

# Rice 'Heat MAGIC' mapping

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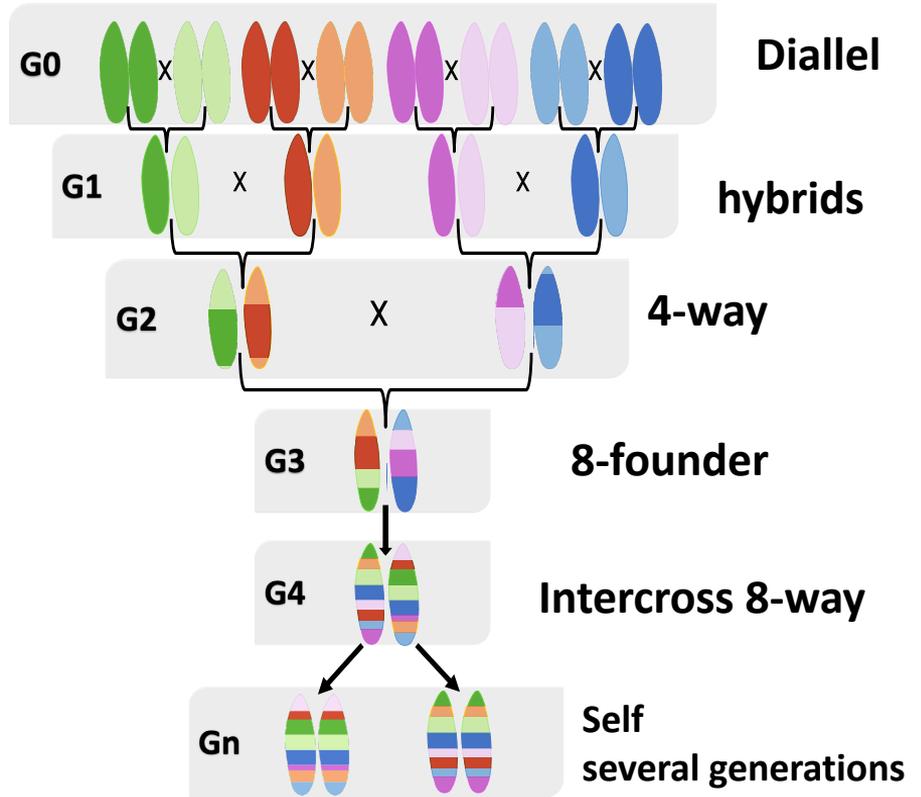
# Why rice? Why heat?

- Half the world's population derives a significant proportion of their caloric intake from rice.
- Unlike the other major cereals, more than 90% of rice is consumed by humans.
- It provides 21% per capita energy and 15% per capita protein globally.
- Rice yield is expected to decrease by 7-10% for every one degree rise in temperature.
- To develop diverse temperature stress tolerant rice varieties.



# MAGIC populations

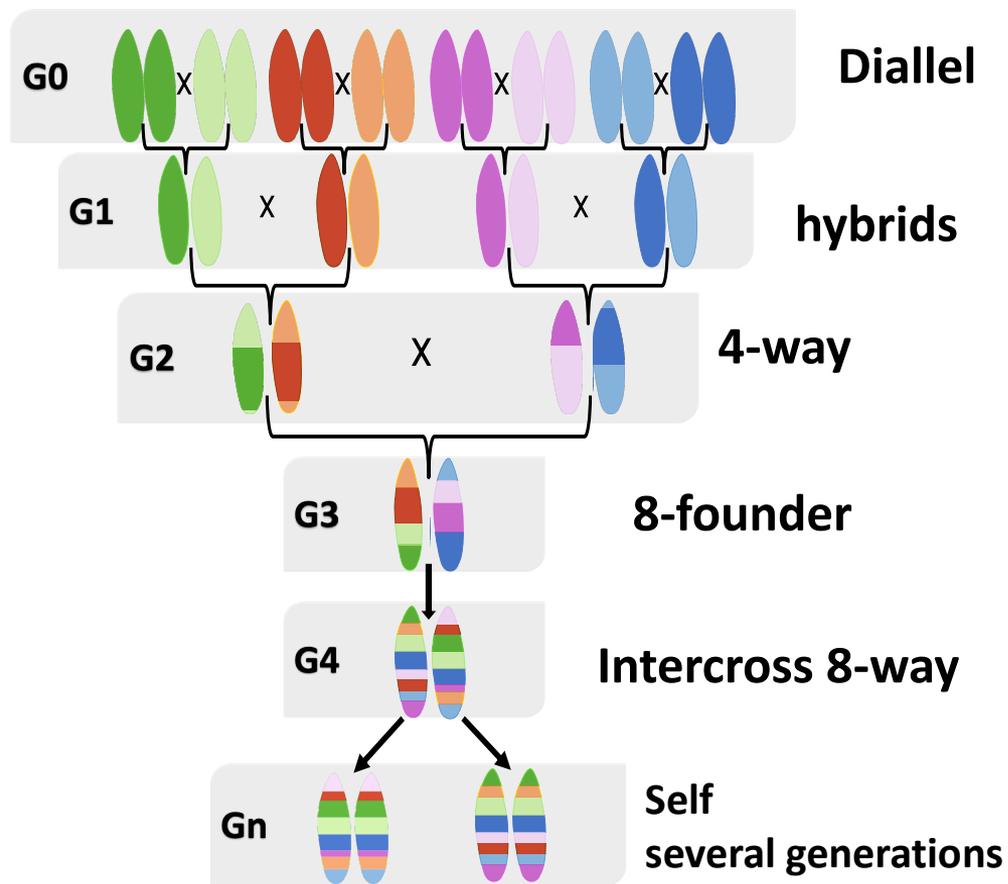
- **M**ulti-parent **A**dvanced **G**eneration **I**nter-cross.
- MAGIC line genomes are mosaics of all founders.
- The population is highly recombined.
- Highly diverse.
- Without population structure.
- High power for trait detection.



# The Rice *Heat* MAGIC population

➤ 844 MAGIC lines

➤  $S_{6-7}$



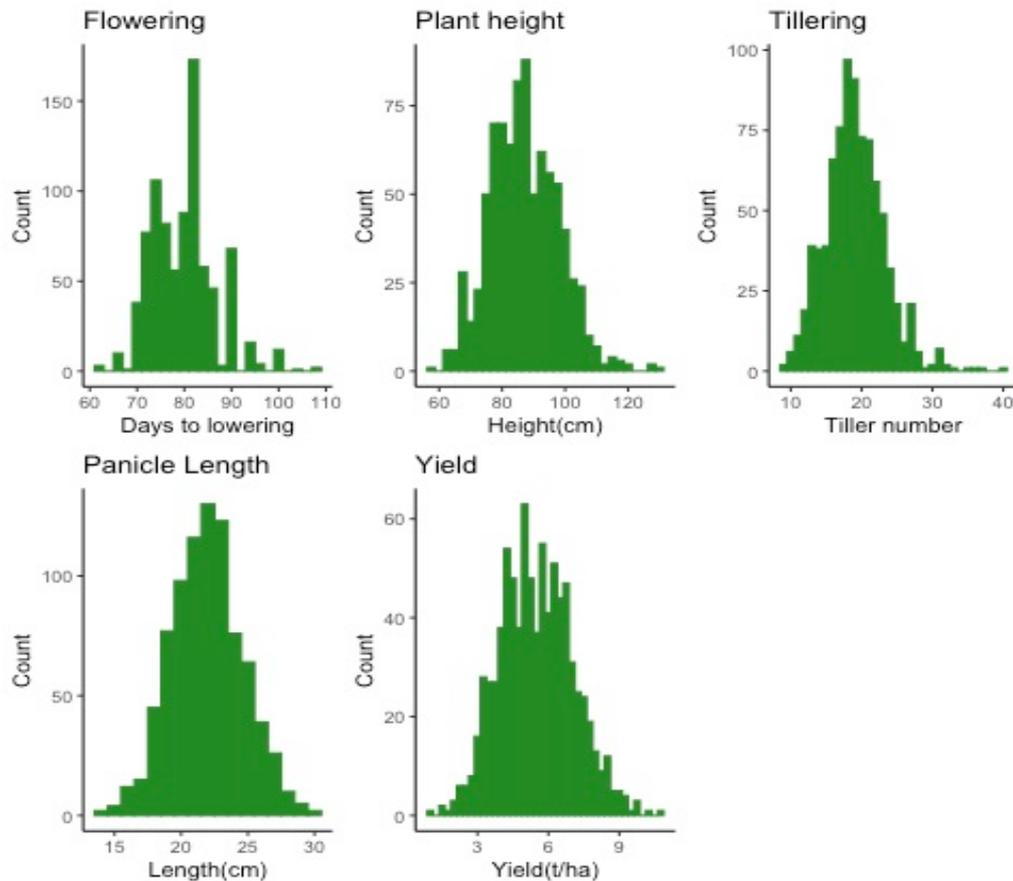
# Rice Heat MAGIC Founders



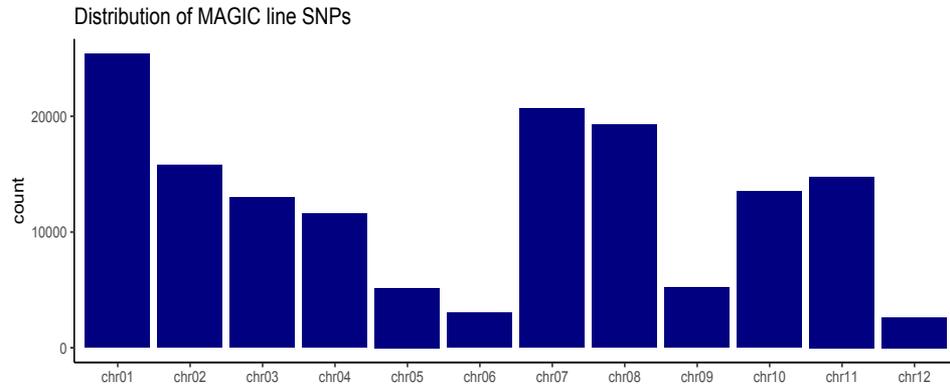
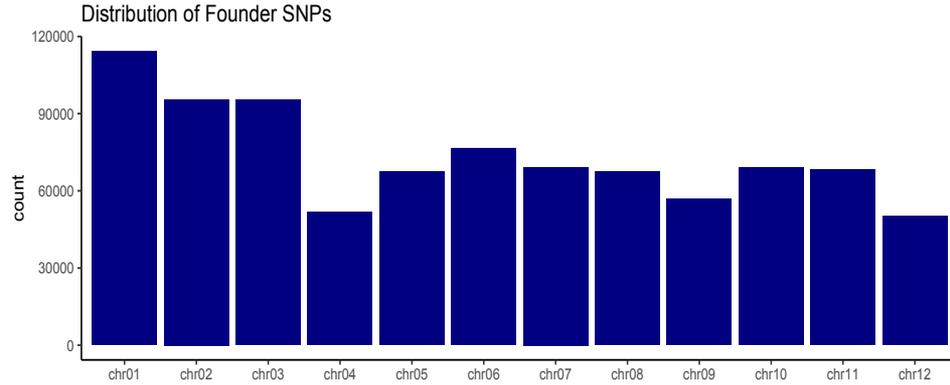
Variety	Varietal type	Origin	Agronomic Relevance
IR 64	Indica	IRRI	Mega-variety in Asia with wide adaptability
GIZA 178	Indica /Japonica cross	Egypt	Popular rice variety in Egypt with high level heat tolerance
MILYANG 23	Indica /Japonica cross	S. Korea	Very popular variety in Korea with wide compatibility and moderate tolerance to heat and cold
Chengcheong	Japonica	S. Korea	Cold tolerant variety from Korea with poor heat tolerance
Dasan	Japonica	S. Korea	Cold tolerant variety from Korea as well as heat tolerant in Japan
Hokuriku76	Japonica	Japan	Cold tolerant variety
IR72	Indica	IRRI	High yielding variety
N22	Aus	India	Highly heat tolerant variety

# Phenotypes

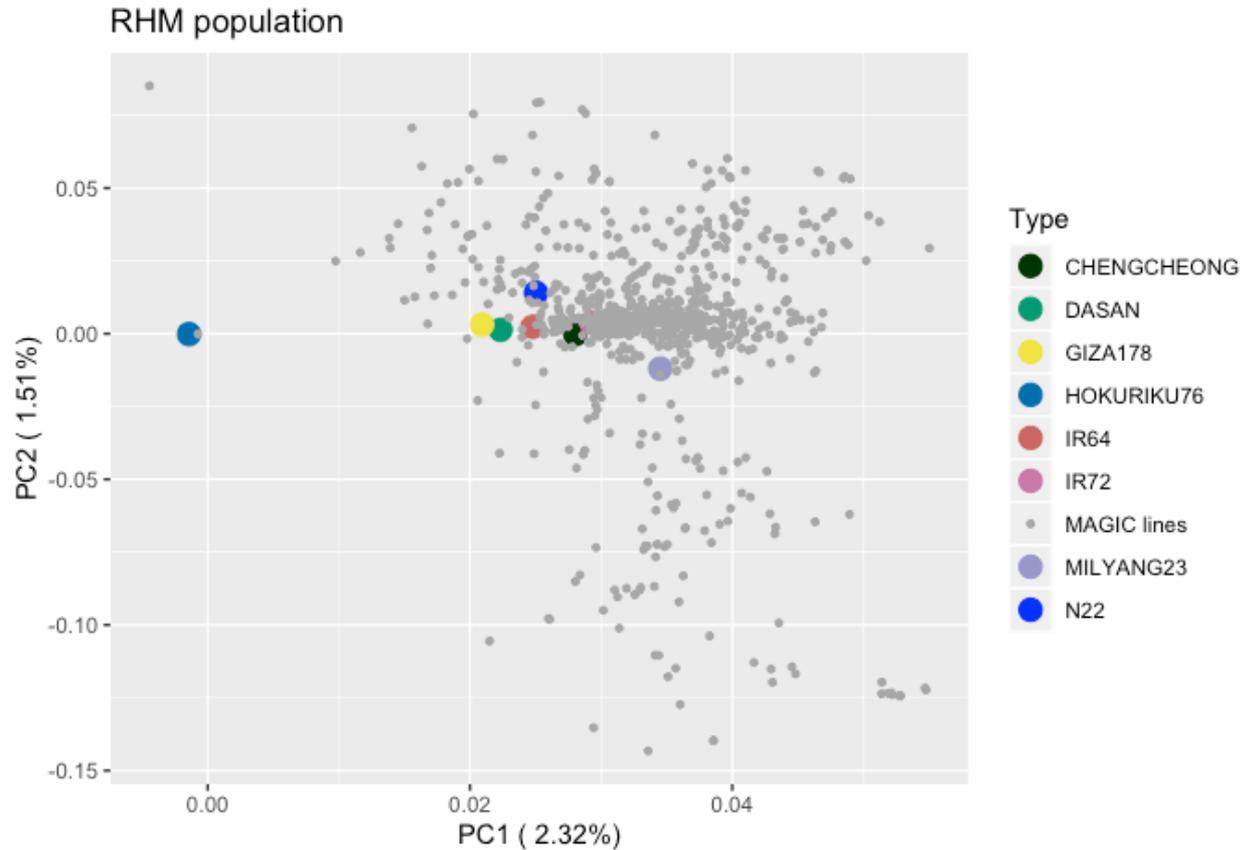
- IRRI Philippines
- Dry season 2017
- Irrigated field conditions



- Founders sequenced at coverage 11x to 15x paired end, average 13.5x.
- Over 2 million sites were called in founders.
- ~800,000 snps homozygous and polymorphic (maf = 0.125) in founders imputed MAGIC lines – STITCH.
- MAGIC lines sequenced at coverage 0.3x to 1x paired end, 345 above 1x coverage, average 1.4x.
- 6 MAGIC lines sequence coverage less than 0.3x and
- ~150,000 polymorphic snps maf = 3% and 836 MAGIC lines coverage  $\geq 0.3x$  used in analysis used for GWAS

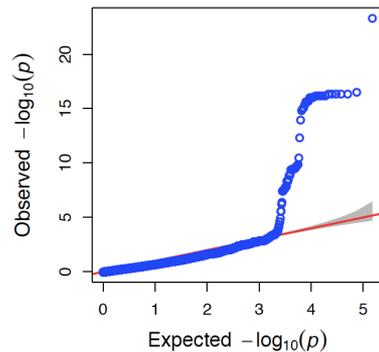
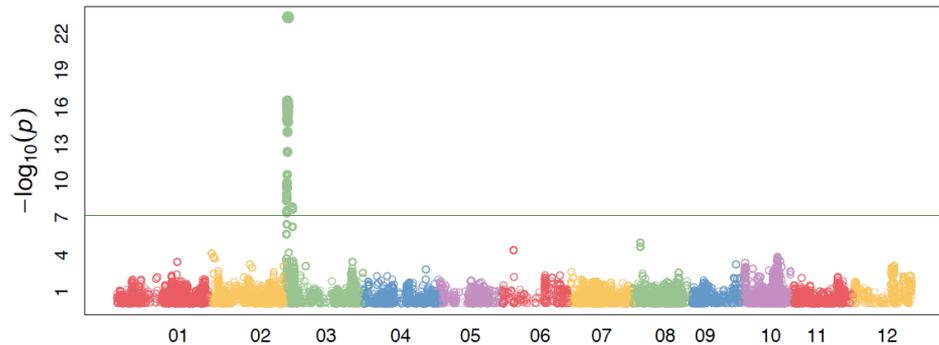


# Population variation

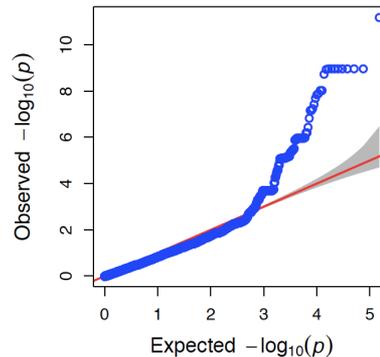
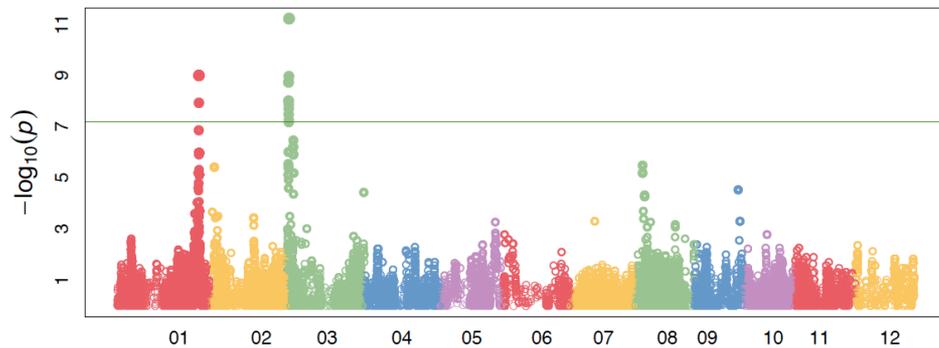


# Association mapping

## Days to flowering

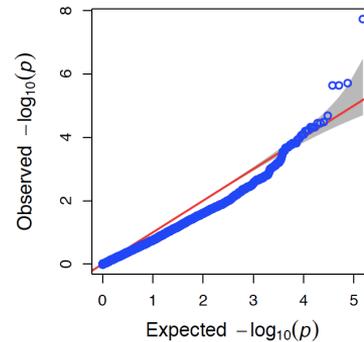
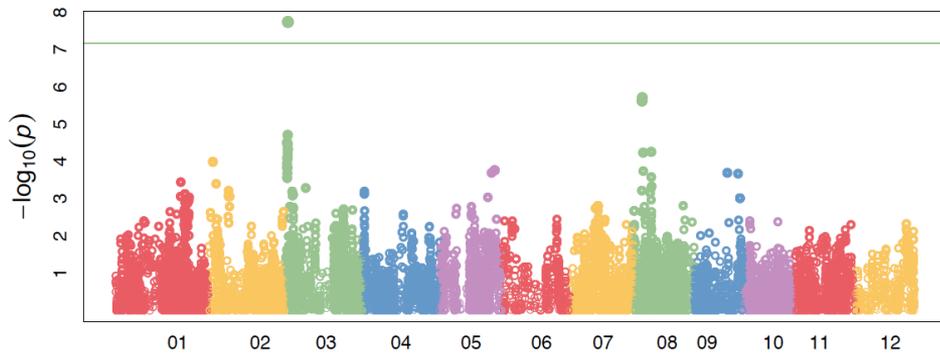


## Plant Height

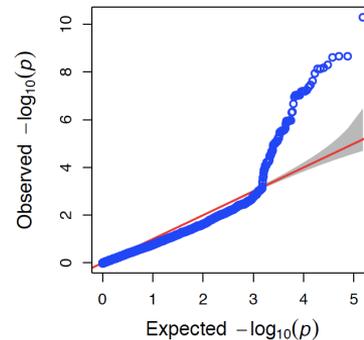
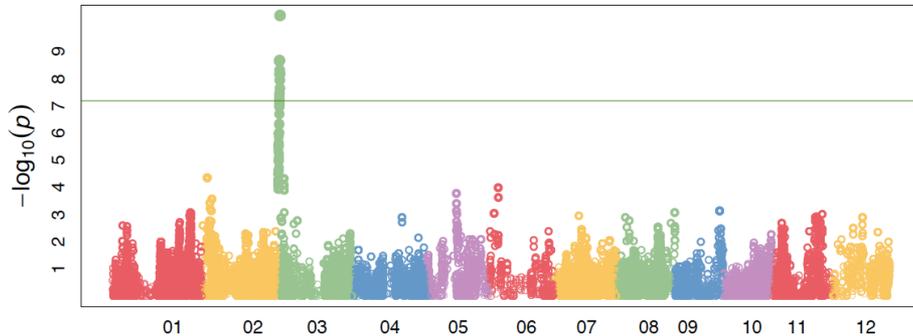


# Association mapping

## Yield

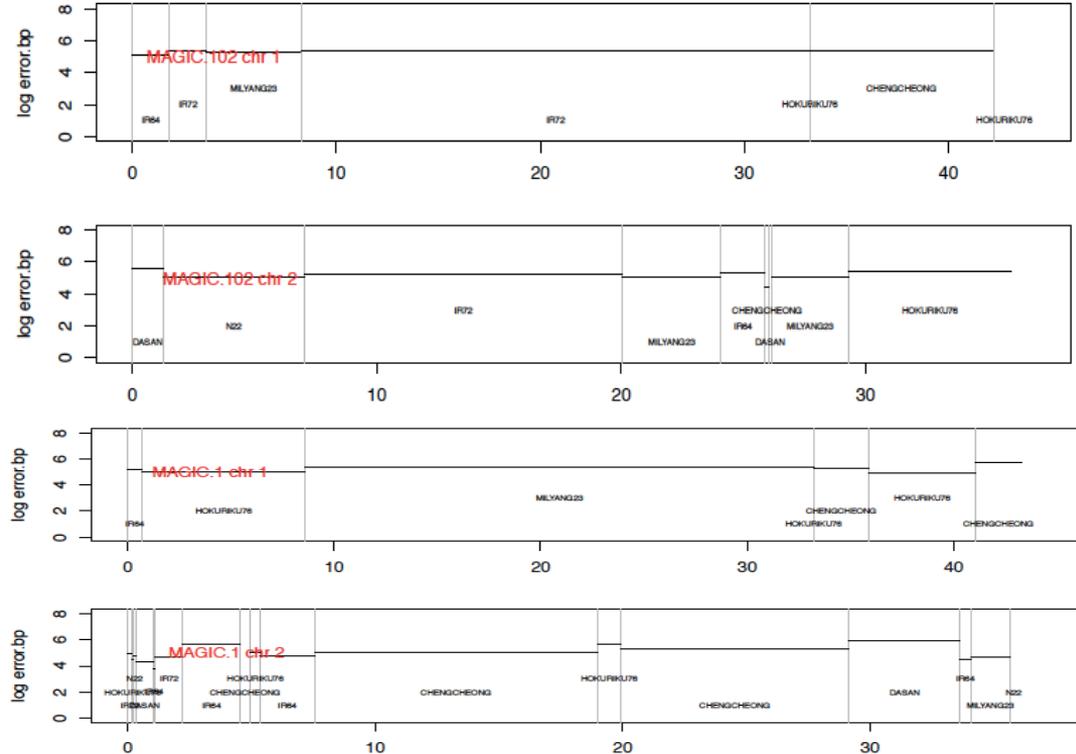


## Panicle length



## Reconstruction

- Estimates recombination break-points in the MAGIC lines.
- Impute founder haplotypes in the MAGIC lines.
- Perform SNP and haplotype GWAS on the imputed genome



STITCH - Founder snp dosage estimation at 800, 000 SNPs

- Genome-wide dosage mapping
- Haplotype dosage mapping – mixed model analysis

Reconstruction

- infer breakpoints from low-coverage sequence data
- impute the genomes of the MAGIC lines

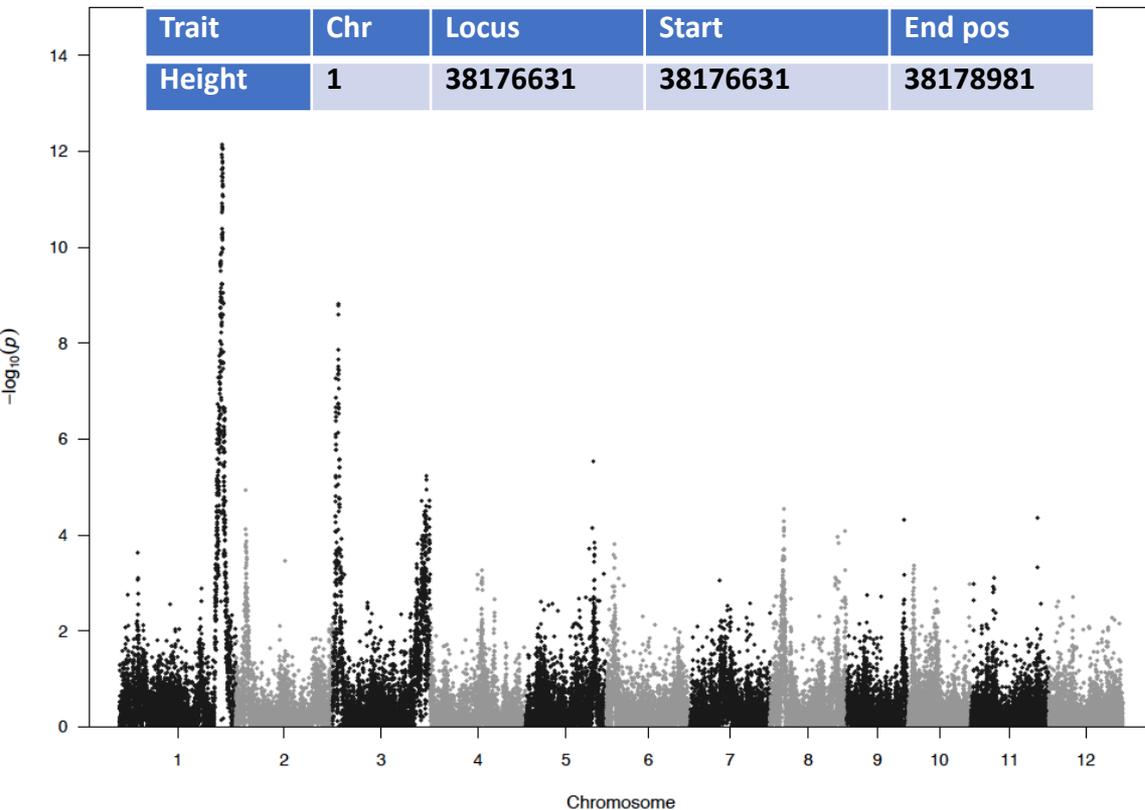
Genome scan

- perform SNP and haplotype association mapping on the imputed genome

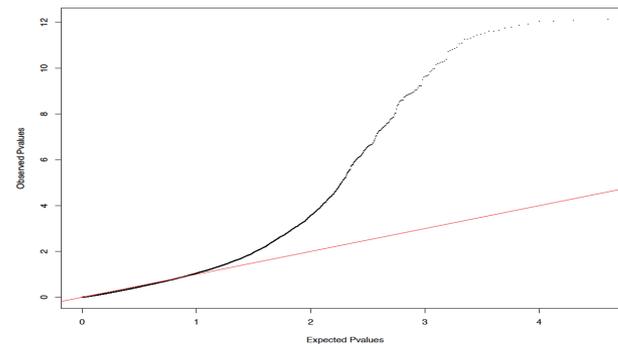
<http://mtweb.cs.ucl.ac.uk/mus/www/19genomes/MAGICseq.htm>

# Haplotype association mapping

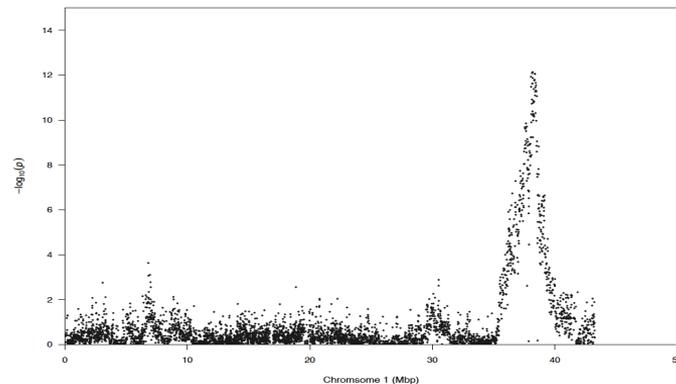
Height dosage GWAS



Height dosage QQplot



Height dosage GWAS\_Chrom1



- Low coverage sequence data in the MAGIC lines were imputed using genotype datasets
- QTLs have been identified underlying key morphological traits.
- QTLs consistently mapped using data from different imputation methods.

## Ongoing work

- Phenotyping and identification of QTLs underlying temperature stress related traits.

# Acknowledgements



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RK Singh



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**Thanks for listening**