

Rice ‘Heat MAGIC’ mapping

Funmi Ladejobi, Rakesh K. Singh*†, Kenneth McNally*, Hei Leung*, James Cockram**, Keith Gardener**, Richard Mott***

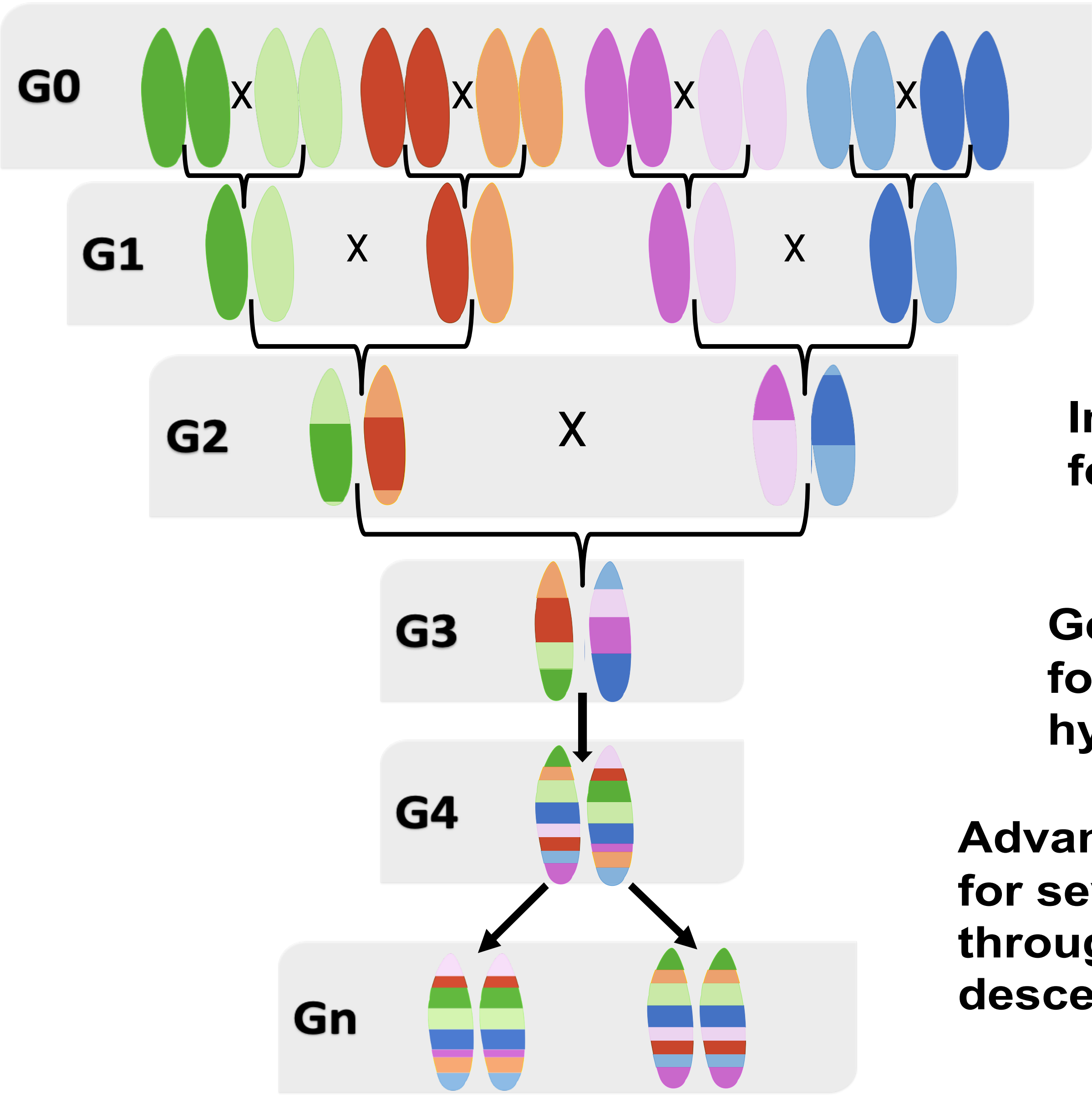
International Rice Research Institute (IRRI), Philippines; †International Centre for Biosaline Agriculture (ICBA), Dubai;

NIAB, Cambridge; *University College London



- The eight population founders were selected to capture temperature stress tolerance traits in the resulting population.
- Population recombined over four generations and inbred for several generations.
- Phenotype data for five agronomic traits collected in irrigated field conditions at IRRI, Philippines in dry season 2018/2019

Founders of the Rice Heat MAGIC population	
Variety	Agronomic Relevance
IR 64	Mega-variety in Asia with wide adaptability
GIZA 178	Popular rice variety in Egypt with high level heat tolerance
MILYANG 23	Very popular variety in Korea with wide compatibility and moderate tolerance to heat and cold
Chengcheong	Cold tolerant variety from Korea with poor heat tolerance
Dasan	Cold tolerant variety from Korea as well as heat tolerant in Japan
Hokuriku76	Cold tolerant variety
IR72	High yielding variety
N22	Highly heat tolerant variety



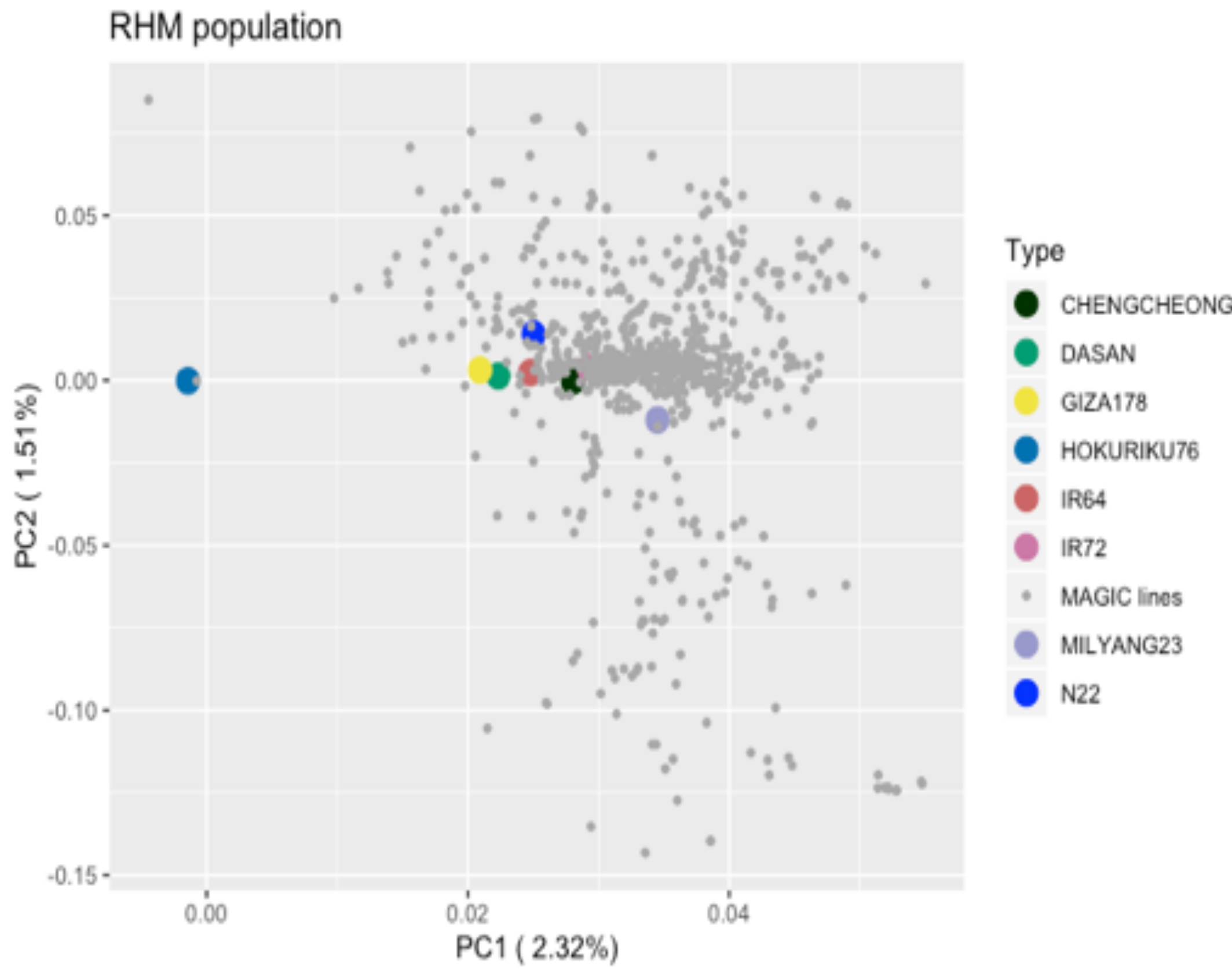
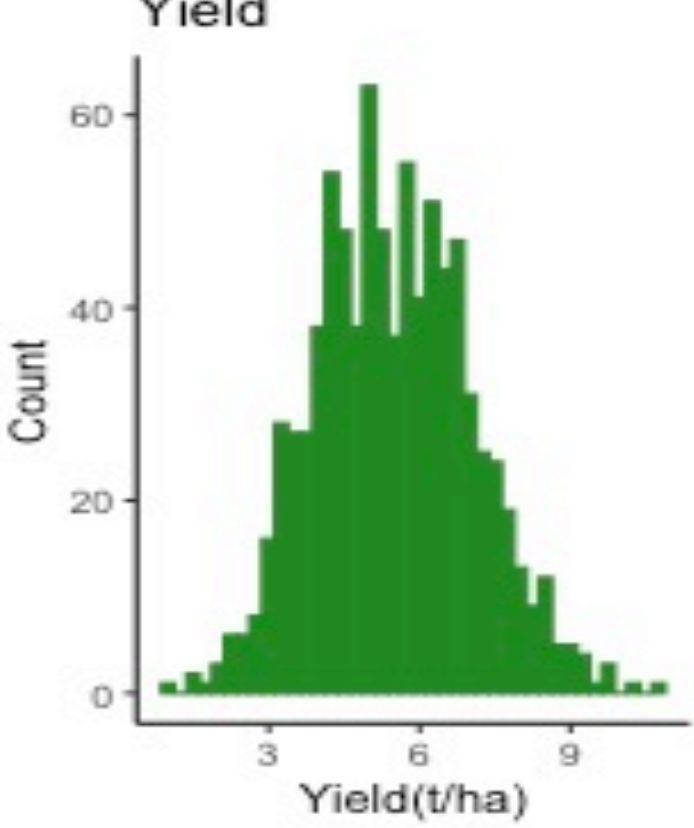
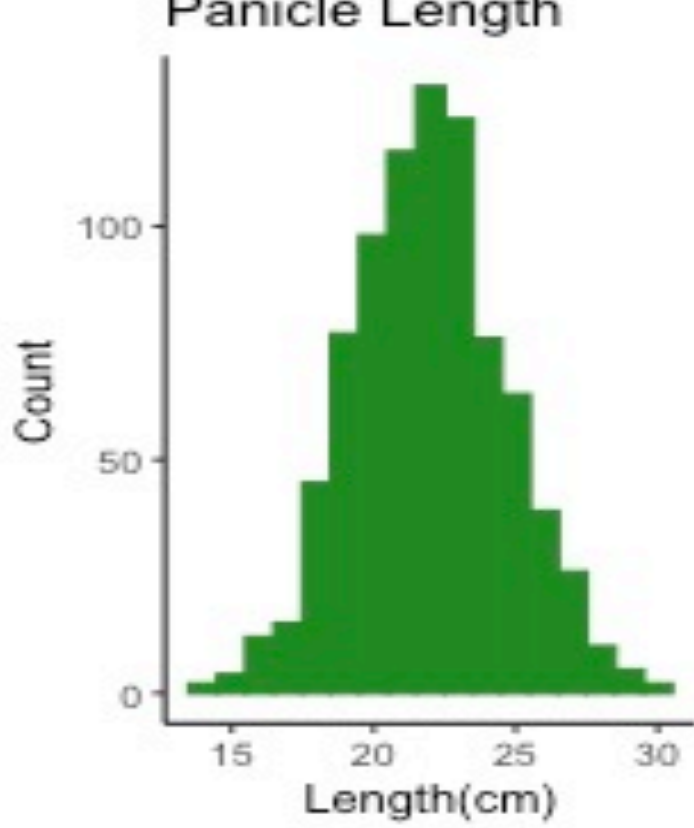
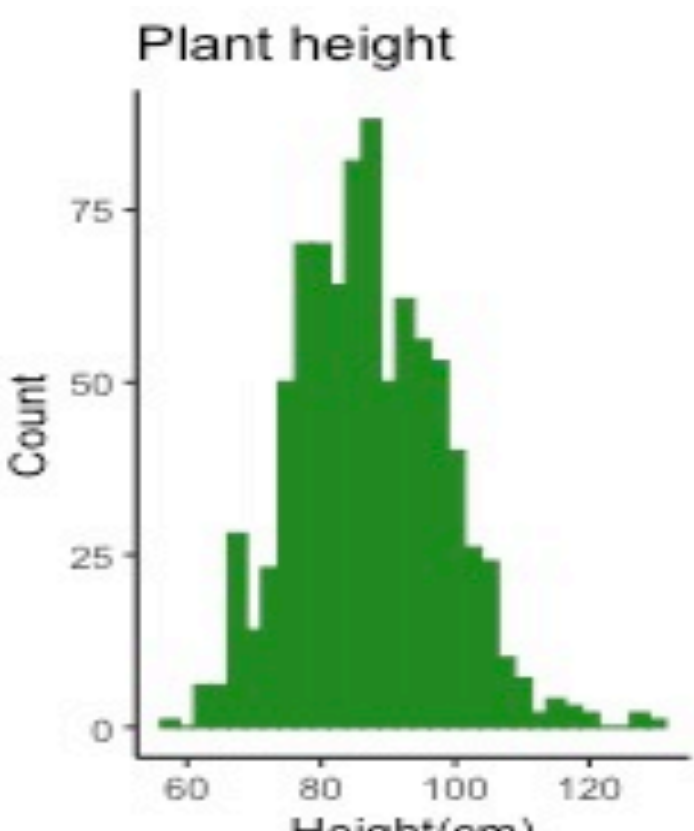
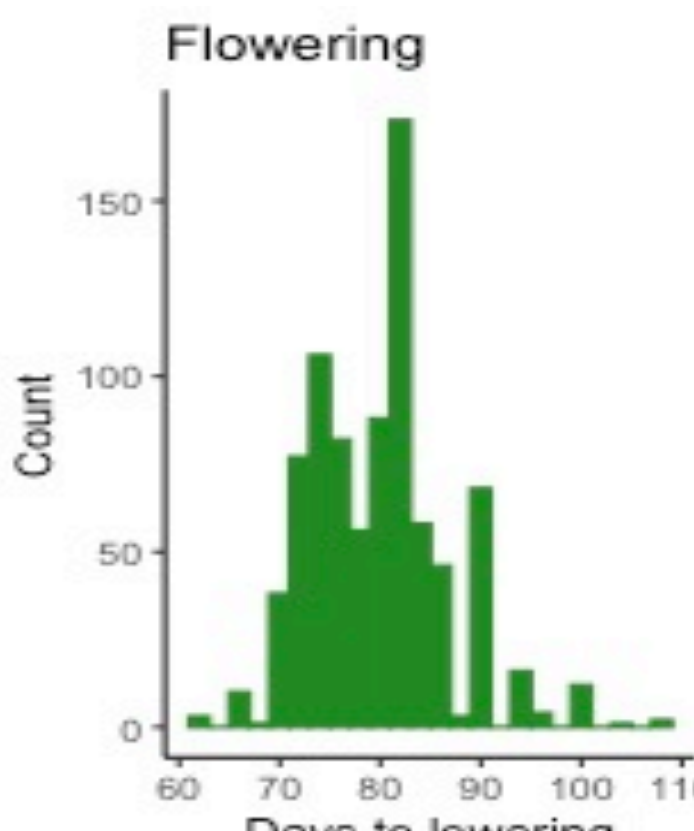
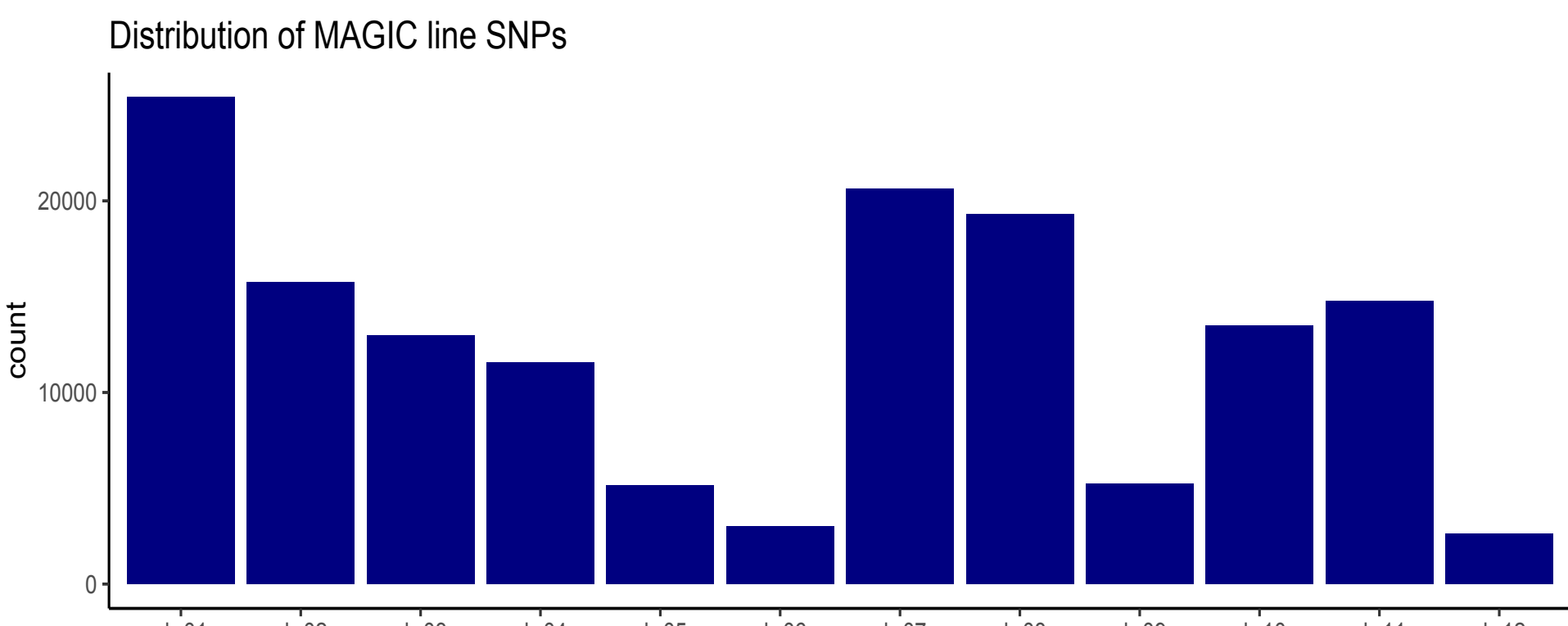
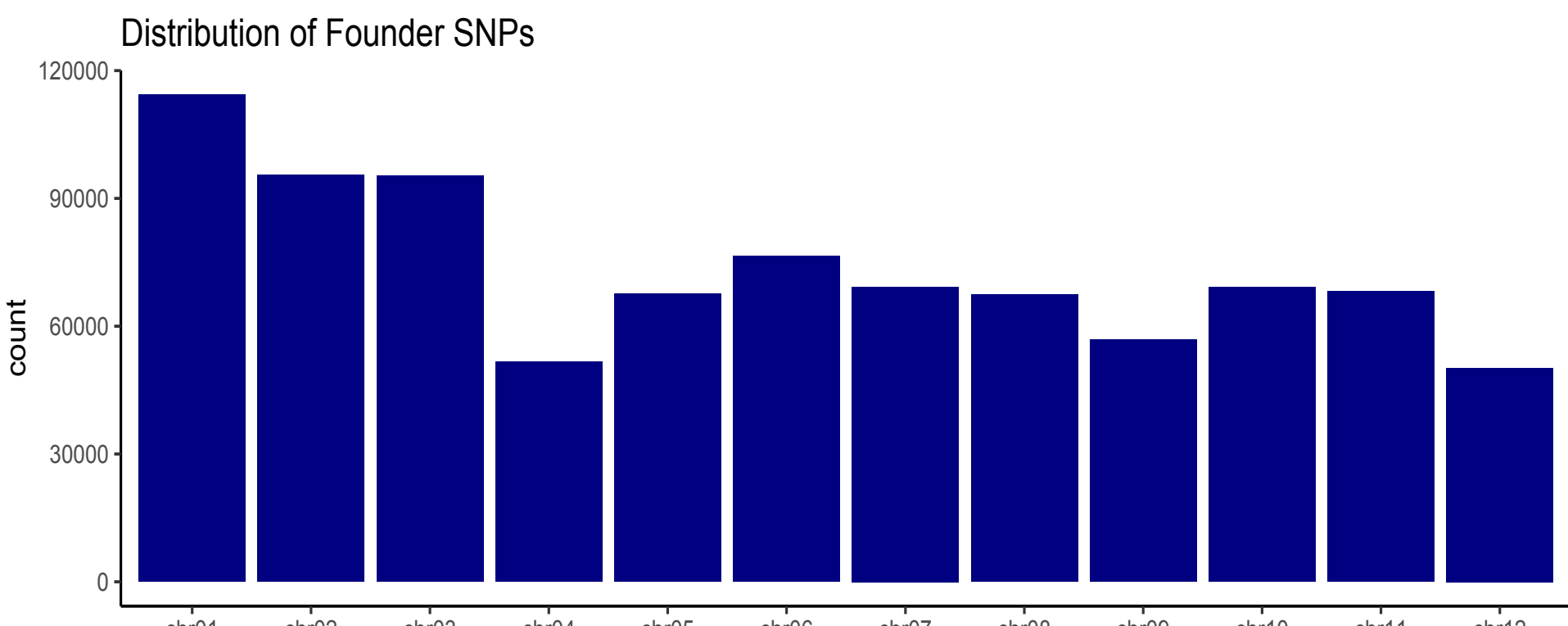
Half di-allele mating of founder lines to develop 28 hybrids

Intercross 28 hybrids

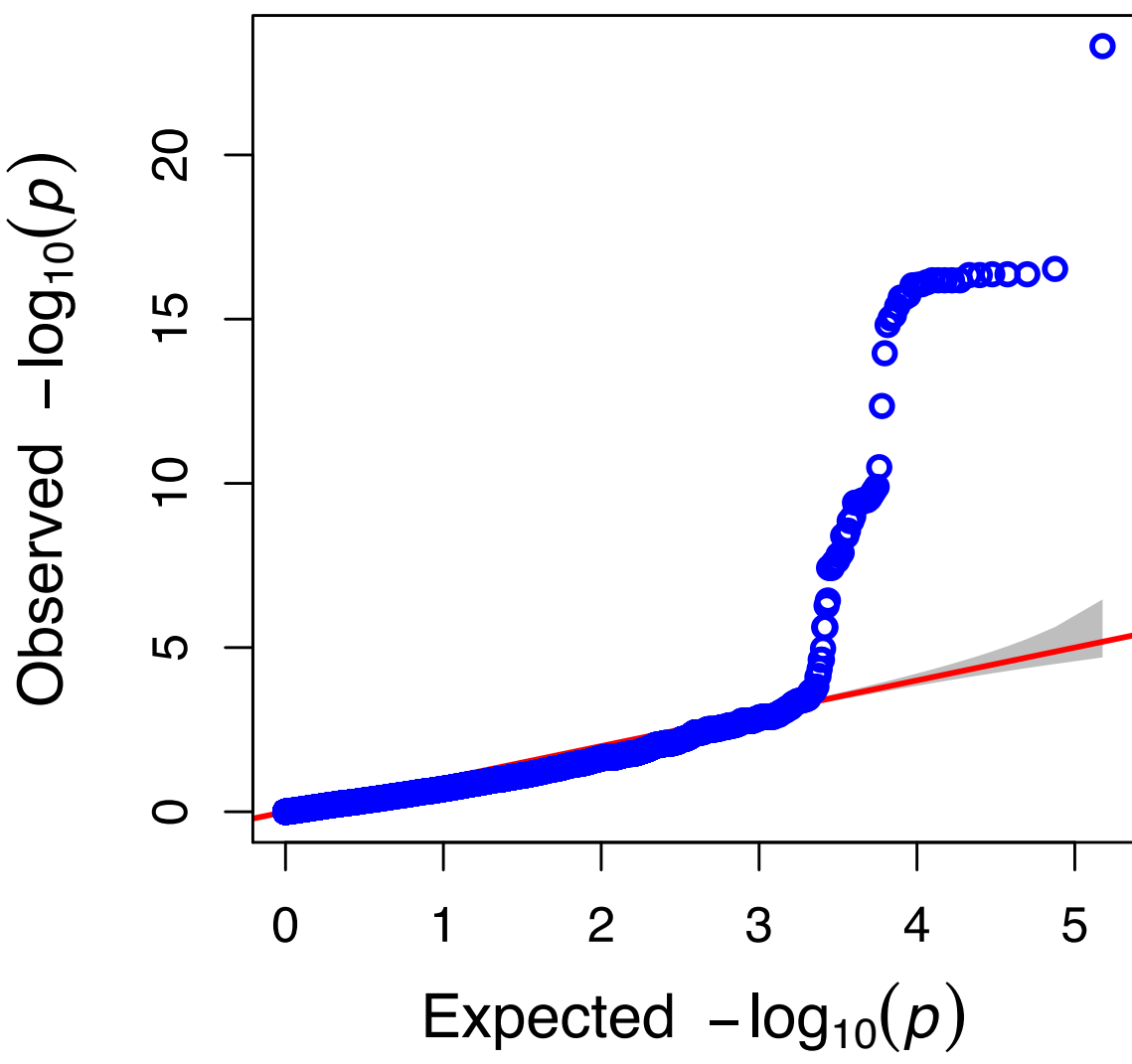
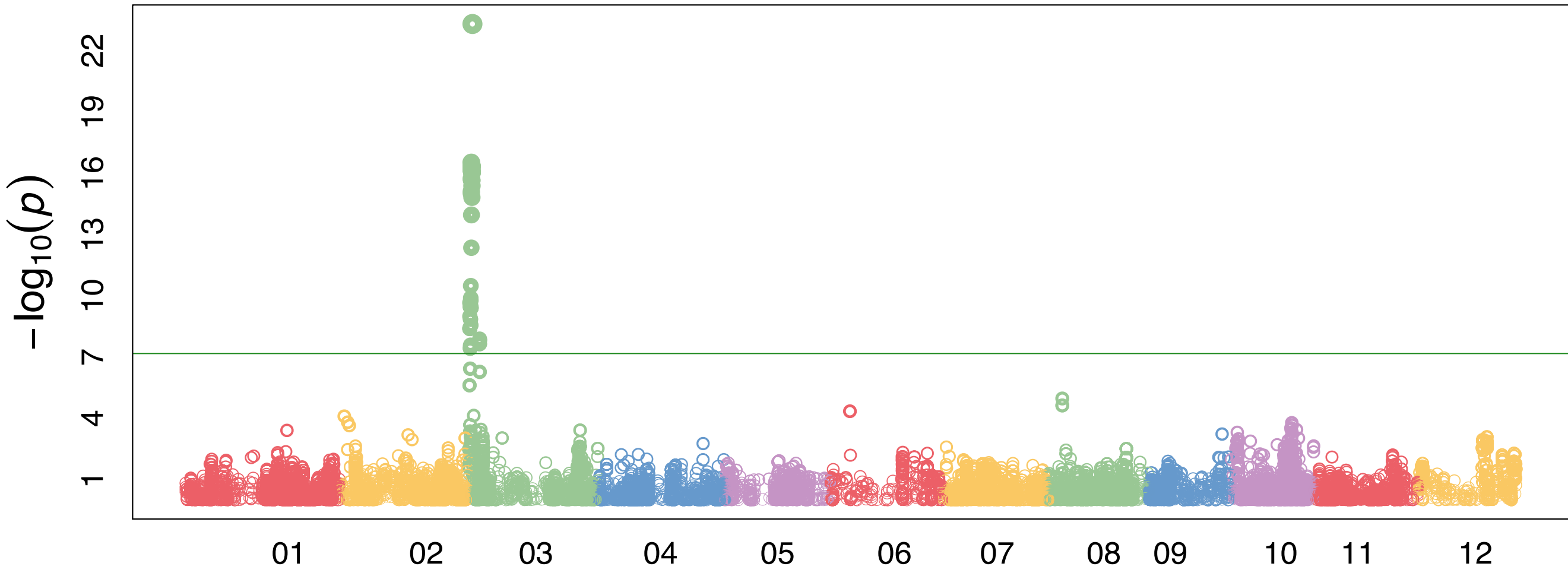
Intercross 70 4-founder hybrids

Generate 60 8-founder hybrids

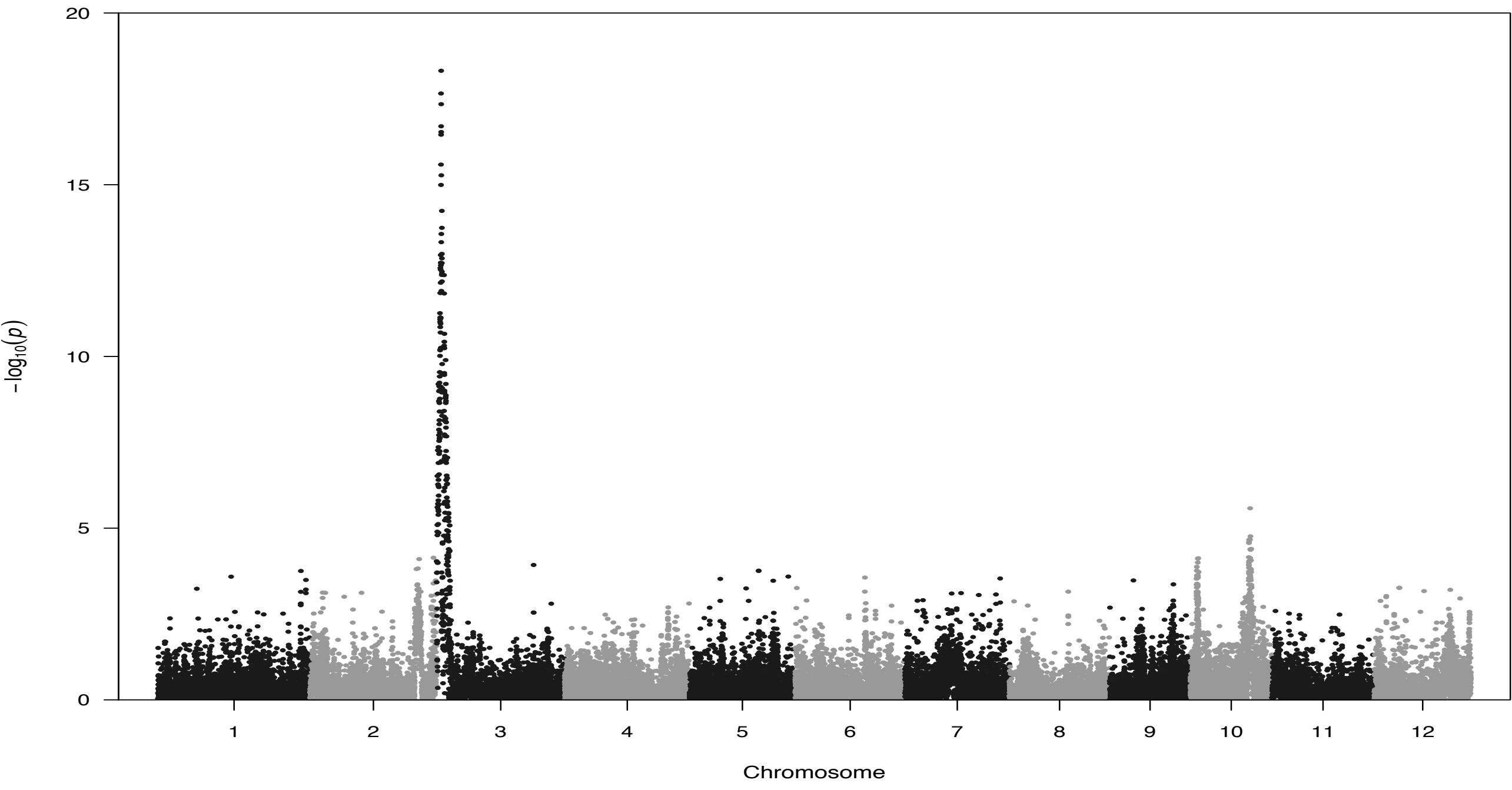
Advance 8-founder hybrids for several generations through single seed descent



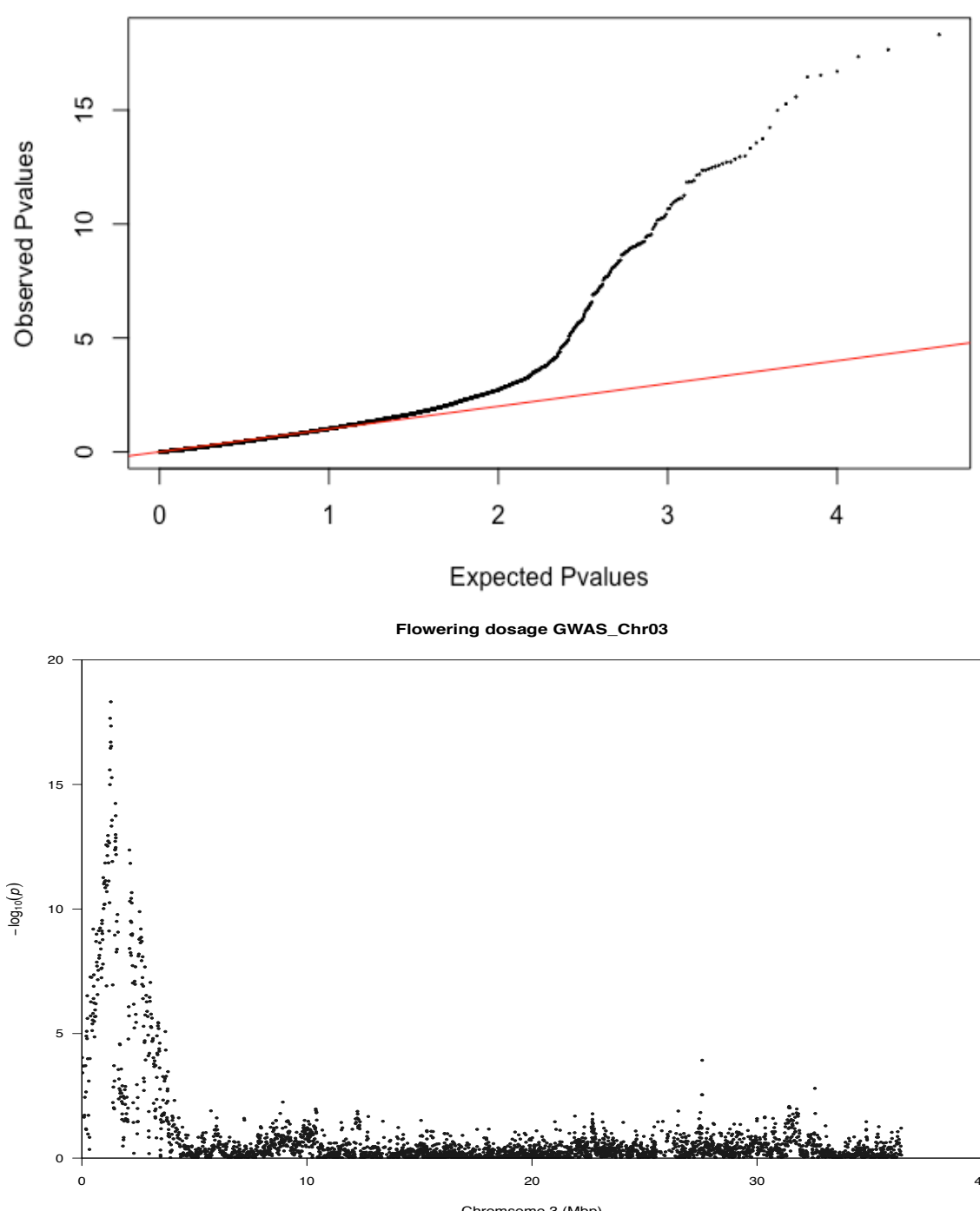
Days to Flowering



Flowering dosage GWAS



Flowering dosage QQplot



Genome-wide association mapping

- Founders sequenced at coverage 10x to 15x paired end.
- MAGIC lines sequenced at coverage 0.3x to 1x average coverage 1.4x paired end.
- ¹STITCH used to impute founder genotypes in the MAGIC lines.
- MAGIC lines SNPs filtered on 3% minor allele frequency.
- ²SNP based mixed linear modelling and ³haplotype based methods used to map QTLs to the same regions.
- Ongoing: Analysis of temperature-stress data in heat stressed and cold stressed environments.

References

1. Davies et al. 2016 – STITCH imputation
2. Lipka et al. 2012 – GAPIT for GWAS mixed linear modelling
3. Program RECONSTRUCTION – infers recombination breakpoints and conduct GWAS. <http://mtweb.cs.ucl.ac.uk/mus/www/19genomes/MAGICseq.htm>

