



Haplotype-Informed Prediction of Fusarium Head Blight Resistance in USA Wheat Breeding Programs

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Introduction

- Fusarium head blight (FHB) of wheat and barley are caused by *Fusarium graminearum*
- FHB resistance in adapted wheat (*Triticum aestivum*) is a major challenge in wheat production.
- FHB resistance is mainly controlled by minor effect QTLs; therefore, genomic selection (GS) is the most effective approach to simultaneously select for multiple QTLs in breeding programs.
- Practical haplotype graph (PHG) database is used to impute haplotypes and missing variants for skim exome capture sequence breeding lines to identify and map novel QTLs for FHB resistance in breeding programs.

Methods

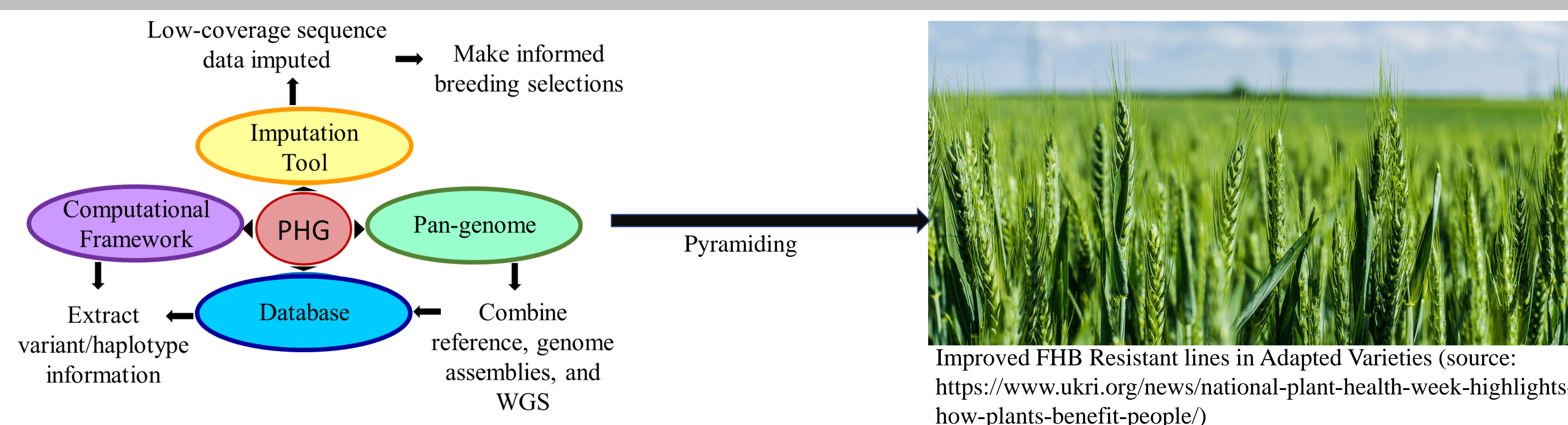


Figure 1: Schematic representation of workflow in building PHG database that carries resistant alleles to identify novel FHB resistant haplotypes/QTLs (PHG= Practical haplotype graph).

Plant Material & *Fusarium graminearum* Field Inoculation

- A panel of 270 wheat cultivars from across the USA (Figure 2) wheat production areas including all market classes: soft, hard, winter, and spring varieties.
- Fusarium graminearum* inoculum was prepared in the laboratory under sterile conditions and inoculated across the experimental plots uniformly in three intervals namely April 15th, May 1st and May 15th.
- Moisture conditions were maintained with sprinklers to get perithecia development and infection.
- These cultivars were grown in the field and evaluated for disease severity (Figure 3A) and fusarium damaged kernel (FDK) (Figure 3B).

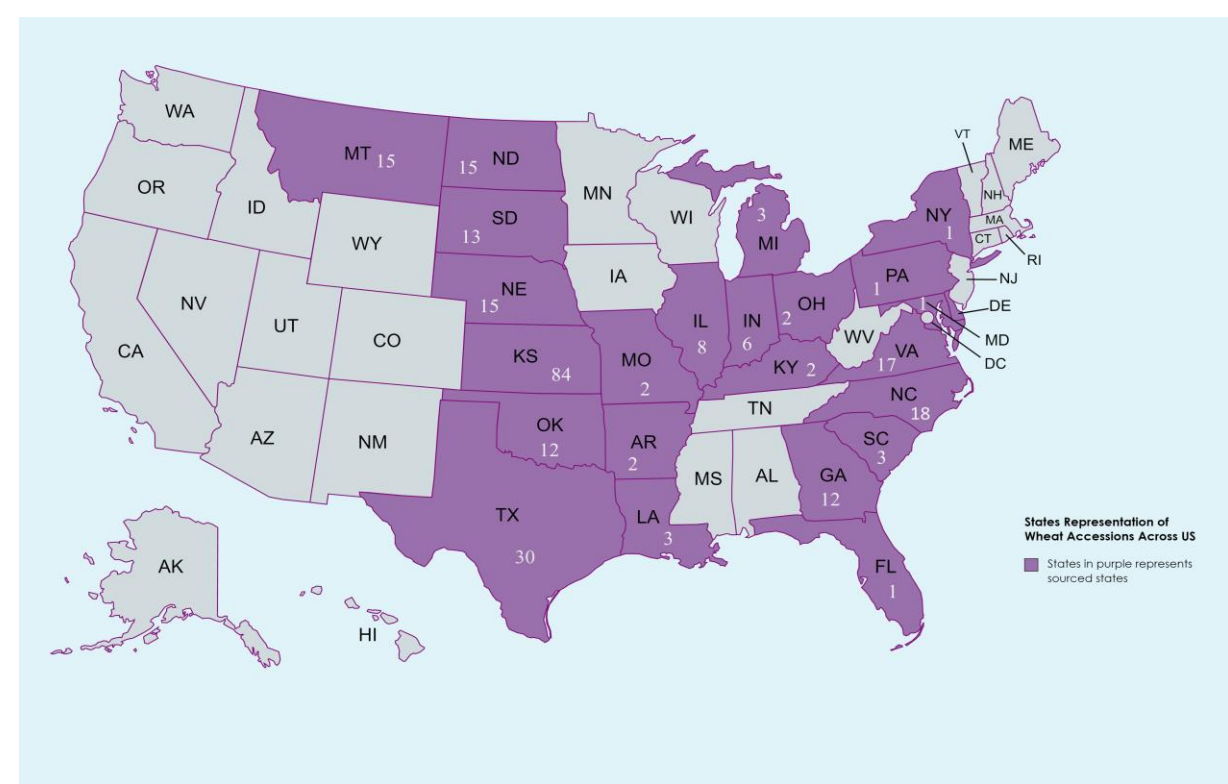


Figure 2: Representation of 270 breeding lines/cultivars by States across US used in this study.



Figure 3: Fusarium infected head=A (AWP KSU, 2022) and Fusarium damaged kernel=B (K-State Agronomy eUpdate, 2015).

Results

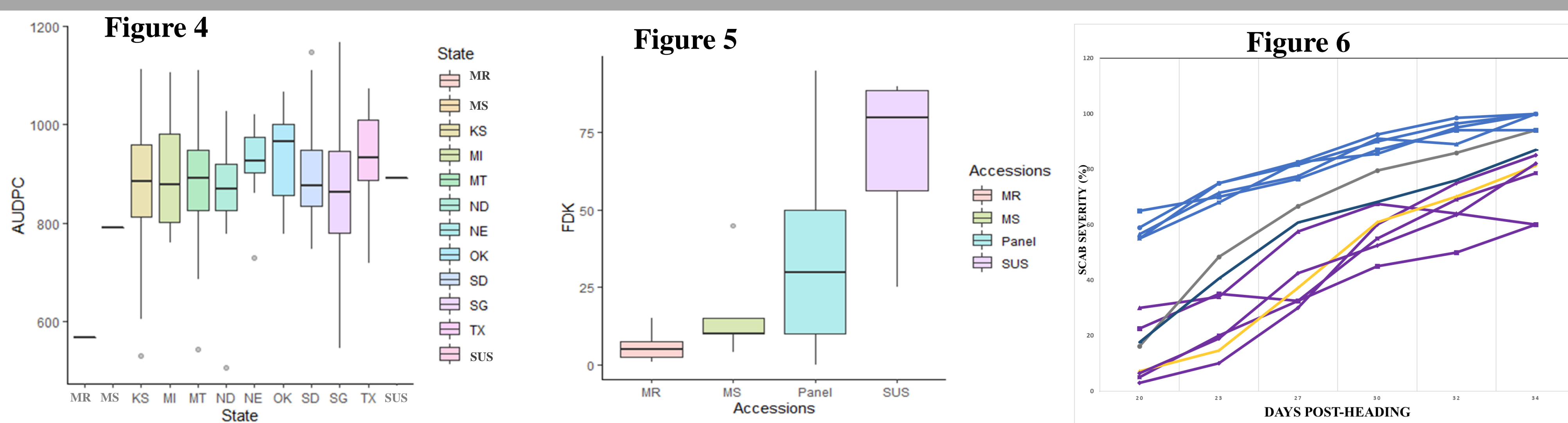


Figure 4: Area under disease progressive curve (AUDPC) of breeding lines across different states in US. AUDPC was calculated using normalized heading dates dataset. Controls: MR=Moderate Resistance (Everest), MS=Moderately Susceptible (Karl92), SUS=Susceptible (Overlay). **Figure 5:** Fusarium damaged kernel (FDK) of the panel breeding lines and controls. MR=Moderate Resistance (Everest), MS=Moderately Susceptible (Karl92), SUS=Susceptible (Overlay). **Figure 6:** Disease severity of top five most resistant (purple) and susceptible (blue) breeding lines with respect to controls: moderately resistant (tan), moderately susceptible (dark blue), and susceptible (gray)

- The normalized area under disease progressive curve (AUDPC), and fusarium damaged kernel (FDK) across wheat accessions including some more resistant than the control (Everest) as shown in figures 4 and 5 respectively (p-value < 0.05).
- The line graph (Figure 6) represents disease (scab severity) progressing lines starting twenty (20) days post-heading dates. Disease severity of selected breeding lines revealed phenotypic diversity wider than the control varieties phenotypic range.

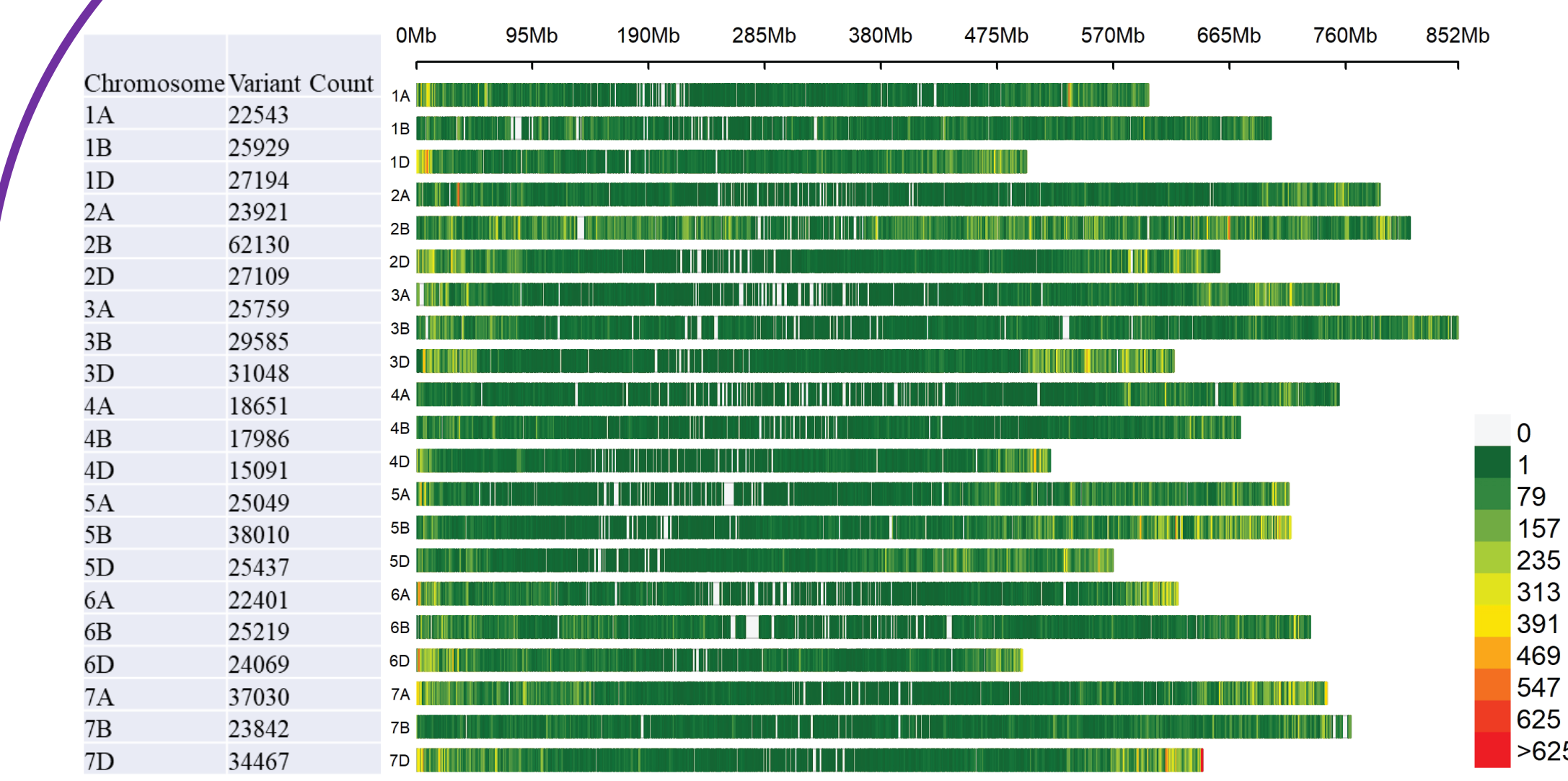


Figure 7: SNP density of ~15x sequencing data of panel mapped to Chinese Spring reference genome using GATK pipeline. Filtered variants present in 80% of lines and binned in 1Mb windows per chromosome. Total of 582,470 variants.

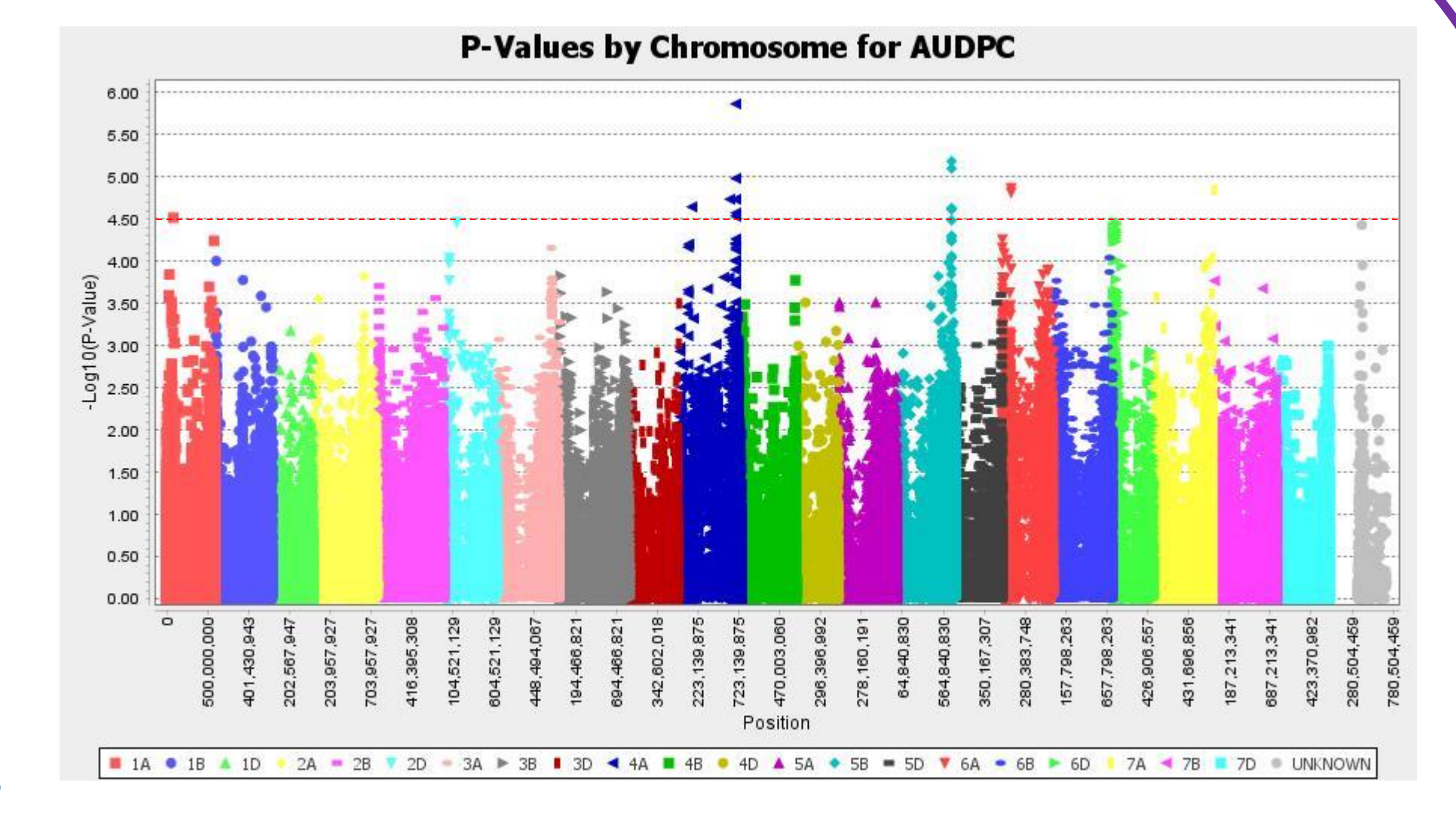


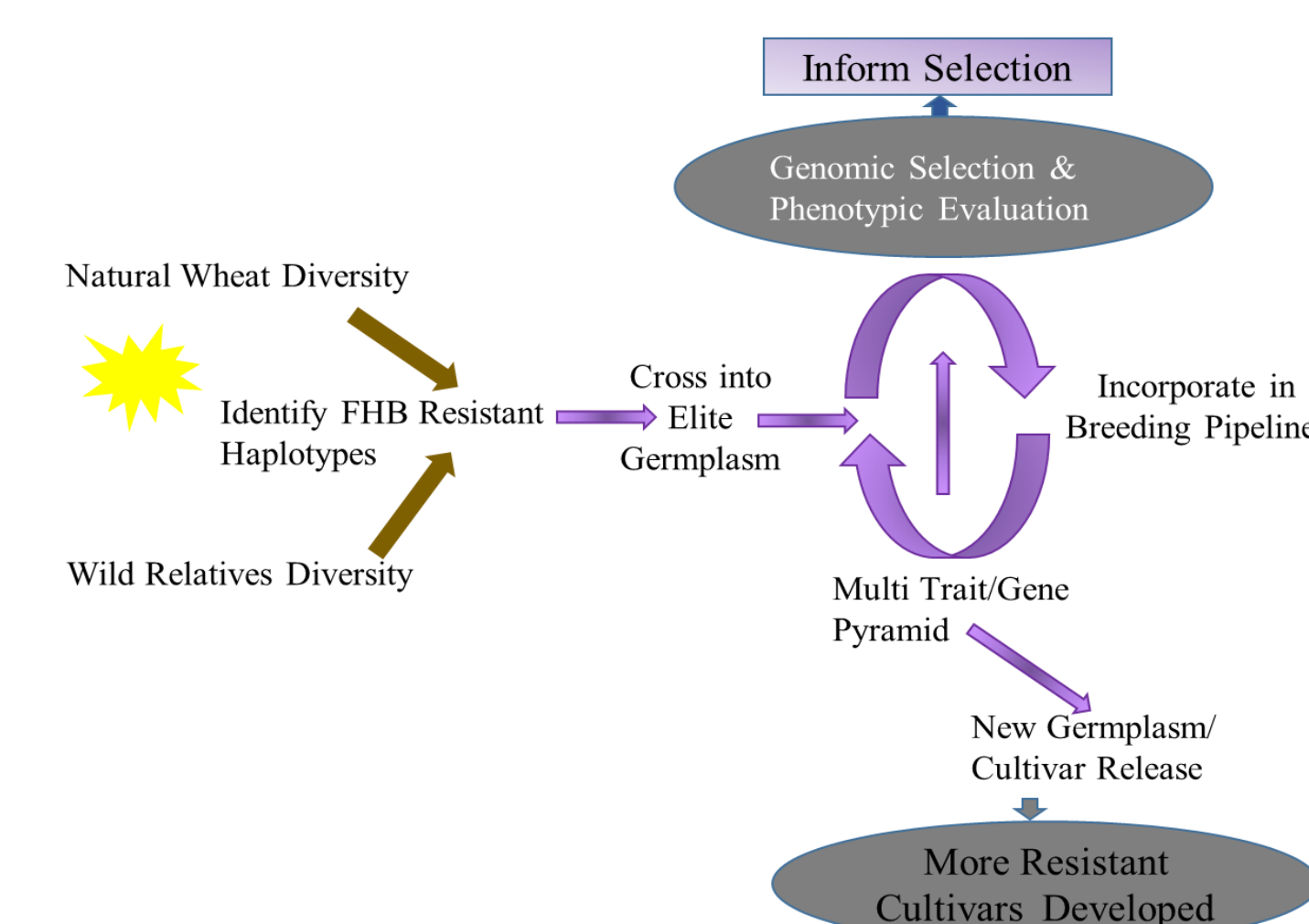
Figure 8: Manhattan plot of normalized AUDPC mapped using mixed linear model (MLM); modeling with kinship in Tassel.

Preliminary Conclusions

- Data analyzed from our experimental field at Rocky Ford station (Manhattan, KS) as shown in figures 4-6 showed phenotypic diversity in our panel of breeding lines.
- Figures 7-8 indicate genetic diversity/variability in the panel.
- We were able to map resistance and susceptibility alleles using this panel of wheat lines spanning most of the US growing regions, using mixed linear models GWAS.
- We are in the process of building a customized PHG database using genic regions as reference ranges and populating it with ~15x sequencing data (Figure 7) of our panel to use to impute breeding lines for our Kansas collaborators.

Vision

- Develop diagnostic markers for marker-assisted breeding in USA breeding programs.
- Use the Wheat PHG database to assist development of adapted resistant wheat cultivars.



Collaborators

Allan Fritz (Kansas State University), Mary Guttieri (USDA-Manhattan), Brett Carver (Oklahoma State University), Francois Marais (North Dakota State University), Gina Brown-Guedira (USDA-Raleigh), Guorong Zhang (Kansas State University-Hays), Jackie Rudd (Texas A & M University), Katherine Frels (University Nebraska-Lincoln), Sunish Sehgal (South Dakota State University), Jason Cook (Montana State University), Shuyu Liu (Texas A& M University), Eric Olsen (Michigan State University), David Van Sanford (University of Kentucky).

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References

K.W. Jordan, P.J. Bradbury, Z.R. Miller, M. Nyine, F. He, et.al. Development of the Wheat Practical Haplotype Graph Database as a Resource for Genotyping Data Storage and Genotype Imputation. G3, 2022, Vol. 12, No.2 <https://doi.org/10.1093/g3journal/jkab390>.



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