

# Imputation and QTL Mapping in Multiparental Crop Populations from Low Coverage Sequence Data

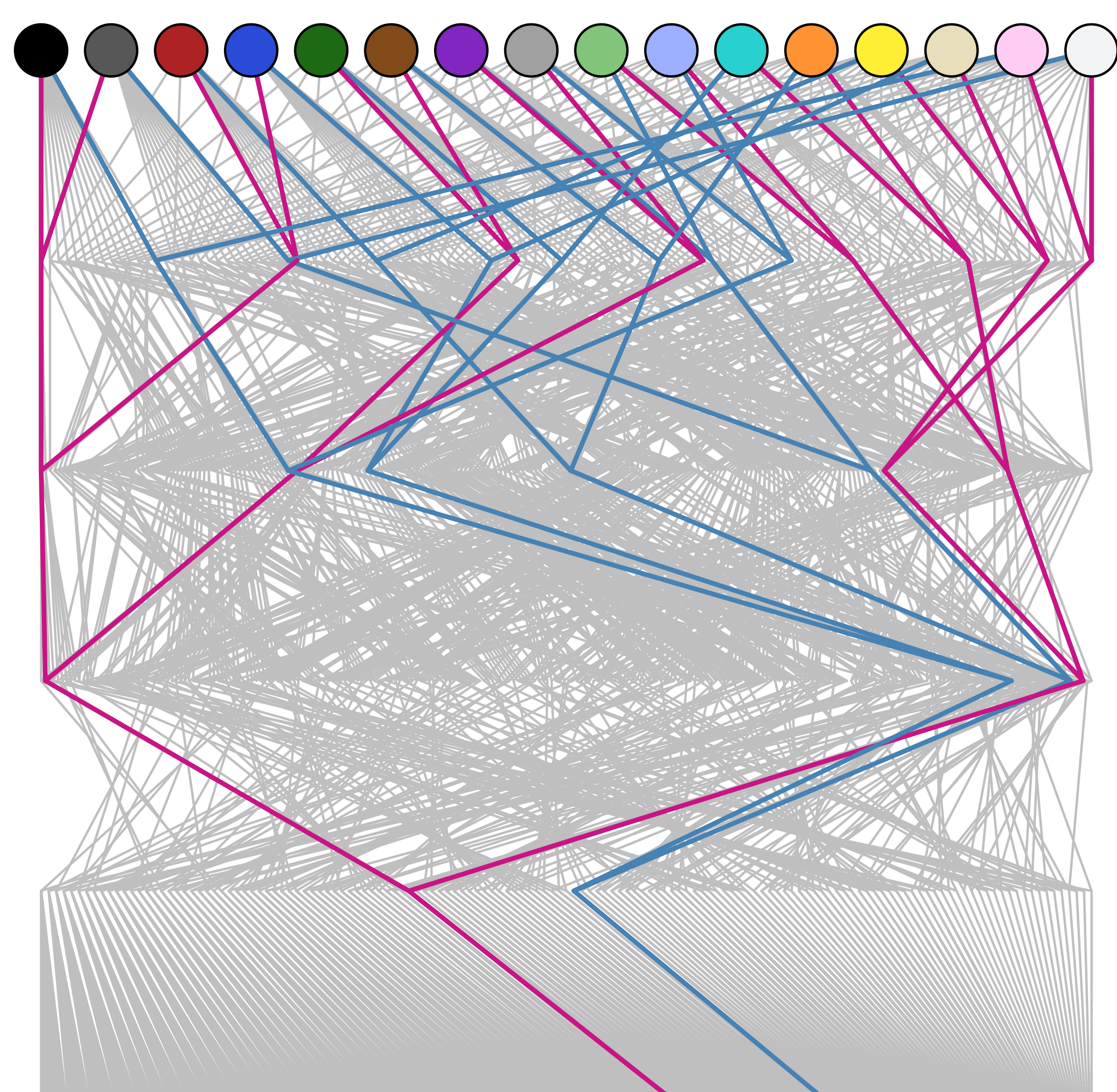
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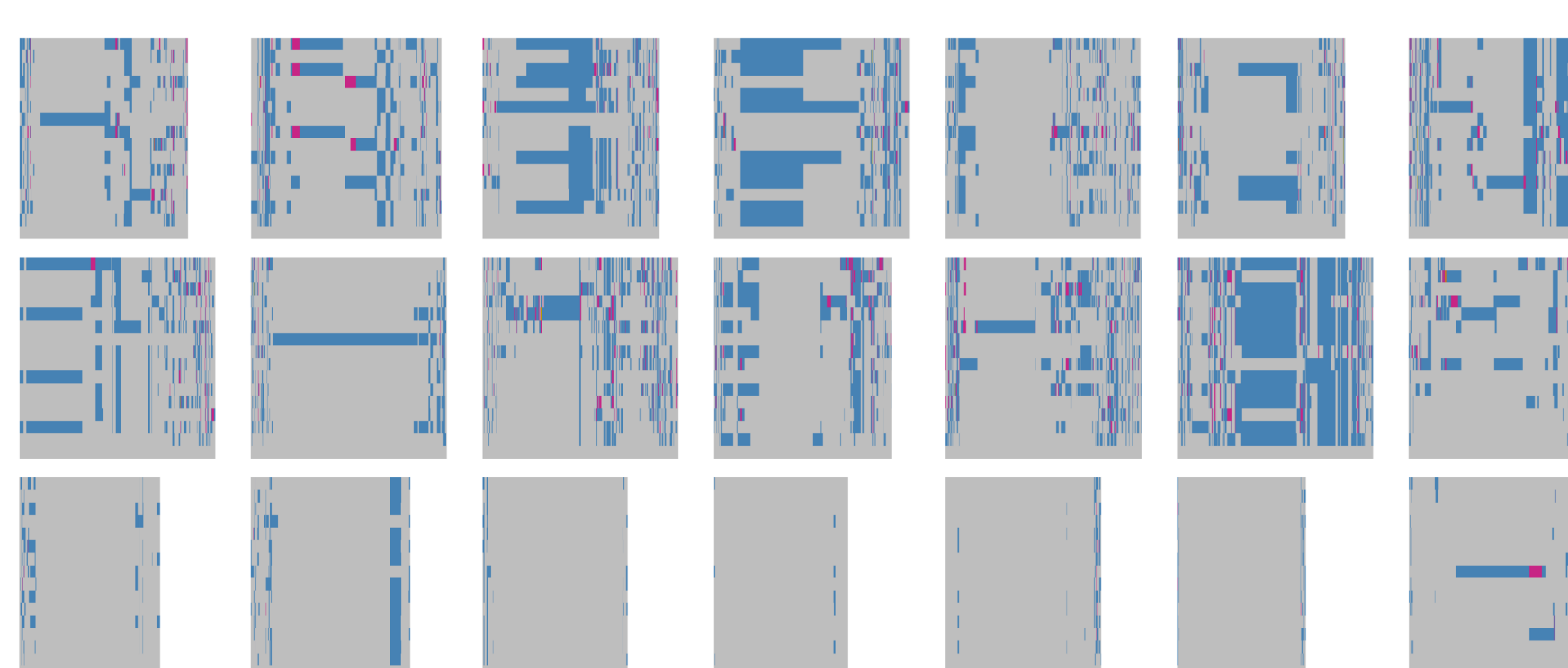


## Multiparental crop populations

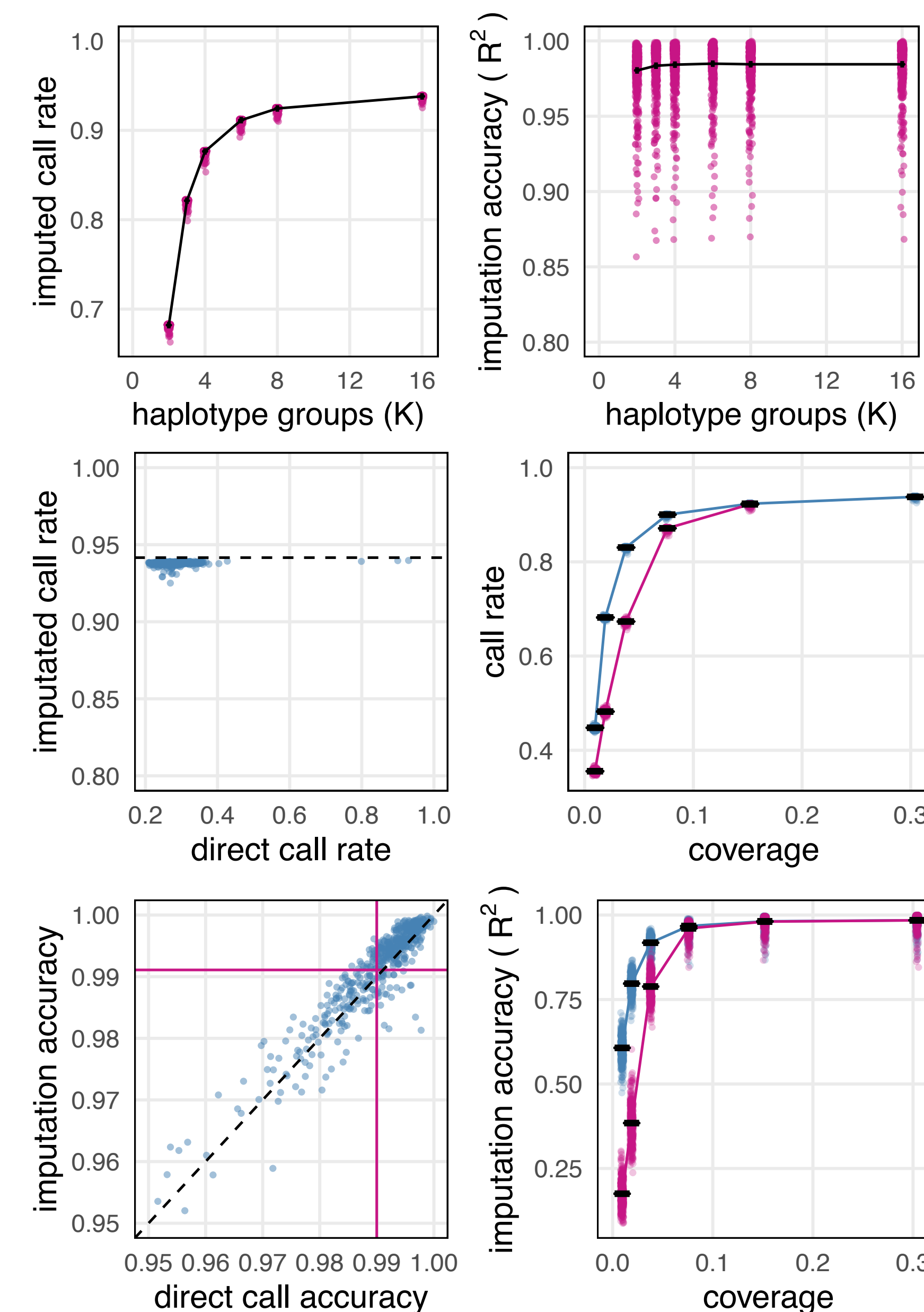
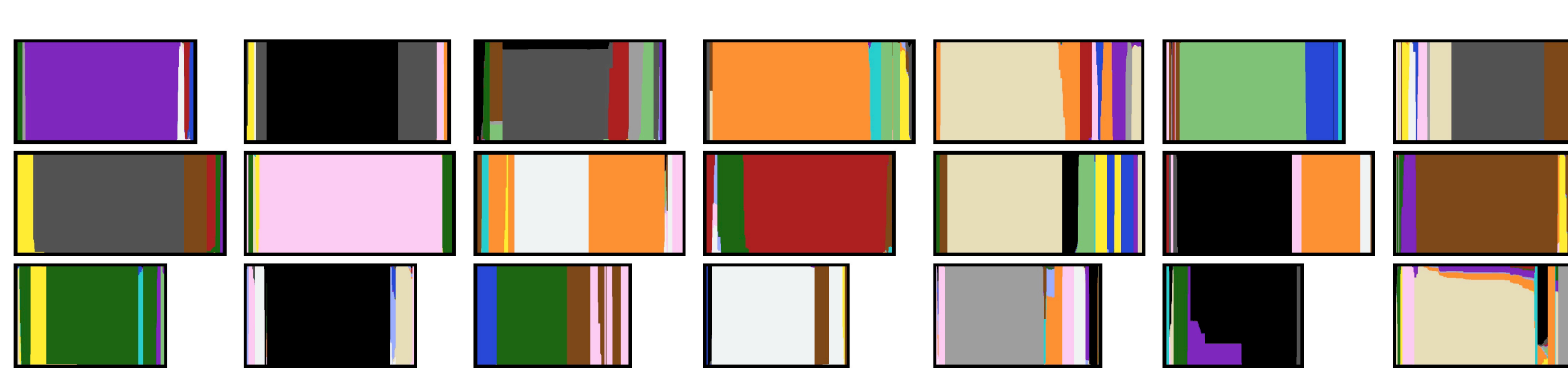
- **NIAB Diverse MAGIC wheat** - 16 founders released between 1935 and 2004 intercrossed in 120 different 'funnels' to produce 504 recombinant inbred lines
- **IRRI Heat MAGIC rice** – 8 founders selected for variation in tolerance to temperature<sup>2</sup>, 836 recombinant inbred lines



**Founders** sequenced using exome capture to 20x (wheat)<sup>3</sup> or WGS to 13.5x (rice)<sup>4</sup>



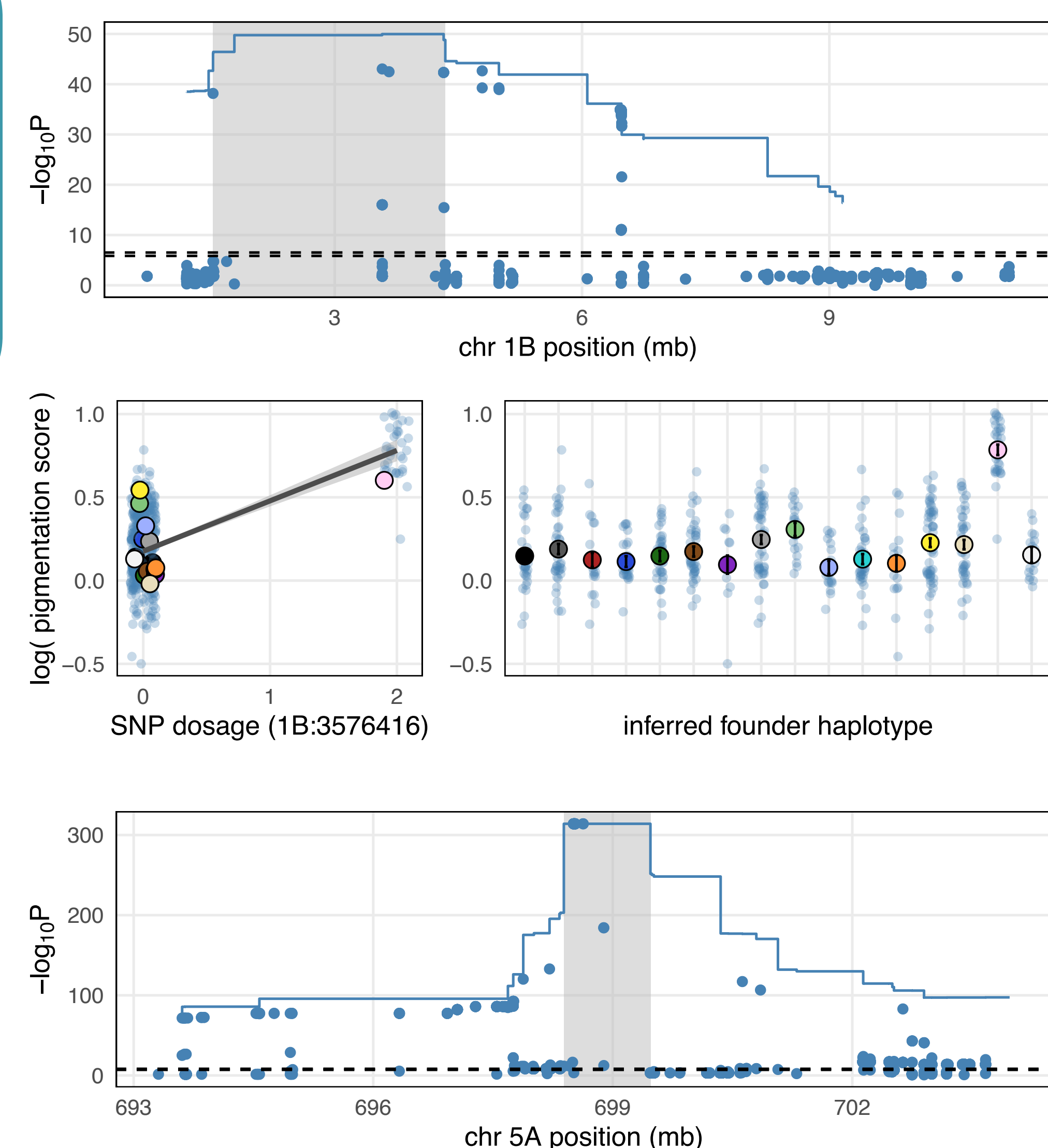
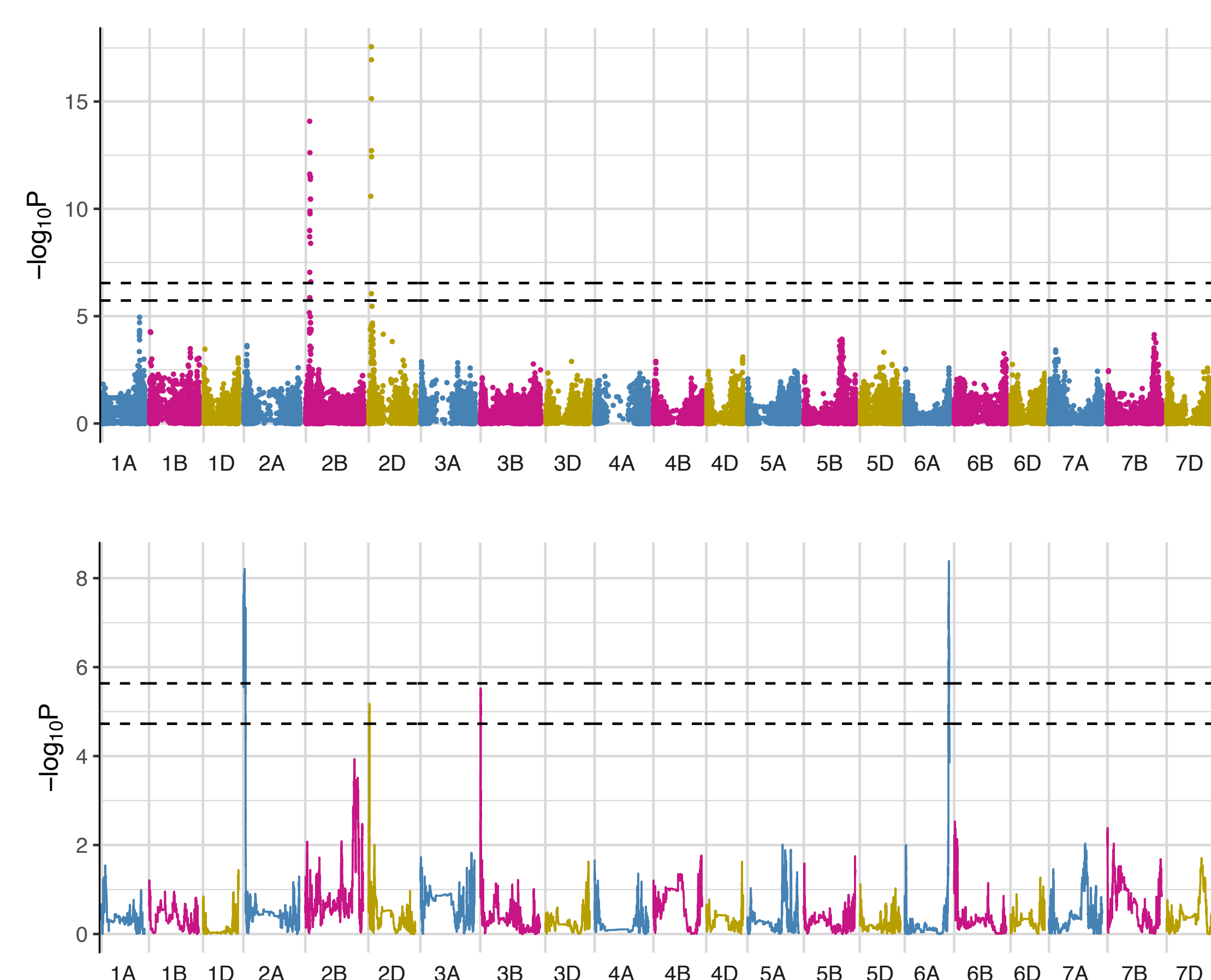
**Low Coverage WGS** of MAGIC lines to ~0.3x (wheat) or 1.4x (rice) used to infer recombination mosaics<sup>5</sup>



- High imputation accuracy **with or without** founder information<sup>6</sup>
- Downsampling indicates coverage as low as 0.1x is sufficient

## Phenotyping and QTL Mapping

- Wheat phenotyped for >50 agronomic traits (yield, phenology, size, seed traits, growth habit, colour, resistance) in replicated yield trials in 2017 and 2018
- Rice phenotyped for yield, height, tillers, flowering time, and panicle length at IRRI, 249 lines also measured at four further locations to characterize heat tolerance<sup>7</sup>



- **Fine-mapping** of known and novel QTLs facilitated by extra generations of recombination in multiparental populations<sup>8</sup>
- Associations with **imputed SNPs** and **inferred founder**



<sup>1</sup>Banco, Bersee, Brigadier, Copain, Cordiale, Flamingo, Gladiator, Holdfast, Kloka, Maris Fundin, Robigus, Slejpner, Soisson, Spark, Steadfast, Stetson.  
<sup>2</sup>IR64, IR72, Milyang23, Dasan, Hokuriku76, N22, IR72, Giza178.  
<sup>3</sup>genic and promoter captures from Gardiner et al. (2019): 1.2m SNPs homozygous and non-missing in all founders.  
<sup>4</sup>800,000 SNP sites homozygous and non-missing in all founders.  
<sup>5</sup>Imputation using STITCH (Davies et al., 2016), filtered to have info score >0.4, MAF>2.5%, and <10% missing  
<sup>6</sup>Accuracy against Affymetrix Wheat Breeders' 35k SNP genotyping array (Allen et al. 2016)  
<sup>7</sup>Lalpur, Bangladesh; Tanore, Bangladesh; Kyaukse, Myanmar; Yezin, Myanmar  
<sup>8</sup>For example, four genes within QTL peak for Awns, including AWNS1, DeWitt et al. (2019)

