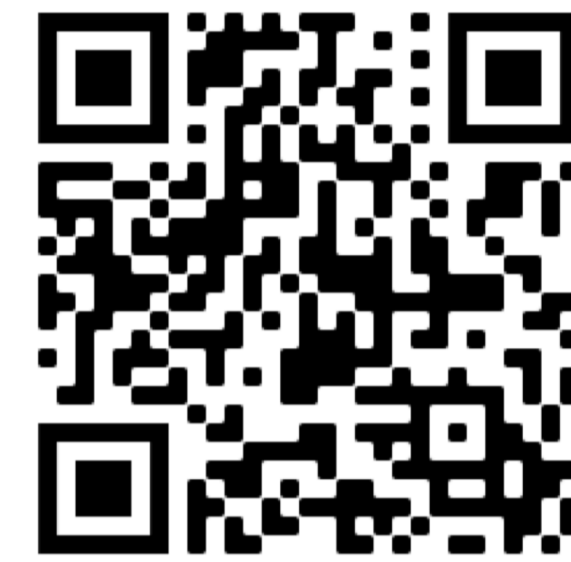
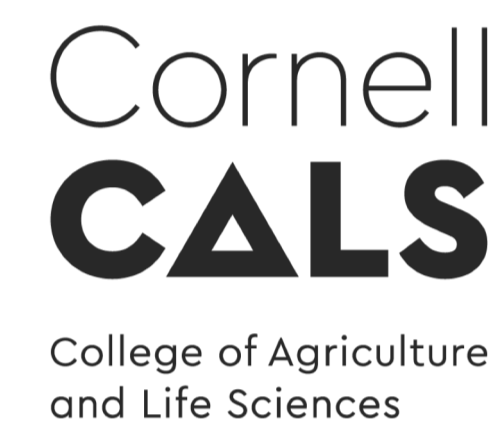


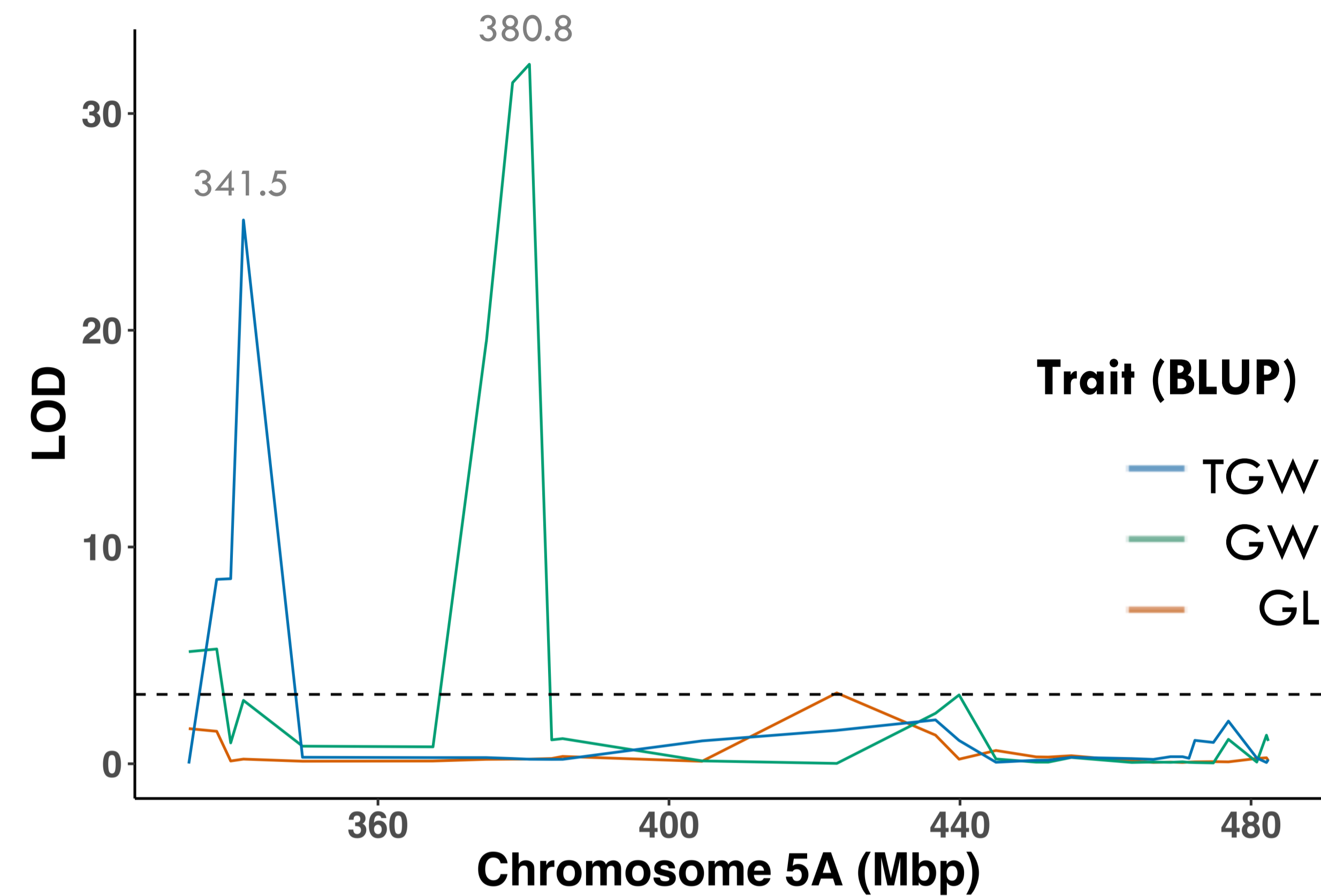
# Integrating Multi-omics Data to Fine-map Wheat Grain Weight and Morphology Genes

**Ella Taagen and Dr. Mark Sorrells**

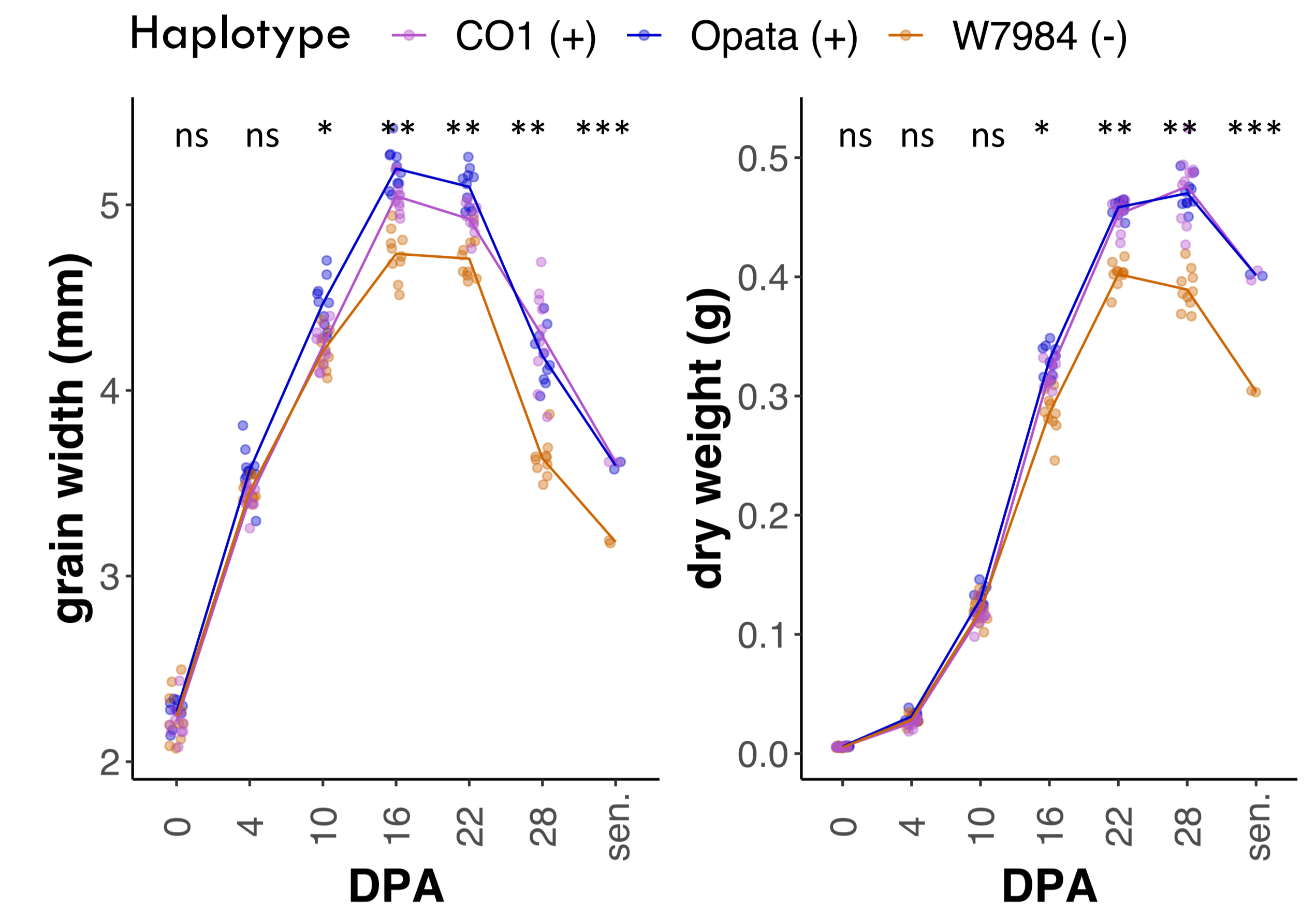
Section of Plant Breeding and Genetics  
Cornell University, Ithaca, NY, USA



**1** Fine-Mapping resolves neighboring QTL for thousand grain weight (TGW) and grain width (GW) on chromosome 5AL W7984 x Opata RILs



**2** Grain development phenotype reveals < 10 days post anthesis (DPA) is optimum time for transcriptome analysis in greenhouse.



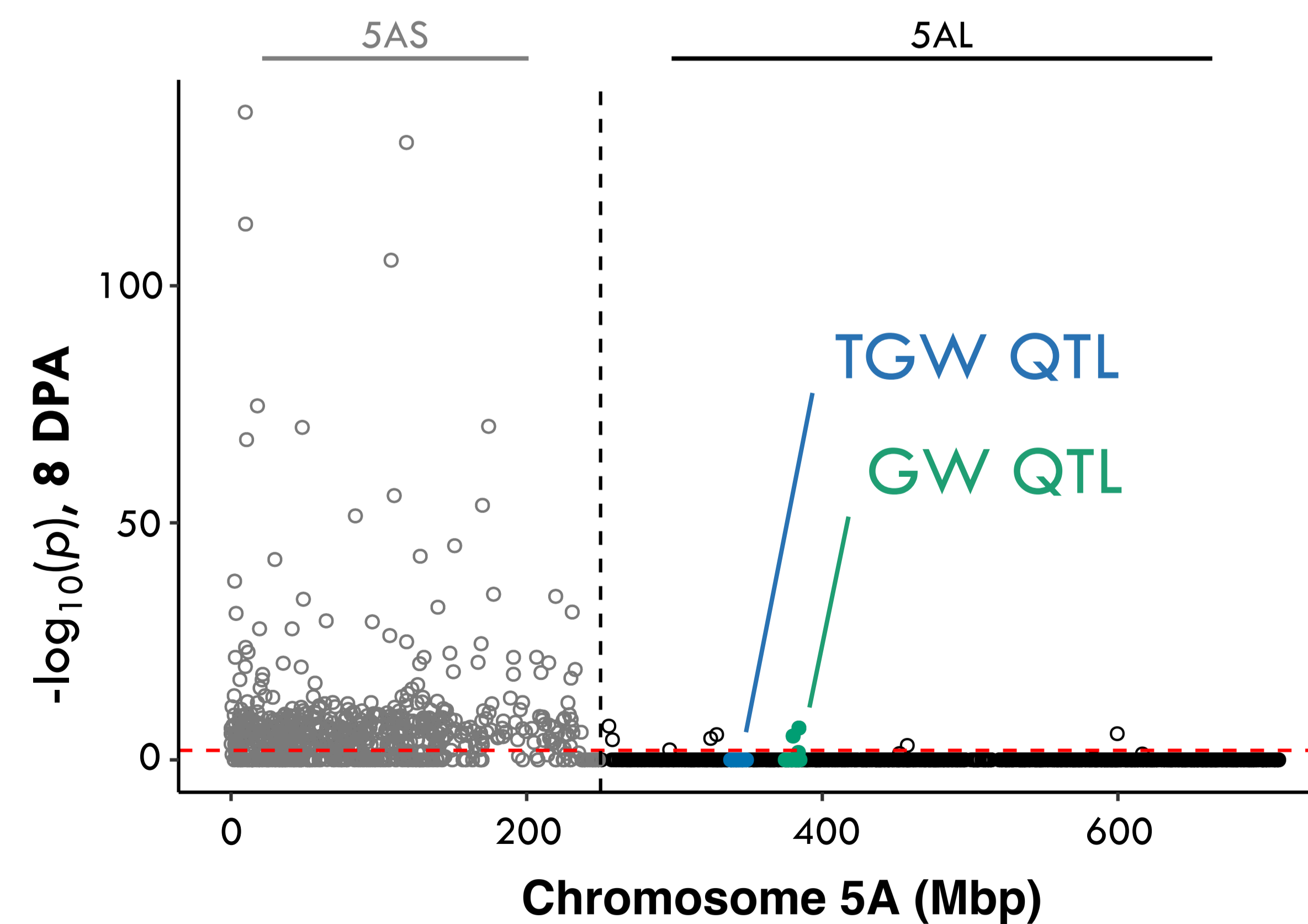
**3** In progress:

Developing grains harvested from **haplotypes** at **4 & 8 DPA**, RNA extracted and submitted to Novogene for RNA-seq.

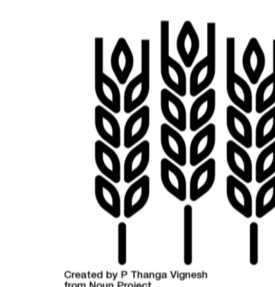
Haplotypes (subset): O: Opata, W: W7984

	334.0	337.8	339.7	341.5	349.6	367.5	374.8	378.5	380.8	383.8	385.3	404.5
Mbp												
Opata	O	O	O	O	O	O	O	O	O	O	O	O
W7984	W	W	W	W	W	W	W	W	W	W	W	W
CO1	O	O	O	O	O	O	O	W	W	W	W	W

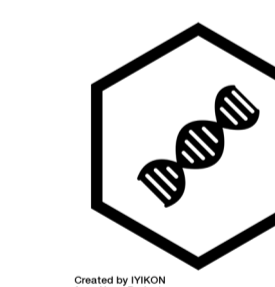
Differential expression for Opata and W7984 haplotype identifies **5AS is missing for W7984**, in agreement with *Gutierrez-Gonzalez et al. 2019*.



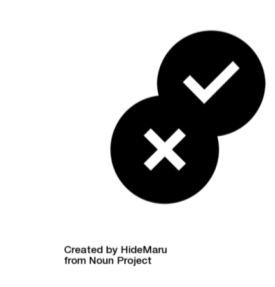
**4** Next steps:



Validation with 2020 field phenotypes



Examine read sequence, signs of post transcriptional modifications?



Impact of 5AS presence/absence on homeologs and genome-wide expression



Ultimately, release selectable marker for wheat breeders