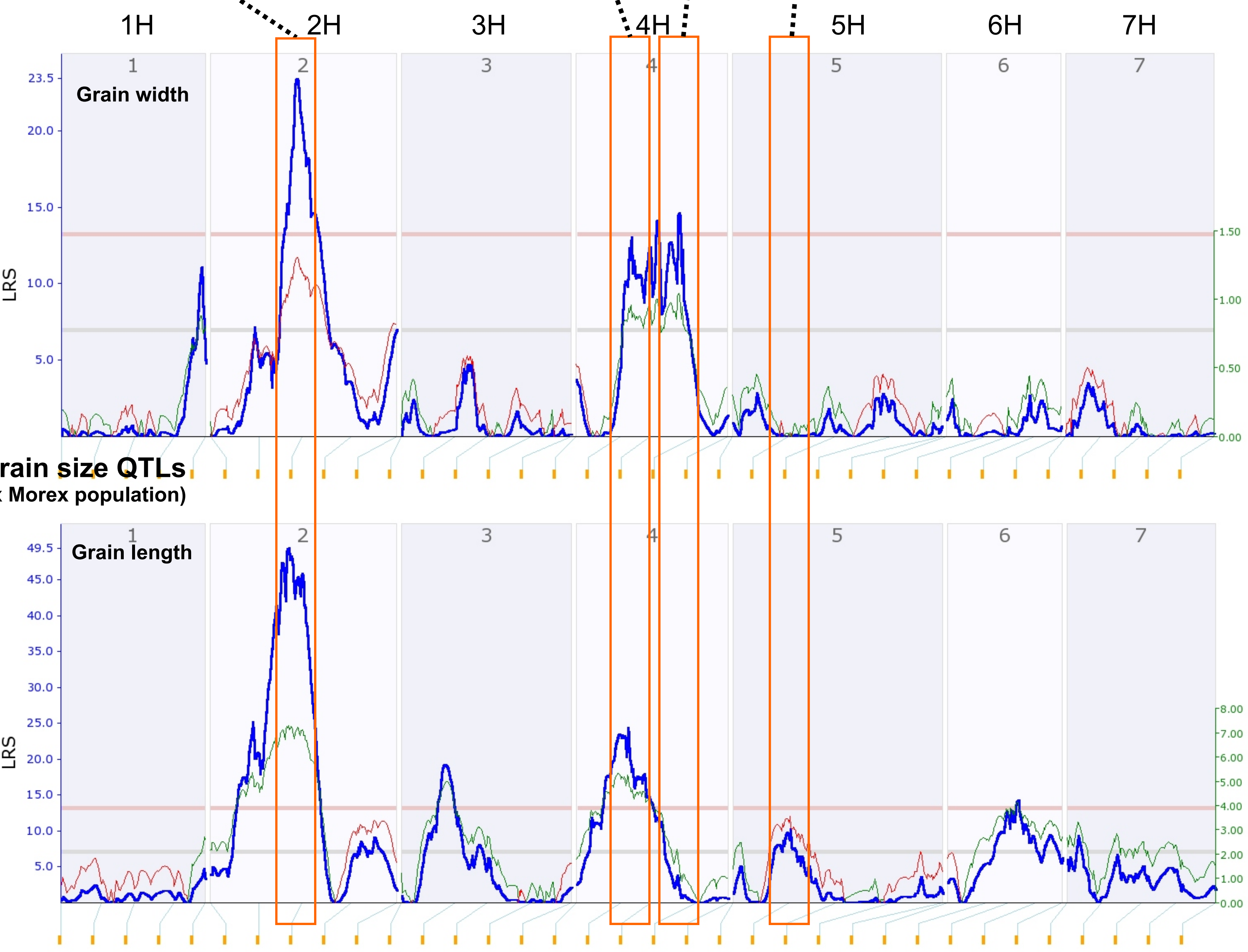
① ② ③

Mapping results of the barley *gigas* and *globosum* mutations*



*several BC1 and BC2 *gigas* lines are not shown; they have multiple introgressions across the genome.

Our primary interest is yield component traits. Grain size is one of such traits. There are about 14 Bowman lines that have been selected specifically based on grain size. Genotypes of 11 *gigas* and *globosum* mutants and their alignment with grain size QTLs are shown here.



Grain size QTLs
(Steptoe x Morex population)

Alignment of the Bowman line genotypes and grain size QTLs identified three major coinciding loci, all involving *globosum* genes.

We selected one of the *globosum* genes for map-based cloning.

WHAT'S SHOWN?

Genotyping:

- ~1,200 POPA markers have known map positions
- they were grouped in 10-15 cM bins
- colours show different than Bowman alleles (red - *gigas*, blue - *globosum*).
- colour intensity reflects number of detected non-Bowman alleles per bin as well as genotyping quality (calculated based on marker scores from the BeadStudio software).

* *gig.2b* has no polymorphic markers, but its location can be inferred from the different line carrying the same mutated gene (*gig2*).

QTL mapping:

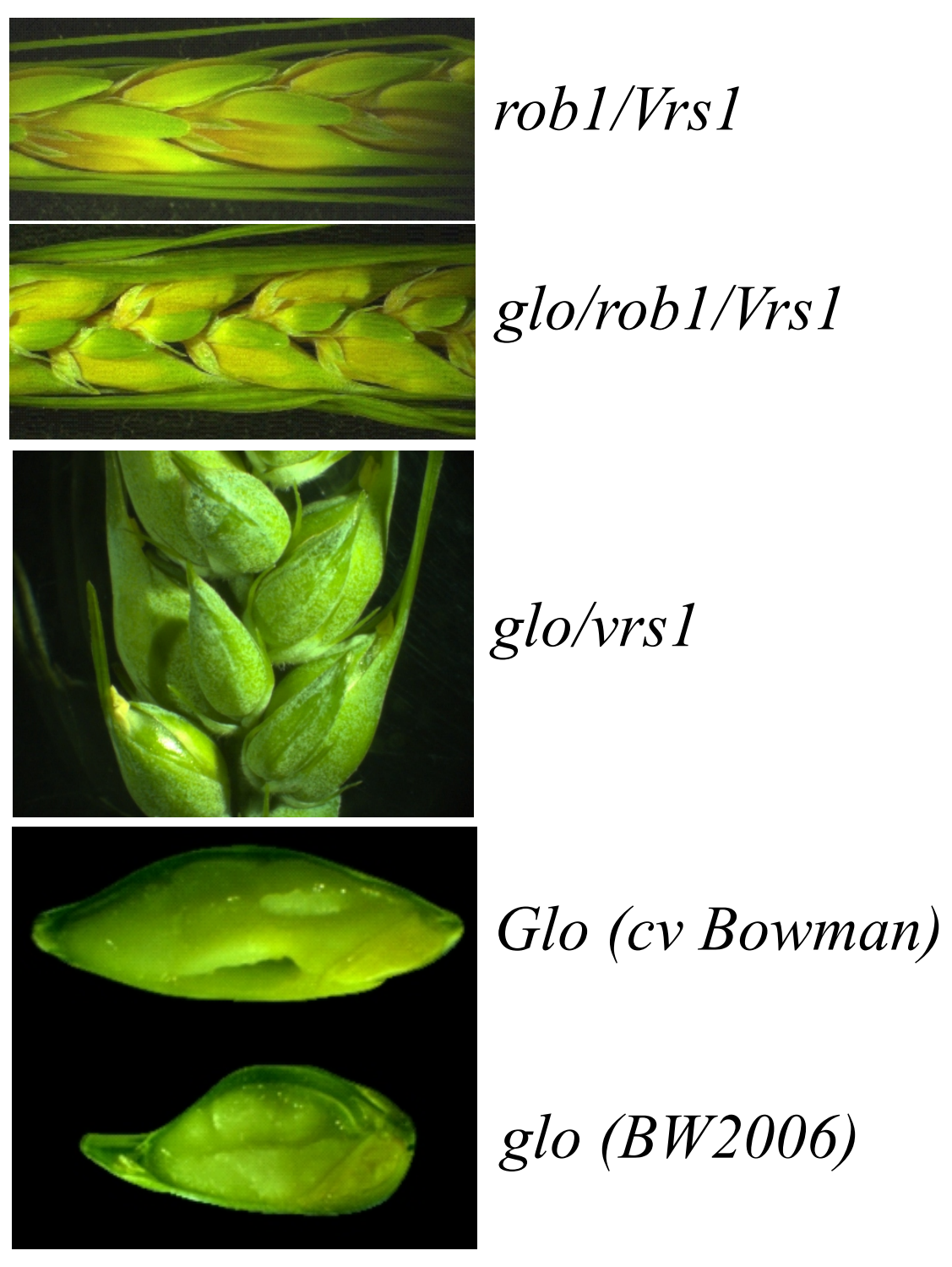
- grain morphometric parameters of the 150 Steptoe x Morex DH lines were obtained by using image capture and analysis system Marvin.
- Interval mapping of grain length and width traits using SNP-based Steptoe x Morex map, that was constructed based on GoldenGate genotyping:

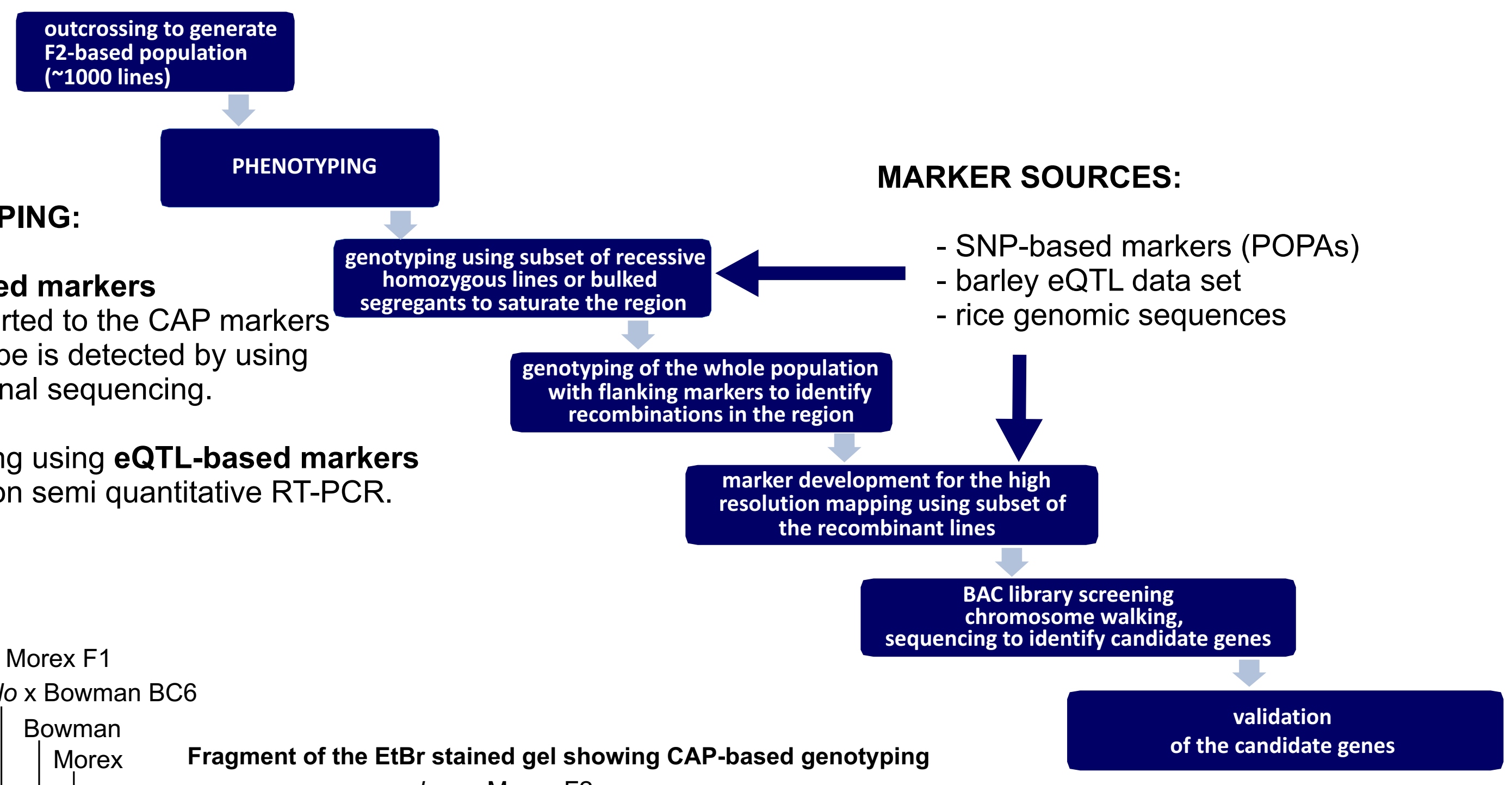
Blue line - Likehood Ratio Statistic (LRS) profile.
Red and green lines show allelic effects.
Horizontal lines (red and grey) - upper and lower significance thresholds calculated based on 1000 permutations.

MAP-BASED CLONING OF THE GLOBOSUM GENE: PHENOTYPE, METHODOLOGY AND THE CURRENT STATUS

④

Bowman and *glo* inflorescences
~1 week before anthesis





outcrossing to generate F2-based population (~1000 lines)

PHENOTYPING

genotyping using subset of recessive homozygous lines or bulked segregants to saturate the region

genotyping of the whole population with flanking markers to identify recombinations in the region

marker development for the high resolution mapping using subset of the recombinant lines

BAC library screening chromosome walking, sequencing to identify candidate genes

validation of the candidate genes

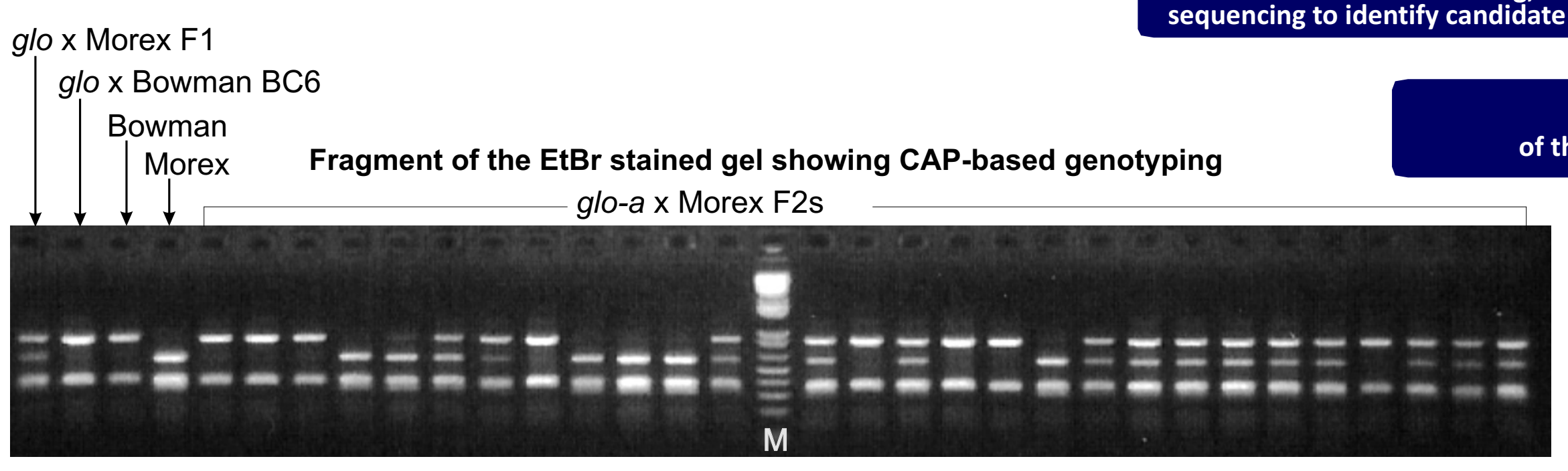
GENOTYPING:

SNP-based markers
are converted to the CAP markers or genotype is detected by using conventional sequencing.

Genotyping using **eQTL-based markers** is based on semi quantitative RT-PCR.

MARKER SOURCES:

- SNP-based markers (POPAs)
- barley eQTL data set
- rice genomic sequences



Fragment of the EtBr stained gel showing CAP-based genotyping