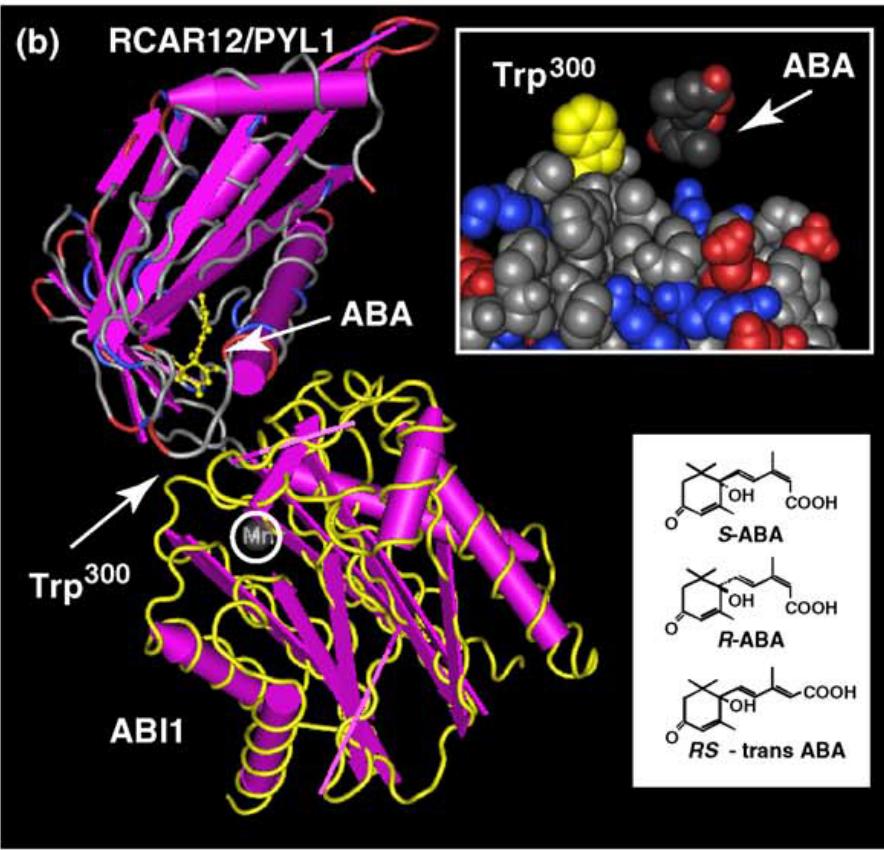


Recent Progress and Future Prospects of the *Arabidopsis* 1001 Genomes Project



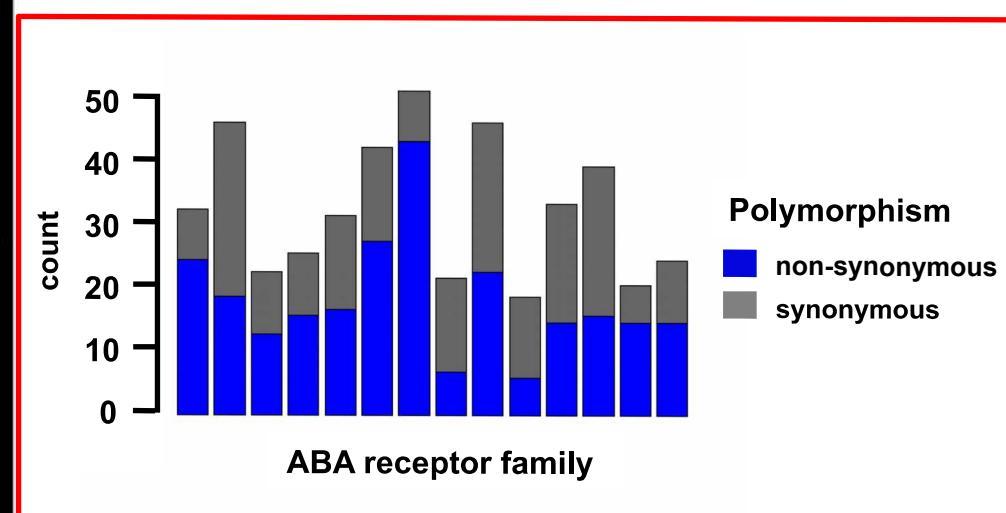
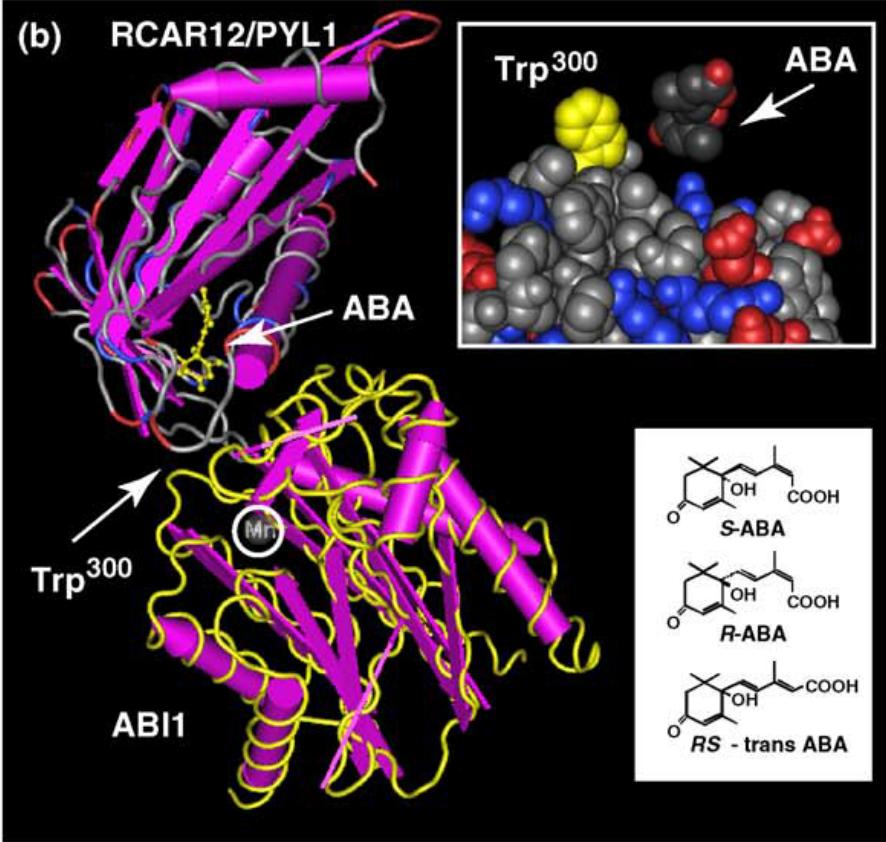
PhD in Molecular Biology



Raghavendra *et al.* 2010, TiPS

Differences in the ABA receptor complex in different natural accessions

PhD in Molecular Biology



Raghavendra et al. 2010, TiPS

Differences in the ABA receptor complex in different natural accessions

Population Genomics

Quantitative Genetics

The 1001 Genomes Project



1001 Genomes

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1001 Genomes

A Catalog of *Arabidopsis thaliana* Genetic Variation.



Tools

Explore the variants. We maintain several tools for data download, visualization, and analysis.

[Go](#)

Download

Visit the Data Center and download whole sets of SNPs, indels, SVs, and genome sequences.

[Go](#)

Get Seeds

Seed sets of natural accessions are available for

Complete set

80 strains (D. Weigel lab, MPI)
195 strains (J. Ecker lab, Salk)
180 strains (M. Nordborg Lab, GMI)

www.1001genomes.org

1001 Genomes Tools

1001 Genomes Tools

Tools for data download, visualization, and analysis.

AraPheno

A public database collection of *Arabidopsis thaliana* phenotypes.

Pseudogenomes

Download sequences for specific genome regions for selected accessions.

Admixture Map

View ADMIXTURE group membership.

VCF Subset

Download Subsets of 1001 VCF Files.

Polymorph 1001

Variant browser for 1135 accessions.

AraGWASCatalog

A public database catalog of *Arabidopsis thaliana* associations from published GWAS studies.

AraGeno

An easy way to identify your *Arabidopsis thaliana* plant.

Strain ID

Upload VCF variants and get closest accession included within the 1135 set.

Polymorph

Variant browser for 80 accessions.

easyGWAS

An integrated interspecies platform for performing and comparing genome-wide association studies.

GWAPP

GWAPP enables researchers working with *Arabidopsis thaliana* to do Genome Wide Association Mapping (GWAS) on their

1001 Proteomes

Non-synonymous SNPs (nsSNPs) browser.

AraGWASCatalog

AraPheno

Data Tools About FAQ

AraPheno

AraPheno is a public database collection of *Arabidopsis thaliana* phenotypes. This Database allows to search and filter for public phenotypes and to obtain additional meta-information.

Search a phenotype, study, trait ontology (e.g. type FRI for phenotype, Atwell for study, or concentration for ontology) or accession r...

Phenotypes

Standardized GWAS pipeline

AraGWASCatalog

Search the catalog

Public GWAS Studies

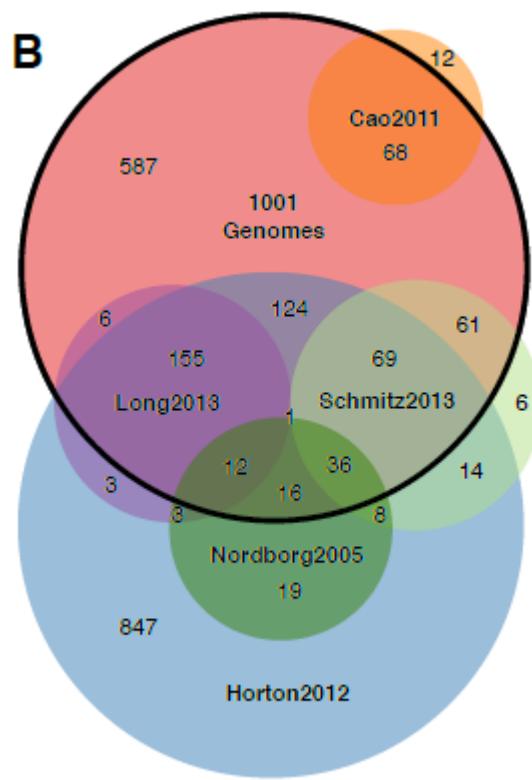
Top Associations

GWAS STUDIES

TOP ASSOCIATIONS

Comparability of the results

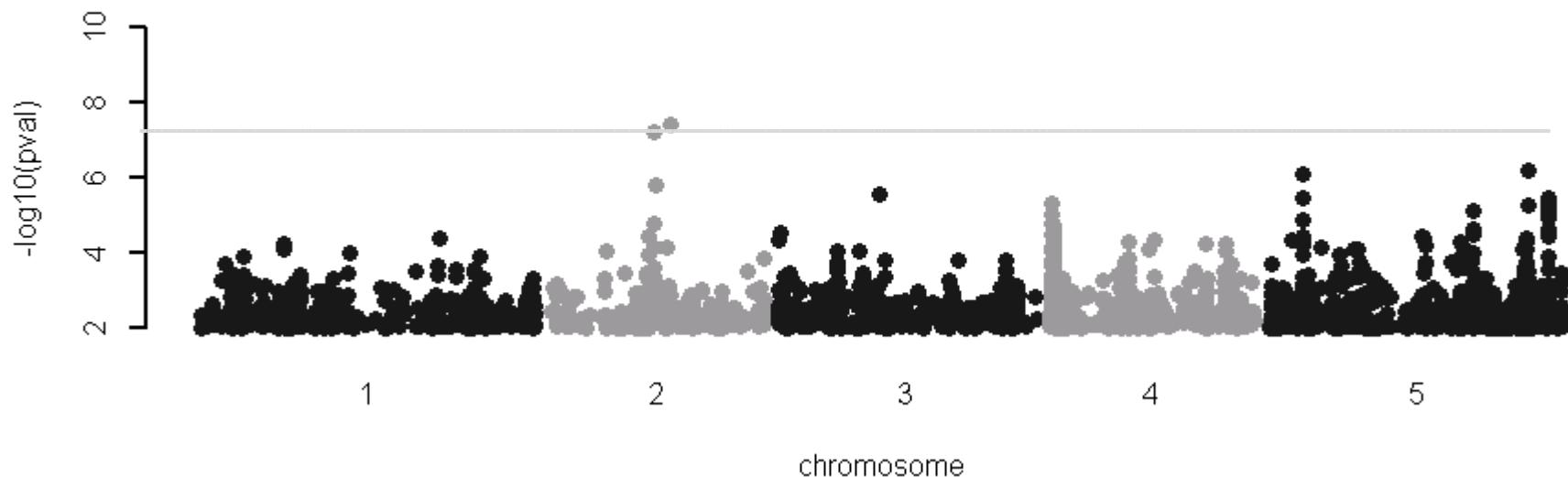
Imputed dataset for GWAS



Full genome data for 1,135 accessions
(10M SNPs)
+
250k SNPs for 1,300 accessions (Horton
et al. 2012)

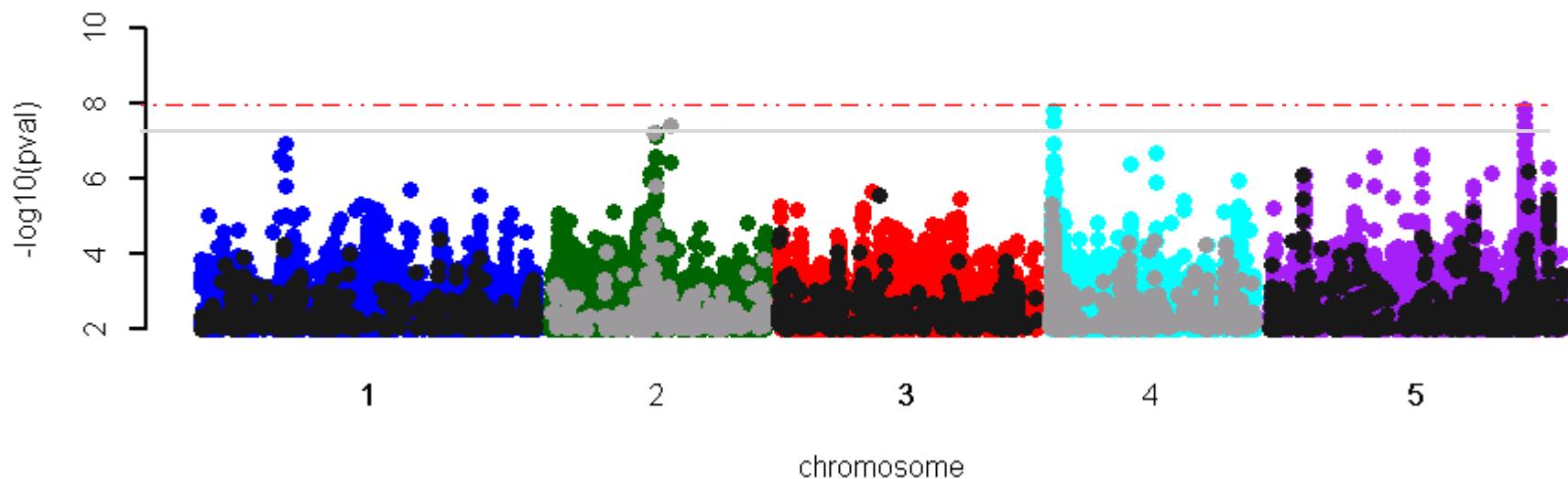
Generation of an imputed data set using
BEAGLE
for 2,029 accessions on 10 M SNPs

GWAS in *Arabidopsis thaliana*



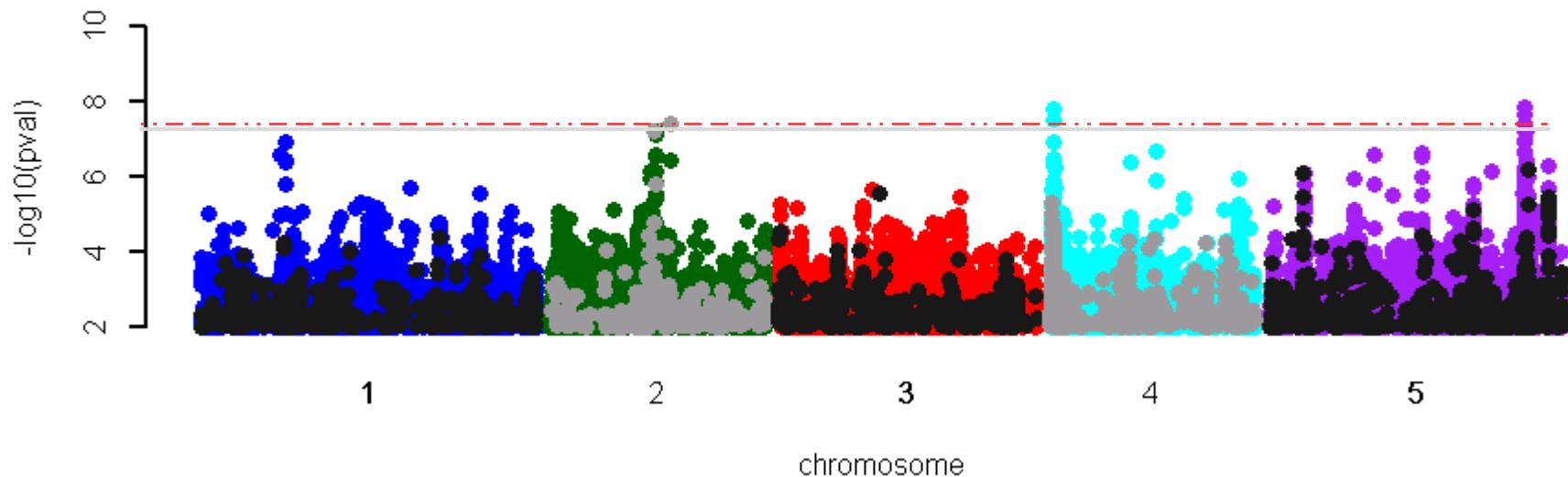
250 K SNPs (1 Marker / 600 bp, Horton et al. NatGen 2012)

GWAS in *Arabidopsis thaliana*



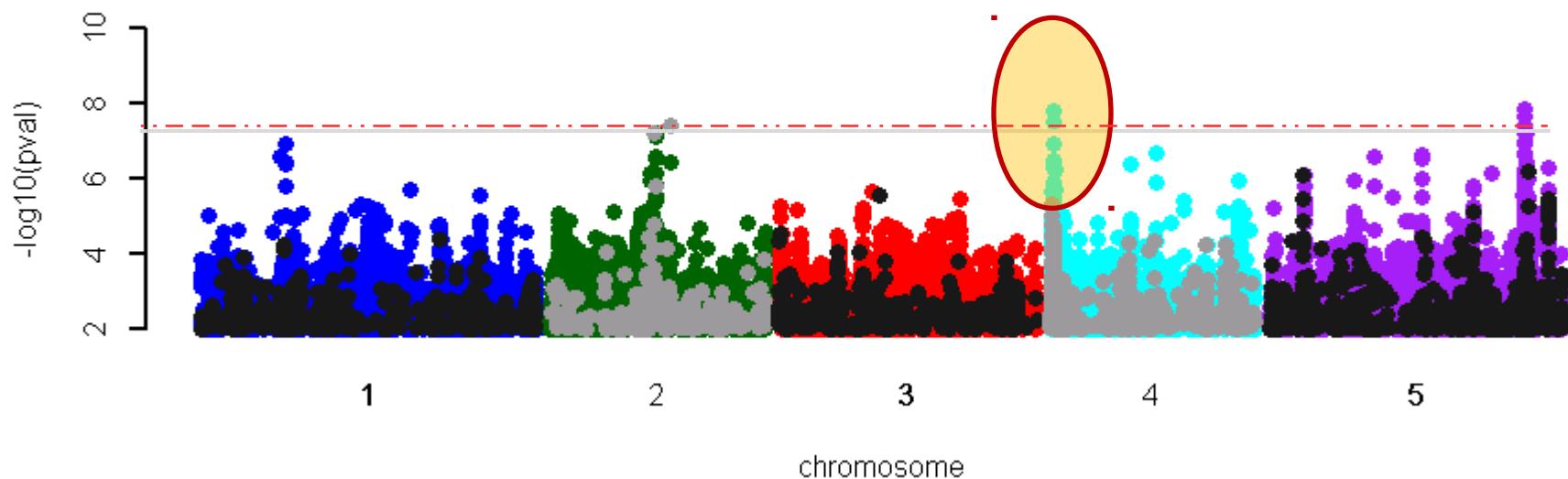
10M SNPs (1 Marker / 15 bp, The1001 Genomes Consortium)

GWAS in *Arabidopsis thaliana*



Permutation-based threshold

GWAS in *Arabidopsis thaliana*

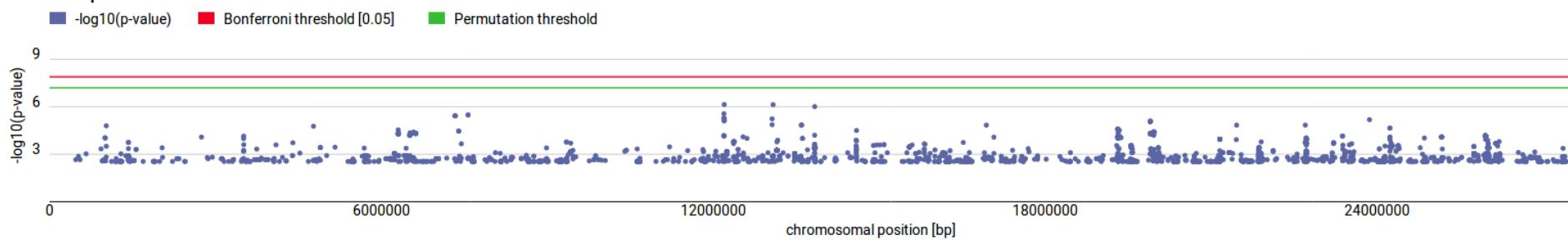


10M SNPs (1 Marker / 15 bp, The1001 Genomes Consortium)

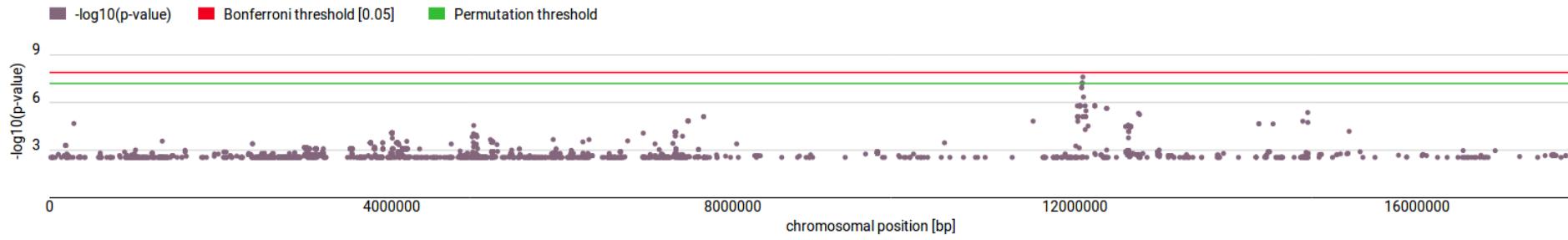
Calcium concentration in leaves

Manhattan Plots

Manhattan-plot for chromosome 1

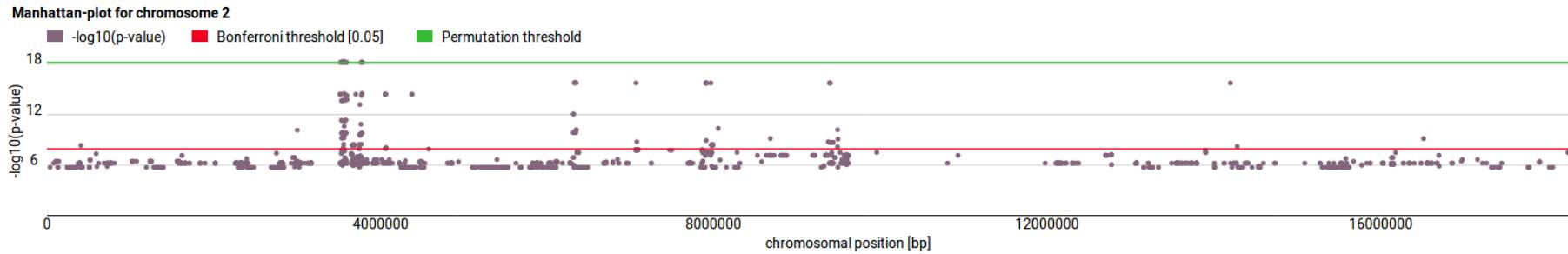
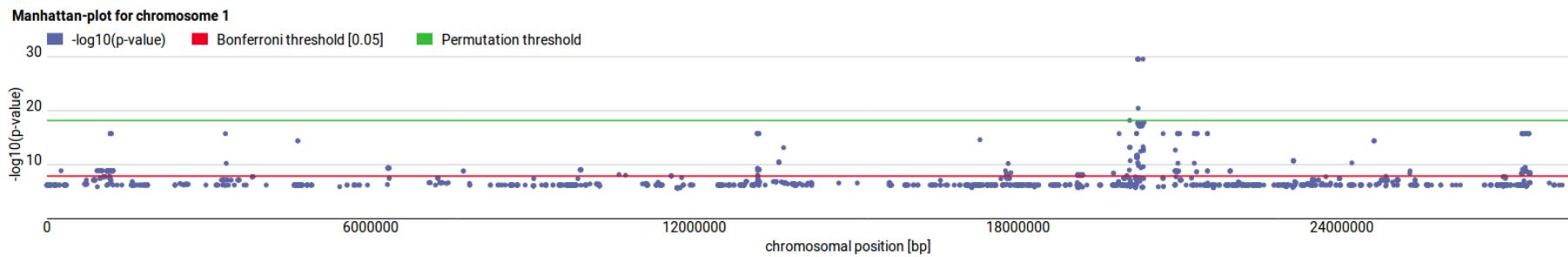


Manhattan-plot for chromosome 2



Chlorosis

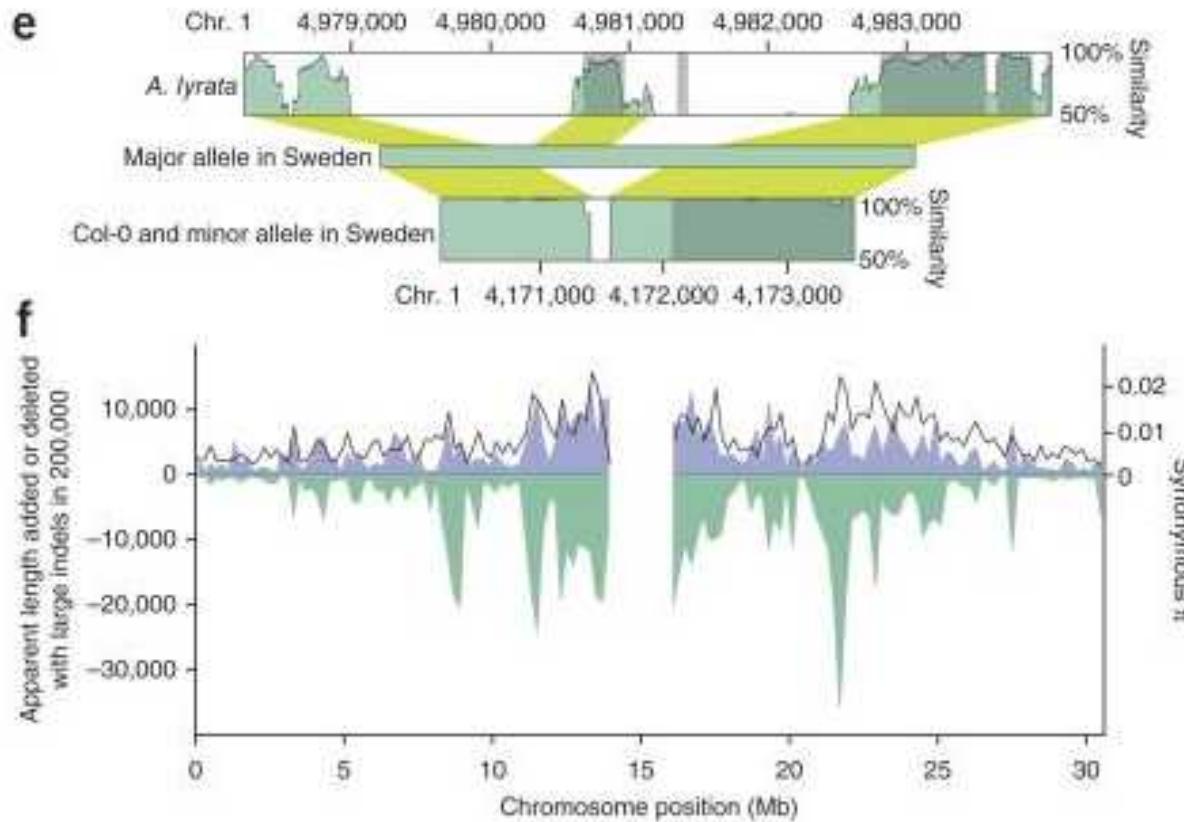
Manhattan Plots



Horizontal GWAS



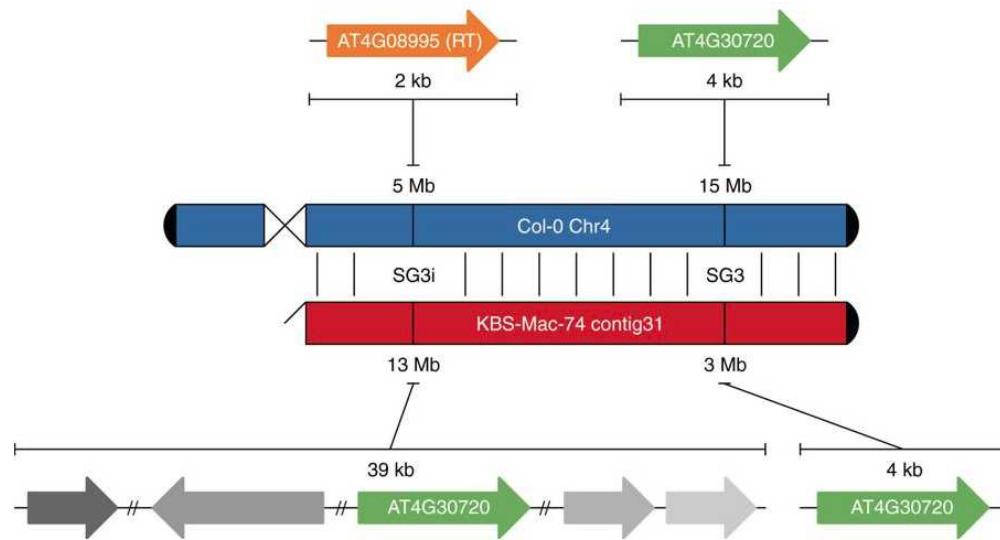
Genomic variation



Genomes are complex

Fig. 4

From: High contiguity *Arabidopsis thaliana* genome assembly with a single nanopore flow cell



SNPs in the *A.thaliana* population (1135 accessions)

10,709,466 SNPs segregate in the population

1,854,599 SNPs are located in coding regions

28,148 SNPs lead to a premature STOP codon



**Nearly 10,000 genes are knock-out
in at least 1 accession**

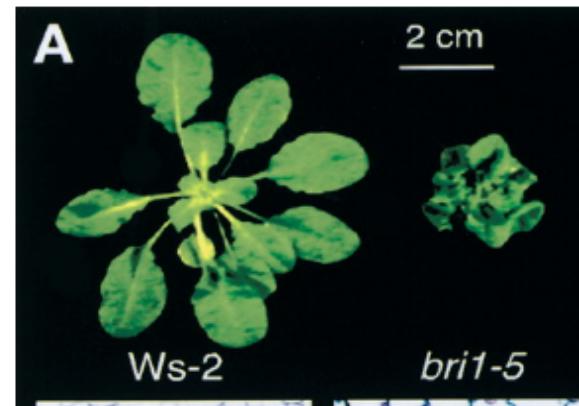
Natural BRI1 knock out in an accession from Portugal (IP-Alo-0)



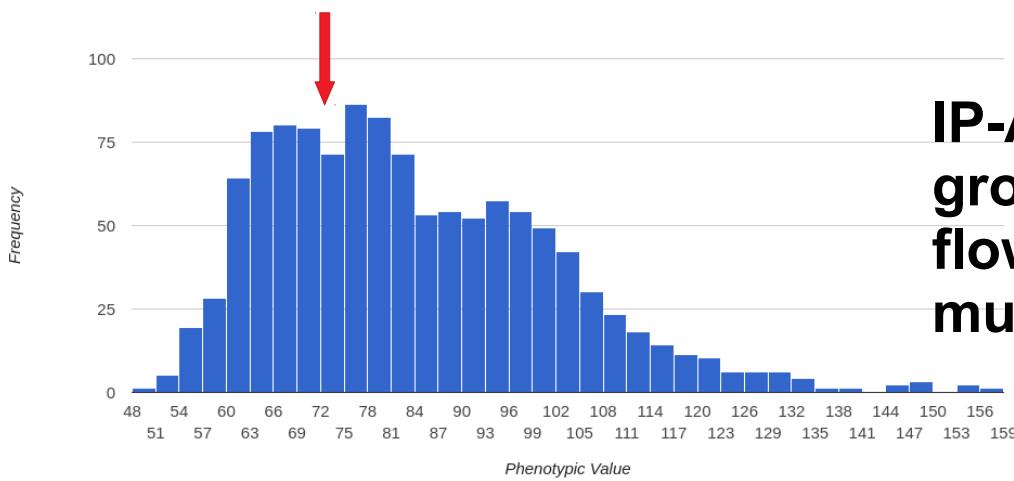
Natural BRI1 knock out in an accession from Portugal (IP-Alo-0)



Natural *BRI1* knock out in an accession from Portugal (IP-Alo-0)

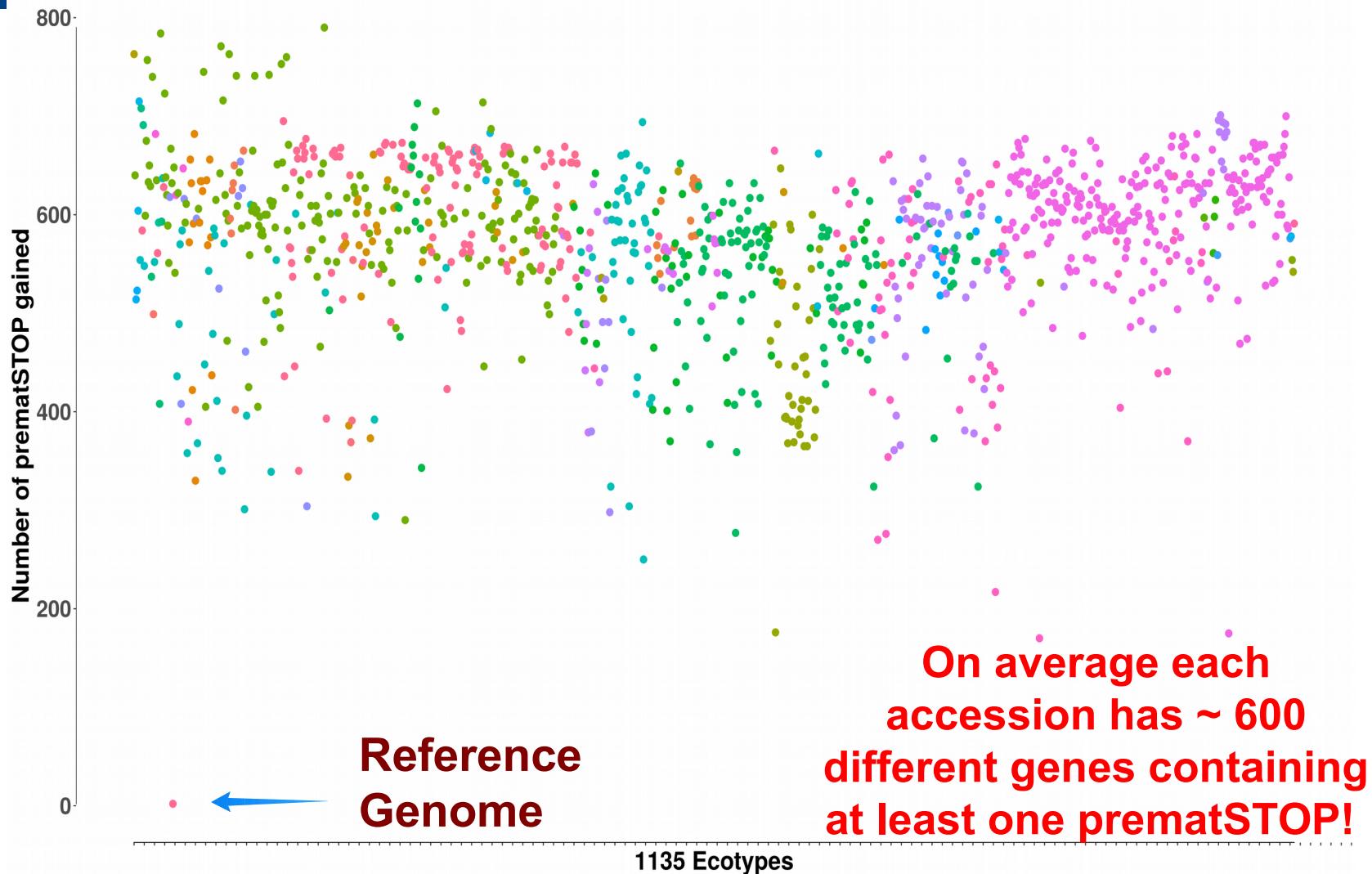


Santiago Mora-García et al. 2004, Genes Dev.

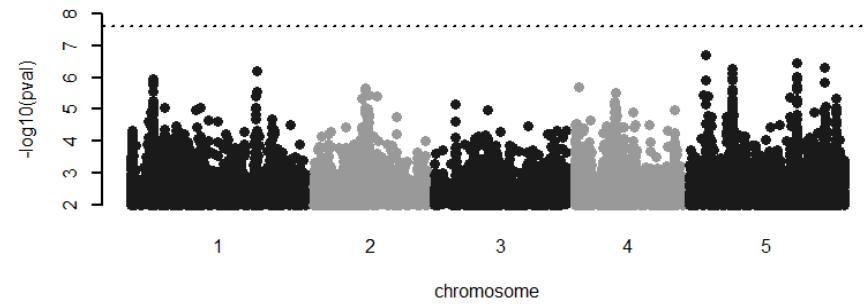
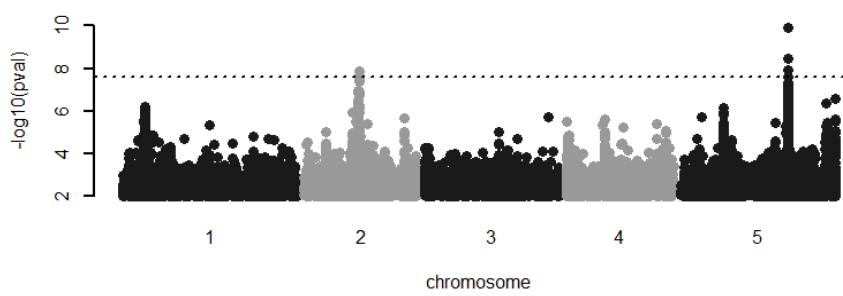
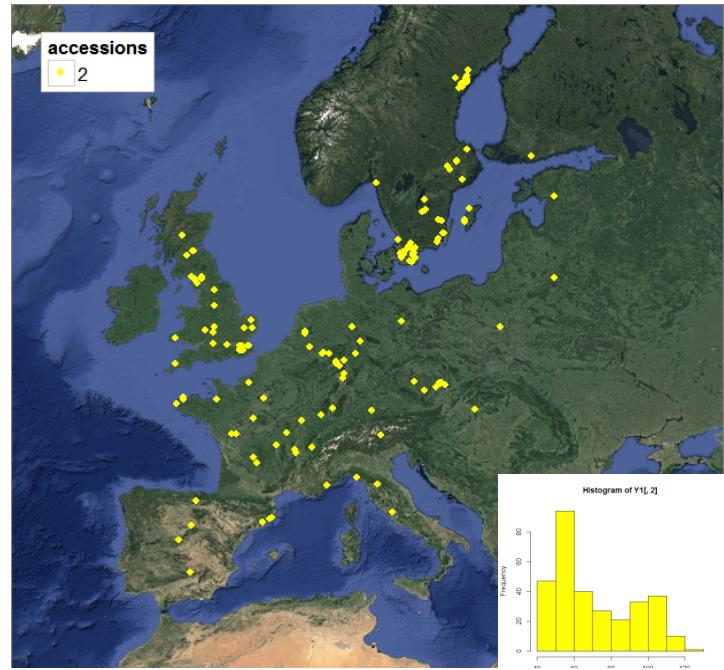
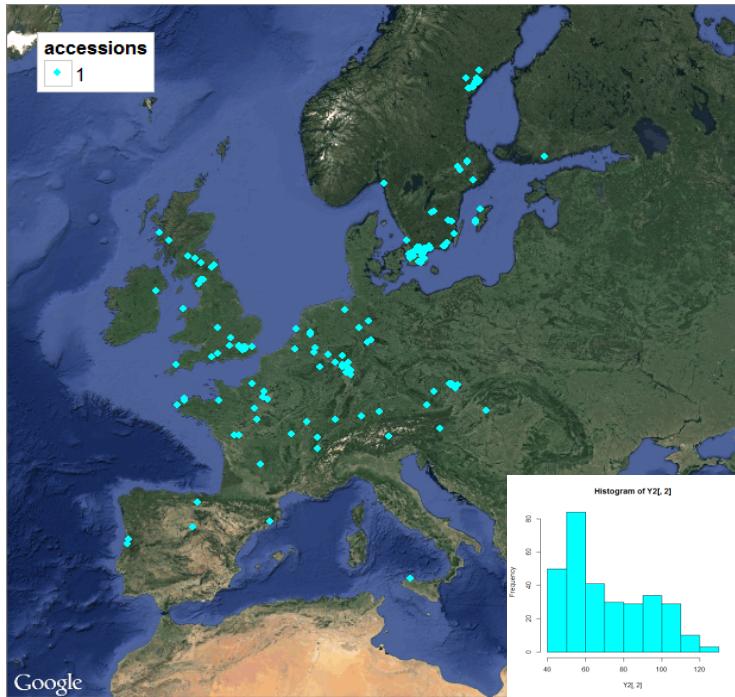


IP-Alo-0 does neither show the growth defect nor the delay in flowering time observed in *bri1* mutants

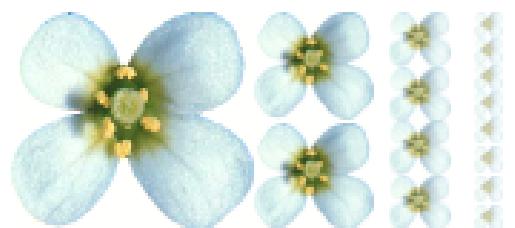
Frequency of prematSTOP codons by accessions



It's complicated



Acknowledgement



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and Theoretical Biology