



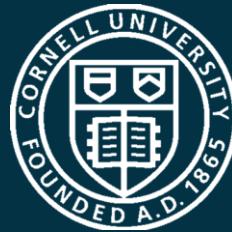
Chasing Genes and Making an Impact Where it Matters

Shantel A. Martinez, PhD

USDA-ARS Lincoln, NE

2019.11.20

ACKNOWLEDGMENTS



Cornell University

USDA ARS Wheat Health Unit
Steber, Garland Campbell Groups
Carter, Pumphrey Groups
Uauy Lab

Cornell Small Grains Group
Jannink & Sorrells Labs

PROJECT FUNDING

Education and Workforce
Development (EWD)



United States
Department of
Agriculture

National Institute
of Food and
Agriculture

Proposal #2017-07109



Eastern Washington Raised



Eastern Washington Raised



BS Bioengineering
MS Crop Sci
PhD Mol Plant Sci



Dr. Camille M. Steber

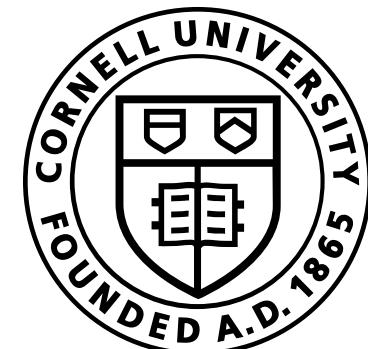


Dr. Kimberly A.
Garland Campbell

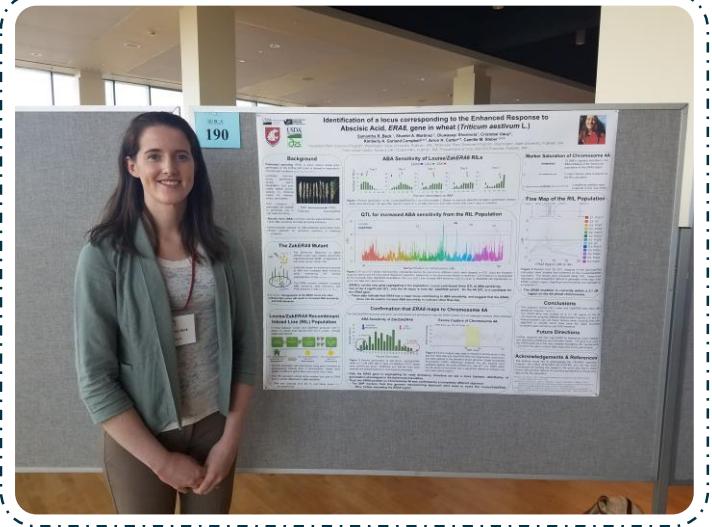
USDA NIFA EWD Fellowship



Dr. Mark E. Sorrells



SERVICE & OUTREACH



Recruiter, volunteer,
mentor (6 years)

A screenshot of a social media profile for "Shantel Amealia". The profile picture shows a person with glasses. The bio reads: "A snippet of stories from your friendly Indigenous scientist who shares all things food, wheat, walking, cat, data, and IPAs". Below the bio are several circular icons representing different interests: "Conf Prep", "It's Conf. Ti...", "Lecture Zone", "Wheat", "Students", "Fieldwork", and "Data". At the bottom of the profile are navigation links for "POSTS", "IGTV", "SAVED", and "TAGGED". Below these are three small thumbnail images: a person with glasses, a landscape with clouds, and a person wearing a "USDA WHEAT" cap.



Public Engagement
@s_amealia

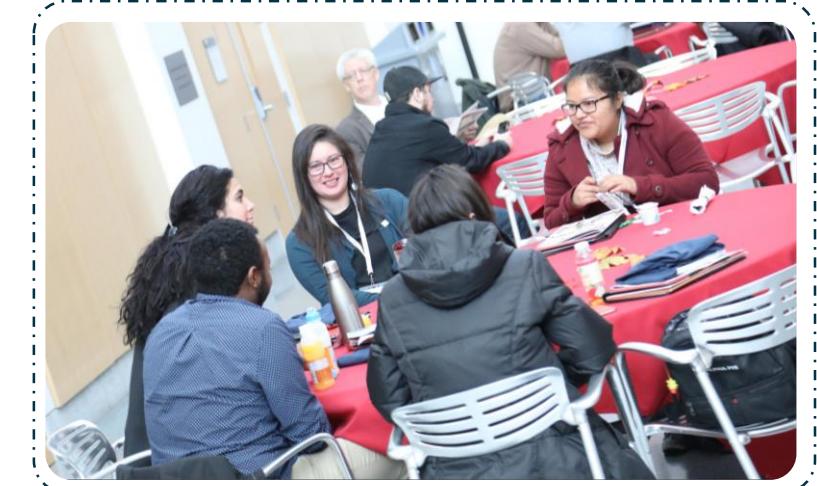


Mentoring women
in science (3 years)

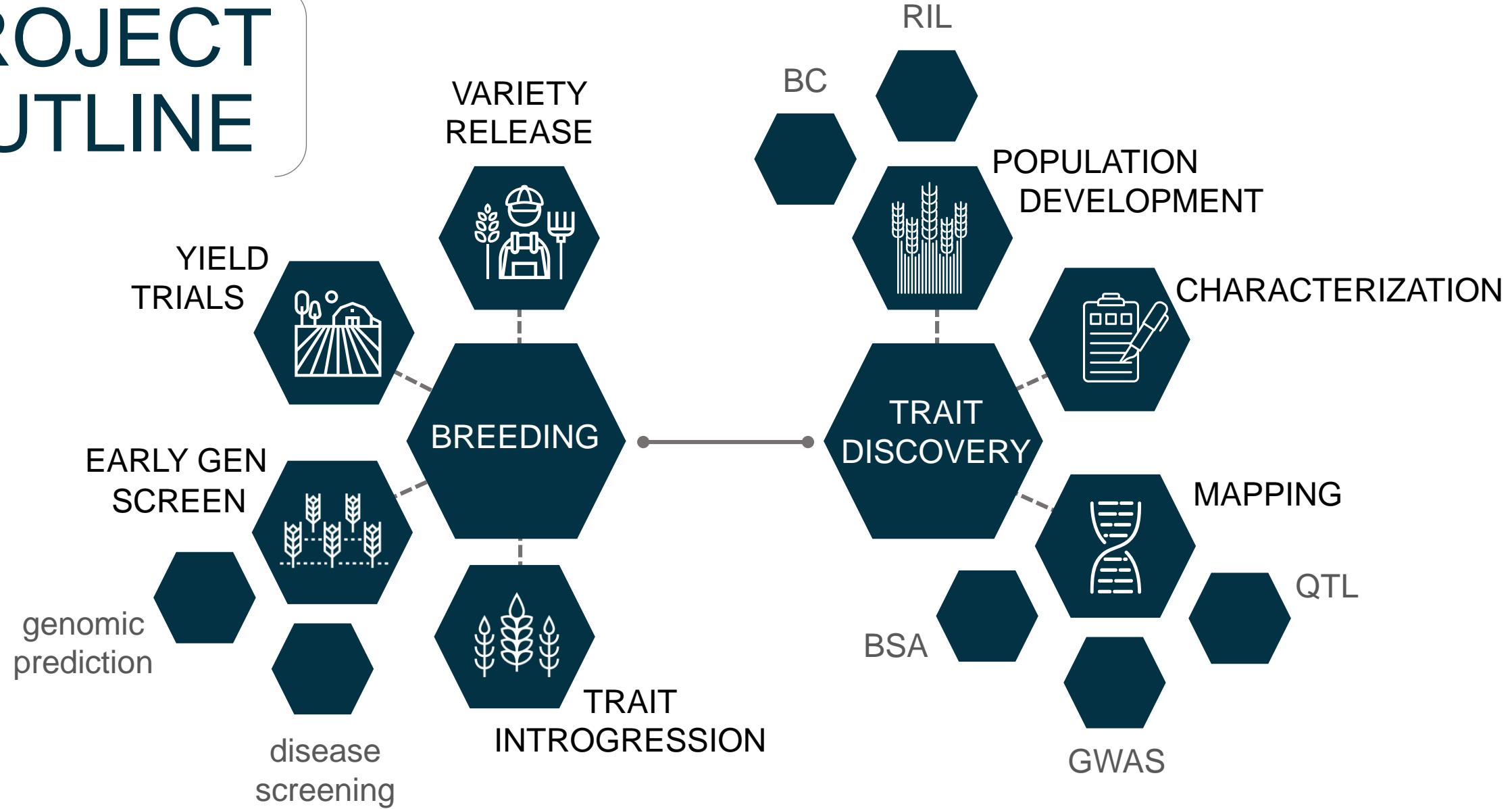


Louis Stokes Alliance for Minority Participation

Volunteer, mentor (5 years)



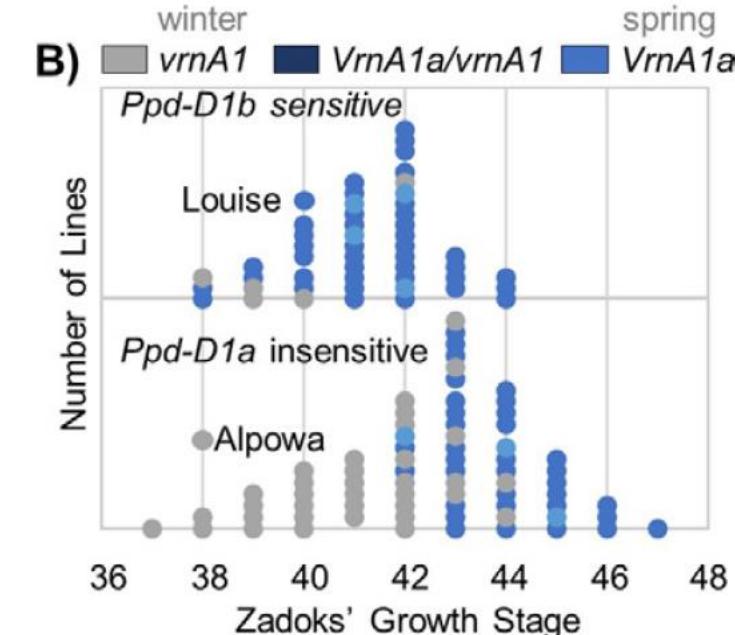
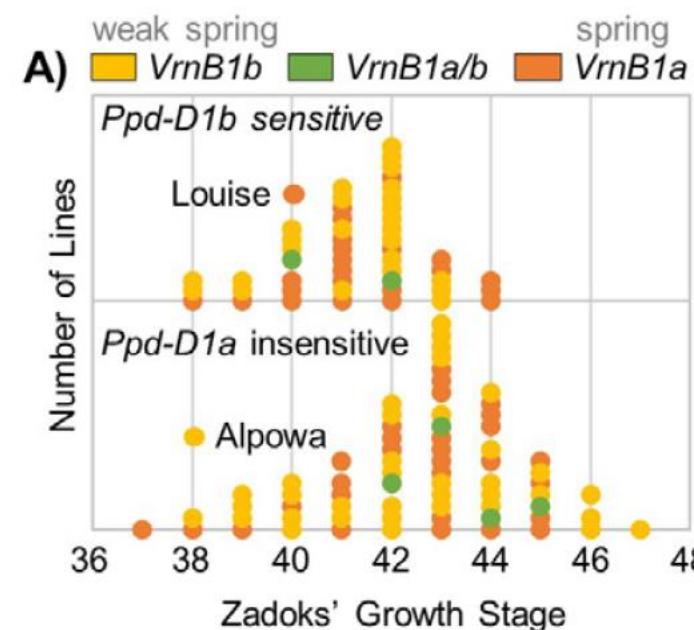
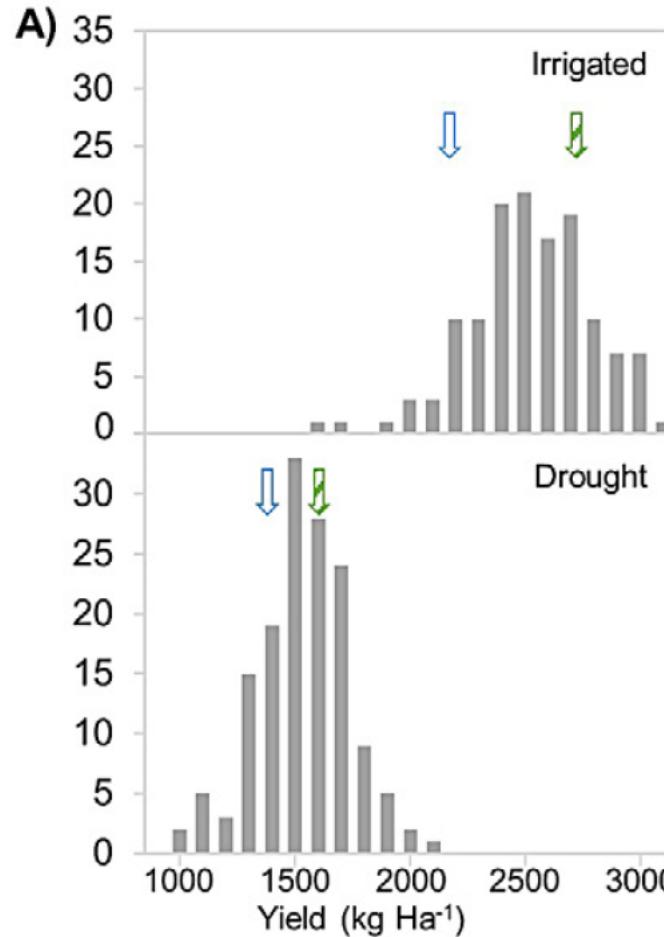
PROJECT OUTLINE



Mapping Population Release



Developed RIL population Louise x Alpowa for potential drought mapping studies



JOURNAL OF PLANT REGISTRATIONS

MAPPING POPULATION

Registration of the Louise/Alpowa Wheat Recombinant Inbred Line
Mapping Population

Shantel A. Martinez, Alison L. Thompson, Nuan Wen, Lesley Murphy, Karen A. Sanguinet,
Camille M. Steber, and Kimberly A. Garland Campbell*

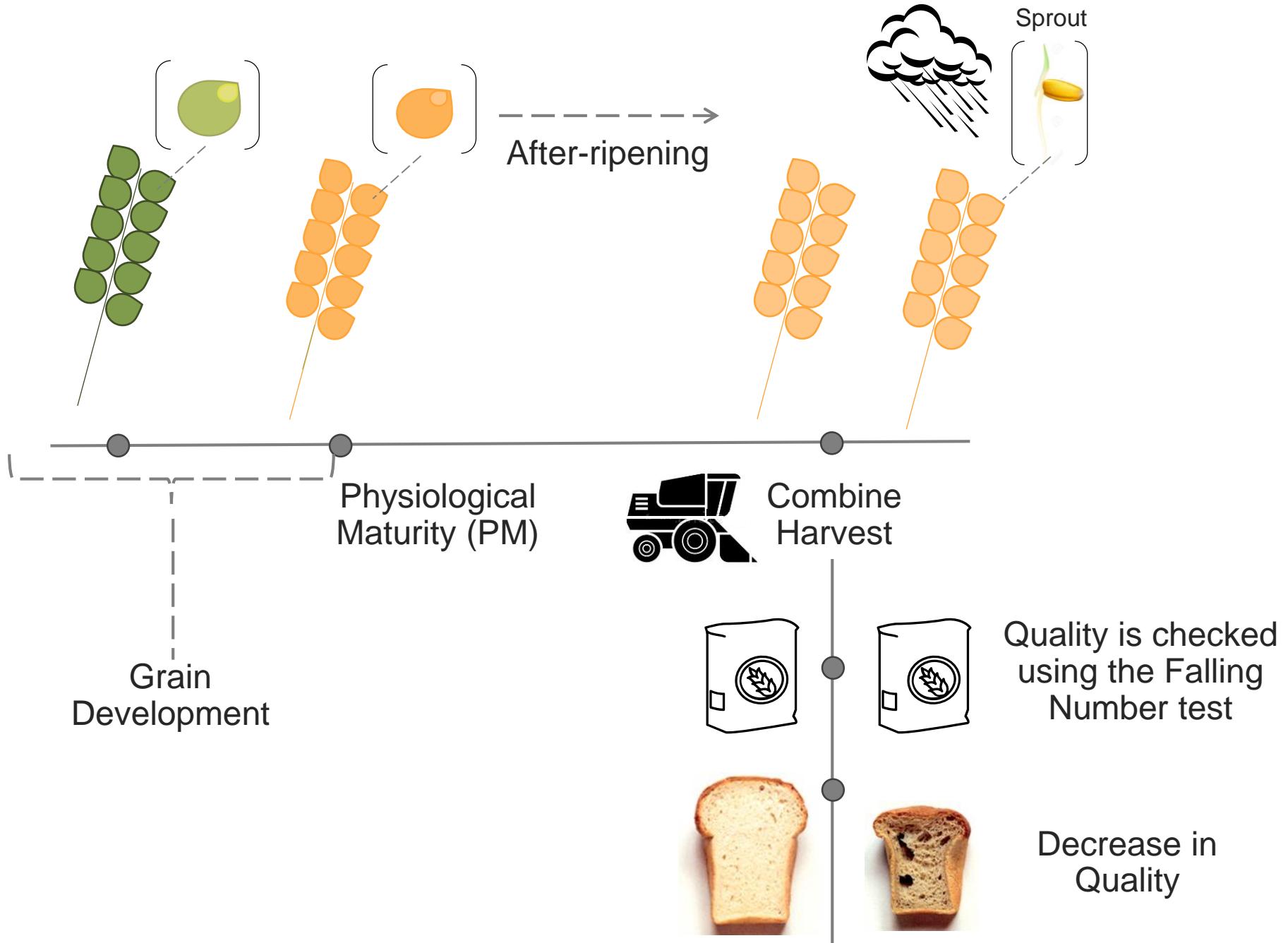
Abstract

A mapping population was developed from the cross of soft

THE INLAND northwest of the United States is a major wheat (*Triticum aestivum* L.)-producing region com-

Martinez et al., 2018a

Preharvest Sprouting



Wheat has
quite a bit of
genetic
variation



Unfortunately, rain events do occur during harvest

England



I guess this is what you'd call pre-harvest sprouting #Harvest18



Jim Thompson
@jimt_farmer

Think rain has stopped play #wheatharvest18
@AllpressF @LumleySean @coostiebarrey
@chrisbettinson2



Twitter

Kansas



Kyler Millershaski
@Shaski92

Follow

I'm always happy to have rain, but not the view I want during #WheatHarvest18 #kswx



3:36 PM - 22 Jun 2018

5 Retweets 37 Likes

Comment 1 Retweet 5 Like 37 Share



37



Share

Nebraska



Chris Cu11an
@ChrisCullan1

Follow

On the edge. #wheatharvest18



5:06 PM - 12 Jul 2018

1 Retweet 40 Likes

Comment 1 Retweet 1 Like 40 Share



1



1



Like 40



Share

Canada



Fermes Chauvin Farms Ltd.
@MoeChauvin

Follow

#wheatharvest18 started here at fermeschauvinfarms.com in StoneyPoint. Decent yields for no rain ... #OntAg #AgMoreThanEver #goodineverygrain



Pacific Northwest



Farms.com

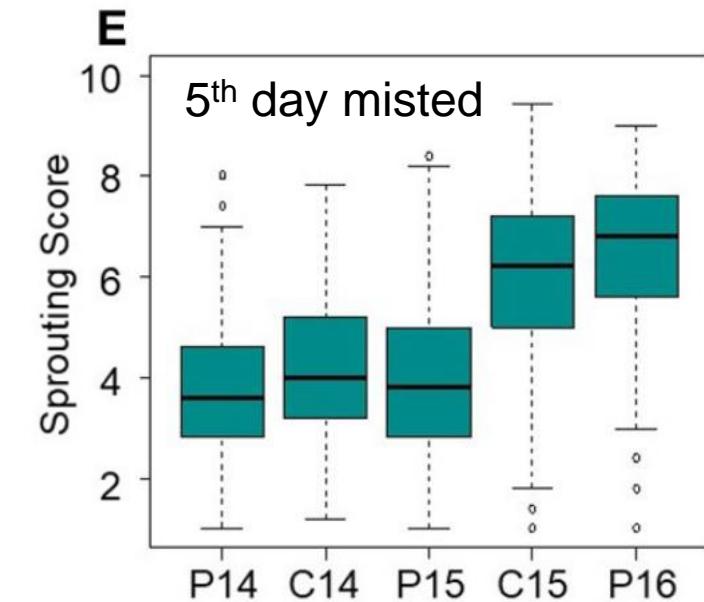
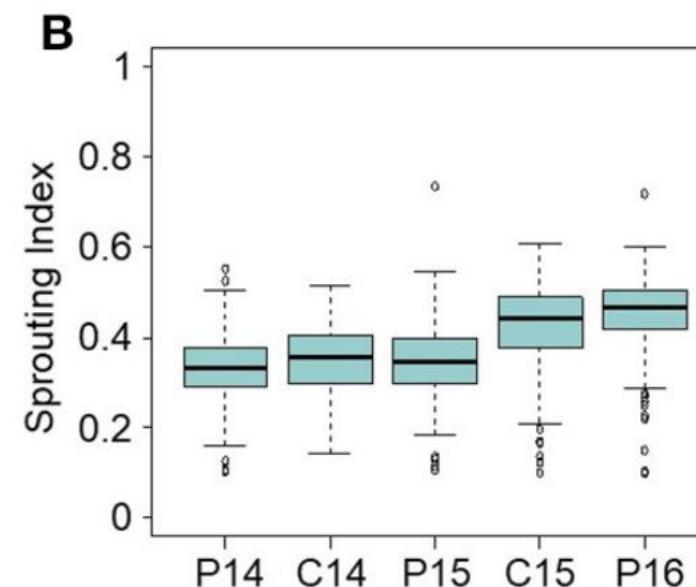
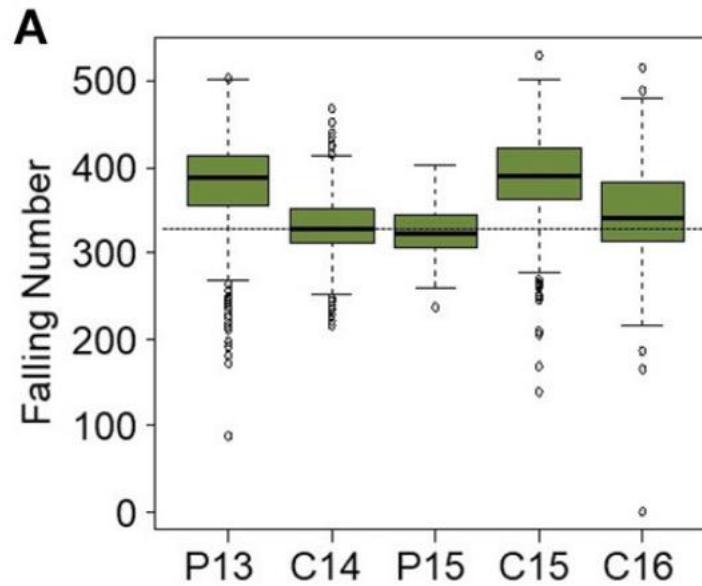


“...in 2016 when losses [*due to low FN*] were staggering, in the tens of millions of dollars.” - Alex McGregor

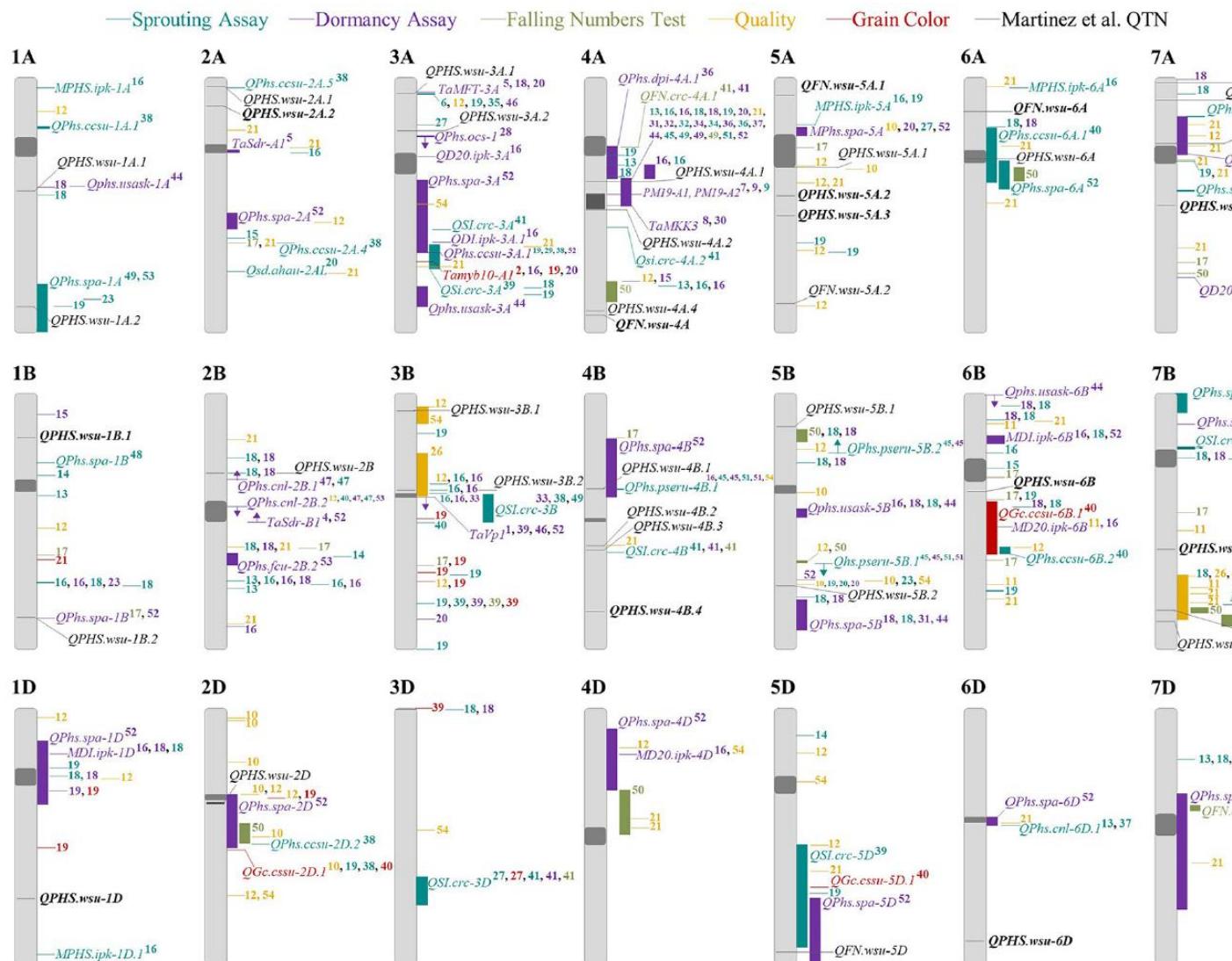


“...September 2016, as the dismal FN results came in, **growers, scientists, agencies, state legislators and Rep.** Cathy McMorris Rogers (R-Wash.) met make sure the FN challenge didn’t fall off the radar screen down the road as other issues came to the fore. It hasn’t.”

GWAS: PNW germplasm



6 MTA were found in multi-env



19 / 34 *QPHS.wsu* loci and
4 / 9 *QFN.wsu* loci
co-localized with (54) previously
published studies

How does this study help?

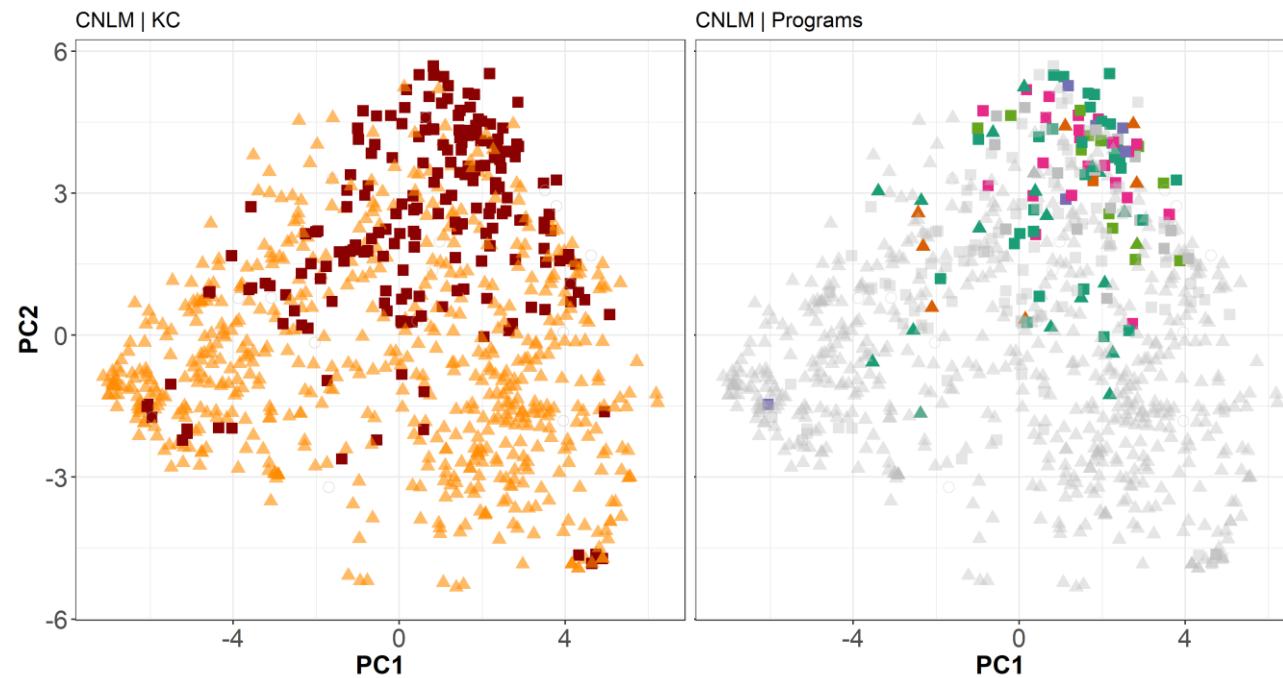
6 MTA made into KASP
markers for breeder selection

Identified germplasm that were
high in FN quality and/or PHS tolerant
versus germplasm that was too low in either

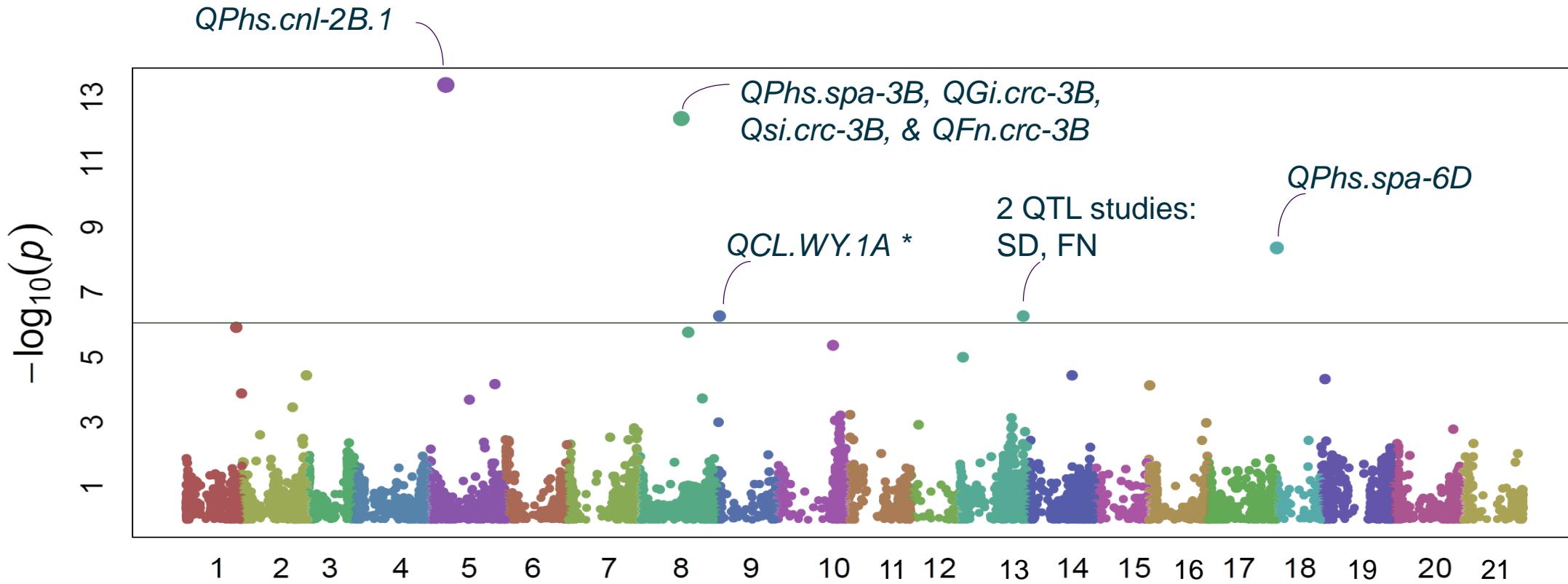
GWAS: Northeast germplasm



White Red

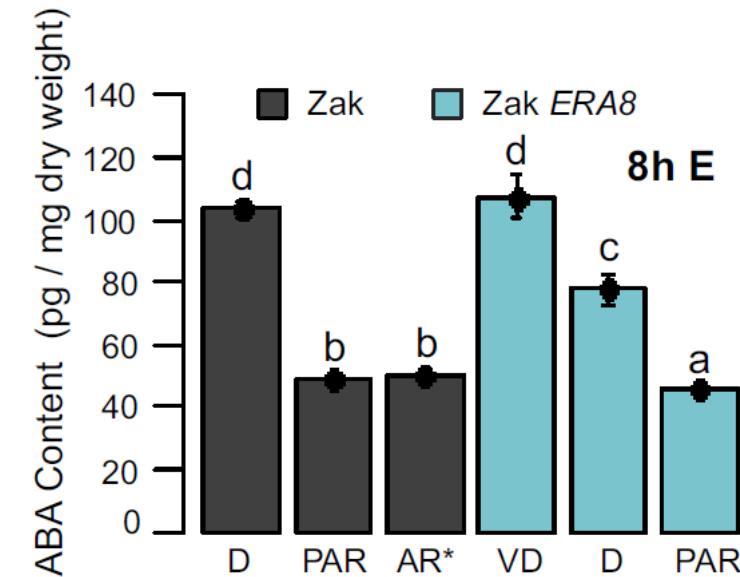
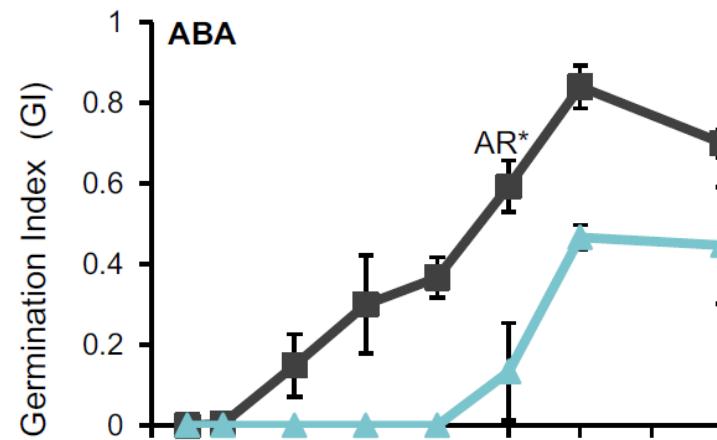
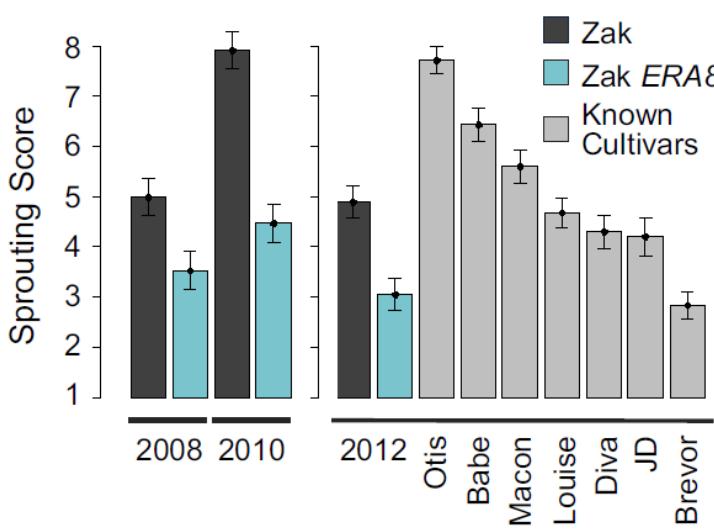


GWAS: Northeast germplasm



Zanetti et al., 2000; Munkvold et al. 2009; Fofana et al. 2009; Zhang et al. 2013;
Kumar et al. 2015; IWGSC, 2018; Martinez et al. 2018; Zuo et al., 2019

ERA8 Mutant Characterization



Euphytica
DOI 10.1007/s10681-016-1763-6

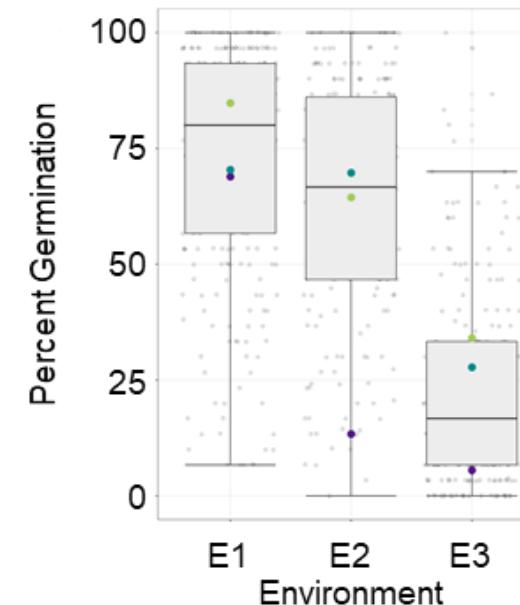
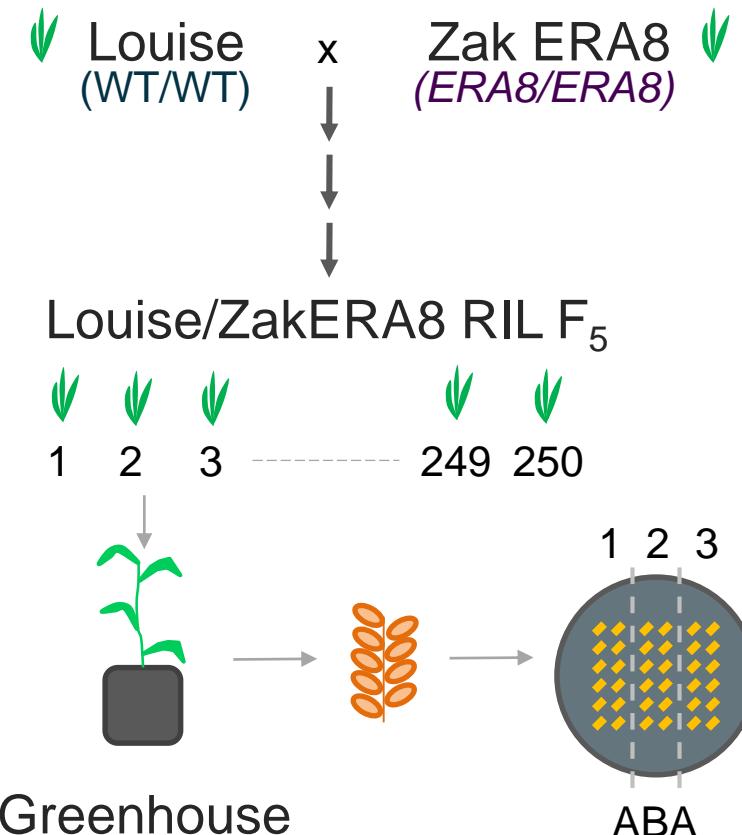


The wheat ABA hypersensitive *ERA8* mutant is associated with increased preharvest sprouting tolerance and altered hormone accumulation

Martinez et al., 2016

Shantel A. Martinez · Keiko M. Tuttle · Yumiko Takebayashi ·
Mitsunori Seo · Kimberly Garland Campbell · Camille M. Steber

RIL Population Development



Genetic cultivar differences in addition to the *ERA8* gene.

New Results

Exome sequencing of bulked segregants identified a novel *TaMKK3-A* allele linked to the wheat *ERA8* ABA-hypersensitive germination phenotype

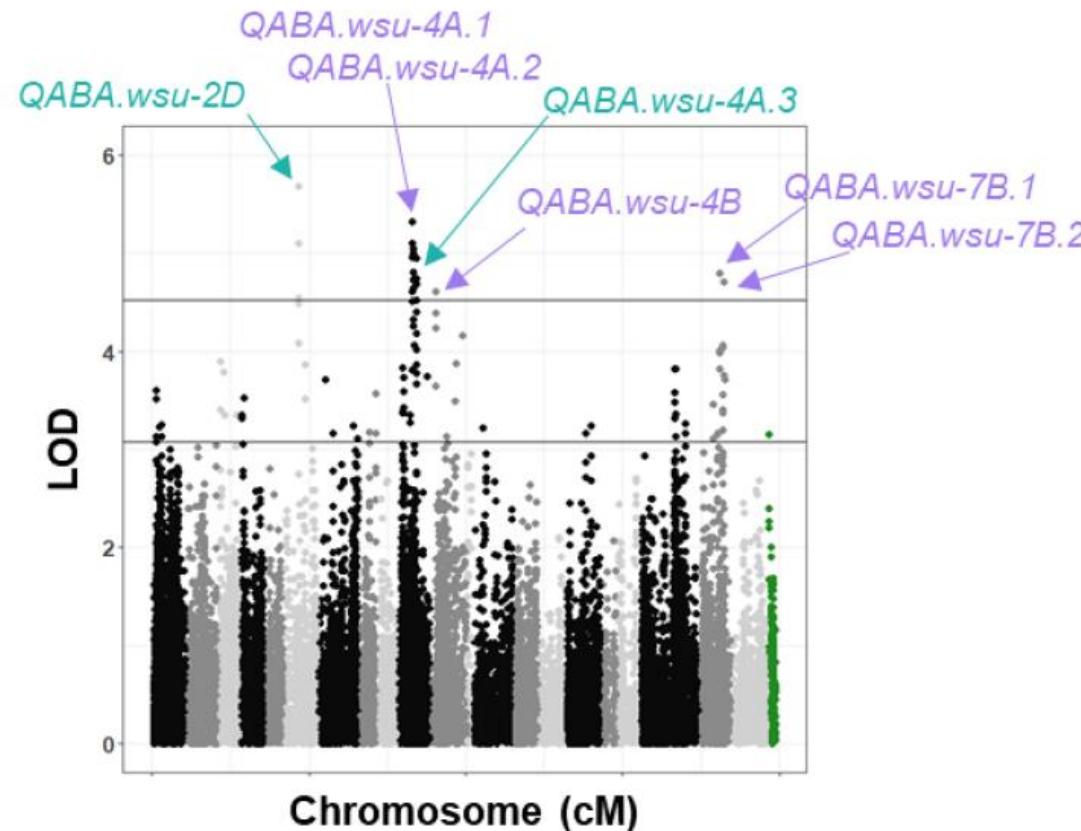
Shantel A. Martinez, Oluwayesi Shorinola, Samantha Conselman, Deven See, Daniel Z. Skinner, Cristobal Uauy, Camille M. Steber
doi: <https://doi.org/10.1101/784652>

This article is a preprint and has not been certified by peer review [what does this mean?].

QTL Mapping



- A Genome • B Genome • D Genome • Unknown



Multiple ABA sensitive QTL (increased dormancy) were found throughout the genome, contributed by either Louise or ERA8

Agronomic Characterization



Although technically ‘not significant’, still concerned about a slight dip in yield

Table 3. Comparisons of agronomic and quality traits for soft white spring wheat Zak *ERA8* and wild-type Zak from field experiments conducted at Pullman, WA.

Trait	Year	Zak <i>ERA8</i>		Zak		<i>p</i> value†
		Mean	SE	Mean	SE	
Zadoks' stage	2012	46.2	0.66	45.8	0.66	0.68
Plant height, cm	2011	85.8	1.4	85.6	1.4	0.92
	2012	67.2	1.4	71.4	1.4	0.048
Yield, kg ha ⁻¹	2011	3988	263	4725	263	0.065
	2012	2952	263	3545	263	0.13
Test weight, kg m ⁻³	2011	789	6.4	770	6.4	0.048
	2012	756	6.4	753	6.4	0.75
Grain protein concentrations, %	2011	9.79	0.58	9.54	0.58	0.77
	2012	14.19	0.26	13.05	0.26	0.014
Hardness, %	2011	13.30	3.12	5.10	3.12	0.10
	2012	18.18	1.40	18.70	1.40	0.80
1000 kernel weight, g	2011	44.6	2.0	45.5	2.0	0.75
	2012	27.6	0.9	27.3	0.9	0.83

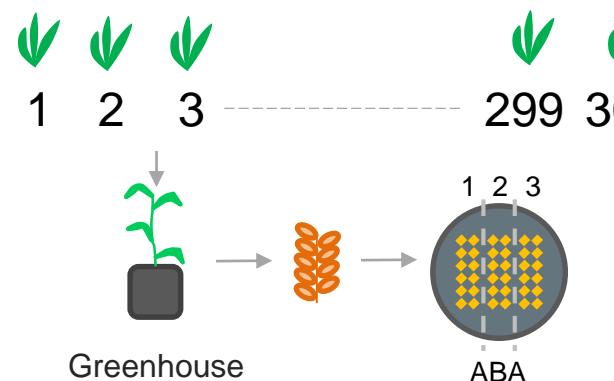
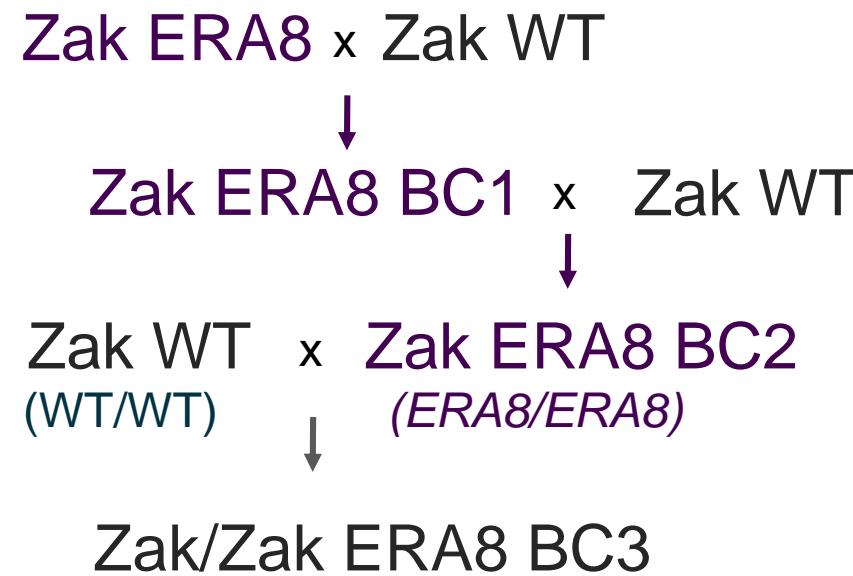
Martinez et al., 2014

Registration of Zak *ERA8* Soft White Spring Wheat Germplasm with
Enhanced Response to ABA and Increased Seed Dormancy

Shantel A. Martinez, Elizabeth C. Schramm, Tracy J. Harris, Kimberlee K. Kidwell,
Kimberly Garland-Campbell, and Camille M. Steber*

BC Population Development

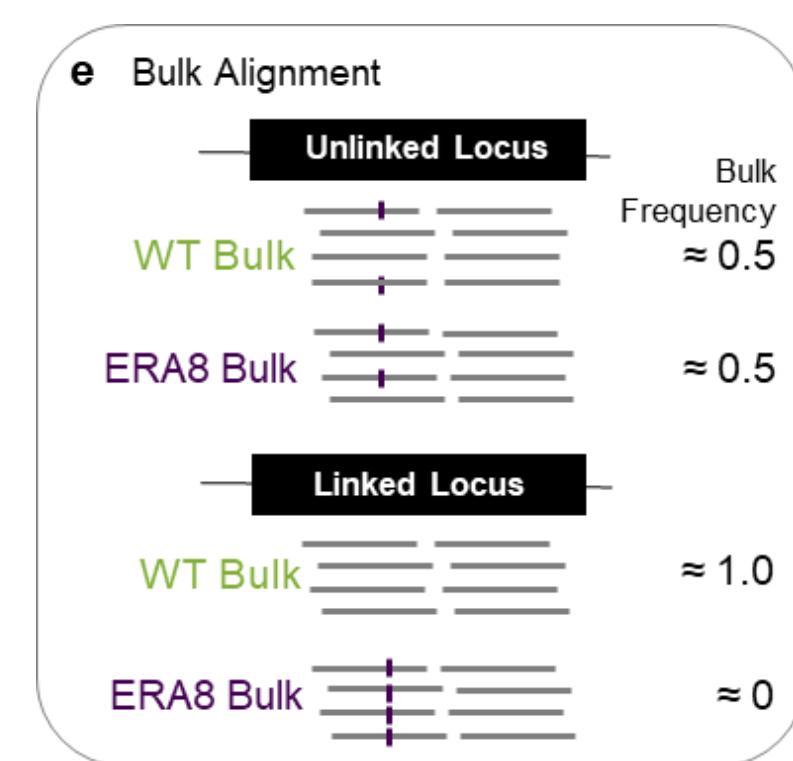
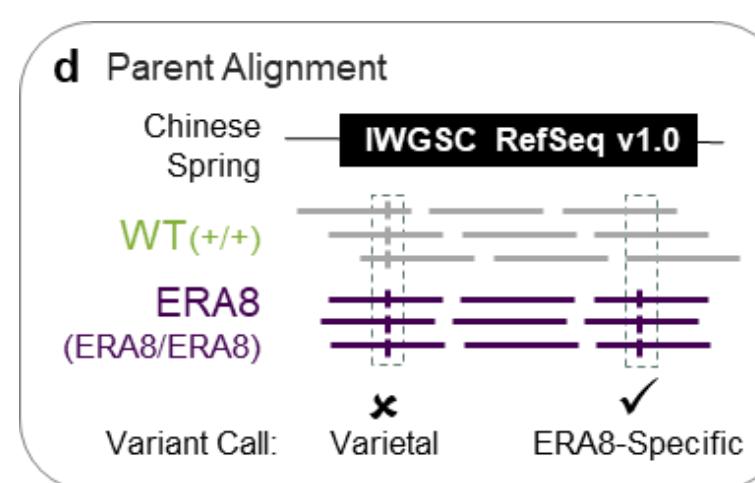
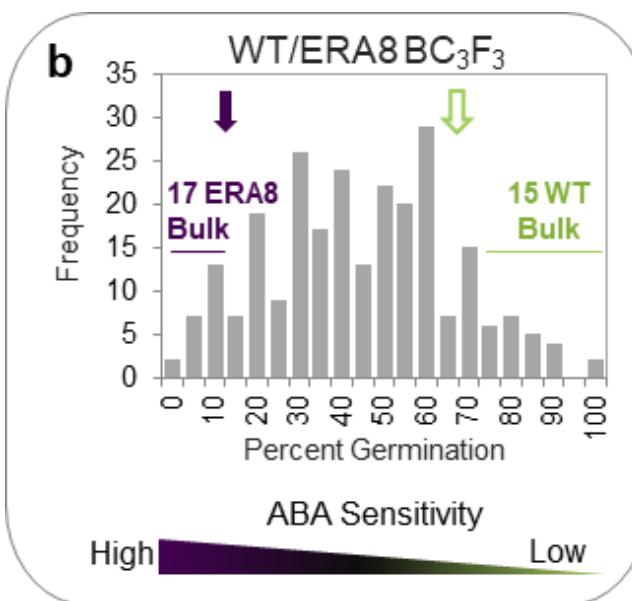
To clean up background EMS mutations not related to our trait of interest

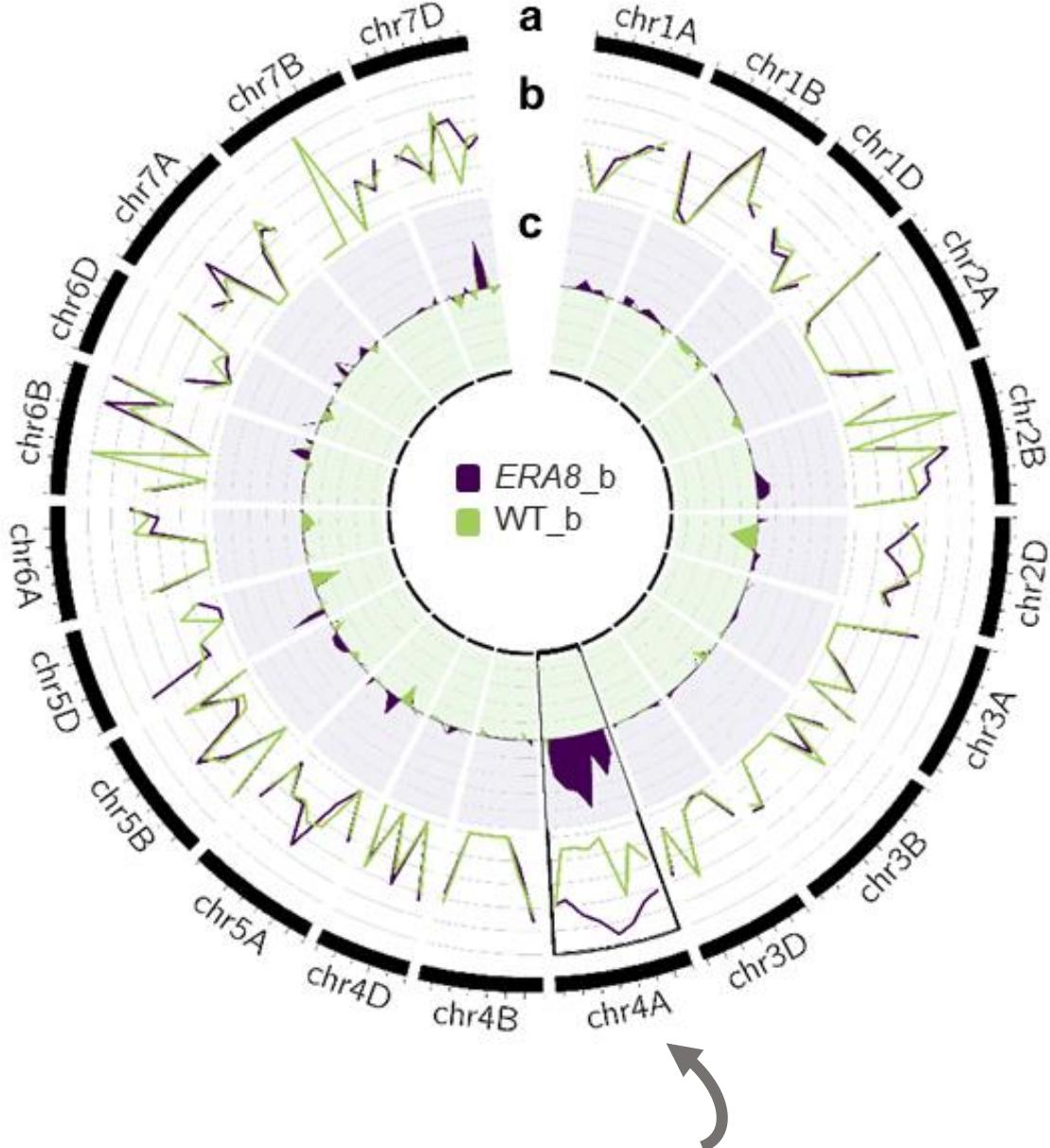


Only mutagen induced differences

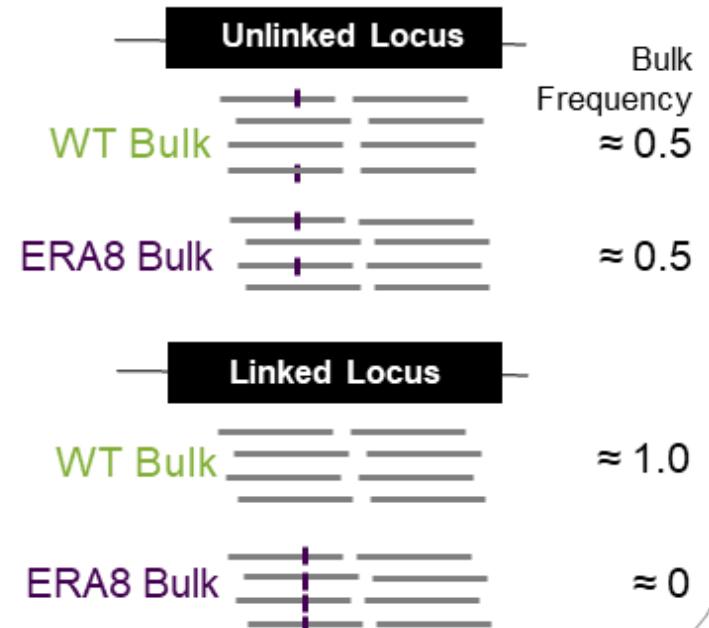
Bulked-Segregant Analysis

using exome-capture DNA sequencing





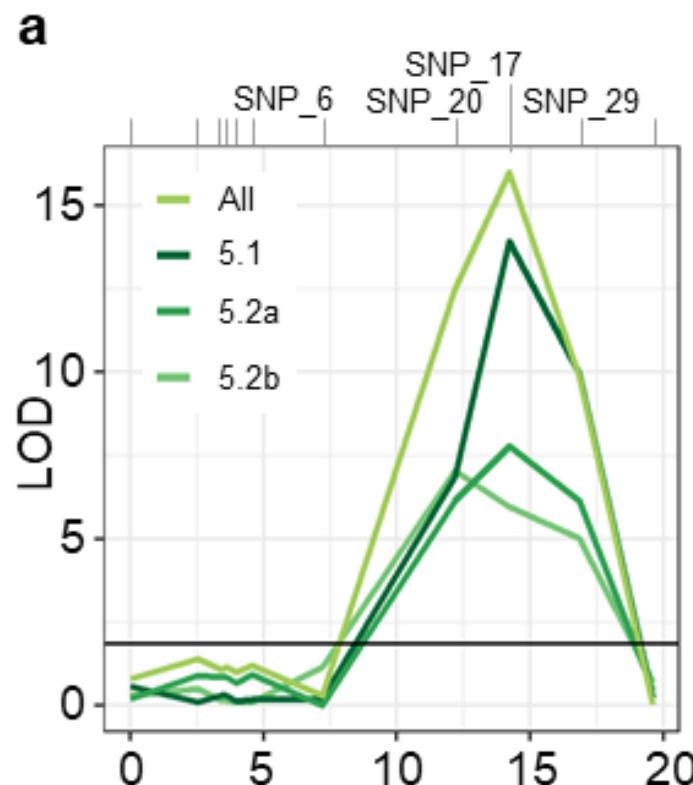
e Bulk Alignment



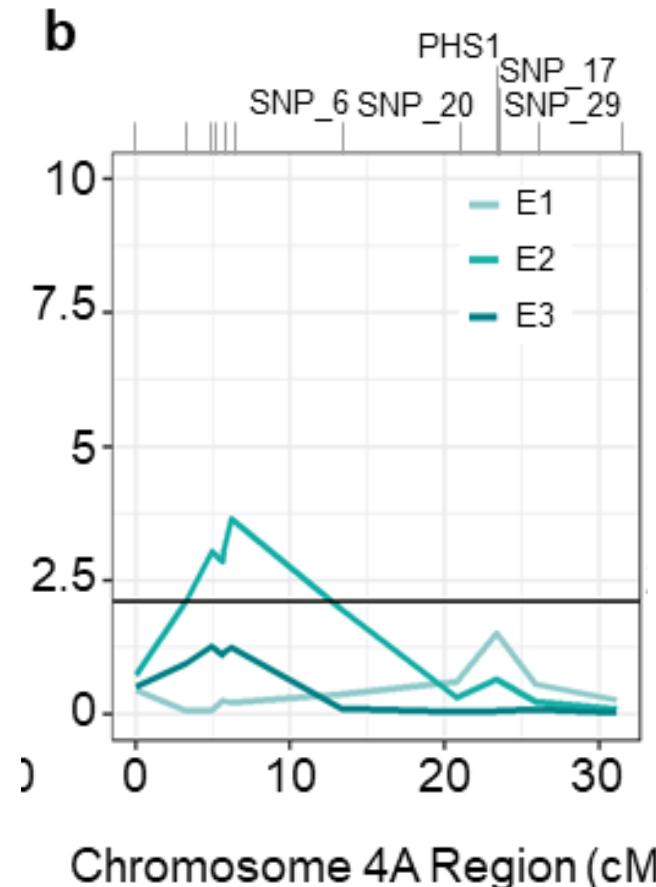
Fine Mapping in *ERA8*



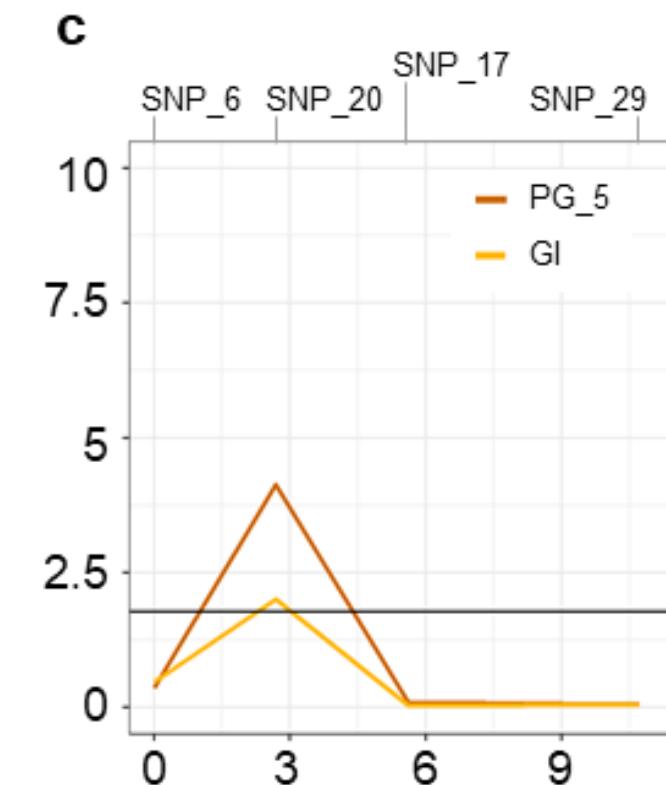
Additional
Zak/ZakERA8 BC



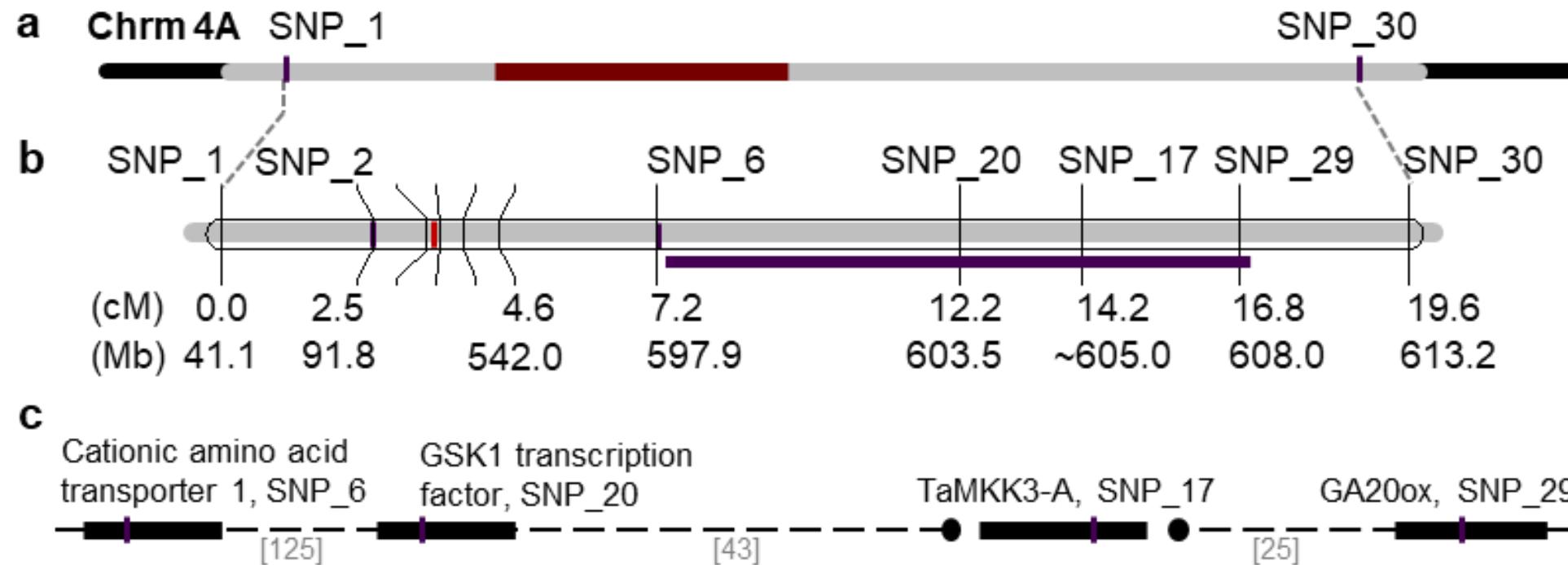
Louise/ZakERA8 RIL



Otis/ZakERA8 F2:F3



Fine Mapping in *ERA8*



Trait Introgression of *ERA8*



JOURNAL OF PLANT REGISTRATIONS

GERMPLASM

Martinez et al., 2014

WSU Winter Wheat

5 crosses
female/ (BC₁ERA8/male)
(~200)

20 crosses
(BC₁ERA8/male) / male
(~200)

USDA Club Wheat

24 crosses
Jasper / BC₃ERA8 (~800)
Bruehl / BC₃ERA8 (~800)
Kaseberg / BC₃ERA8
Brevor / BC₃ERA8
X010263-3C / BC₃ERA8
ARS010719-4L / BC₃ERA8

WSU Spring Wheat

3 crosses
Otis / BC₂ERA8 (529)
Louise / ERA8
x5 (698)
x12 (286)
BC₁ERA8 / Diva

RAGT Seed, UK

In collaboration with JIC

f Genome-specific KASP primers
Allele 1 FAM-CCTCTGCTATTGCTTAATCTCTc
Allele 2 HEX-CCTCTGCTATTGCTTAATCTCTt
Common GGACTTGGCAGCATATGTCA

Martinez et al., 2020

Fine Mapping *QPhs.cnl-2B.1*



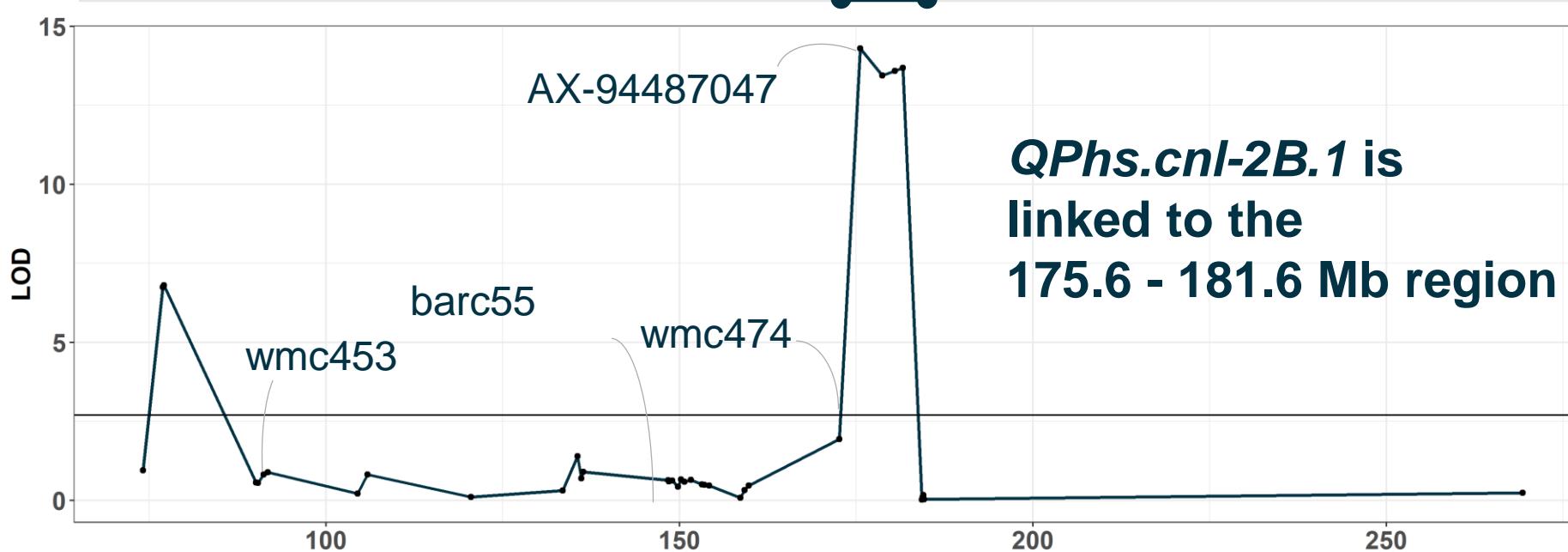
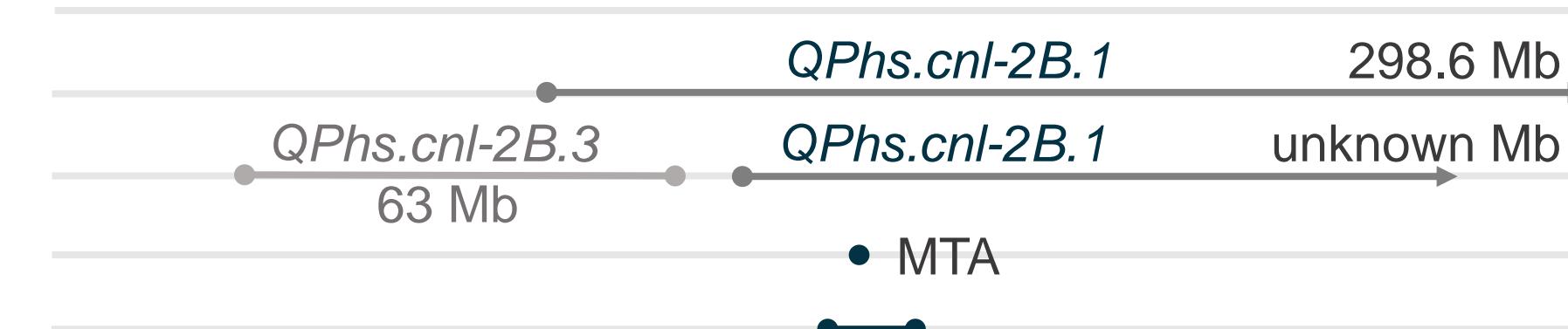
Chrm 2B

Munkvold et al. 2009

Somyong et al. 2014

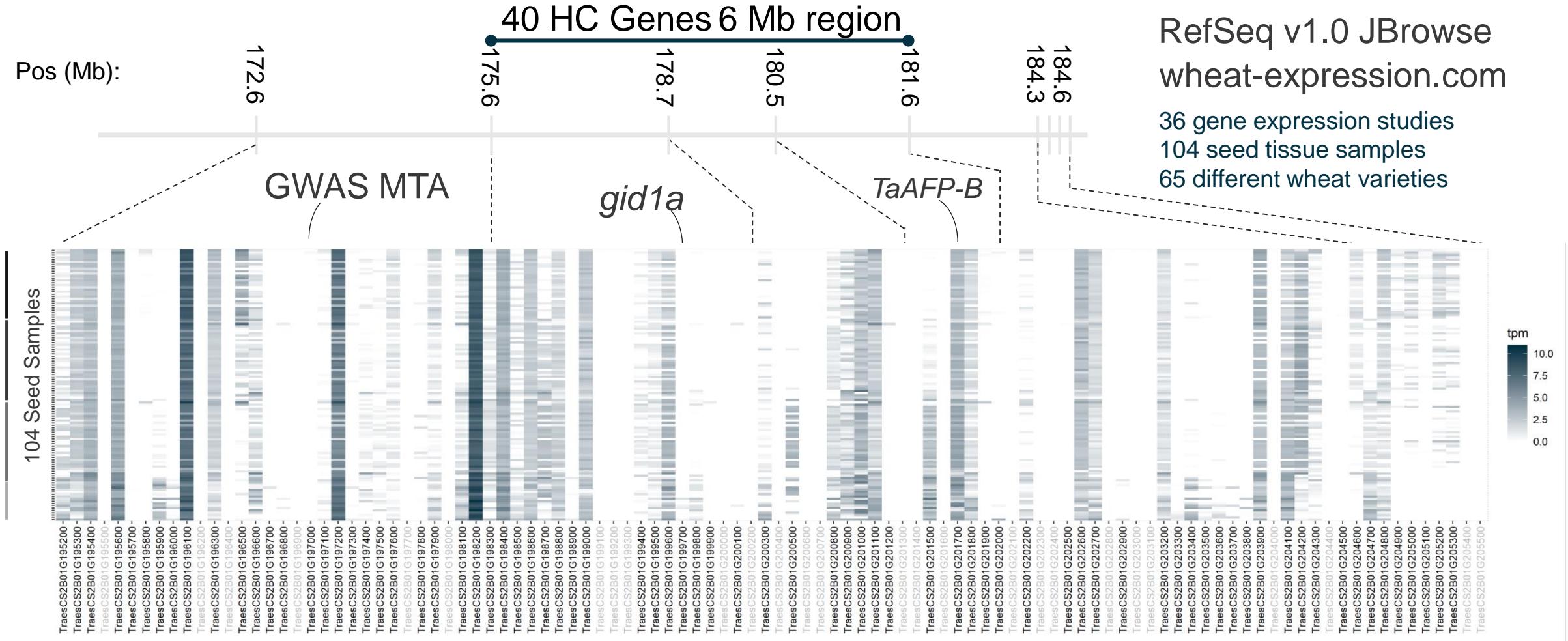
GWAS

QTL Analysis



430 BC1F5:8
PHS BLUP Score;
7 environments
SSR, Axiom, KASP markers
'cim' of qtl package in R

Fine Mapping *QPhs.cnl-2B.1*



Trait Introgression *QPhs.cnl-2B.1*



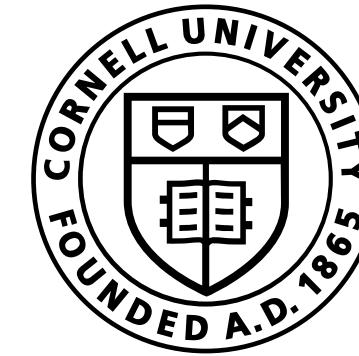
Club wheat



WA winter



NY winter



158 lines
elite nursery
past 10 years

Japanese Germplasm



'Tamaizumi'



Can we integrate genomic prediction
in the breeding program to make more
accurate decisions?

Genomic Prediction

Observations/Phenotype

$$\mathbf{u} \sim N(0, K\sigma_g^2)$$

\mathbf{u} is the vector of breeding values
with estimated relationship matrix K

Models can calculate K differently:

Ridge Regression

Gaussian Kernel

$$y_{\text{obs}} \sim \text{Loc} + \text{Yr} + \text{HarvDate}$$

fixed
effects

random
effects

\mathbf{u} : GEBV

$$\mathbf{WZu} + \boldsymbol{\epsilon}$$

design
matrix

e : experimental error



$$+ (1|\text{variety})$$

Genomic Prediction

Prediction Accuracy (PA)

$\text{cor} (y_{\text{obs}}, \text{GEBVs}_{\text{model}})$

$\text{cor} (y_{\text{obs_test}}, \text{GEBVs}_{\text{test}})$

1.0 Perfect Prediction

0.0 Inaccurate

Prediction Model

- Gaussian kernel
- Ridge regression

Output:
GEBVs_{train+test}



Five-fold CV

Phenotype

	80% Train	20% Test	All Env	total n
All Env	Both	1287		
Red	369			
White	904			

```
graph TD; A[All Env Both] --- B[80% Train]; A --- C[20% Test]; A --- D[1287]; E[Red 369] --- F[80% Train]; E --- G[20% Test]; E --- H[369]; I[White 904] --- J[80% Train]; I --- K[20% Test]; I --- L[904];
```

Genomic Prediction

Prediction Accuracy (PA)

$\text{cor} (y_{\text{obs}}, \text{GEBVs}_{\text{model}})$

$\text{cor} (y_{\text{obs_test}}, \text{GEBVs}_{\text{test}})$



Prediction Model

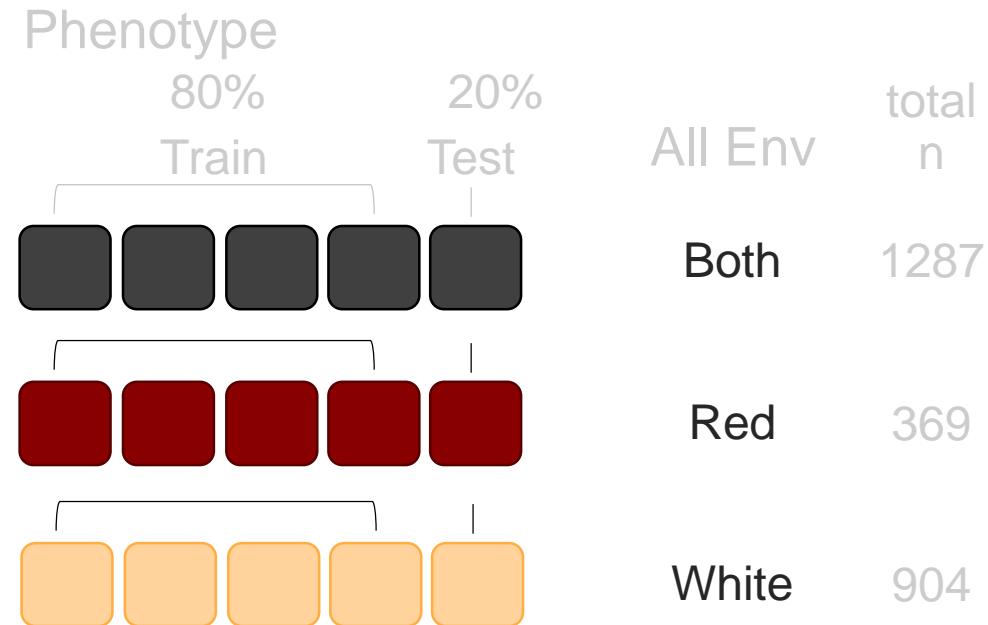
- Gaussian kernel
- Ridge regression

Output:
GEBVs_{train+test}

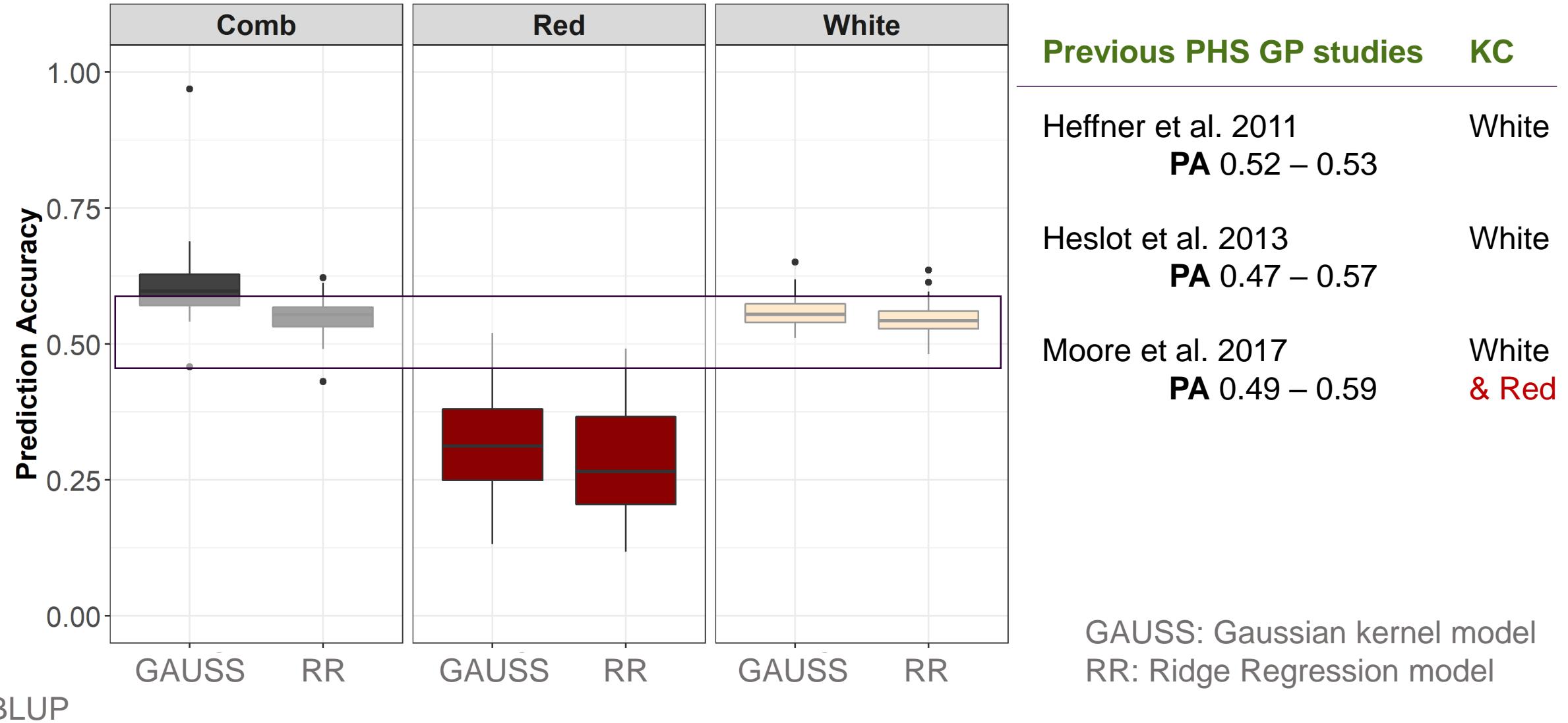
Both $y_{\text{obs_both}} \sim \text{Loc} + \text{Yr} + \text{HarvDate} + \text{KColor} + (1|\text{variety})$

Red $y_{\text{obs}} \sim \text{Loc} + \text{Yr} + \text{HarvDate} + (1|\text{variety})$

White $y_{\text{obs}} \sim \text{Loc} + \text{Yr} + \text{HarvDate} + (1|\text{variety})$



A comparison of Ridge Regression and Gaussian kernel models across seed coat colors



What does an accuracy of 0.6 even mean?

Accuracy of an phenotypic estimate (without genetic data)

$$PA = \text{cor}(\text{Obs_EnvA}, \text{Obs_EnvB})$$

$\text{cor}(\text{Obs2008}, \text{Obs2009})$

.

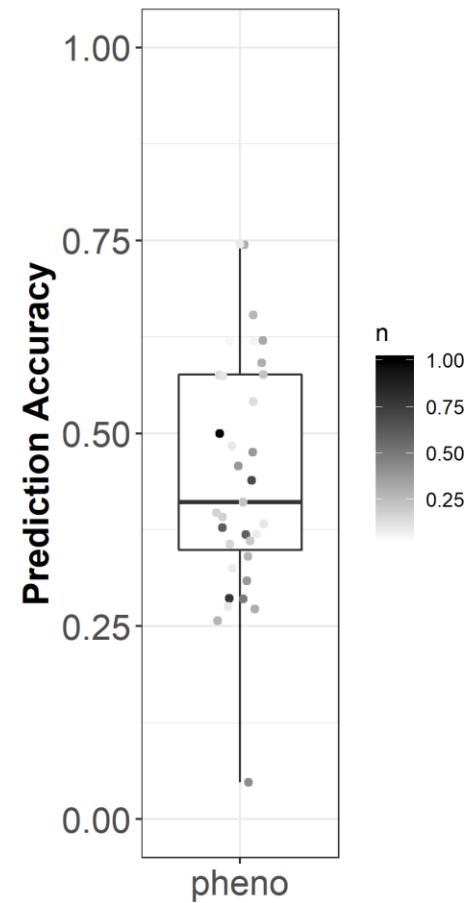
.

.

$\text{cor}(\text{Obs2015}, \text{Obs2017})$

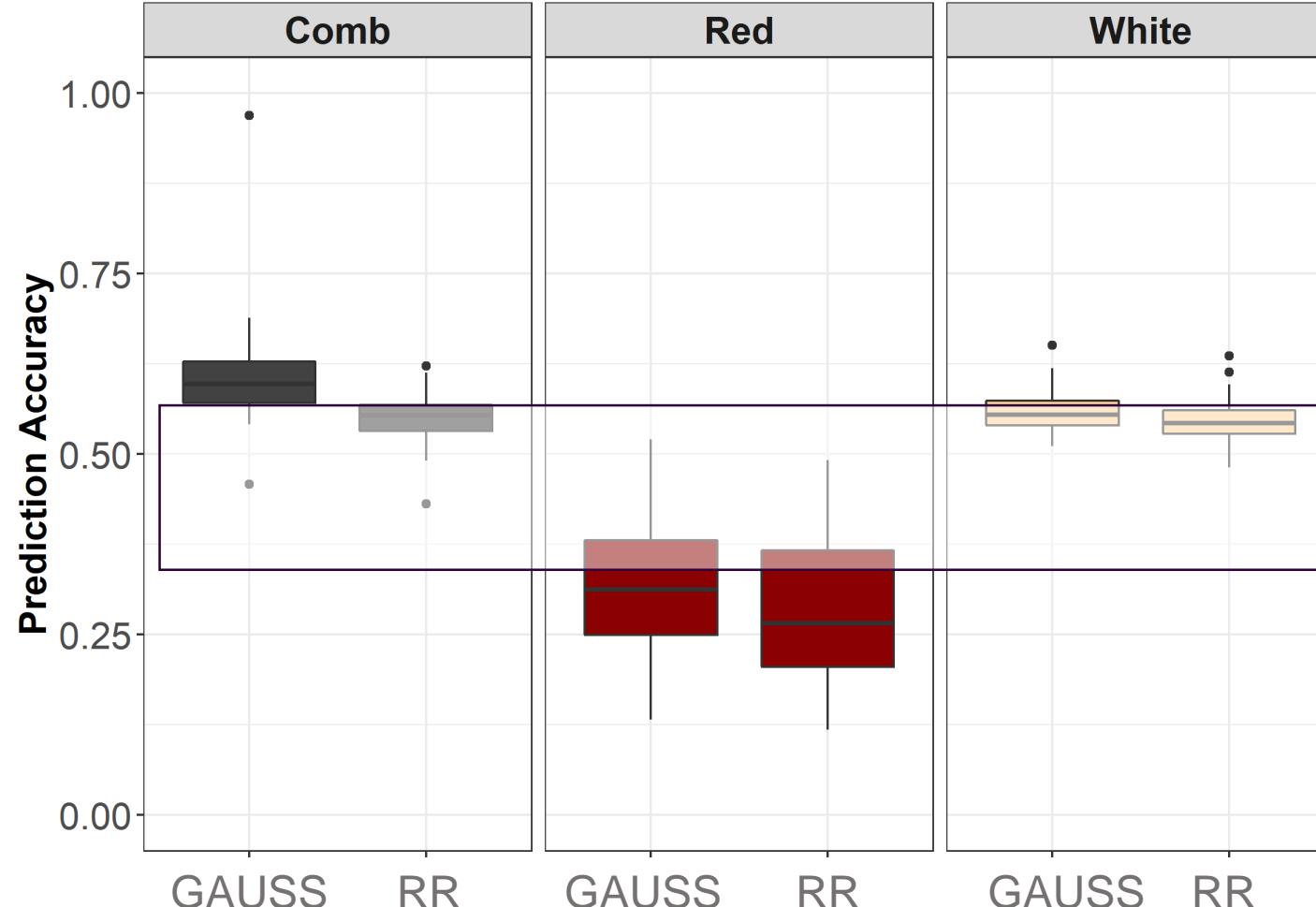
Average PA
0.45

PA_{pheno}

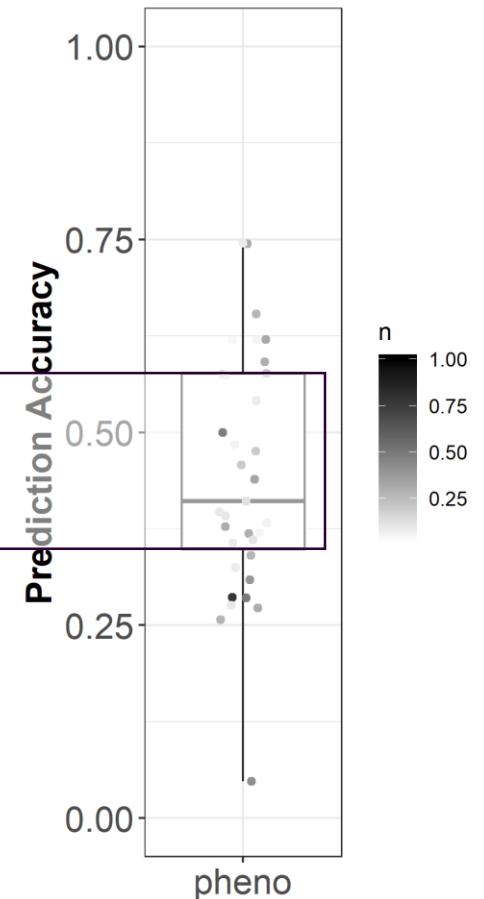


The correlation (PA) from one environment to another environment is comparable, to genomic prediction accuracies.

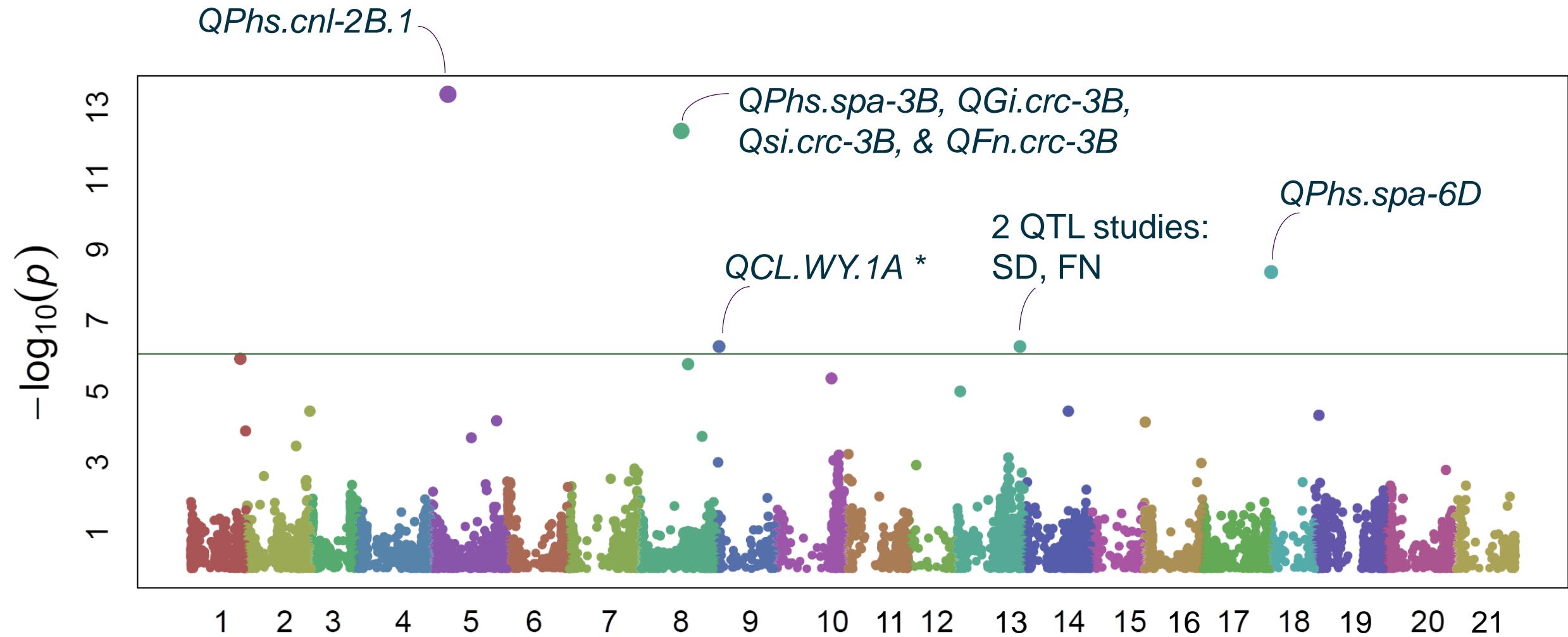
PA_{pred}



PA_{pheno}

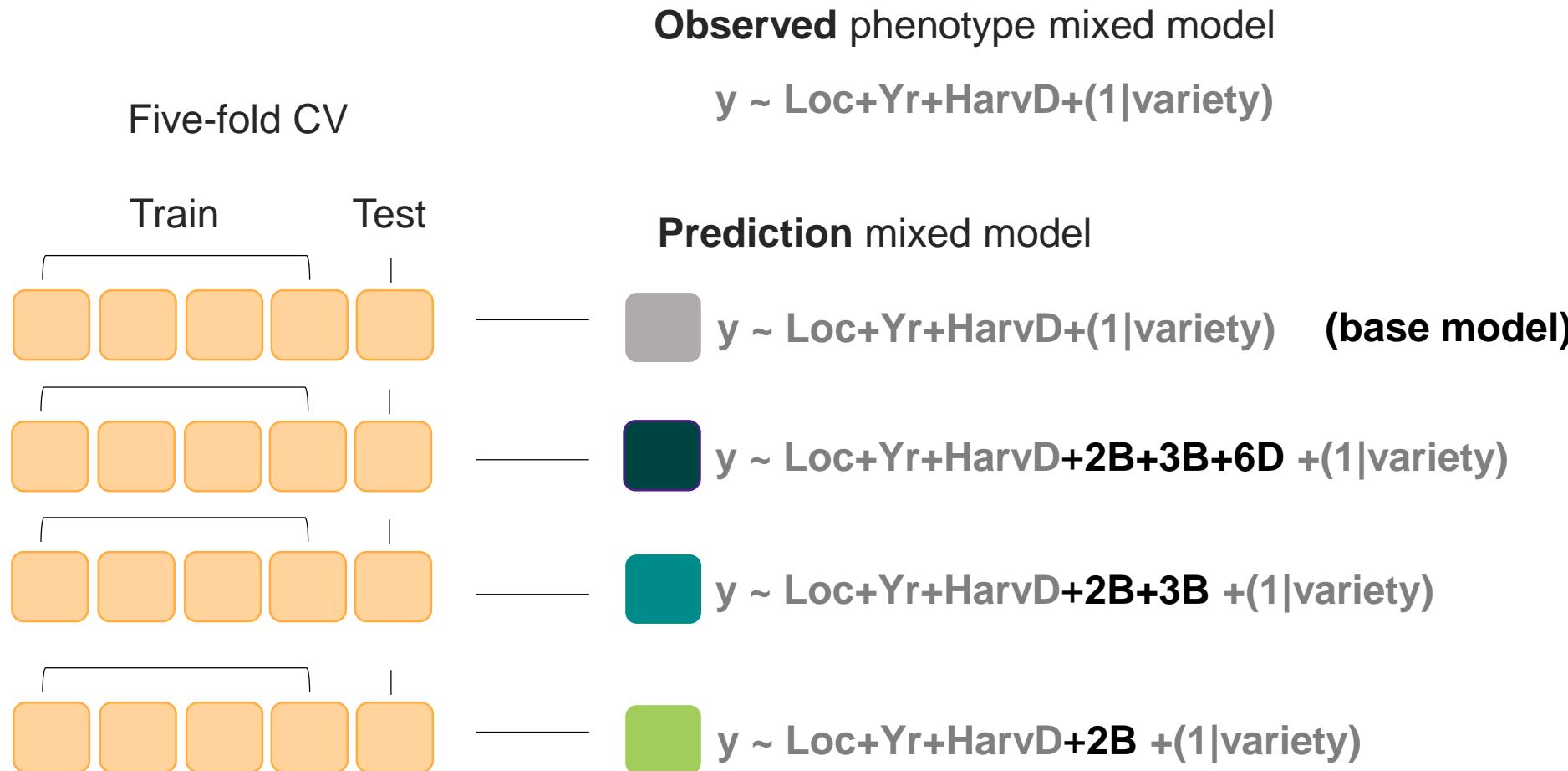


White kernel GWAS found multiple significant loci



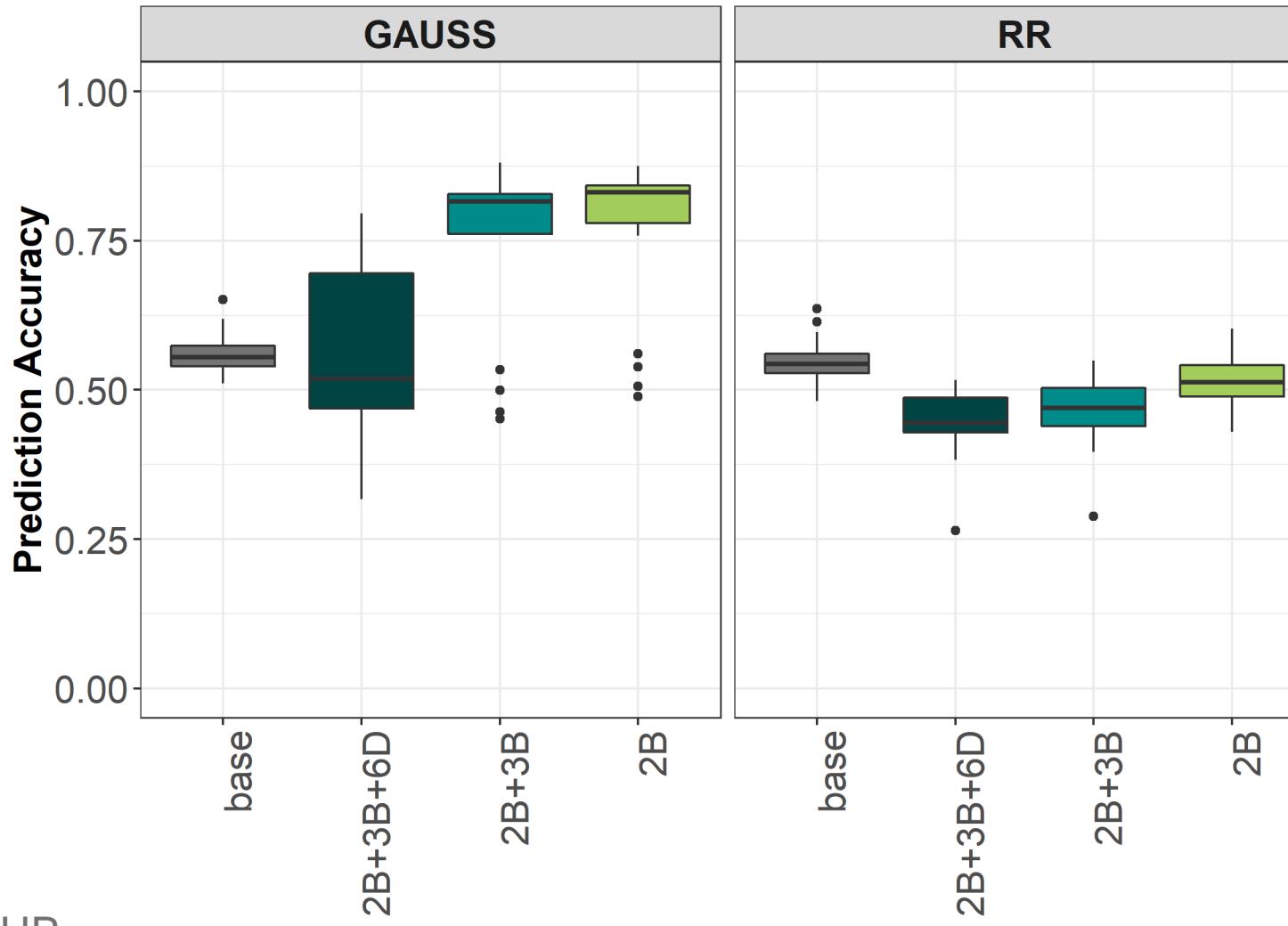
Zanetti et al., 2000; Munkvold et al. 2009; Fofana et al. 2009; Zhang et al. 2013;
Kumar et al. 2015; Martinez et al. 2018; Zuo et al., 2019

Will associated QTL improve prediction?



$$PA = \text{cor} (y_{\text{obs_test}}, \text{GEBVs}_{\text{test}})$$

Adding significant QTL as fixed effects seems to improve accuracy for Gaussian kernel model



GAUSS additive + non-additive
RR only additive

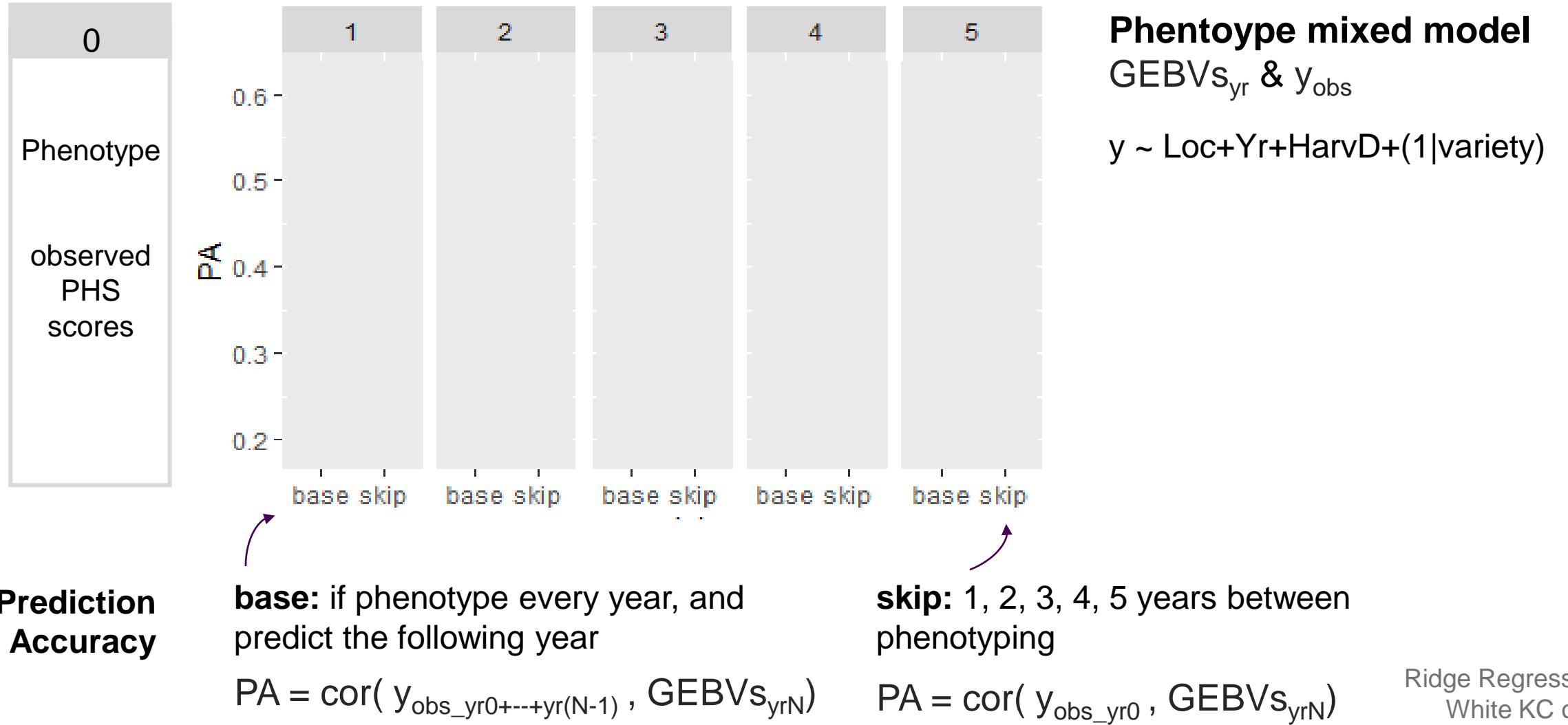
GAUSS vs RR

The real question is, what do you want to use it for?

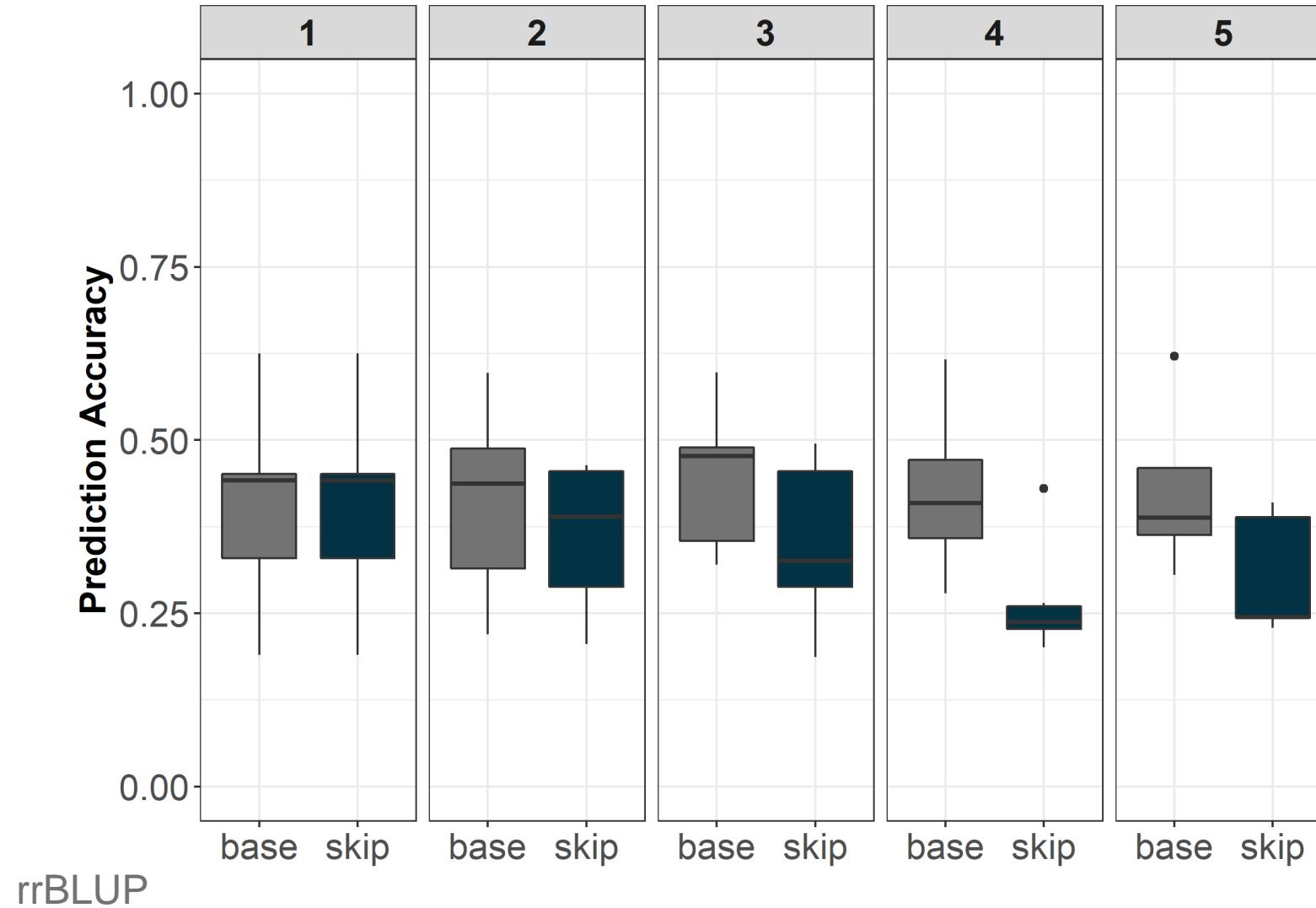
- Want additive RR for selection
- Want +non-add for prediction

Need to investigate if adding significant QTL markers as a fixed effect is overfitting the model?

How many years between phenotyping can a breeding program skip without losing substantial PA?



How many years between phenotyping can a breeding program skip without losing substantial PA?



It may be possible to phenotype for PHS tolerance every couple of years, without effecting accuracy

Something to consider:

- Increased genetic diversity year to year will reduce ability to accurately calculated GEBVs
- Year to year GEBV calculations tend to have lower PA than GEBV calculated from hundreds of individuals over multiple environments

Ridge Regression
White KC only



Why use genomic prediction for this trait?

Phenotyping occurs at the end of the growth cycle

No “mid-cycle” selections before harvest

These phenotypic hurdles are not exclusive to PHS screening



Very labor intensive

Precise sampling



Disease Screening



Traits dependent on inoculation, severity, etc can benefit from genotypic predictions of the phenotype

FHB (2 field seasons)



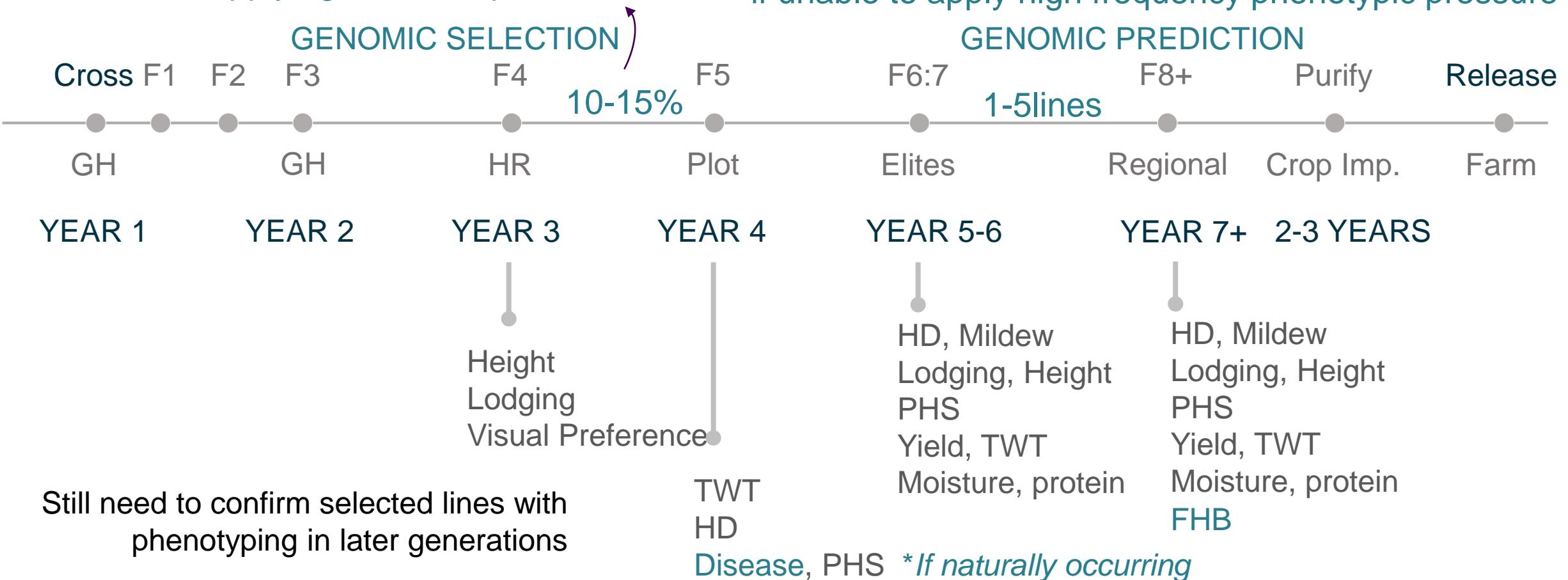
Stripe Rust (7 field seasons)



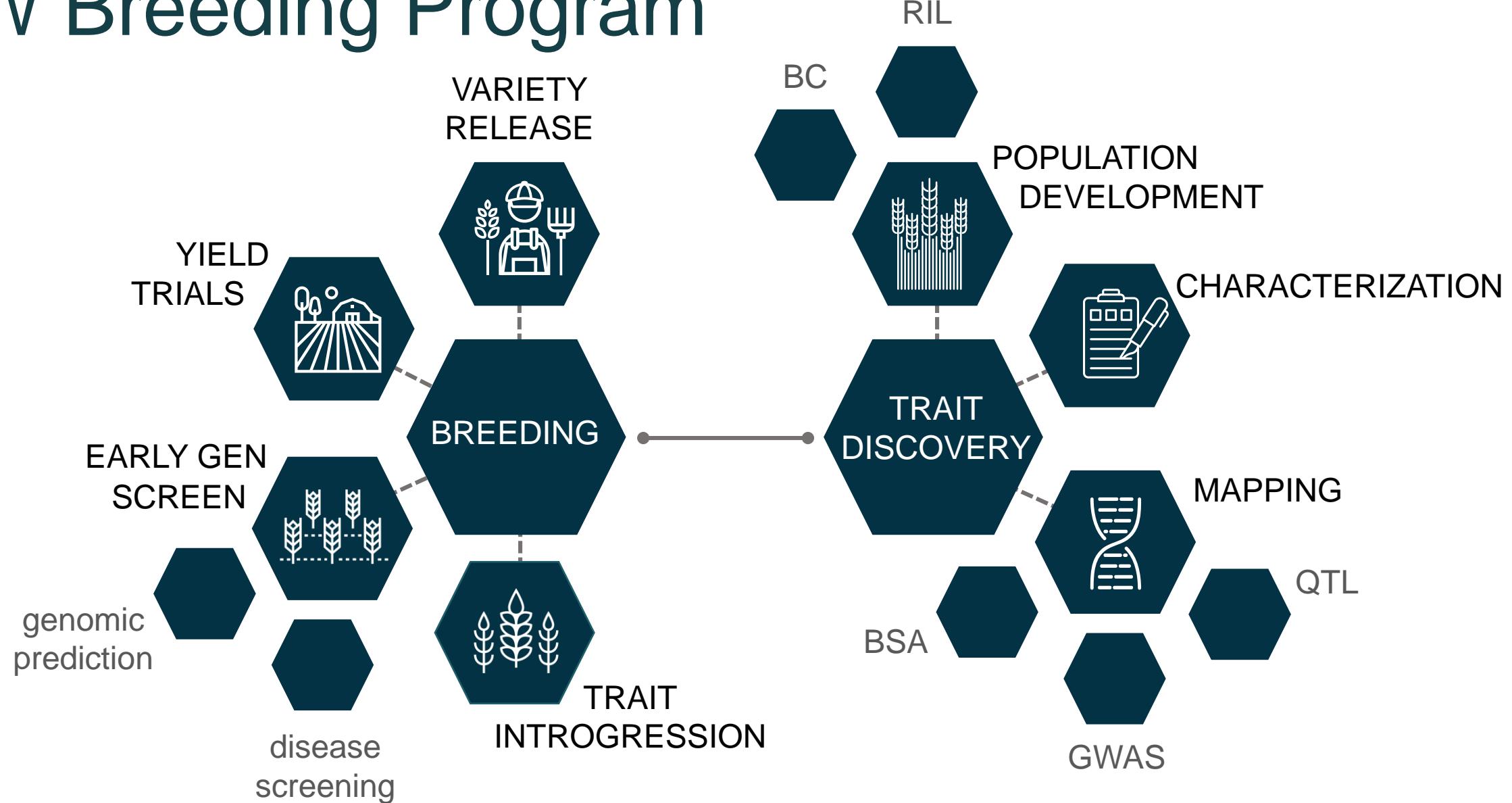
Breeding with Genomic Prediction



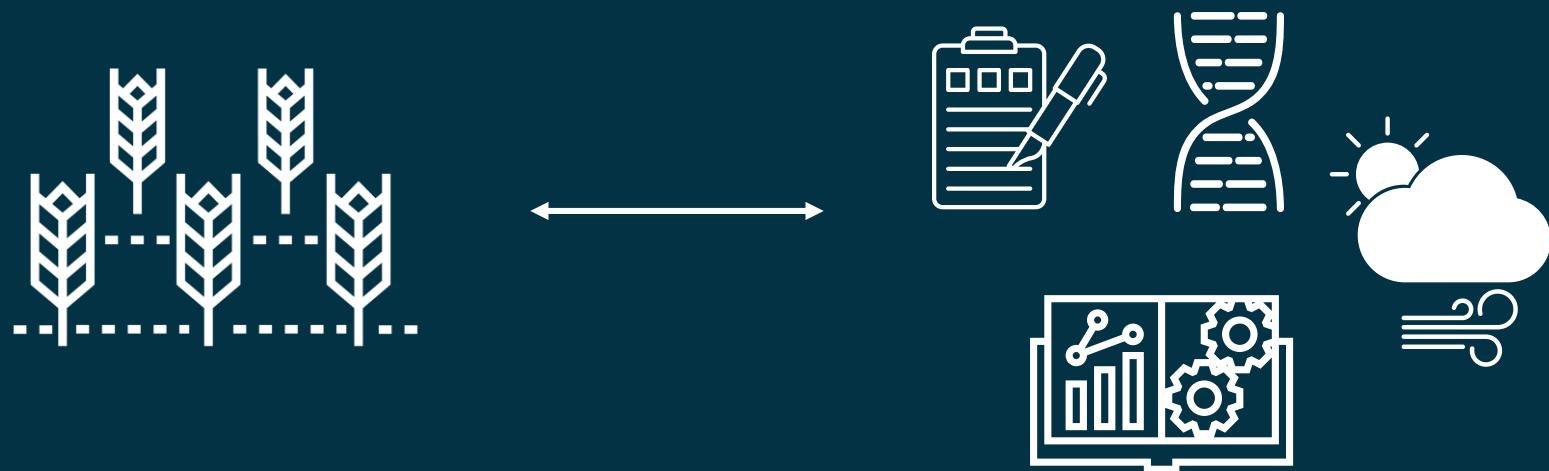
GEBVs can help guide selection; less likely to throw out PHS Tolerant lines when applying selection pressure



HRW Breeding Program



As your next generation plant breeding:
aim to fuse wheat breeding with predictive analytics



Thank you for your attention

LinkedIn



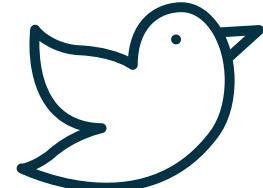
Website



Email



Twitter



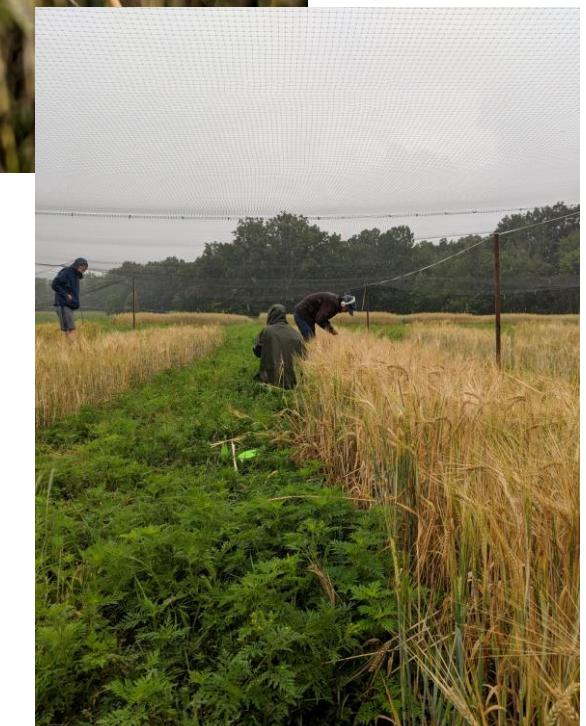
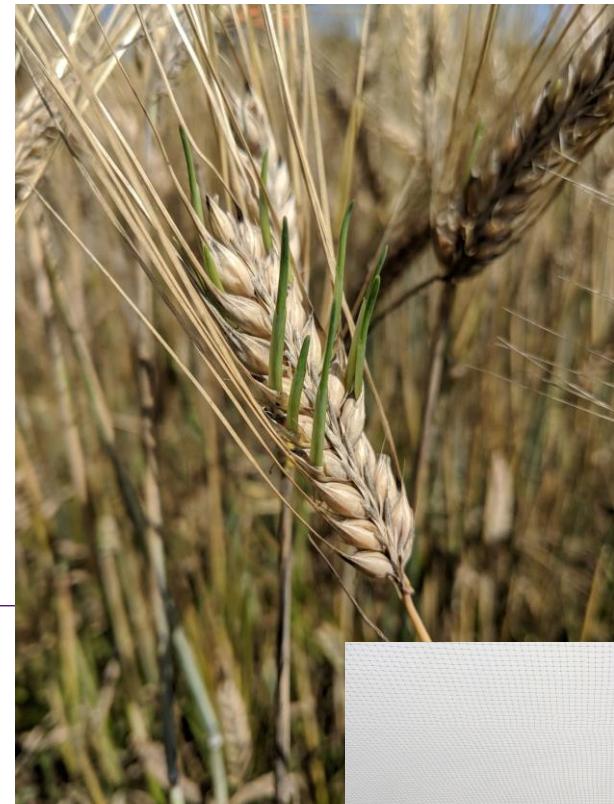
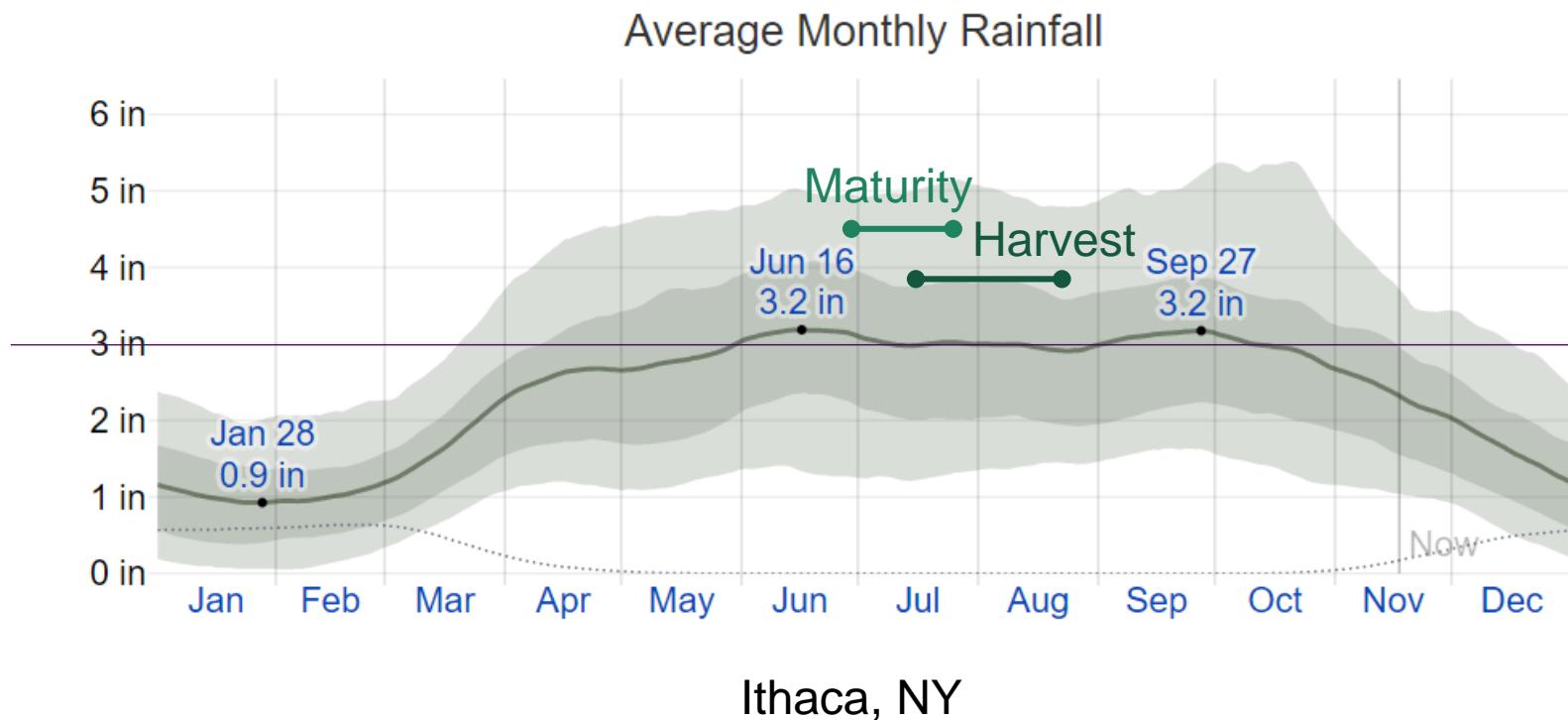
shantel-a-martinez

shantel-martinez.github.io

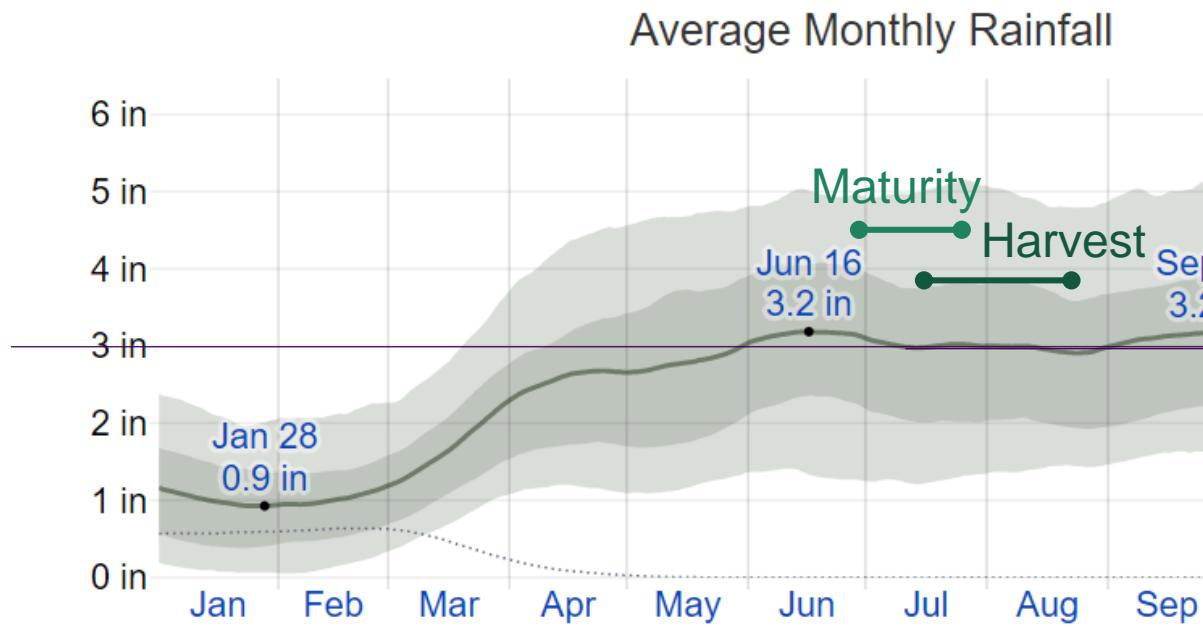
shantel.a.martinez@gmail.com
sam594@cornell.edu

@s_amealia

How can my PHS skills be used?

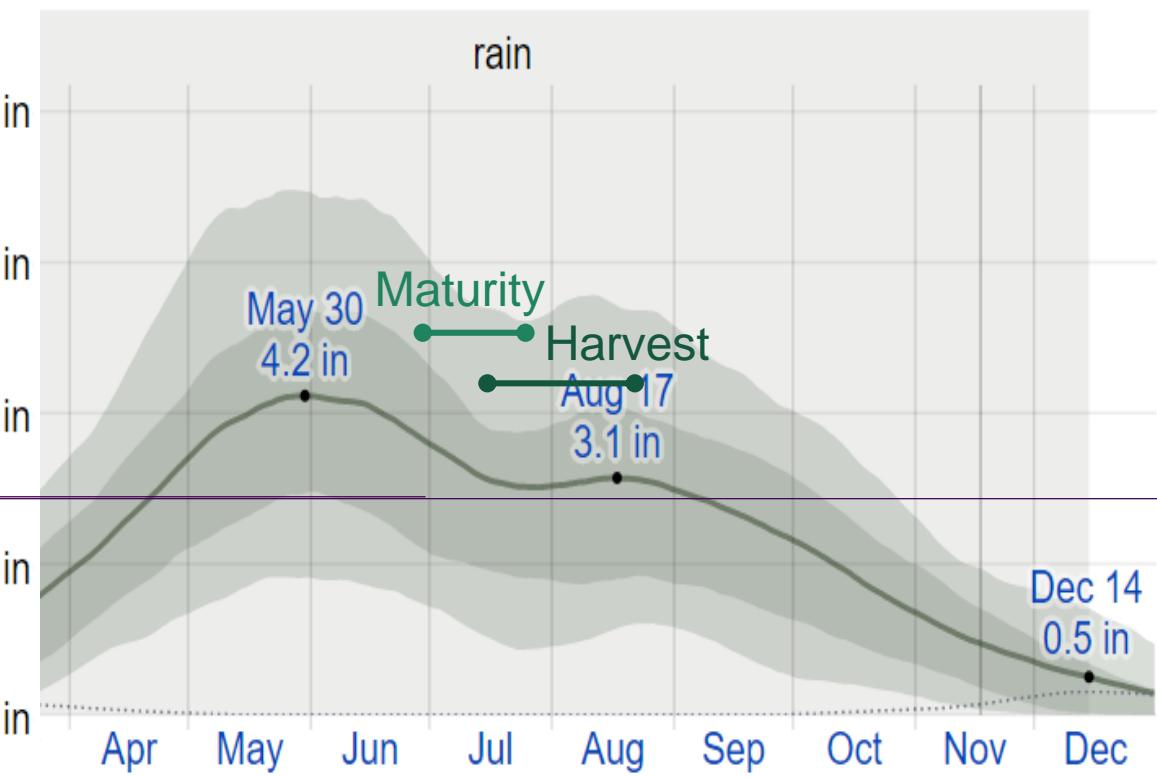


My experience can be useful if a program starts growing malting barley in NE



Ithaca, NY

Average Monthly Rainfall



Lincoln, NE

Mixed Model

Observations/Phenotype

$$y = \mu + X\beta_{loc} + X\beta_{yr} + X\beta_{harv} + Zg + \epsilon$$

population mean

fixed
effects

loc: location

yr: year

design
matrix

harv:
sampling
date

random
effects

$$g: BLUP \quad y_{obs}$$

e: experimental error

design
matrix

$$y_{obs} \sim Loc + Yr + HarvDate$$

$$+ (1|variety)$$