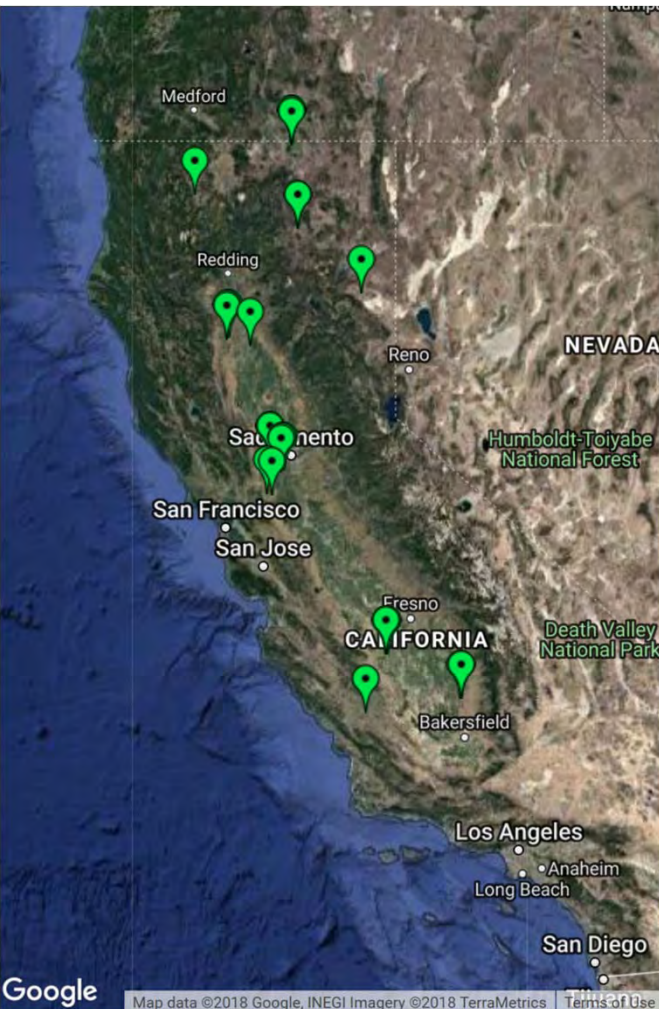




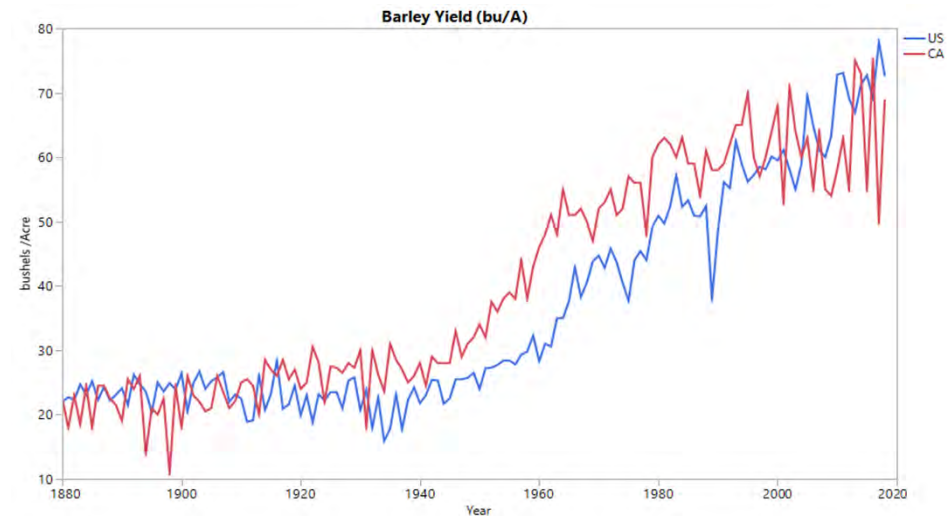
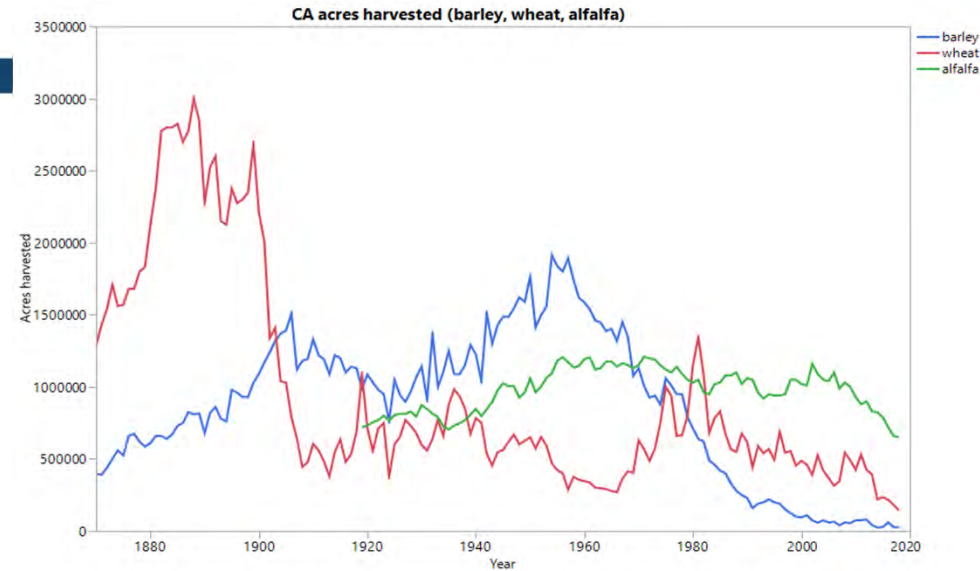
UC Davis Genomics-Assisted Barley Breeding

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California Barley



- Sacramento and San Joaquin Valley
 - Fall planted, partially irrigated
- Foothills & S Central Coast
 - Fall planted, rainfed
- Tulelake basin
 - Spring planted, irrigated
- S Desert Region
 - Fall planted, irrigated



Genomic Selection (GS) for malting barley

Goals:

1. Genetically characterize the current malting barley germplasm
2. Test ability of GS models to predict malt quality traits
3. Incorporate GS and MAS into CA barley breeding

Genomic Selection

- Uses a statistical model to *predict* the phenotype of a plant based on genome wide markers (SNPs)
Genomic Estimated Breeding Value (GEBV)

- Training Population

Genotype + phenotype

used to:

train the model

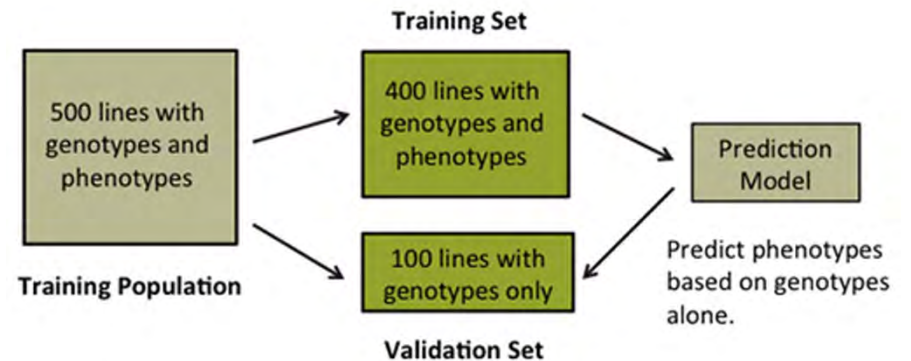
predict marker effects

test accuracy through cross validation

- Prediction Population

Genotype only

GEBVs predicted by model



Phenotypic Correlations in Training Population

	Kernel weight	Plumpness	Malt Extract	Barley Protein	Wort Protein	S/T	Diastatic Power	α -Amylase	β -Glucan	FAN	Wort Color	Wort Clarity
Year	**	***	***				***		**	***		
Barley color	-0.24	-0.12	0.21	-0.20	0.14	0.24	-0.22	0.13	-0.02	0.12	0.03	0.30
Wort Clarity	0.07*	0.10	0.09	-0.10	0.04	0.09	0.02	0.15	-0.08	0.07	-0.10***	
Wort Color	0.07*	0.00	0.47	-0.08	0.59	0.49	-0.05	0.45	-0.37	0.66***		
FAN	0.02	0.01	0.46***	0.11	0.77***	0.48	0.17	0.71***	-0.45			
β -Glucan	-0.04	-0.10	-0.30	0.15	-0.28	-0.35	-0.40***	-0.55*				
α -Amylase	-0.10	-0.01	0.38	-0.06	0.49	0.42	0.22					
Diastatic Power	0.06	-0.06	-0.37	0.53	0.11	-0.33						
S/T	-0.04	0.15	0.83	-0.65***	0.59***							
Wort Protein	0.03	0.03	0.39	0.20***								
Barley Protein	0.04	-0.19	-0.67***									
Malt Extract	0.10	0.34***										
Plumpness	0.78***											

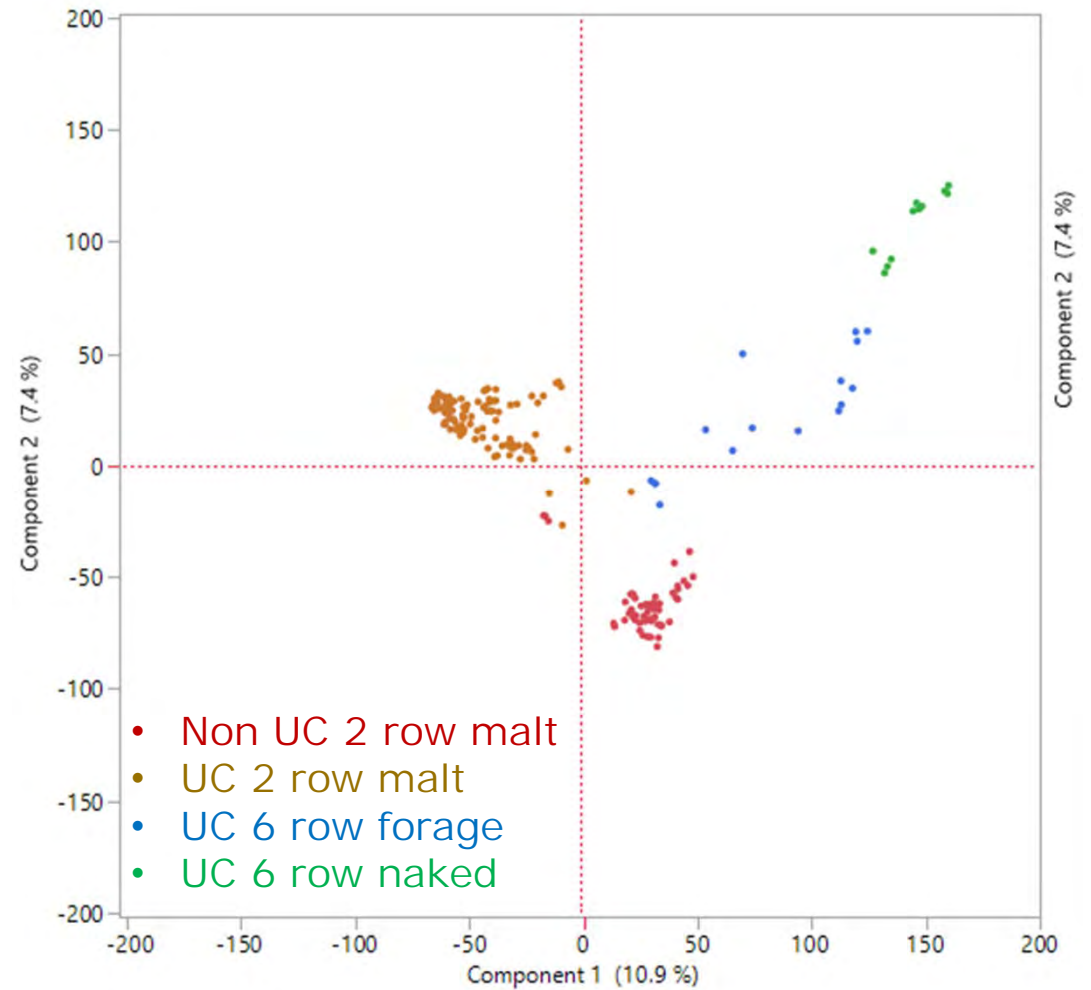
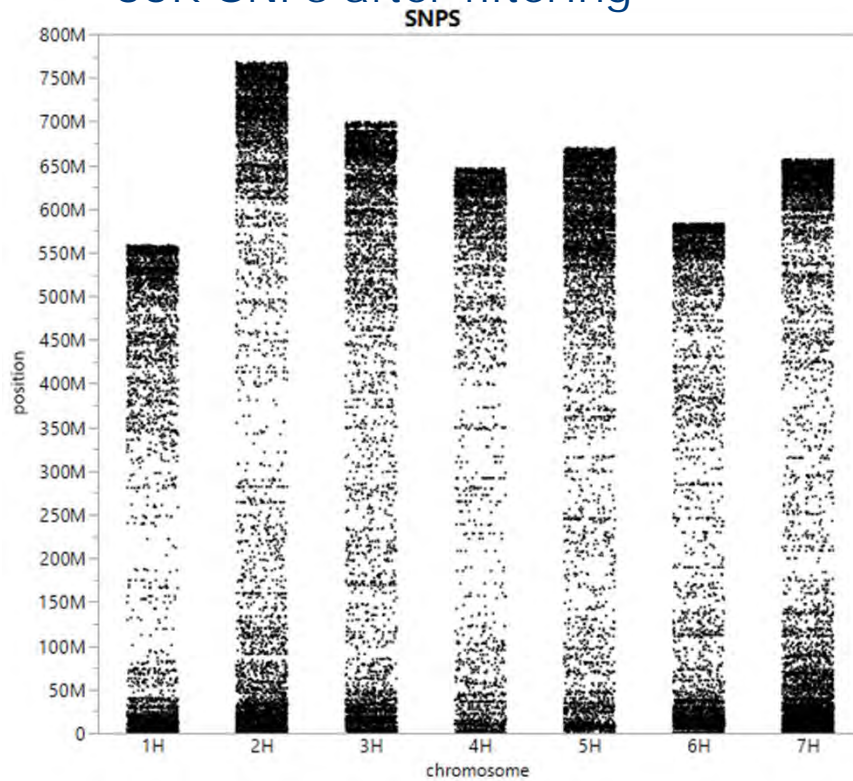
USDA Malt Quality data from 198 lines grown in Davis, CA in 2016-2017

P < 0.01 *
 P < 0.001 **
 P < 0.0001 ***
 High correlation and significance

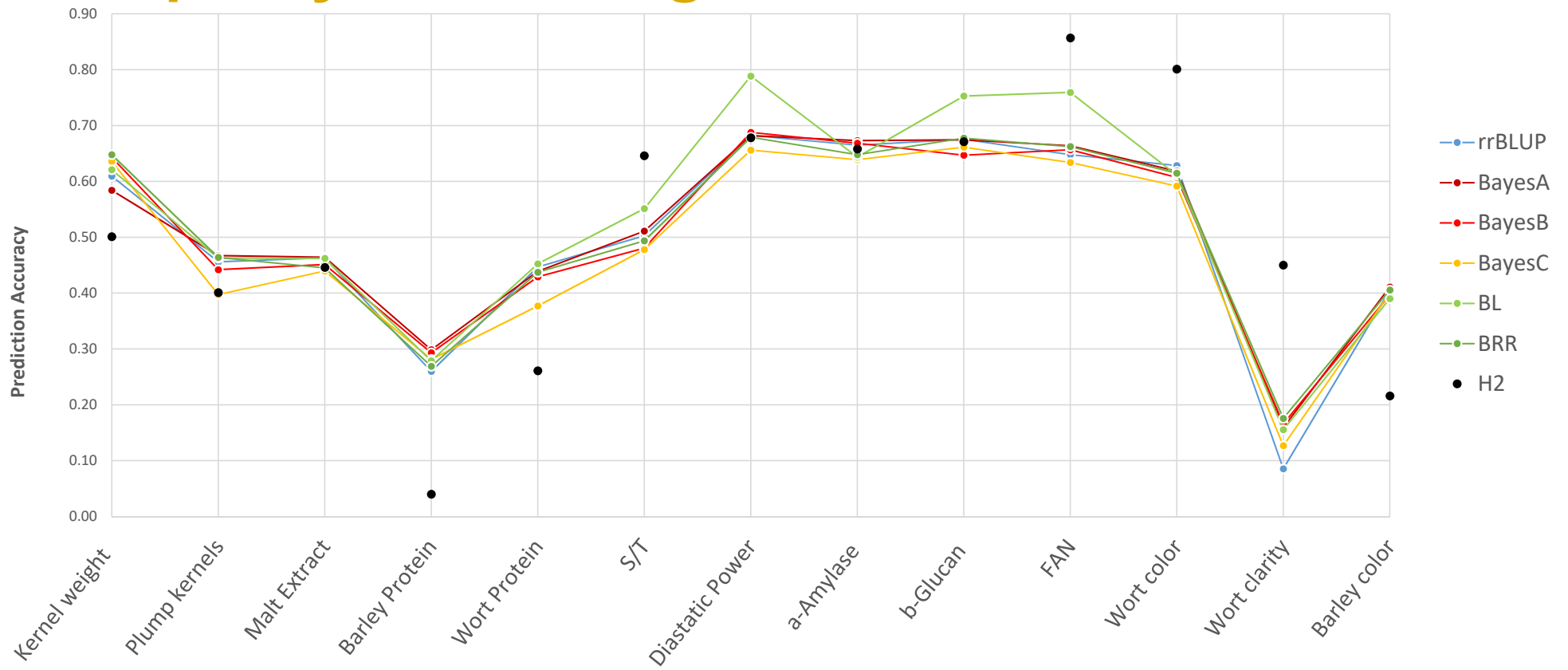
Genetic Diversity

GBS (*PstI-MspI*)

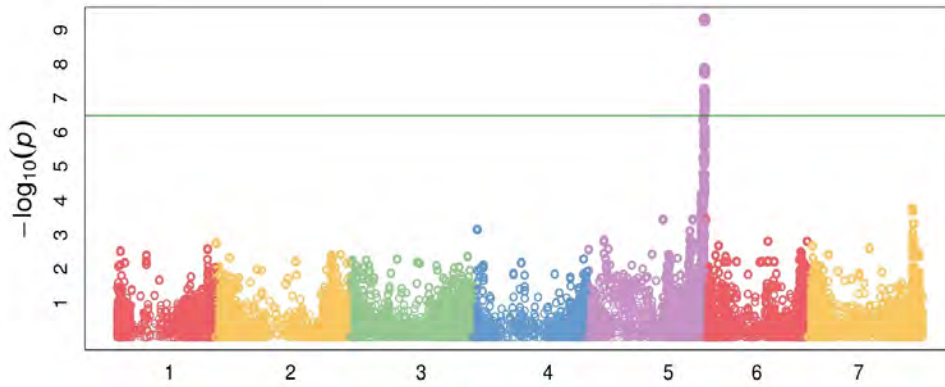
~35K SNPs after filtering



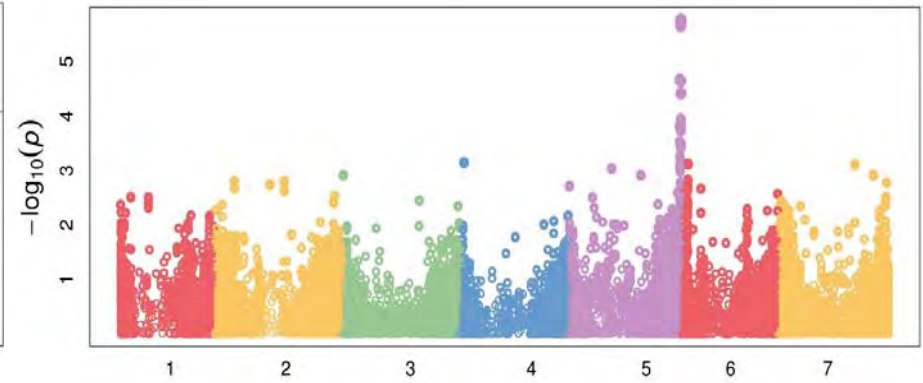
Heritability and prediction accuracy of malt quality traits using different GS models



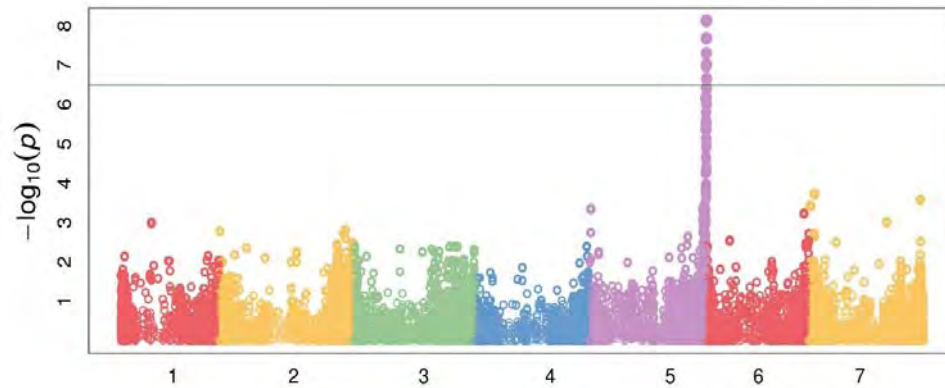
α -Amylase



β - glucan

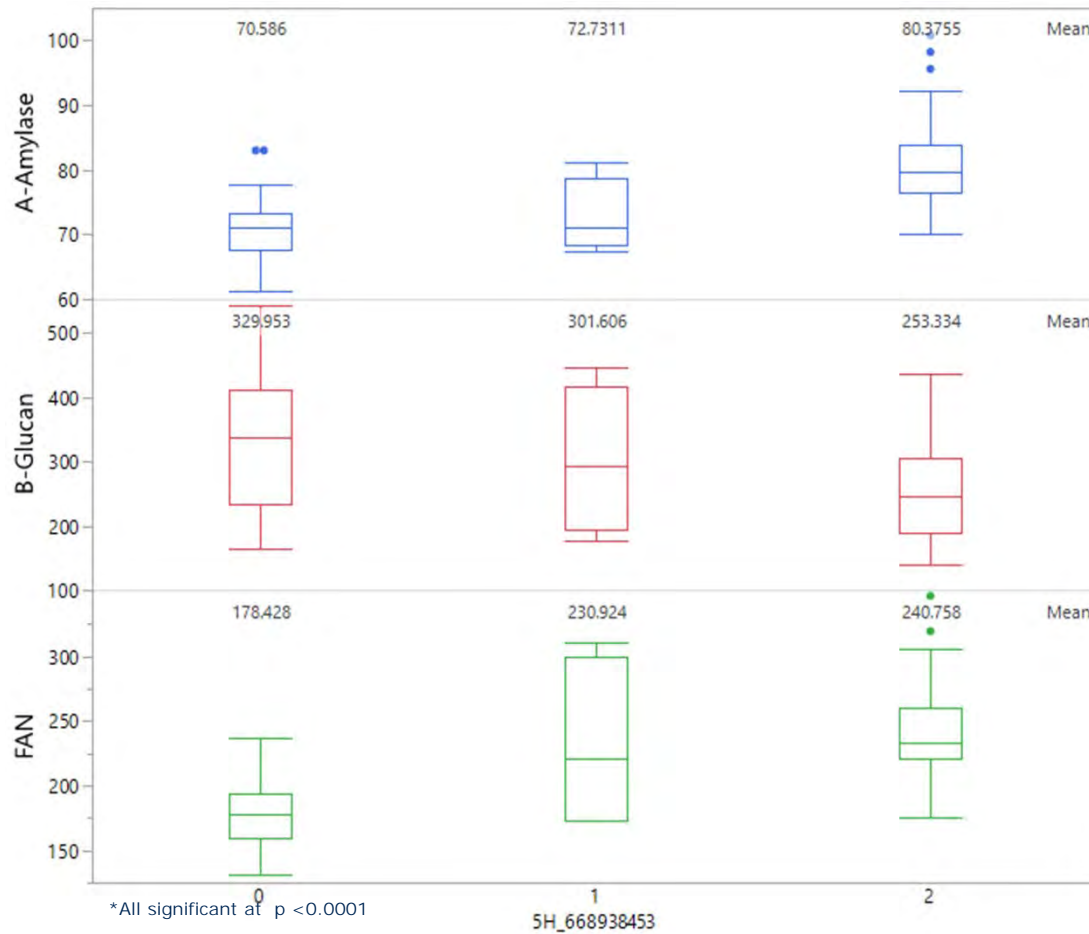


FAN



	α -Amylase	β -Glucan
FAN	0.71***	-0.45
β -Glucan	-0.55*	

SNP effect

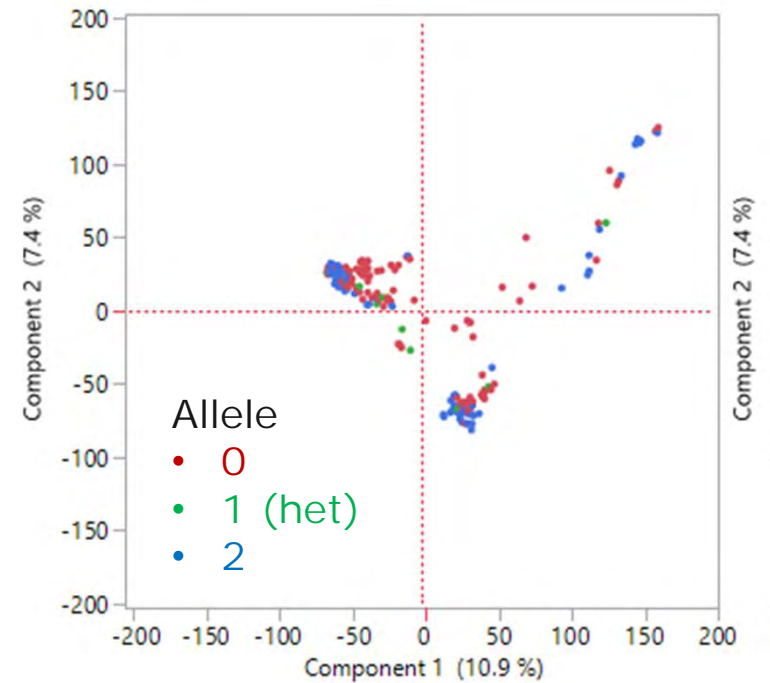


AMBA ideal malt criteria -two row (adjunct, all malt)

β -glucan (<100 ppm)

α -Amylase (> 50, or 40-70 DU)

FAN (> 210, or 140-190 ppm)



Future work

- Develop a marker for α -amylase, β -glucan and FAN.
- Genotype new malting barley lines (breeding program, GRIN, other programs) and use GS to select lines for malt quality analysis.
- Use GS for yield and disease traits.
- Implement GS into the forage and food barley program.