

# Genetic resources for the 16-founder NIAB MAGIC diverse wheat population

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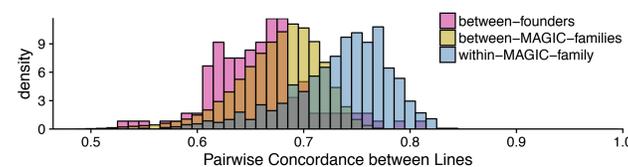
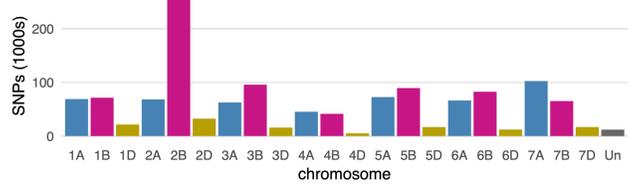
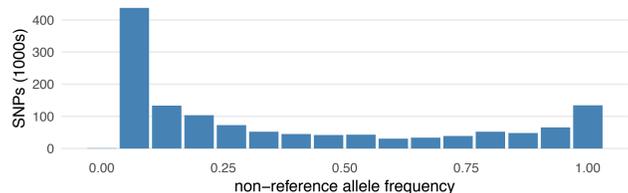
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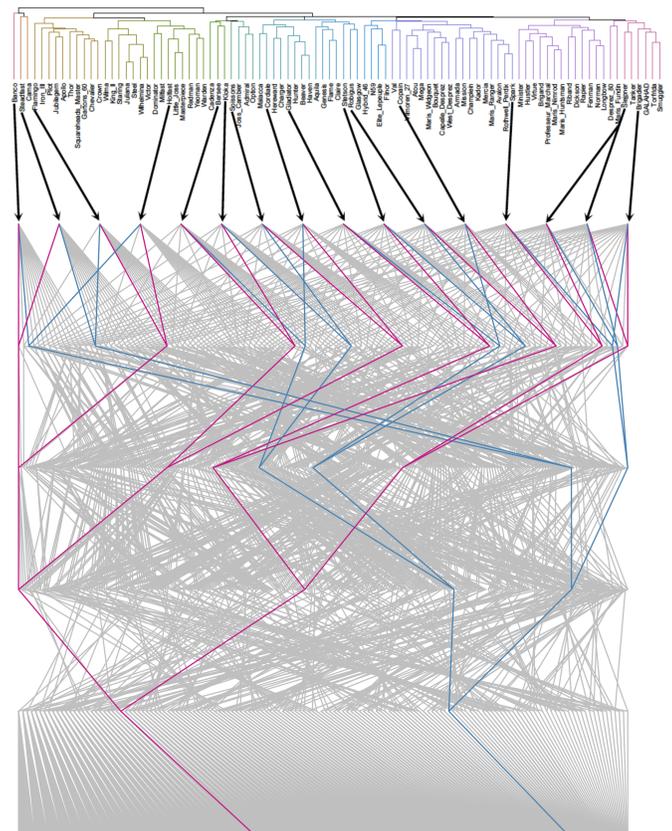
## Multi-parent Advanced Generation Inter-Cross

- 16 founder varieties (released between 1935 and 2004 in Northern Europe)<sup>1</sup> were chosen to maximize diversity captured
- Founders were intercrossed in 120 different ‘funnels’ followed by seven generations of selfing to produce 552 recombinant inbred lines in 120 ‘families’



- **Founders** sequenced to ~20x using exome capture<sup>2</sup>
- **Low Coverage WGS** of MAGIC lines to ~0.3x

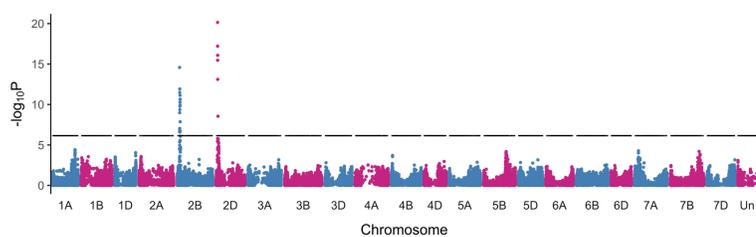
- **STITCH<sup>3</sup>** used to impute 1.1m SNPs with 99.5% call rate
- Median 97.9% concordance (median R<sup>2</sup>=0.944) against array<sup>4</sup>



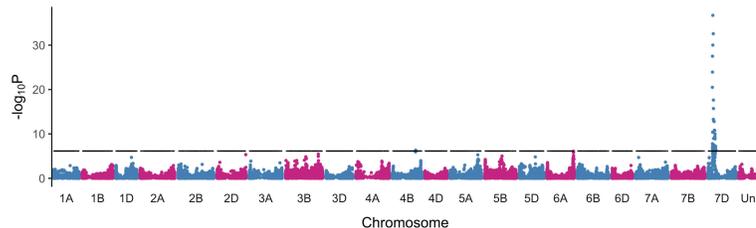
## Phenotyping and QTL Mapping

- Replicated yield trials with/without fungicide 2017/18 (x2 seed rates): 3,620 plots
- **114 phenotypes** for yield, phenology, size, seed traits, growth habit, colour, and yellow rust resistance
- **Germplasm and genotype/phenotype resources available<sup>5</sup>**

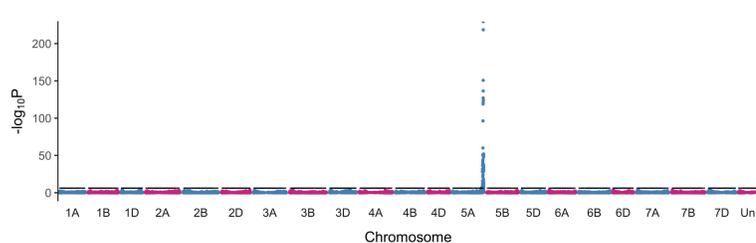
Heading Date



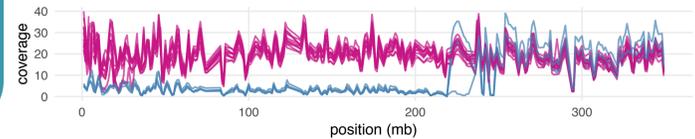
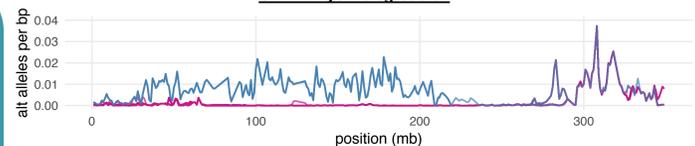
Stem Pigmentation



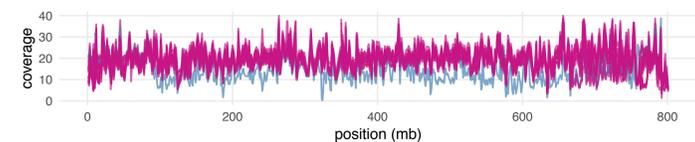
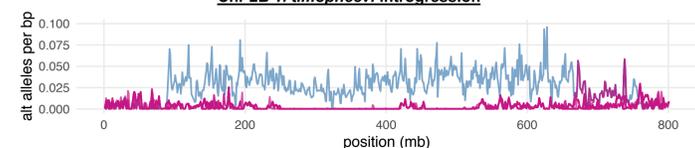
Awn Presence/Absence



Chr 1B Rye introgression

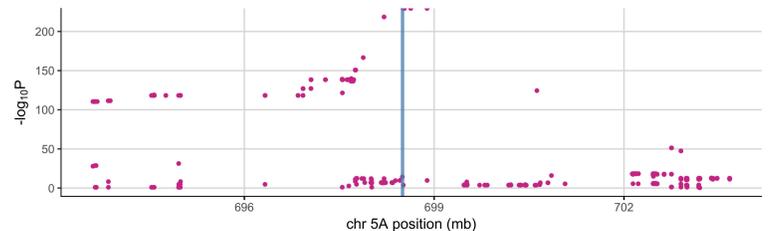


Chr 2B T. timopheevi introgression



- **Large introgressions** display low coverage, non-reference genotypes, co-inheritance and segregation distortion
- **Successfully map known and novel QTL**

mapping AWNS1 locus<sup>6</sup>



<sup>1</sup>Banco, Bersee, Brigadier, Copain, Cordiale, Flamingo, Gladiator, Holdfast, Kloka, Maris Fundin, Robigus, Slejpnor, Soisson, Spark, Steadfast, Stetson

<sup>2</sup>Gardiner et al. (2019), genic and promoter captures. 1.3m SNPs identified after filtering sites with heterozygous or missing calls, requiring that reads are properly paired with PHRED mapping quality scores greater than 30.

<sup>3</sup>Davies et al. (2016), imputed SNPs filtered to have MAF>2.5% and <0.1 missingness

<sup>4</sup>Using Affymetrix Wheat Breeders' 35k SNP genotyping array (Allen et al. 2016)

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<sup>6</sup>Three genes within QTL peak, including AWNS1 (blue) DeWitt et al. (2019)

