NIAB Diverse MAGIC: dissecting trait genetic architecture across 70 years of wheat breeding

Goal

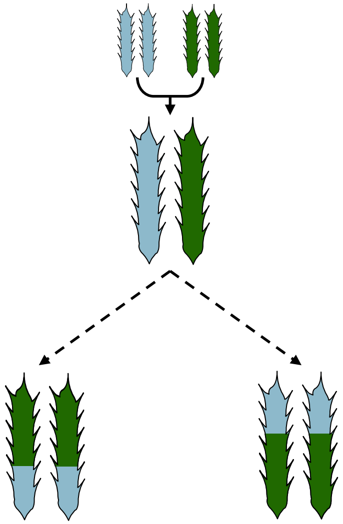
Reveal genomic basis of historical change and assess potential for future improvement

“Linking genotype with phenotype remains the **holy grail** of crop biodiversity studies”

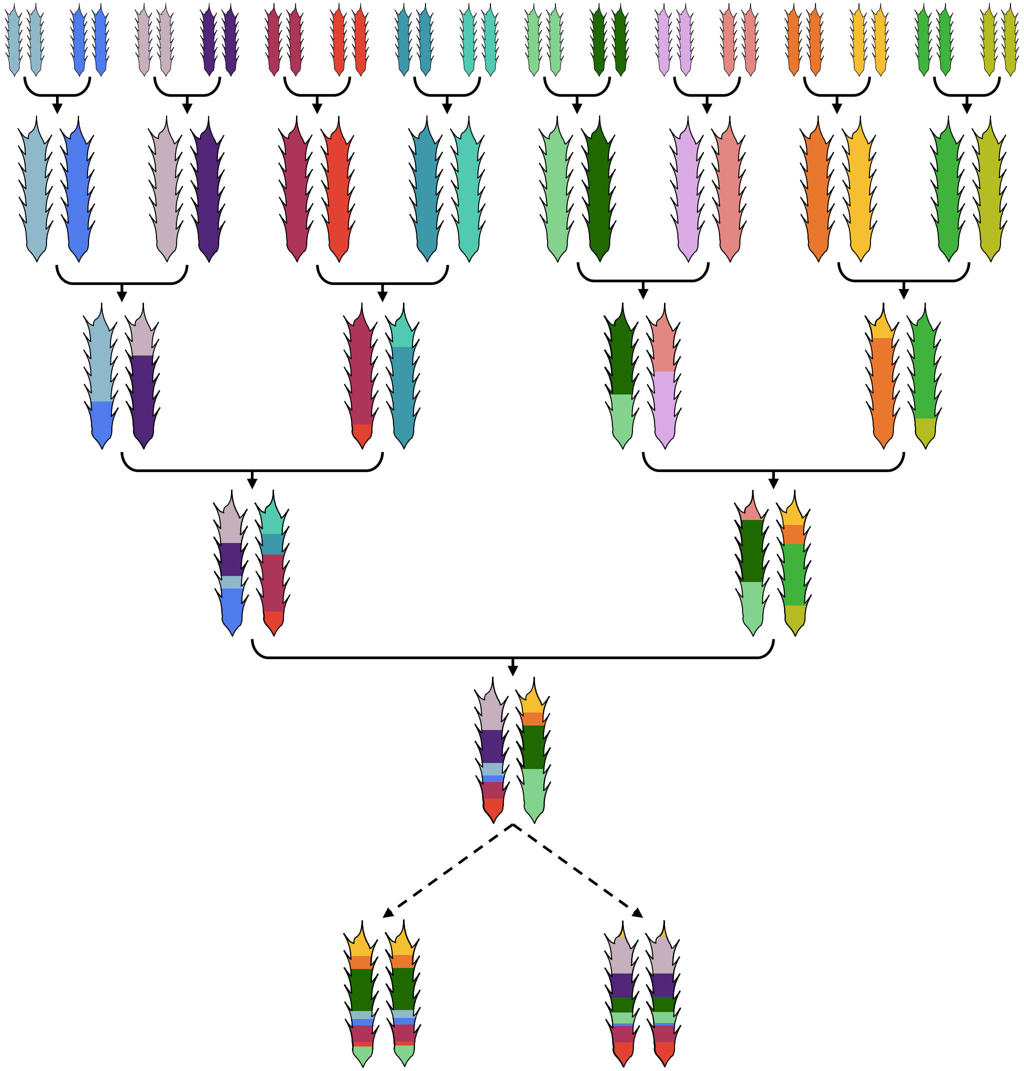
(Hufford et al., 2019)

Linking genotype with phenotype

Bi-parental population



Multi-parental (MAGIC) population



Scott & Ladejobi et al. (2020)

Linking genotype with phenotype

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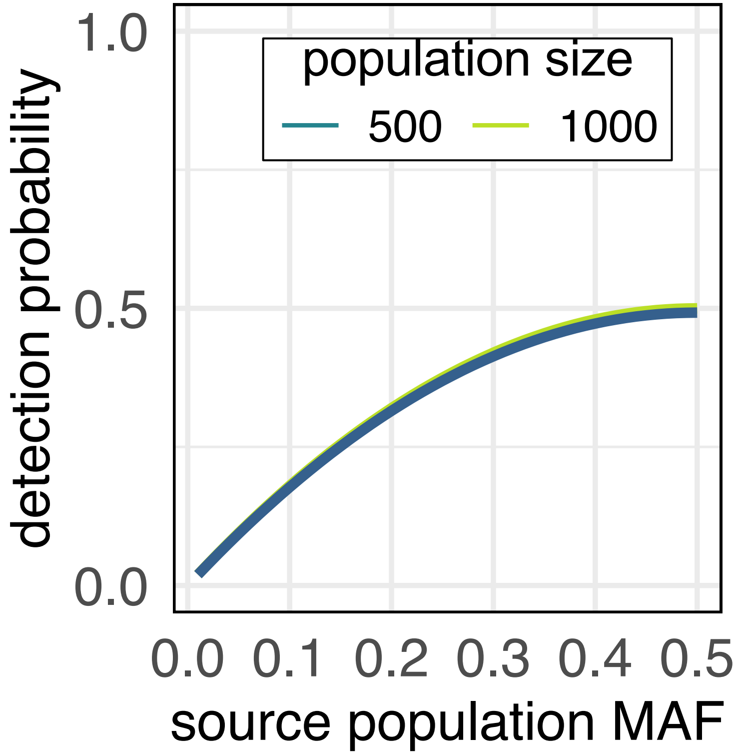

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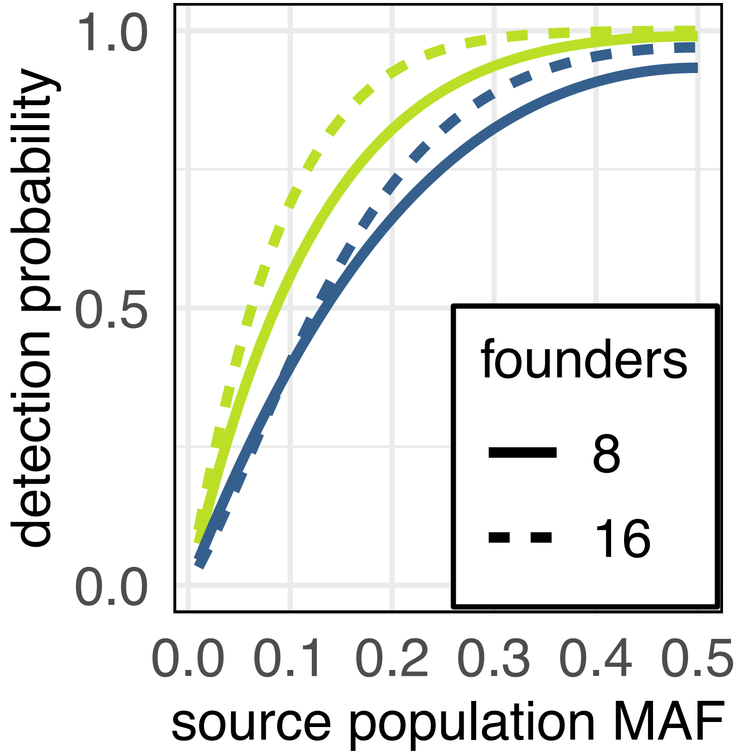

Generic tool for trait mapping, with low population structure

Scott & Ladejobi et al. (2020)

Outline

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- Founder genotyping (promoter & genic capture)
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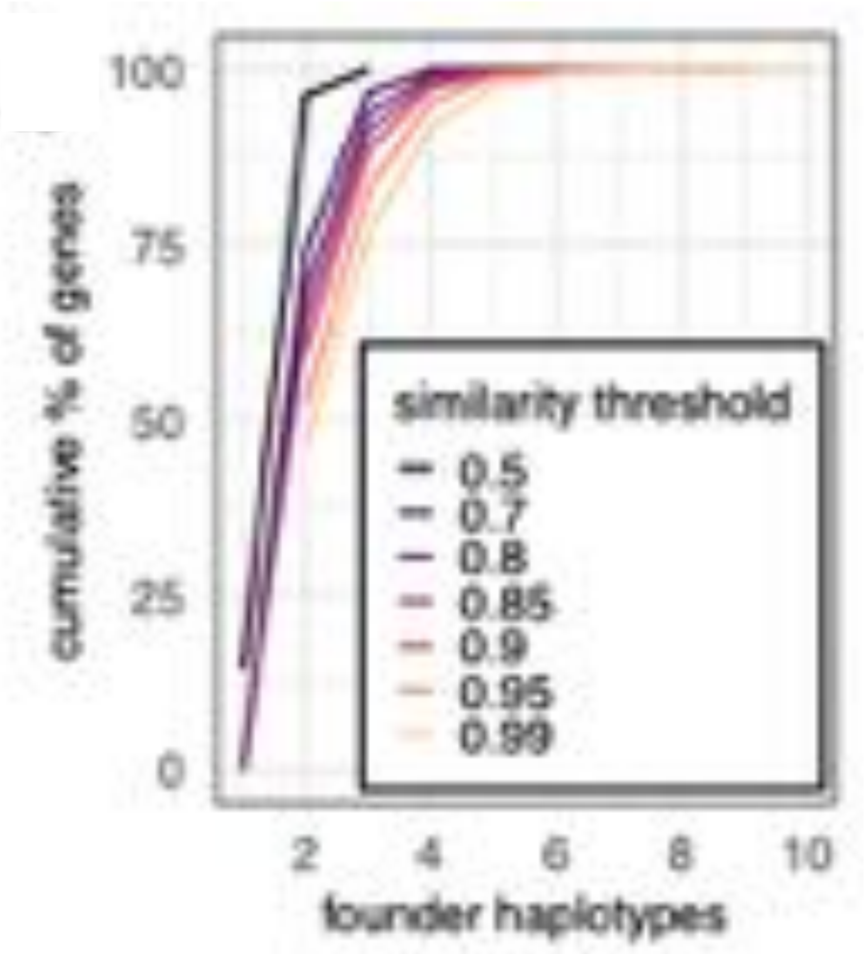
NIAB Diverse MAGIC founders

Founder Variety	Year of Listing	Country of Origin	Yield (t/ha)
Holdfast	1935	UK	5.1
Steadfast	1942	UK	4.6
Bersee	1951	UK	5.4
Banco	1956	Sweden	5.5
Flamingo	1960	Netherlands	5.8
Kloka	1965	Germany/UK	NA
Maris Fundin	1975	UK	6.6
Copain	1980	France	6.6
Stetson	1983	UK	7.0
Slejpner	1986	Denmark	7.9
Brigadier	1993	UK	8.6
Spark	1993	UK	7.6
Soissons	1995	France	7.6
Robigus	2003	UK	9.1
Cordiale	2004	UK	8.9
Gladiator	2004	UK	9.1

- promoters & exomes sequenced to **20x**
- **1.13M SNPs**
- Capture **~73% of global diversity**

Minimal Haplotypic Diversity among sixteen founders



- **No more than 3 haplotypes at ~89% of genes**
- Selection and population bottlenecks reduced UK effective population size before the onset of modern breeding programmes?

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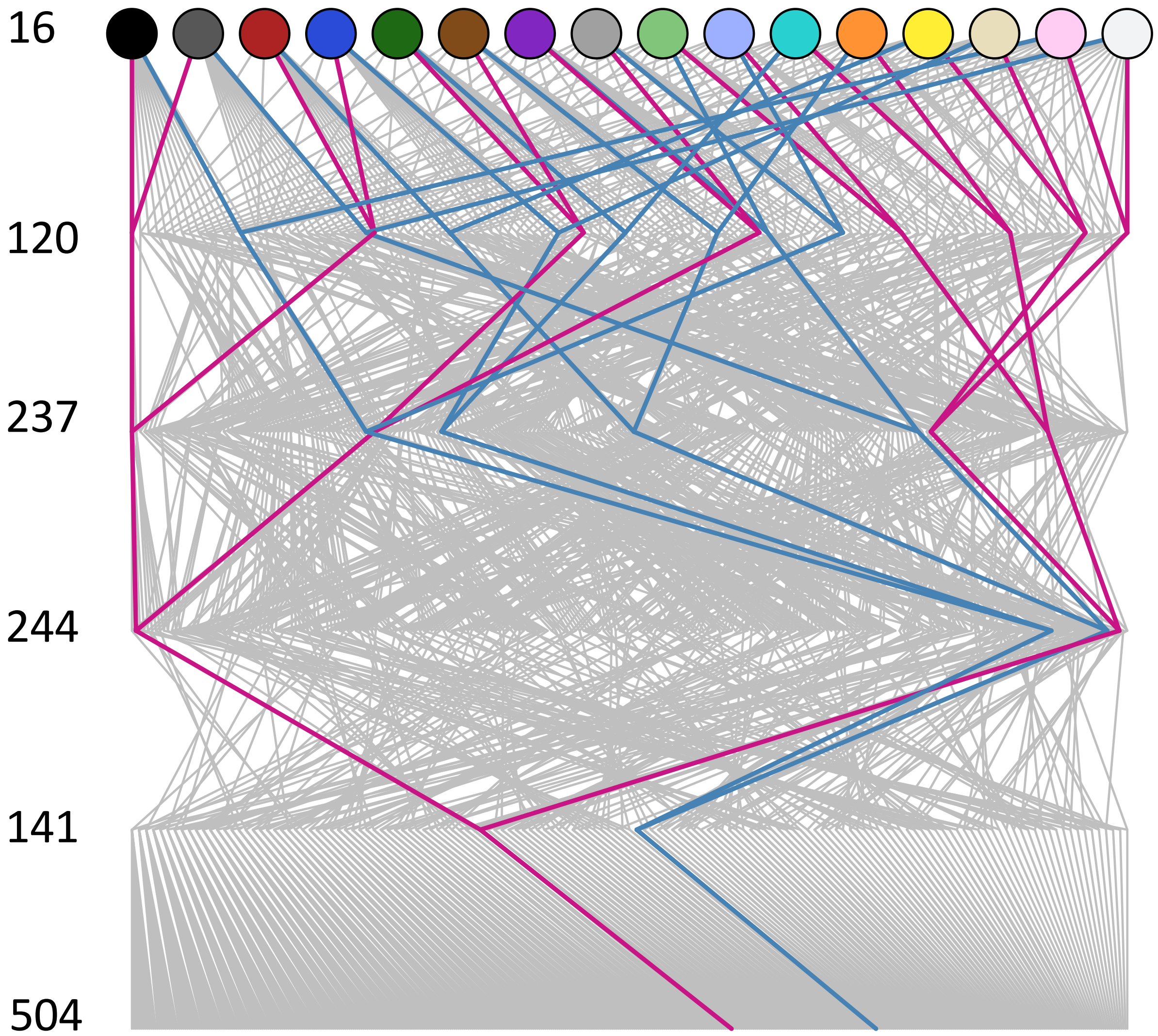
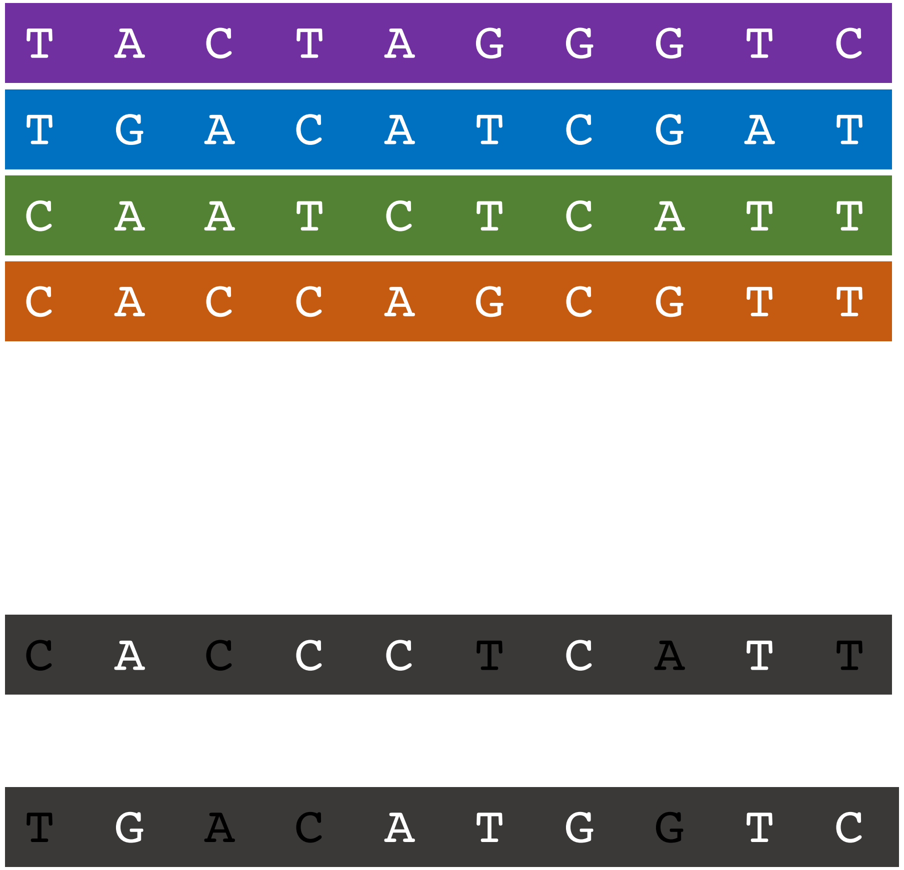
Recombinant Inbred Lines



- **>500** Recombinant Inbred Lines
- **0.3x** Whole Genome Sequencing
- Imputed **1.1M SNP** sites with >**99% accuracy**

Imputation from low coverage WGS

Founder Haplotypes



T A C T A G G G T C

T G A C A T C G A T

C A A T C T C A T T

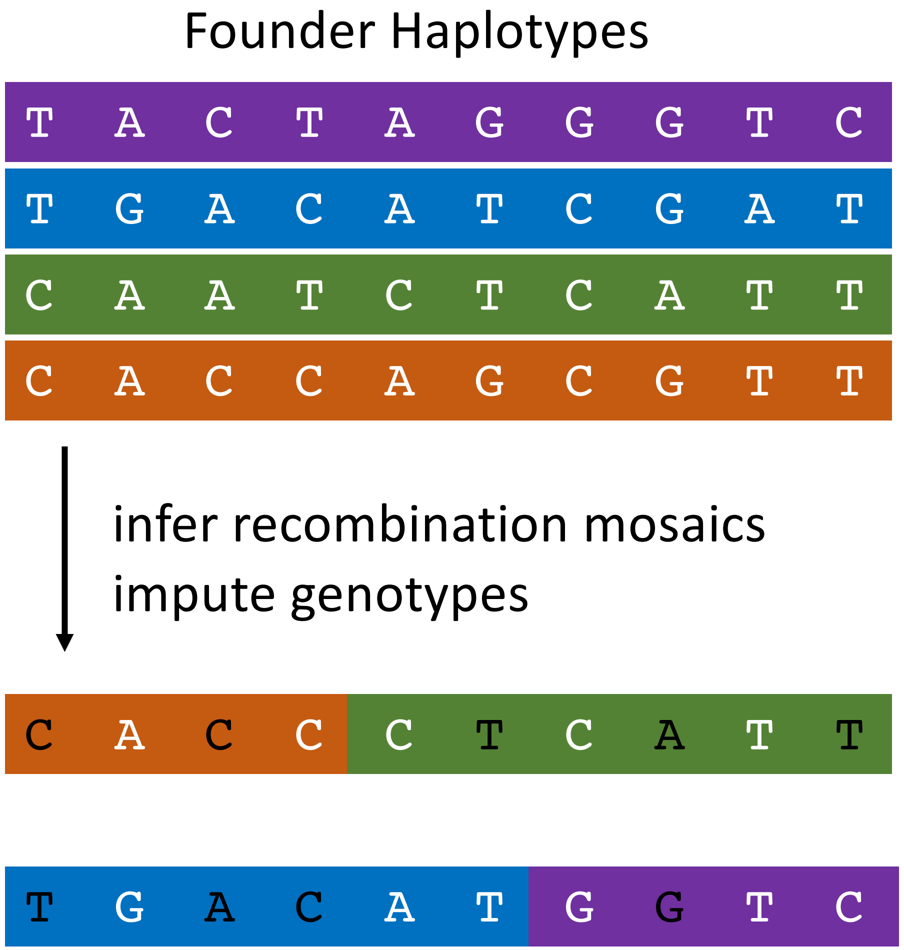
C A C C A G C G T T

C A C C C T C A T T

T G A C A T G G T C

0.3x WGS coverage for 504 inbred lines

Imputation from low coverage WGS



Founder Haplotypes

T	A	C	T	A	G	G	G	T	C
T	G	A	C	A	T	C	G	A	T
C	A	A	T	C	T	C	A	T	T
C	A	C	C	A	G	C	G	T	T

infer recombination mosaics
impute genotypes

C	A	C	C	C	T	C	A	T	T

T	G	A	C	A	T	G	G	T	C

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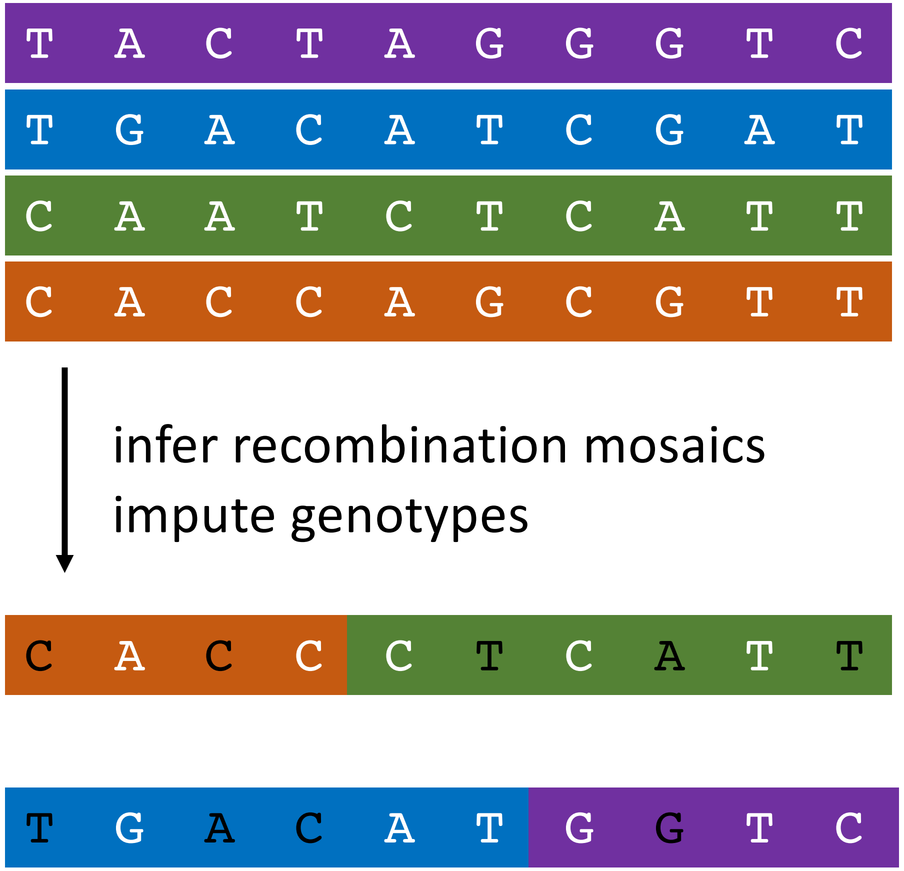
Founder Haplotypes



T A C T A G G G T C

T G A C A T C G A T

C A A T C T C A T T

C A C C A G C G T T

infer recombination mosaics

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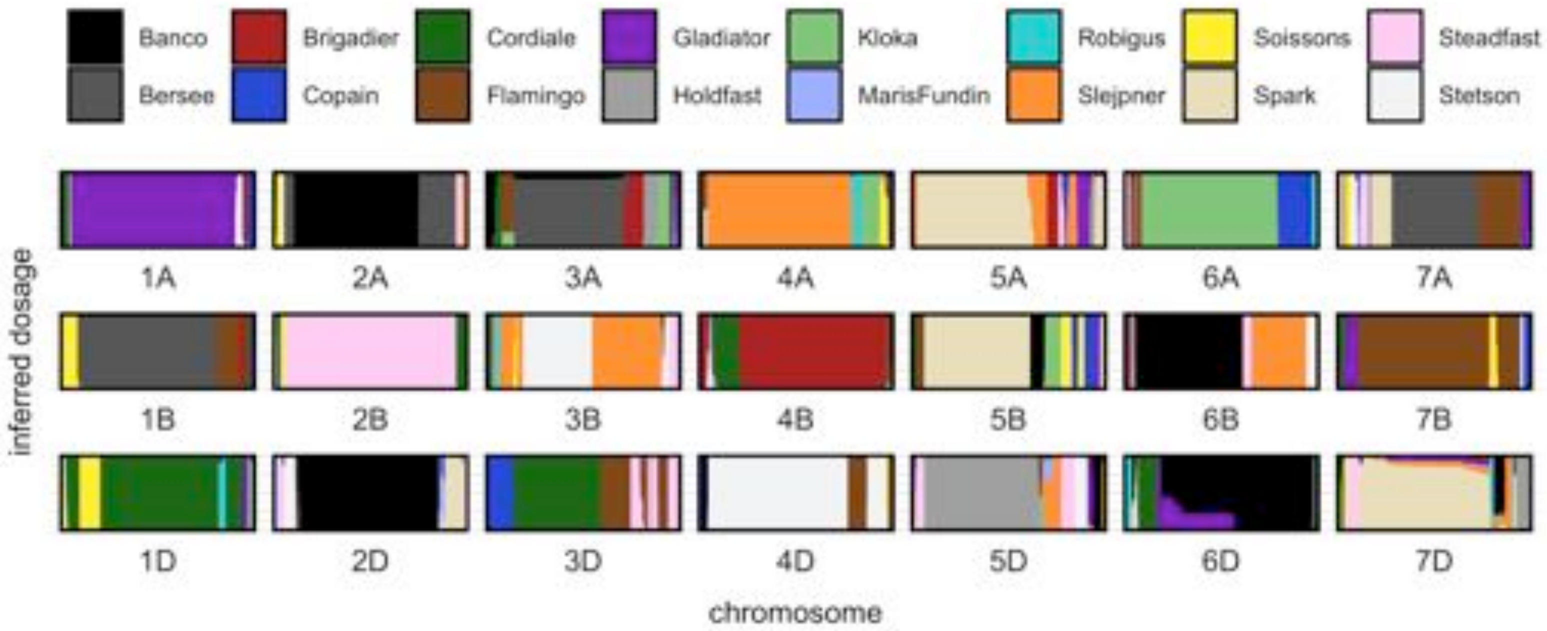
C A C C C T C A T T

T G A C A T G G T C

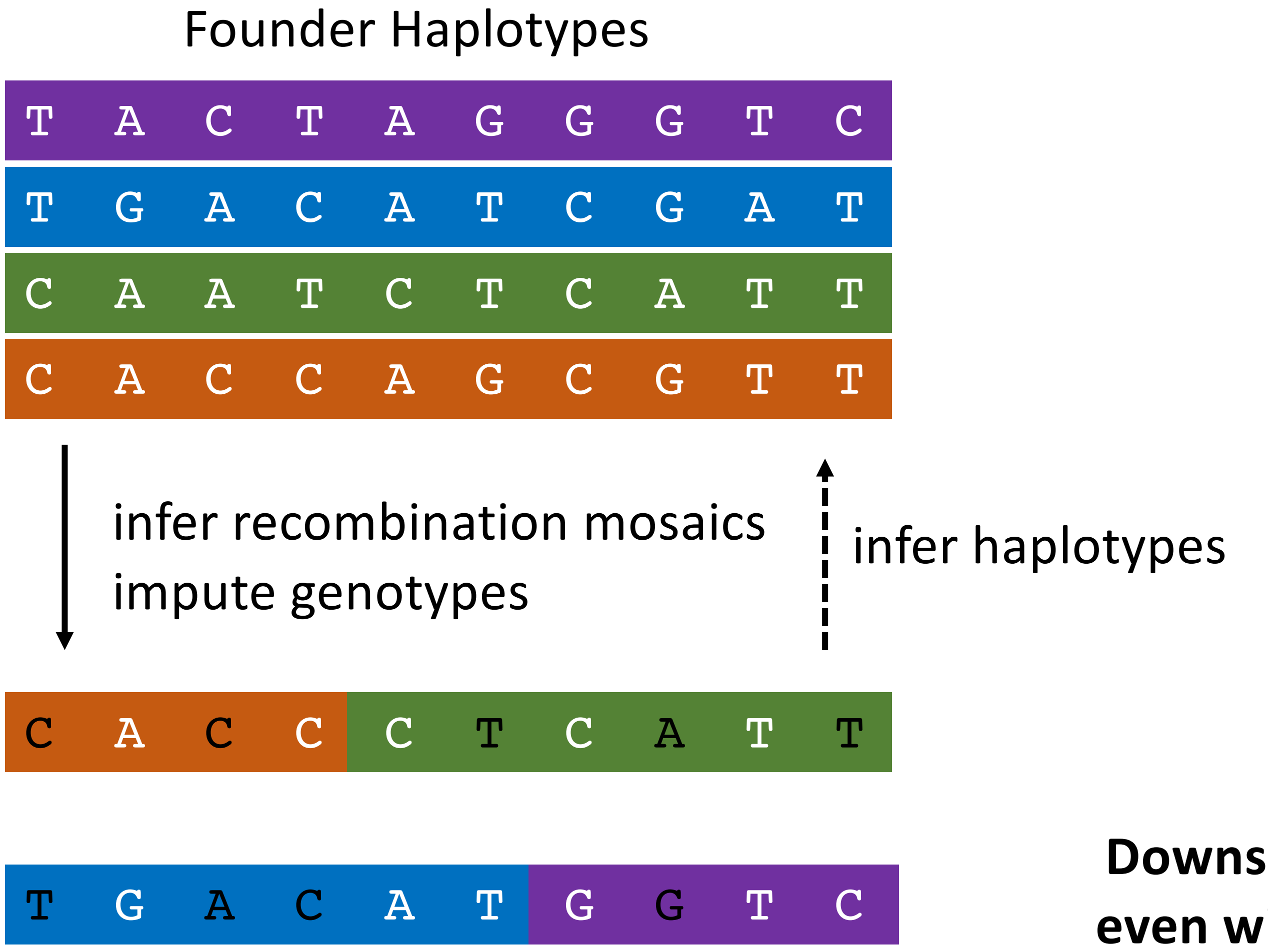


4.9-5.2 recombinants per Morgan (5 predicted)

99.1% accurate against genotyping array data (~5k sites)

0.3x WGS coverage for 504 inbred lines

Imputation from low coverage WGS



Founder Haplotypes

T A C T A G G G T C

T G A C A T C G A T

C A A T C T C A T T

C A C C A G C G T T

infer recombination mosaics
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C A C C C T C A T T

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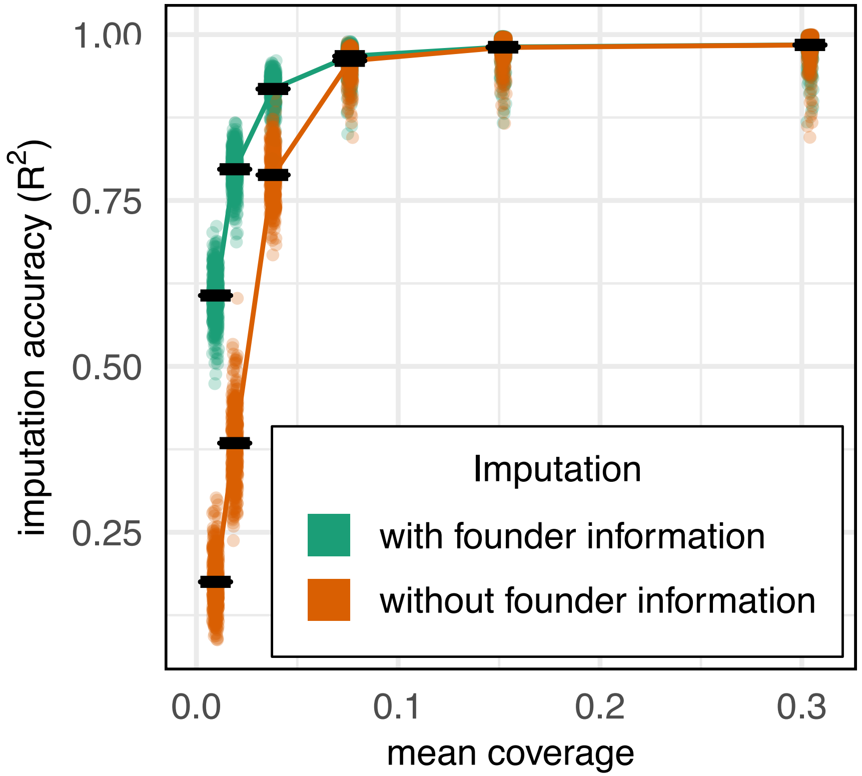

Downsampling indicates accurate imputation from 0.075x even without the founder haplotypes as a reference panel

STITCH software (Davies et al., 2016)

Outline

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Results

- QTL mapping

- Genomic prediction

- Cross-phenotype trends

Phenotyping

- Replicated yield trials with/without fungicide, >2000 plots per year
- 47 traits, of which 25 measured in two years (2017/18)

Phenotype Category	Traits Measured
Yield	Yield, Protein Content, Thousand Grain Weight, Specific Weight
Disease Resistance	Yellow Rust Infection (x3 timings)
Phenology	Germination Rate, Pre-Harvest Sprouting, Heading Date, Flowering Date, Vernalisation, Flag-leaf Emergence Date, Green Leaf Area, Flag Leaf Senescence
Seed Traits	Width, Length, Area, Ear weight, Spikelet Number, Infertile Spikelets
Growth Habit	Growth Habit, Ear Taper, Flag Leaf Angle, Flag Leaf Floppiness, Awn Presence/Absence
Size	Height to Flag Leaf Base, Height to Ear Base, Flag Leaf Ear Distance, Ear Length
Other	Pigmentation, Ear Waxiness, Leaf Waxiness, Lodging

Nick Fradgley

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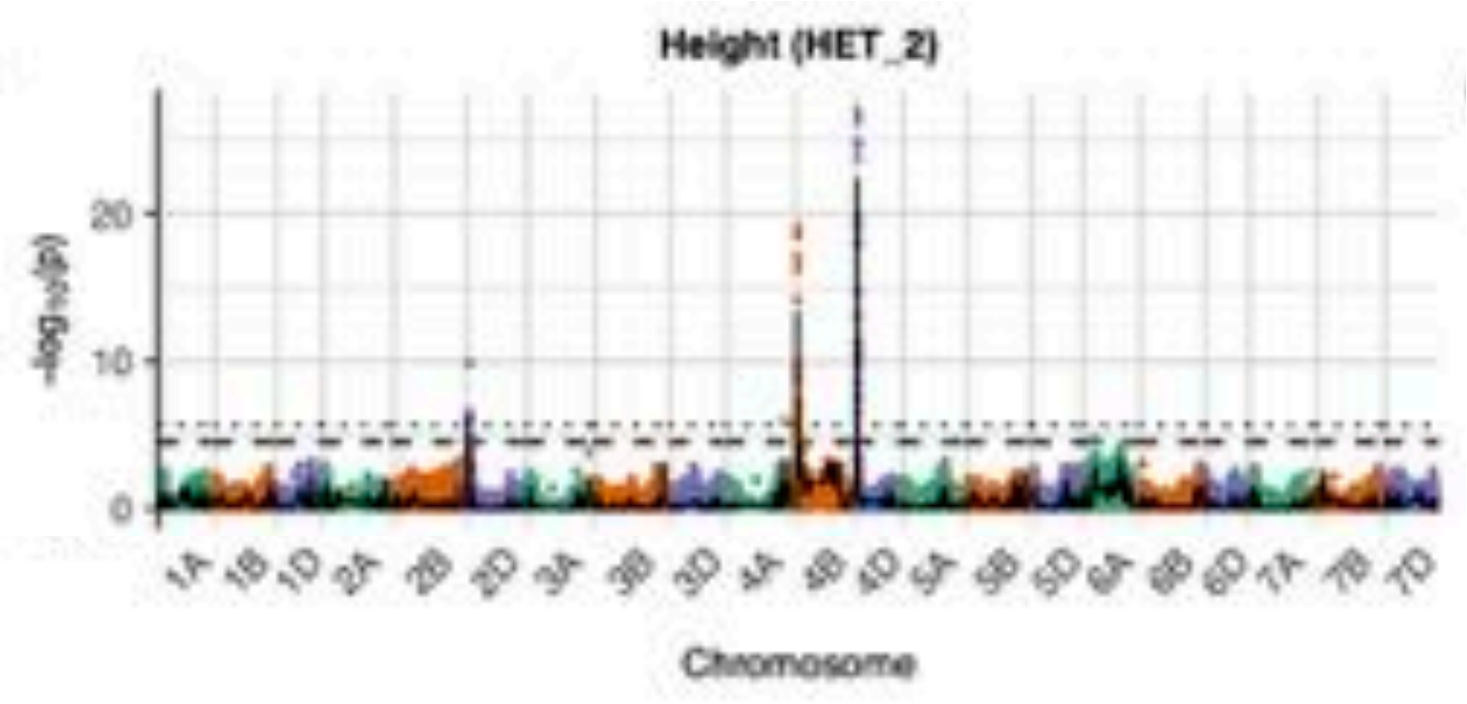
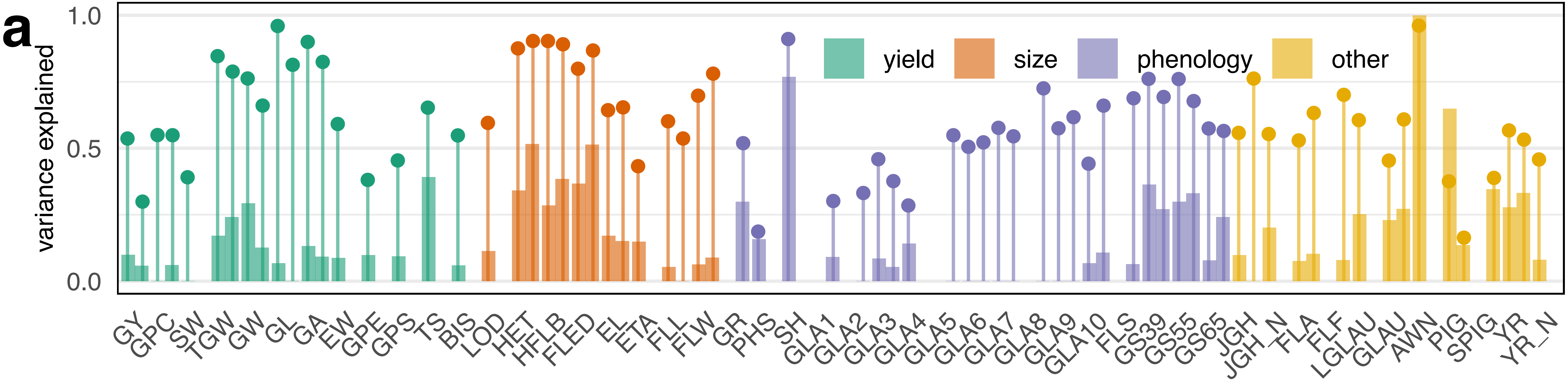
QTL mapping


Height (HET_2)
20
10
0
-log10(p)
1A
1B
1D
2A
2B
2D
3A
3B
3D
4A
4B
4D
5A
5B
5D
6A
6B
6D
7A
7B
7D
Chromosome

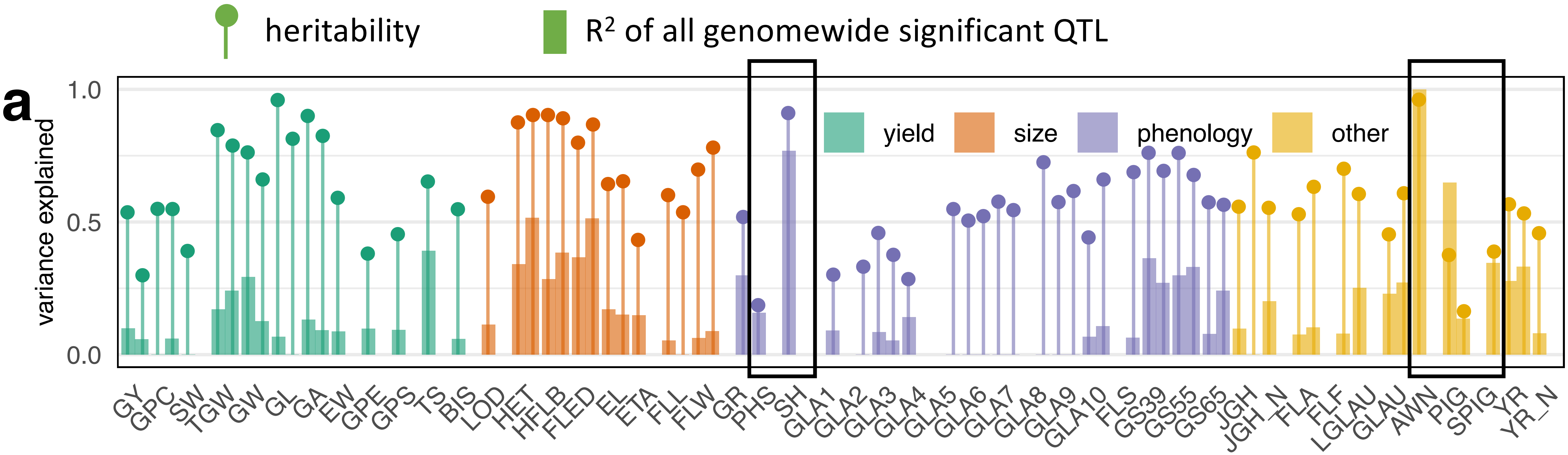
Variety of genetic architectures

● heritability

🟩 R^2 of all genomewide significant QTL



Variety of genetic architectures



- Heritable variation explained by 1-4 QTLs, e.g., Awns, pigmentation, spring habit

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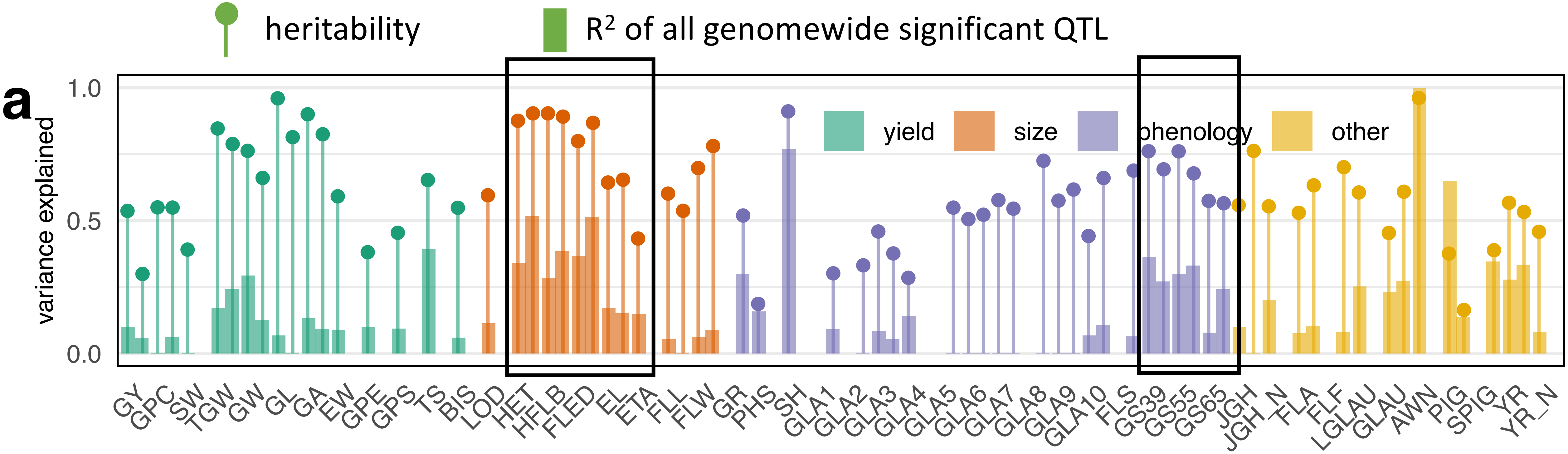
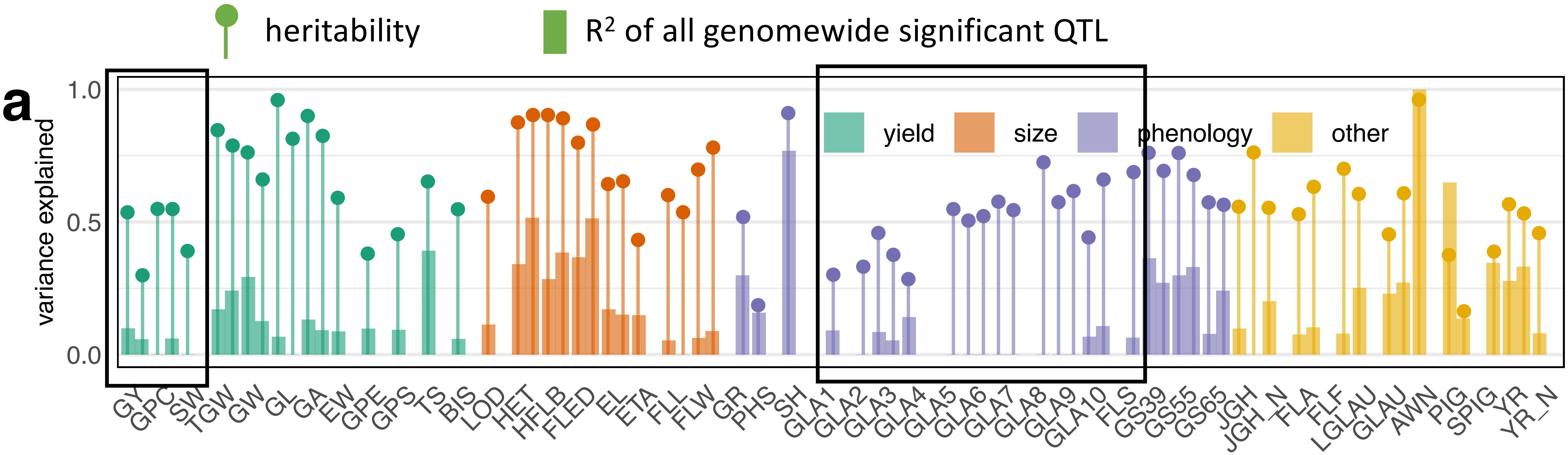


- Heritable variation explained by 1-4 QTLs, e.g., Awns, pigmentation, spring habit
- Mix of large effect QTLs and polygenic loci of smaller effect, e.g., height and heading date

Variety of genetic architectures



- Heritable variation explained by 1-4 QTLs, e.g., Awns, pigmentation, spring habit
- Mix of large effect QTLs and polygenic loci of smaller effect, e.g., height and heading date
- Most heritable variation not explained by large effect QTLs, e.g., yield and green leaf area

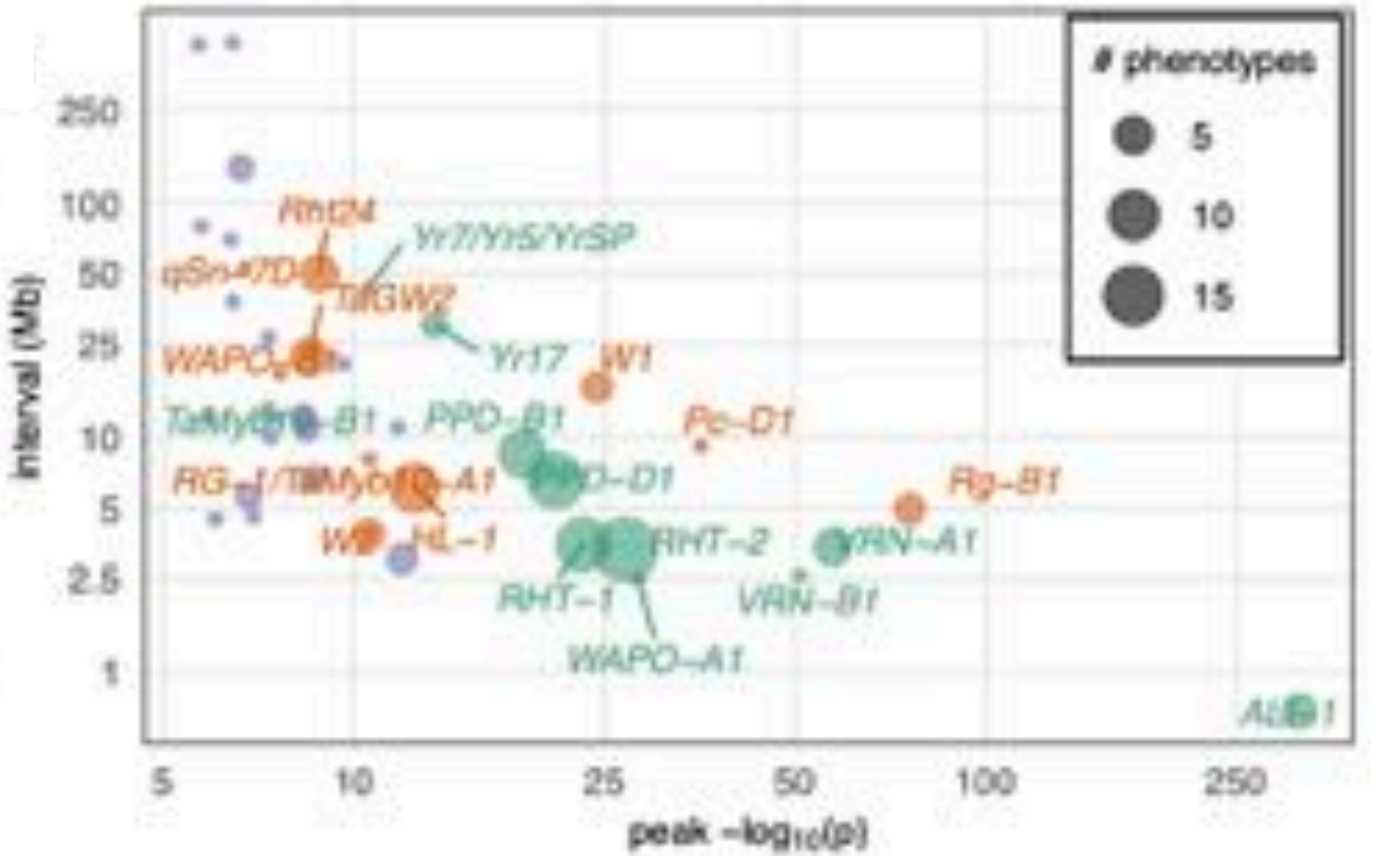
QTL summary

- **136** genomewide significant QTLs
- **42** genomic locations

11 HC colocalisations (e.g., known gene)

10 LC colocalisations (e.g., genetic map)

21 uncertain colocalisation



- Population captures ‘green revolution’ and latitudinal adaptation alleles
- Consistent with a low diversity, well-studied gene pool

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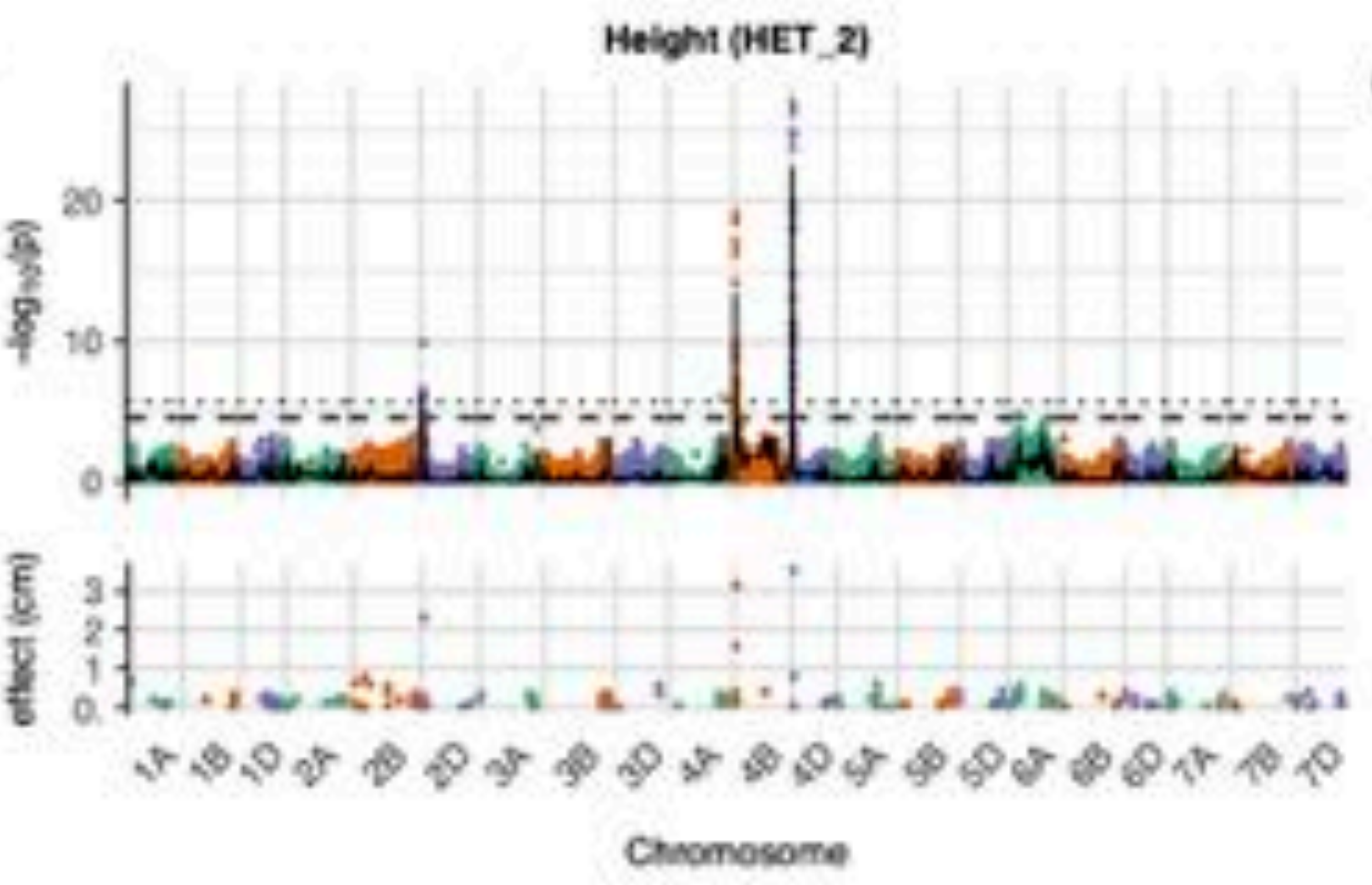
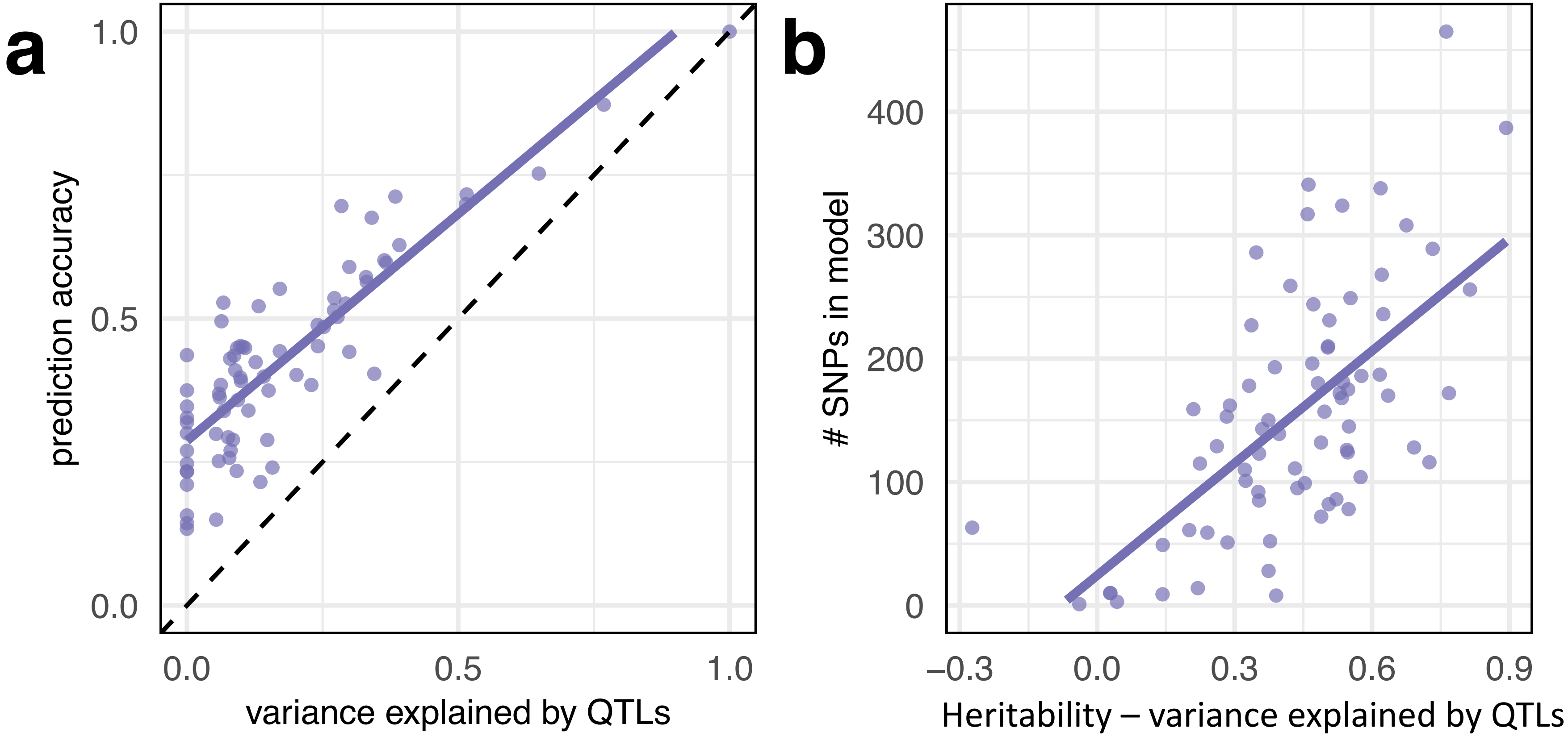
Genomic Prediction



Olu**funmi**layo Ladejobi

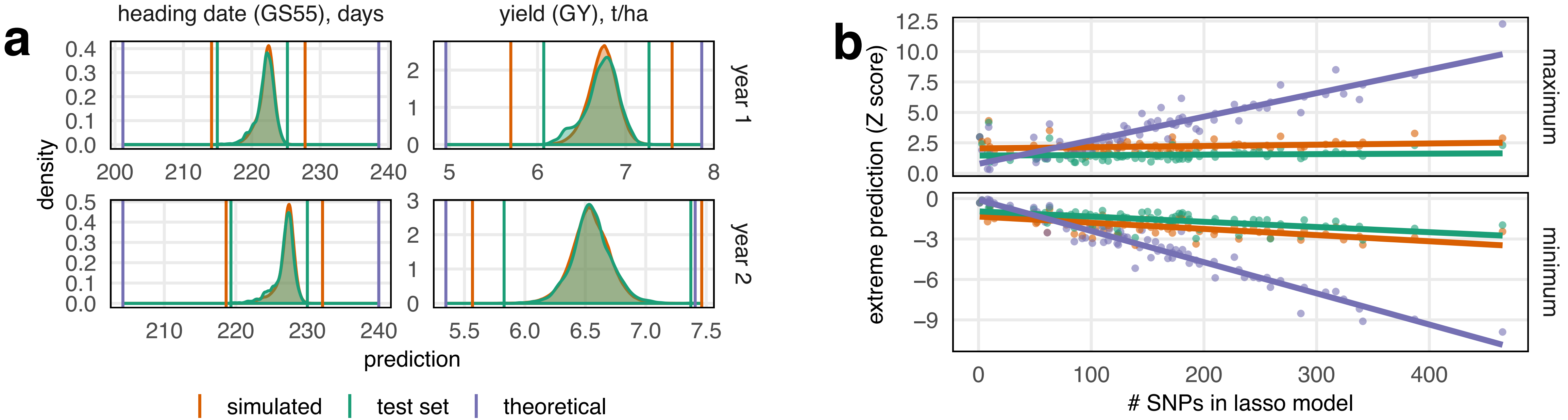
Genomic Prediction Summary

Phenotype prediction accuracy assessed in subset of lines not used to create model



- Reasonable prediction accuracy (mean 0.43)
- **Uses 1-465 SNPs (mean 155)**

Predict potential for improvement



Simulate new population of 20k lines, predict phenotypes in simulated lines to test if new extreme combinations are created.

Estimate predicted phenotype extreme if all positive alleles could be combined

Large phenotypic shifts likely to require selection at dozens of loci

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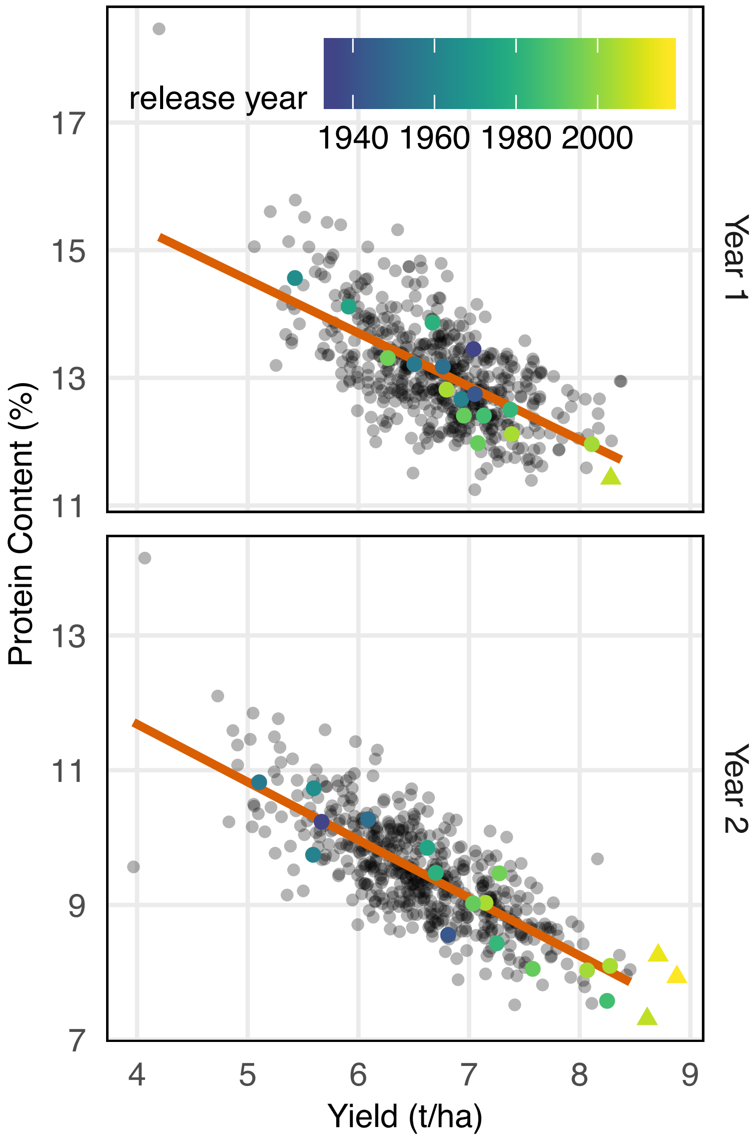
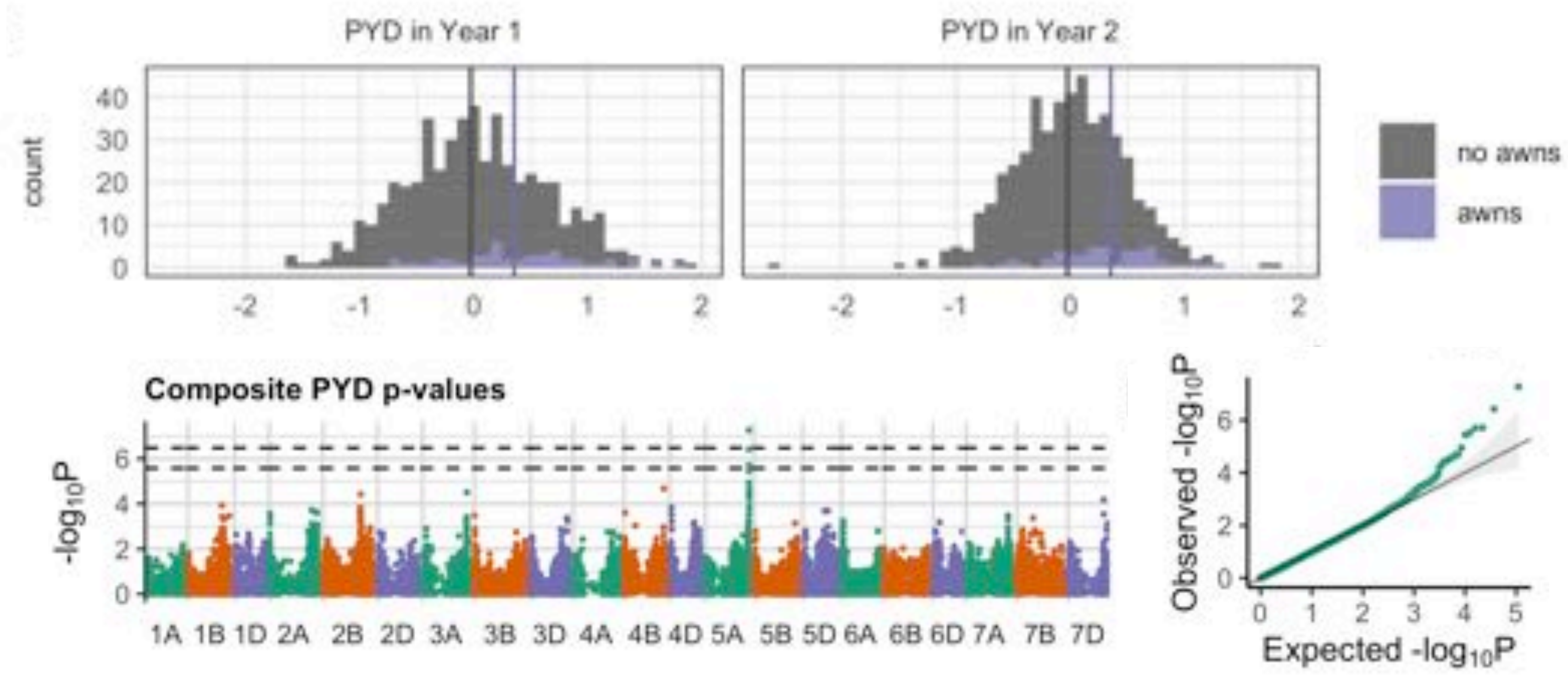
Yield-Protein Trade-off



Improvement in yield has come with reduced protein content

Protein-Yield Deviation is the departure from this regression

Yield-Protein Trade-off



- Higher Protein Yield Deviation in lines with Awns

- Heritability 0.41 (year 1) 0.25 (year 2)
- Prediction accuracy 0.26 (year 1) 0.13 (year 2)

Modest potential for targeted selection to break this trade-off

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Conclusion

Continue selecting from within existing variation (and introgressing selected exotic alleles)?

Or, would it be worth ambitiously expanding the pool of available haplotypic diversity genomewide?

Acknowledgements

Data/Resources Freely Available

Project website:

http://mtweb.cs.ucl.ac.uk/mus/www/MAGICdiverse

Preprint:

Limited haplotype diversity underlies polygenic trait architecture across 70 years of wheat breeding

bioRxiv doi:10.1101/2020.09.15.296533

https://www.biorxiv.org/content/10.1101/2020.09.15.296533v1

Review:

Multi-parent populations in crops: A toolbox integrating genomics and genetic mapping with breeding

Heredity (2020) 125, 396–416

BBSRC bioscience for the future

NIAB

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Earlham Institute

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