shantel-martinez.github.io

Identifying Loci and Genomic Prediction Models for PHS Tolerance in Northeast Soft Wheat Breeding Programs

Shantel A. Martinez

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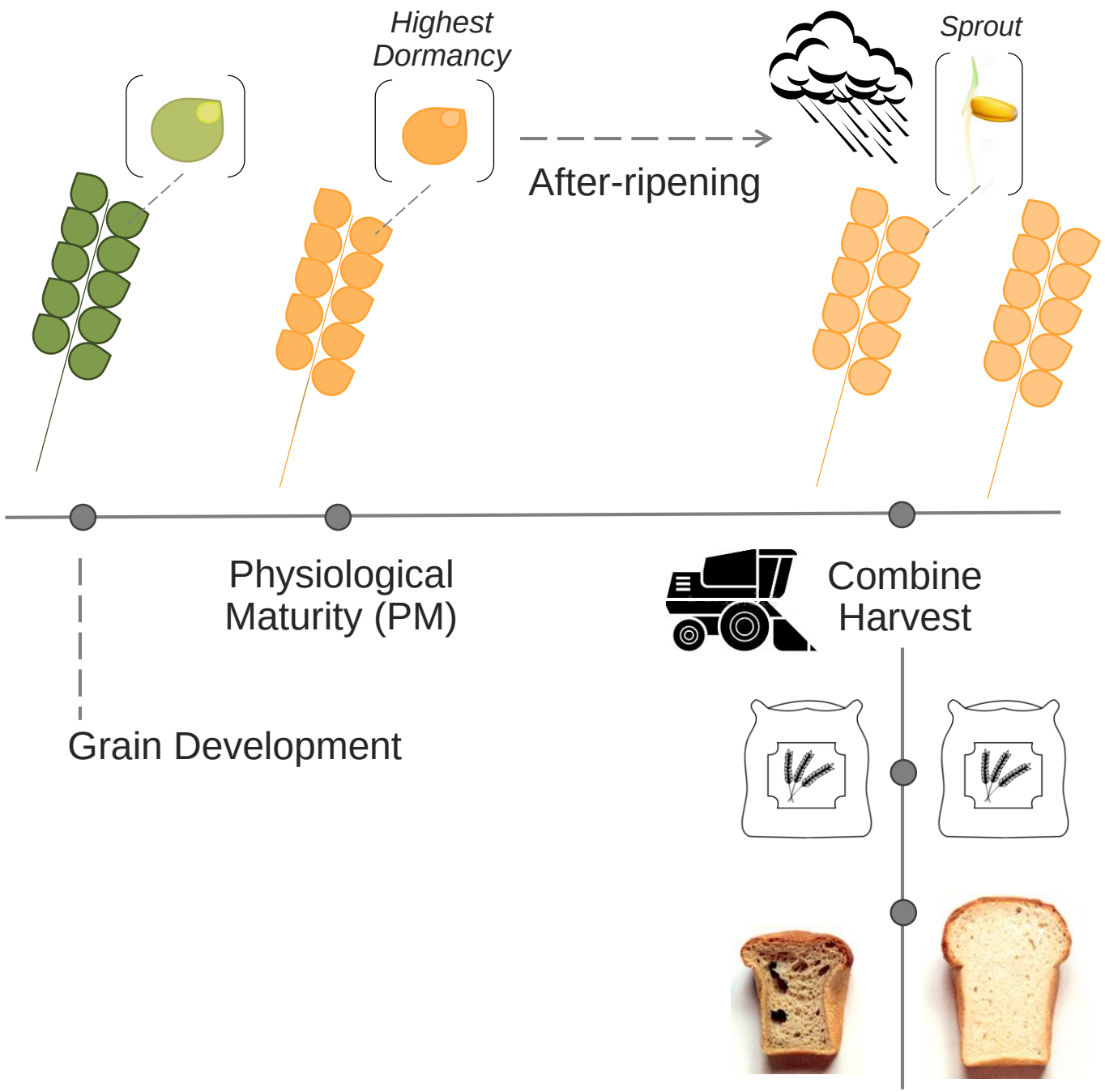
Cornell University

Soft Wheat Quality Meeting

April 23rd, 2019


Highest Dormancy
Sprout
After-ripening
Physiological Maturity (PM)
Combine Harvest
Grain Development

We are not alone - 2018 Preharvest Sprouting

England

Tobias Barber @ekte_Toby — Following

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

2:21 PM - 25 Aug 2018

Jim Thompson @jimt_farmer — Follow

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

9:53 AM - 27 Jul 2018

1 Retweet 8 Likes

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

Rhett Kaufman @rhett_kaufman — Follow

Should have brought the combines to the field 3 months ago. Just need 1 more day #Harvest18

Nebraska

Chris Cu11an @ChrisCullan1 — Follow

On the edge. #wheatharvest18

5:06 PM - 12 Jul 2018

1 Retweet 40 Likes

1 1 40

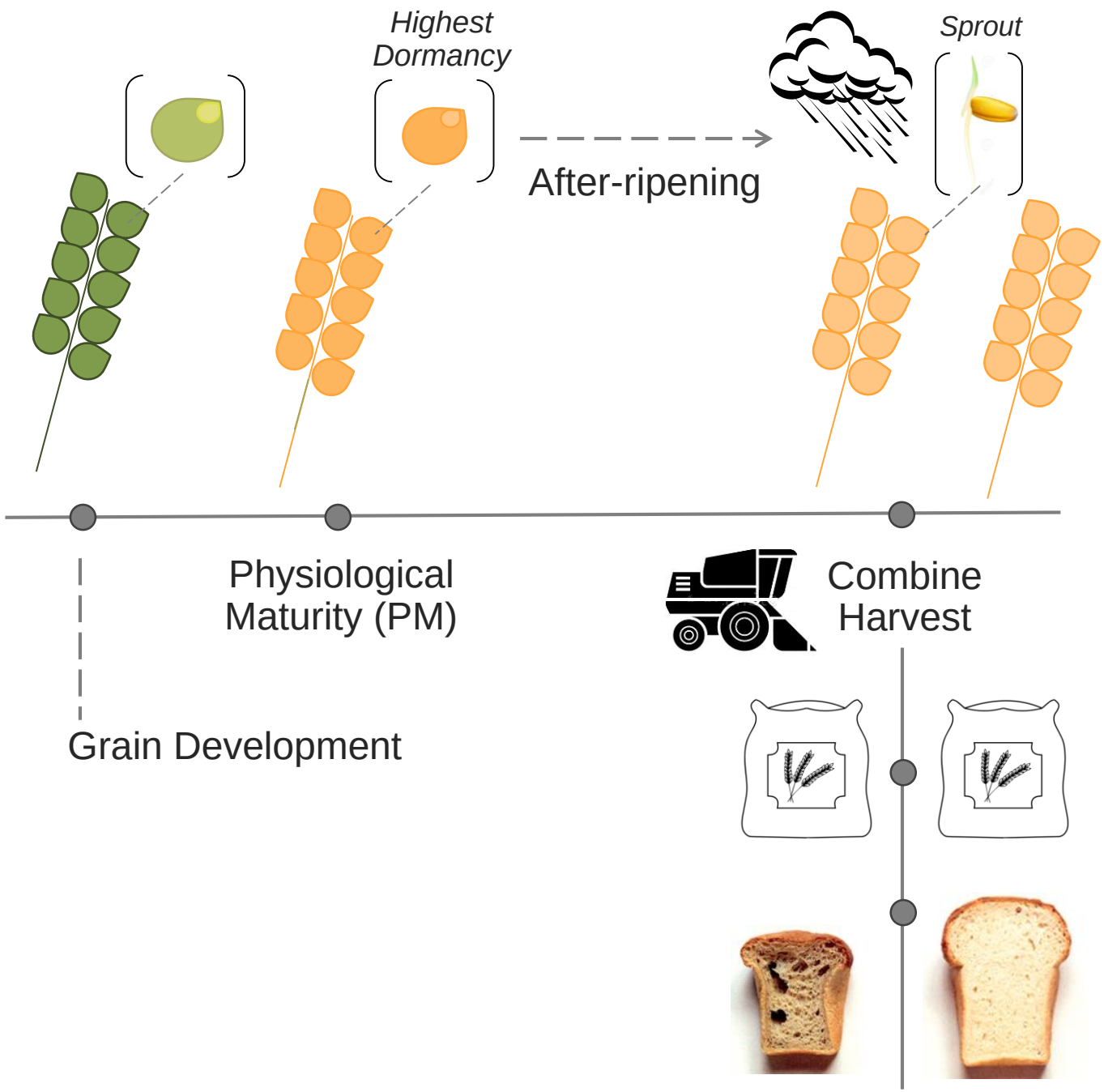
Canada

Fermes Chauvin Farms Ltd. @MoeChauvin — Follow

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

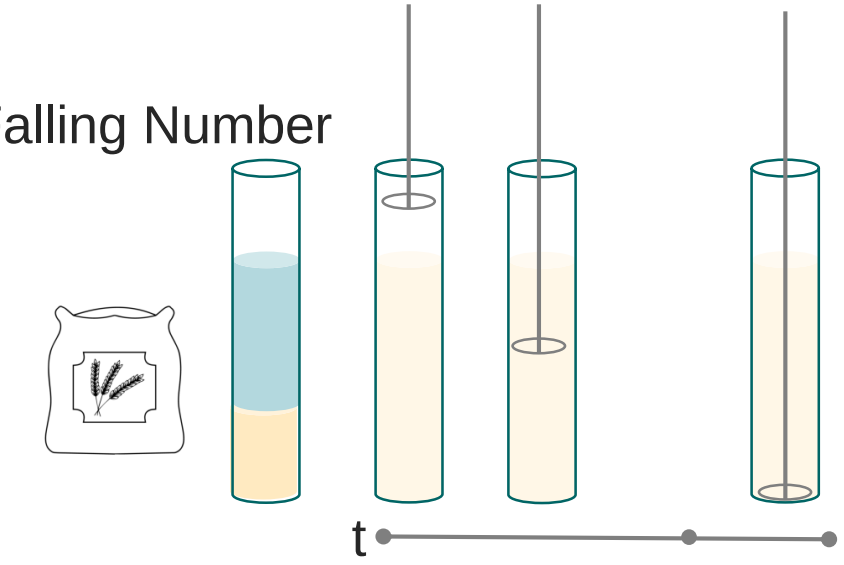
4:51 PM - 5 Jul 2018

Farms.com

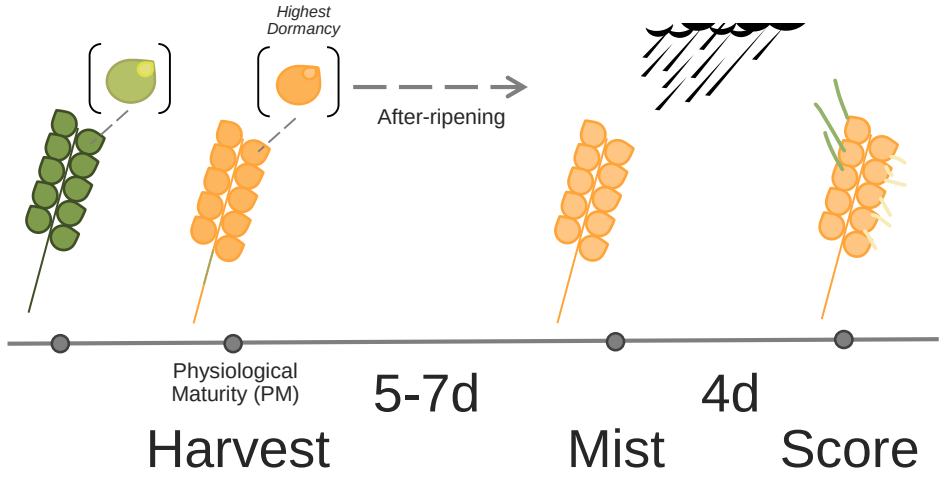


Methods to Screen for PHS

1 Falling Number



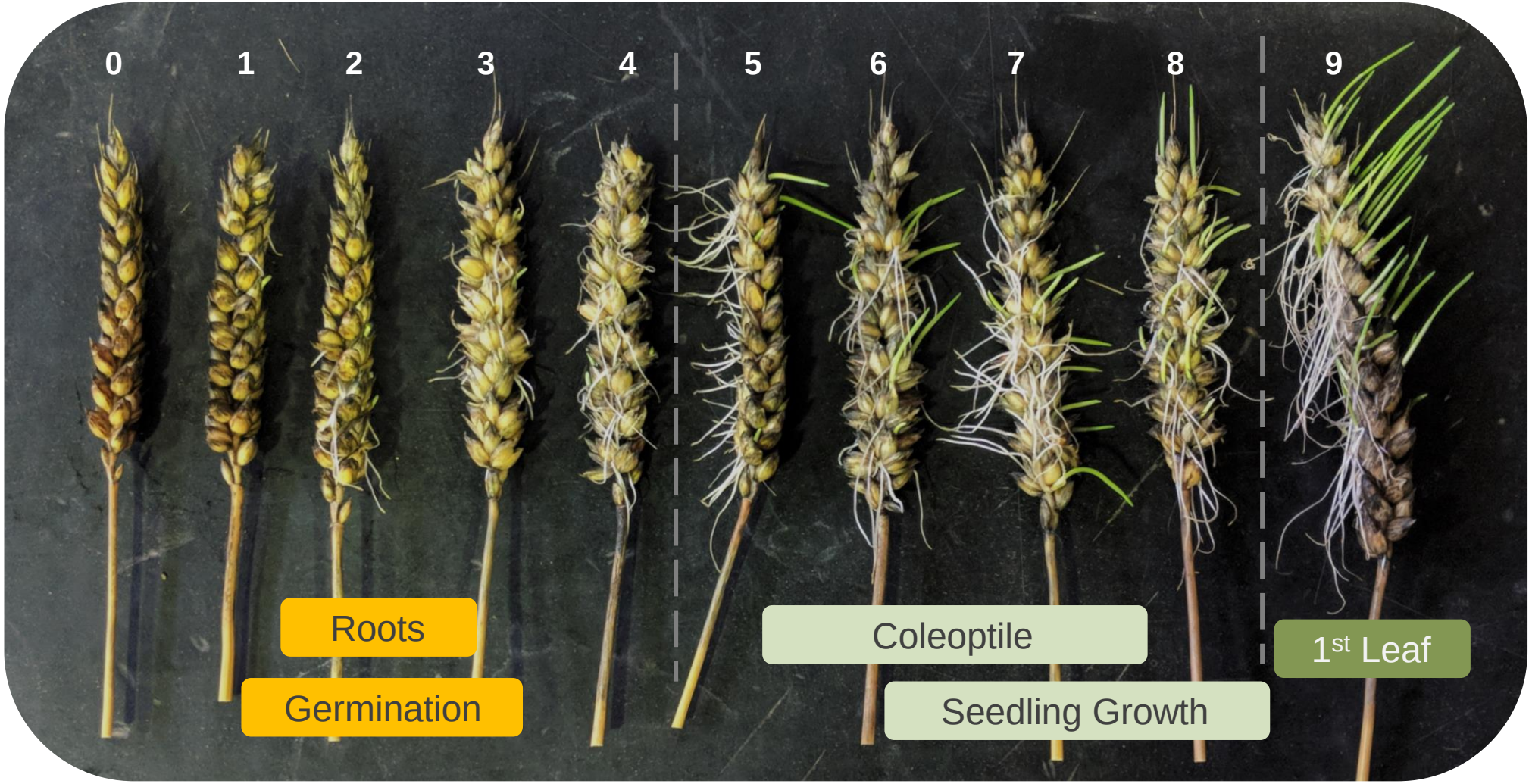
2 Spike Wetting Test



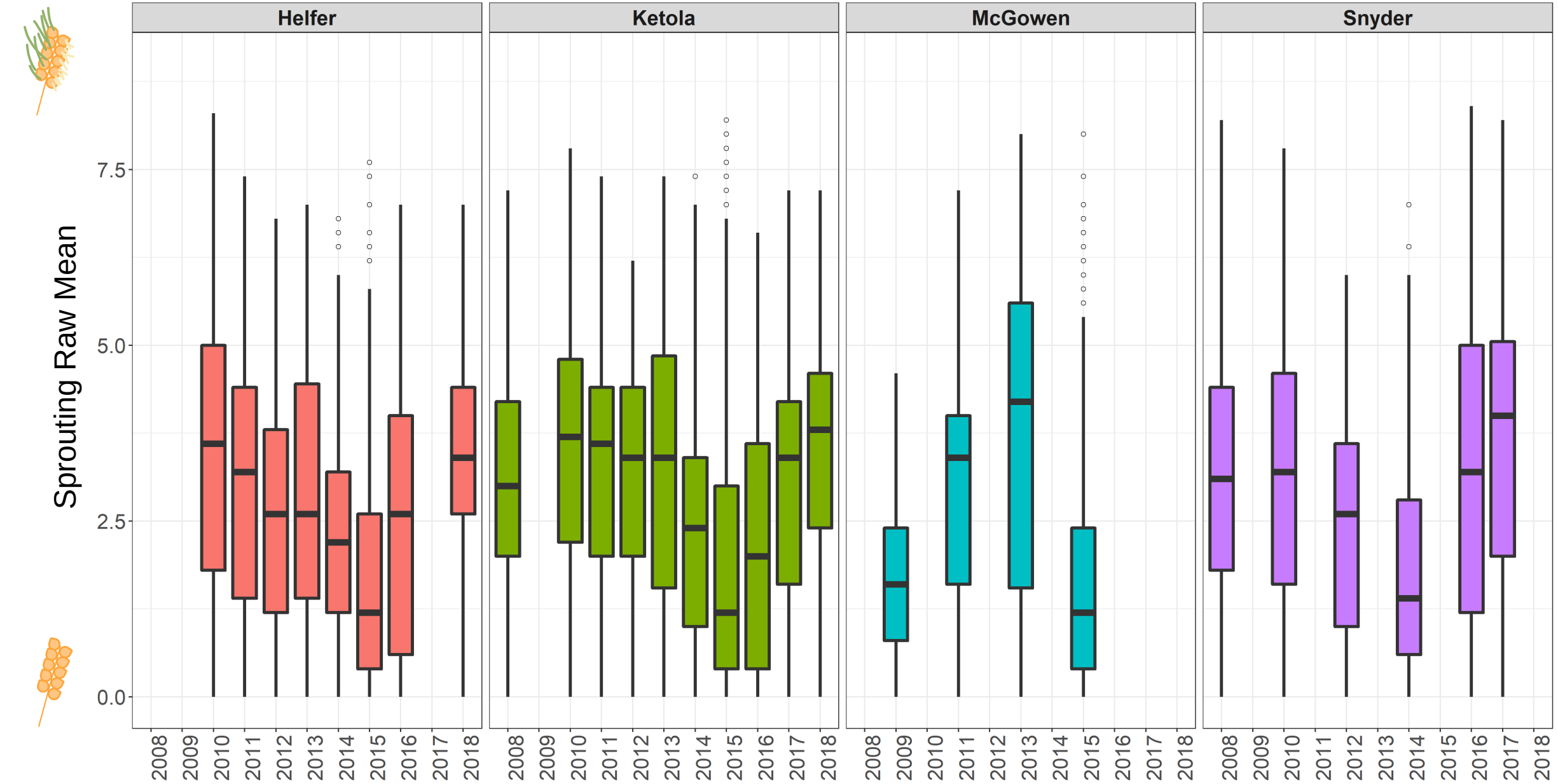
Perten.com | 123rf.com

Visible Sprout Scored

PHS Tolerant ⟷ PHS Susceptible

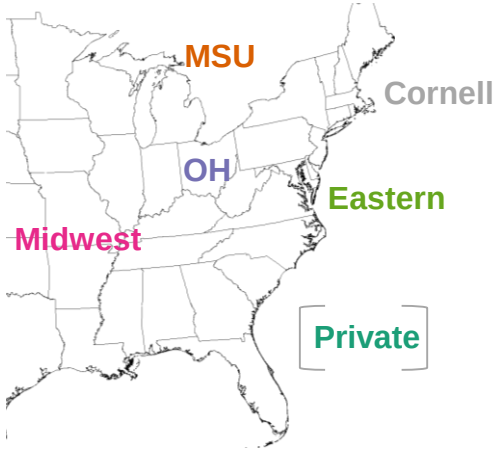


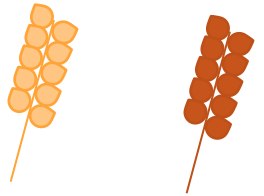
McMaster & Derera *et al*., 1976


Helfer
Ketola
McGowen
Snyder
Sprouting Raw Mean
0.0
2.5
5.0
7.5
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018

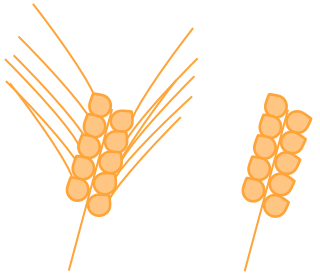
CNL Master Nursery (CNLM)

White Red

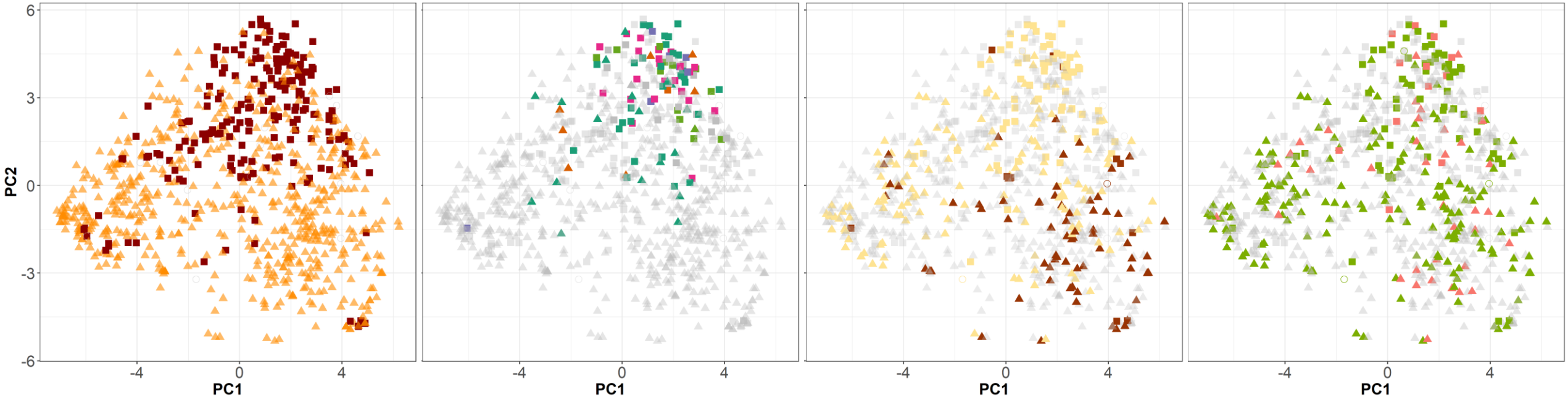




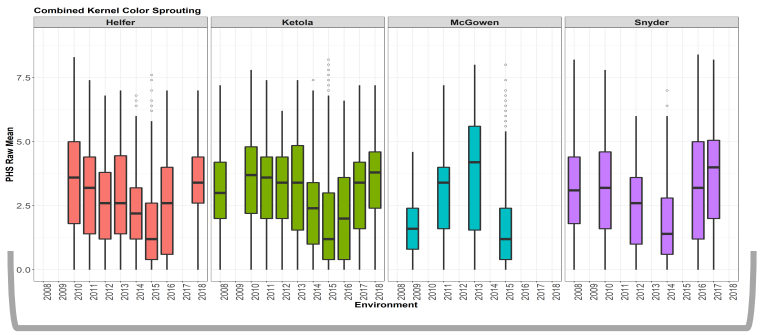
White Amber



Awned Awn-less

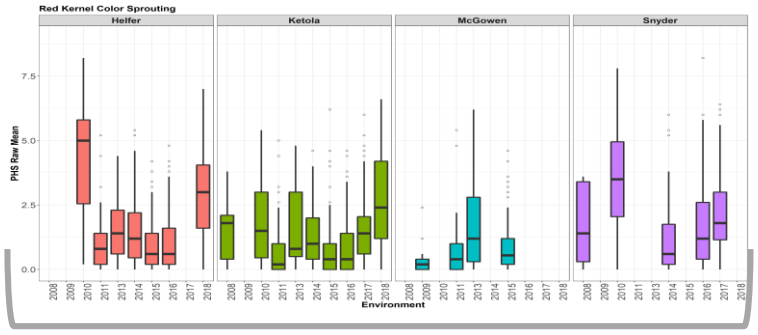


Both



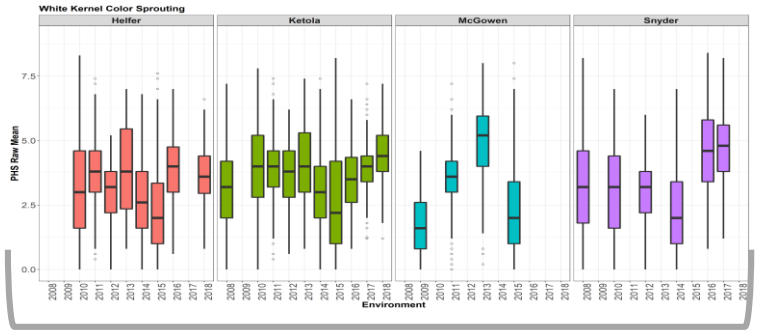
BLUP

Red KC



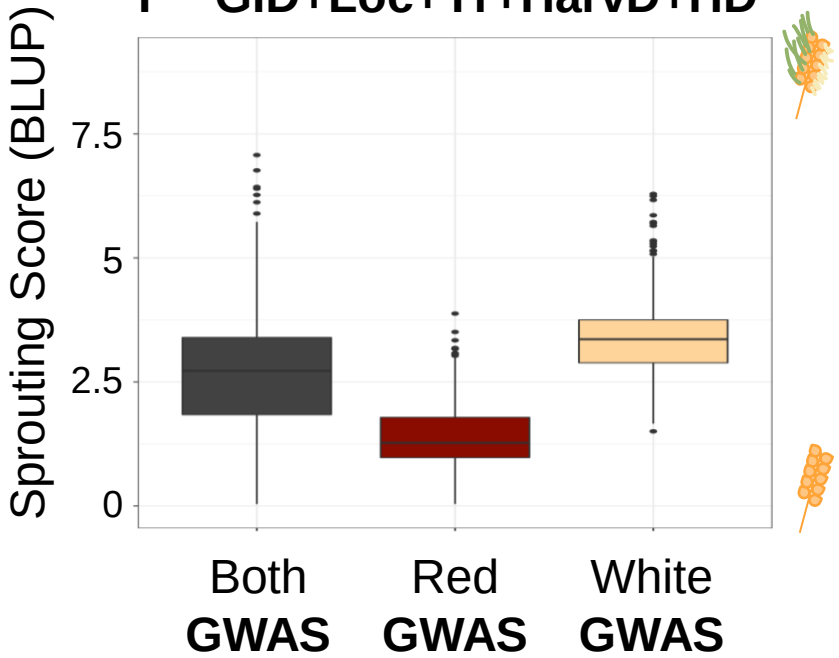
BLUP

White KC



BLUP

Y ~ GID+Loc+Yr+HarvD+HD



GWAS **GWAS** **GWAS**

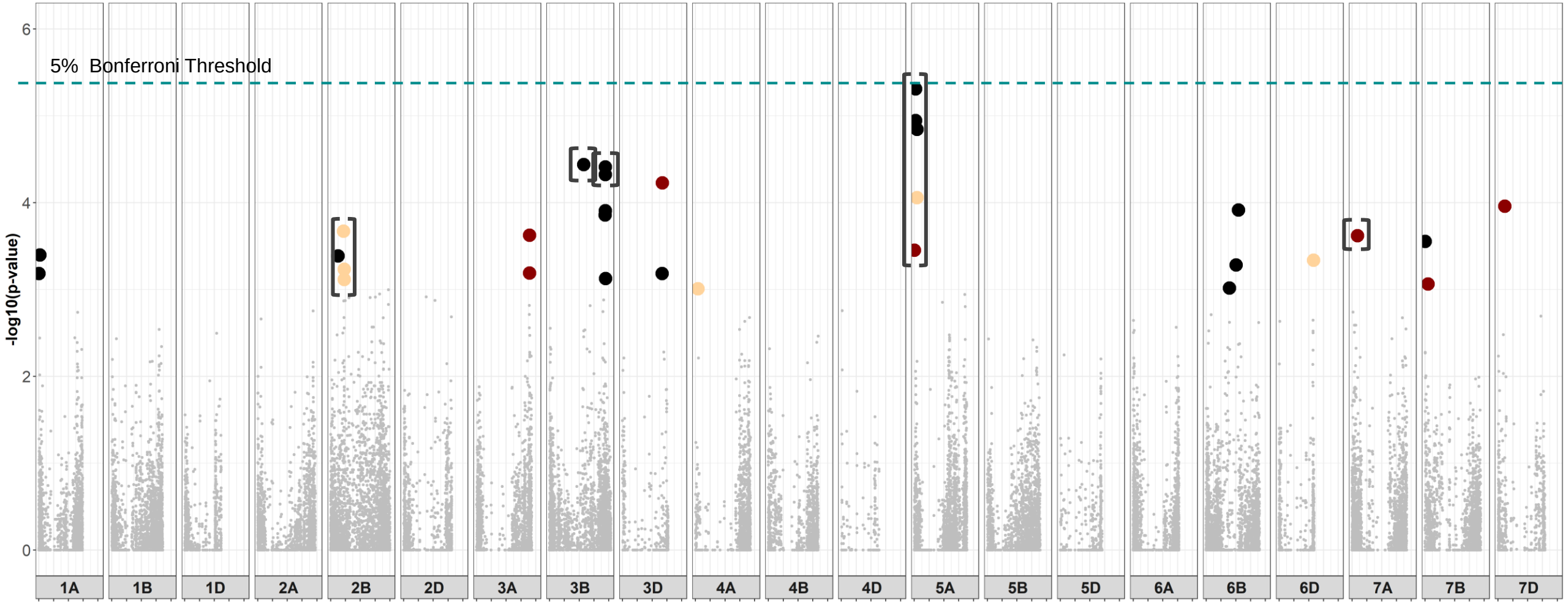
rrBLUP | 4PC | MAF > 0.05

Both

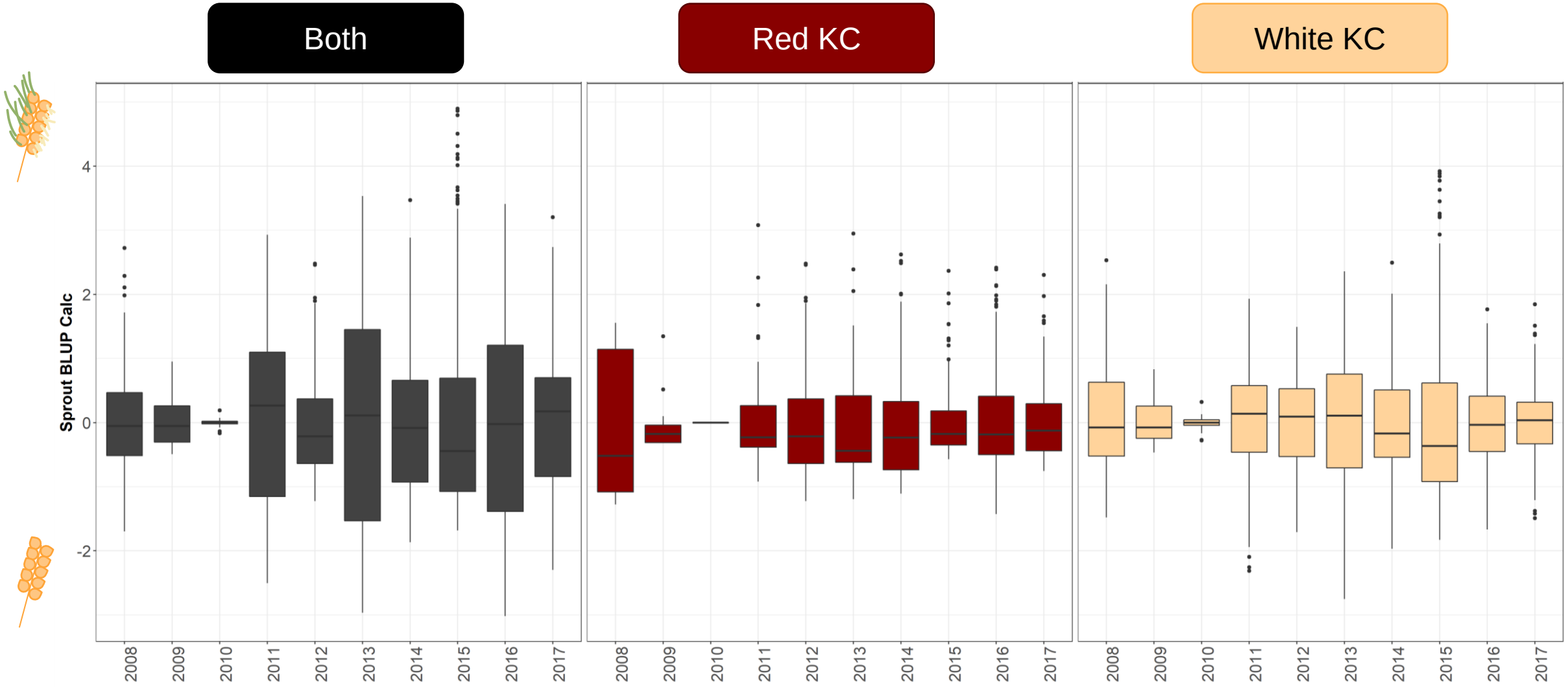
Red KC

White KC

QTN Across All Environments

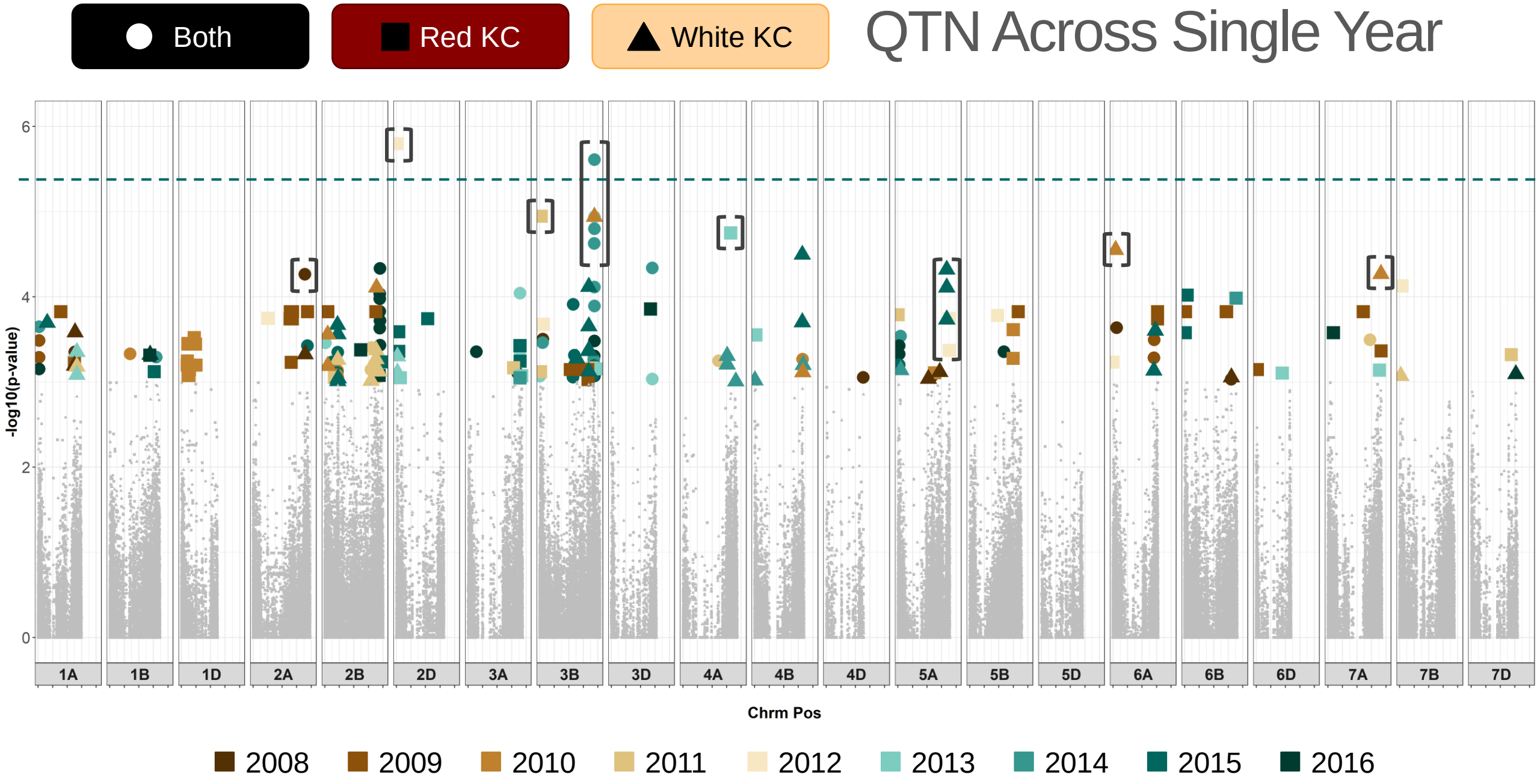


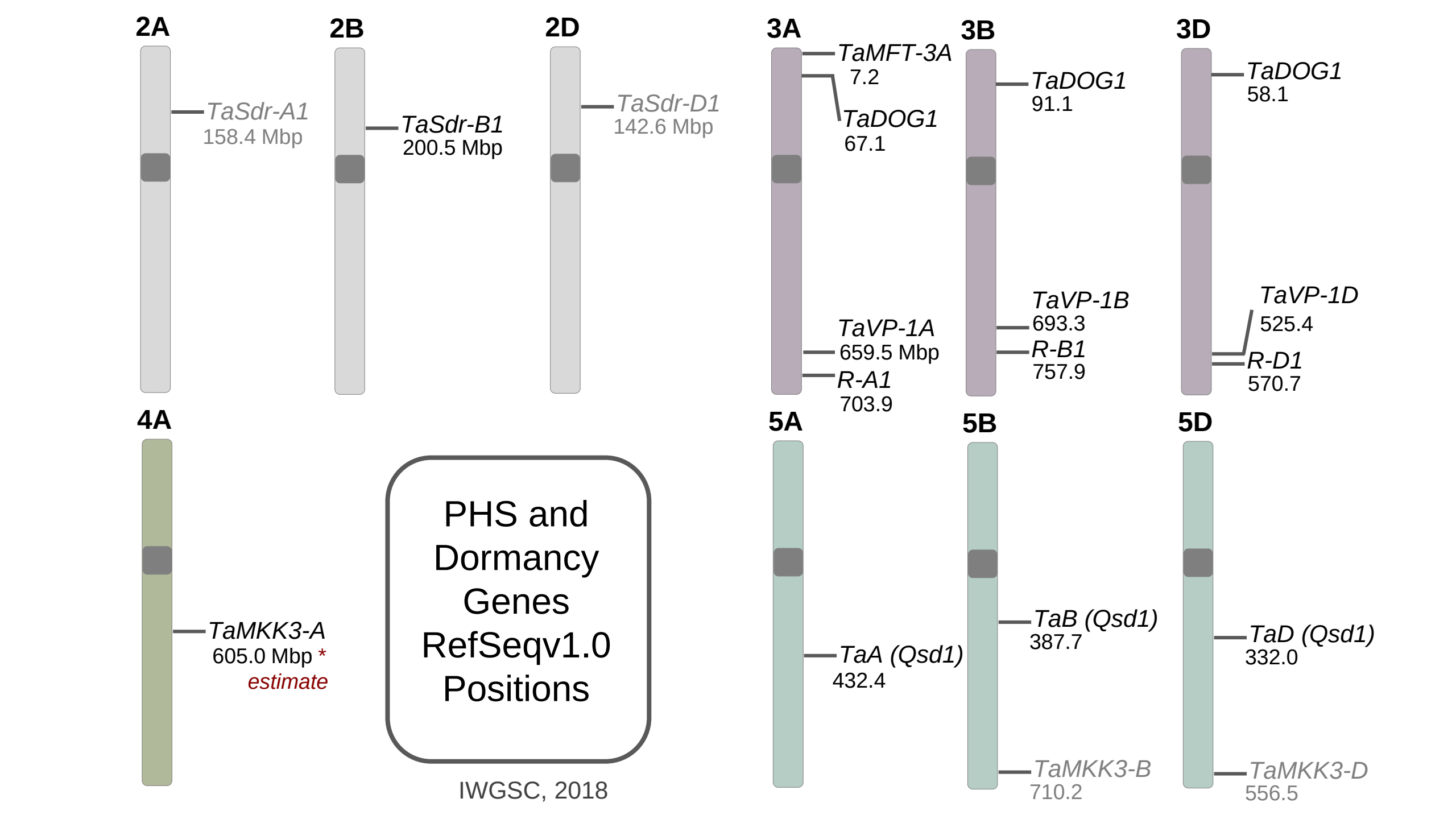
Do We See Different QTN Within a Single Year?



GWAS: rrBLUP | 4PC | MAF > 0.05

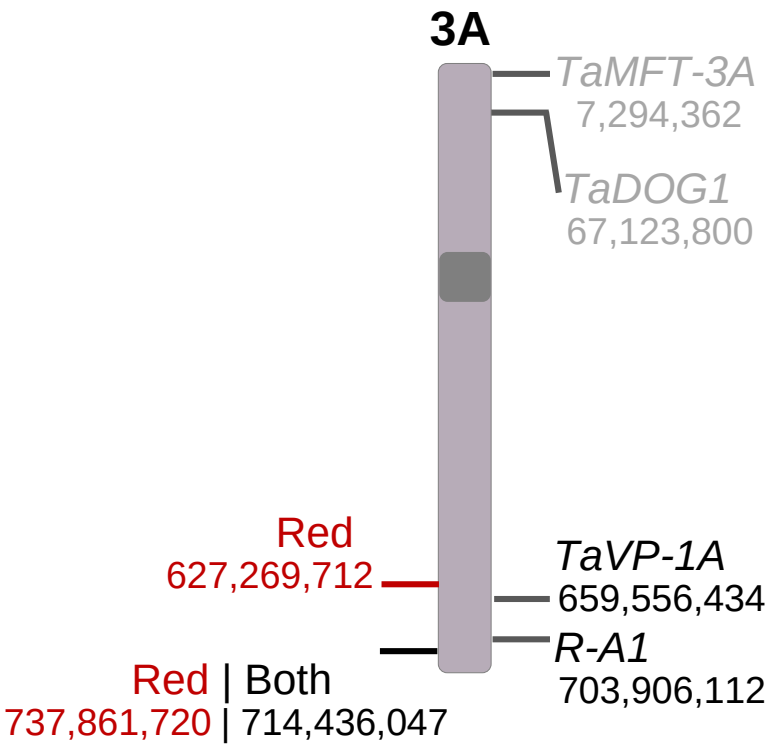
QTN Across Single Year

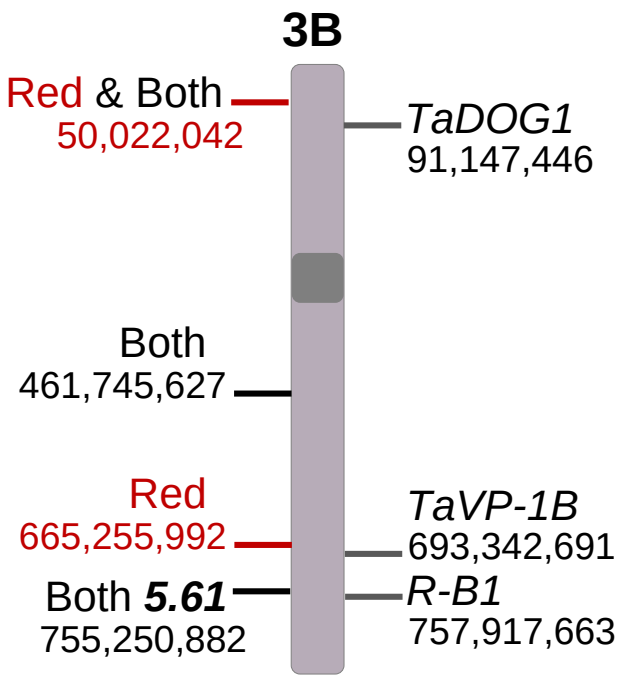


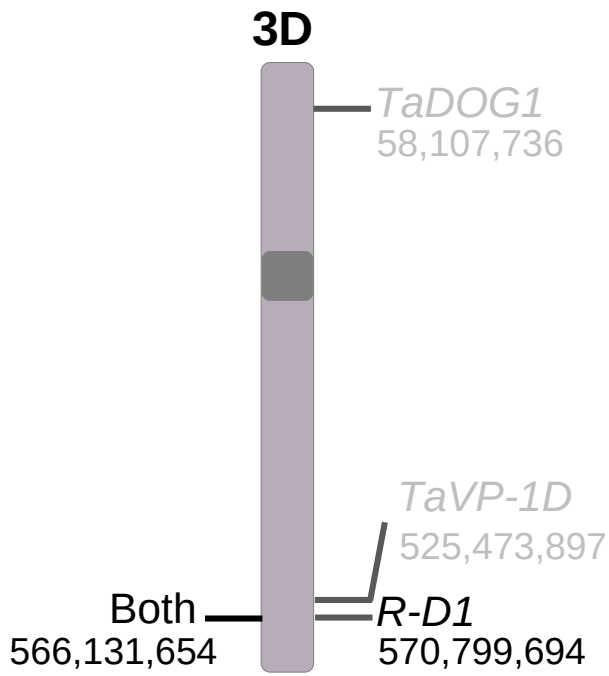

2A
TaSdr-A1
158.4 Mbp
2B
TaSdr-B1
200.5 Mbp
2D
TaSdr-D1
142.6 Mbp
3A
TaMFT-3A
7.2
TaDOG1
67.1
TaVP-1A
659.5 Mbp
R-A1
703.9
3B
TaDOG1
91.1
TaVP-1B
693.3
R-B1
757.9
3D
TaDOG1
58.1
TaVP-1D
525.4
R-D1
570.7
4A
TaMKK3-A
605.0 Mbp *
estimate
PHS and Dormancy Genes RefSeqv1.0 Positions
IWGSC, 2018
5A
TaA (Qsd1)
432.4
5B
TaB (Qsd1)
387.7
TaMKK3-B
710.2
5D
TaD (Qsd1)
332.0
TaMKK3-D
556.5

KC group
sig. marker position

Genes in the Neighborhood

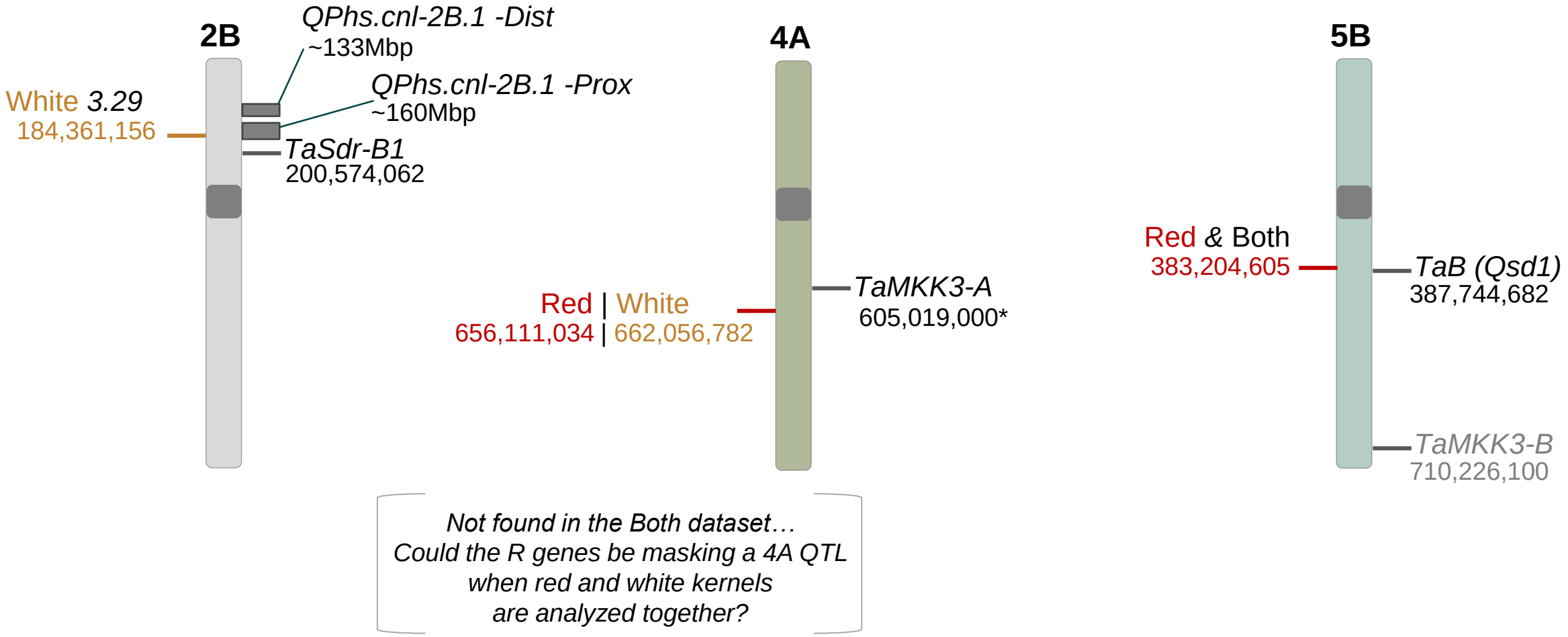




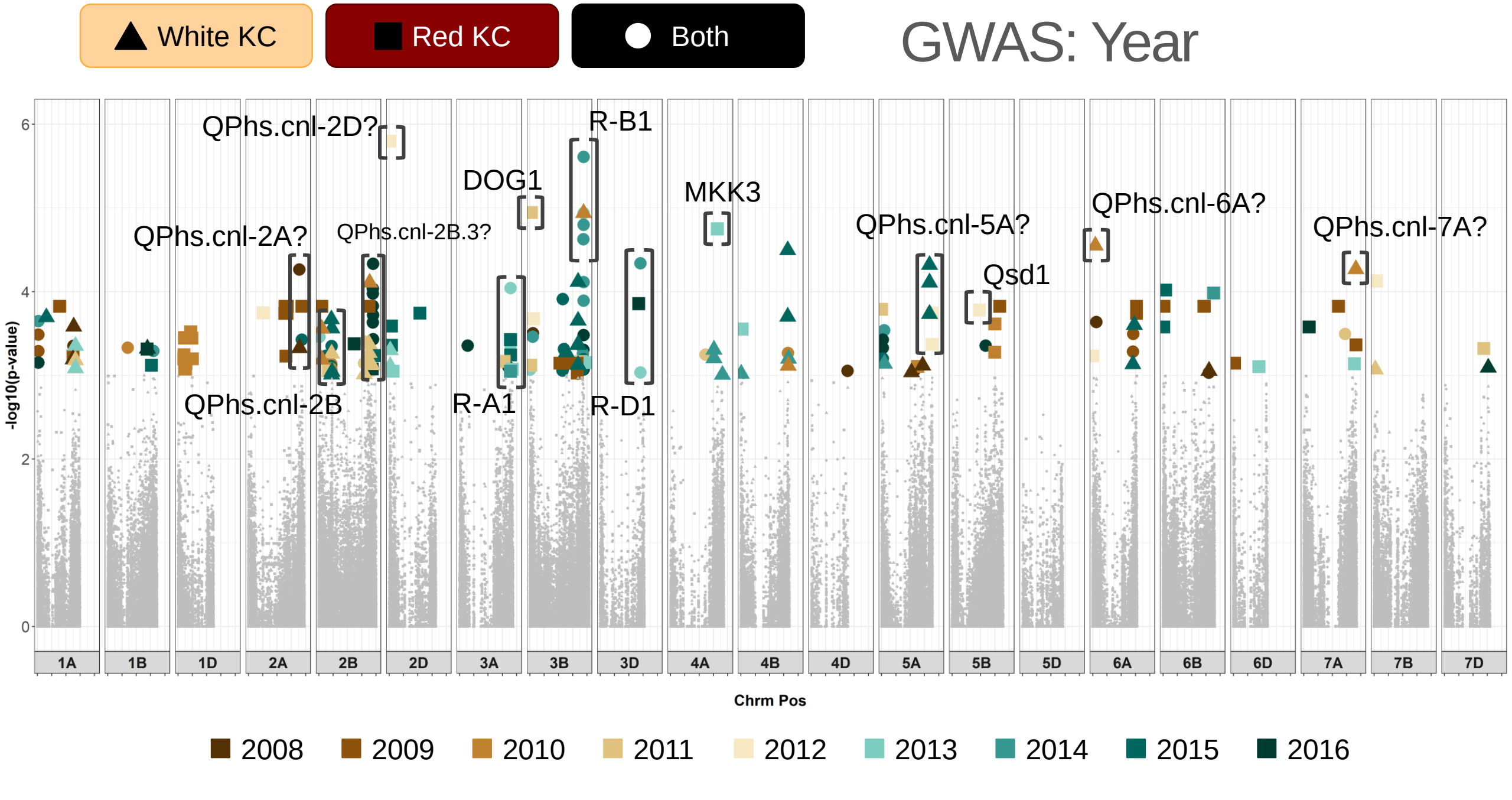


Genes in the Neighborhood

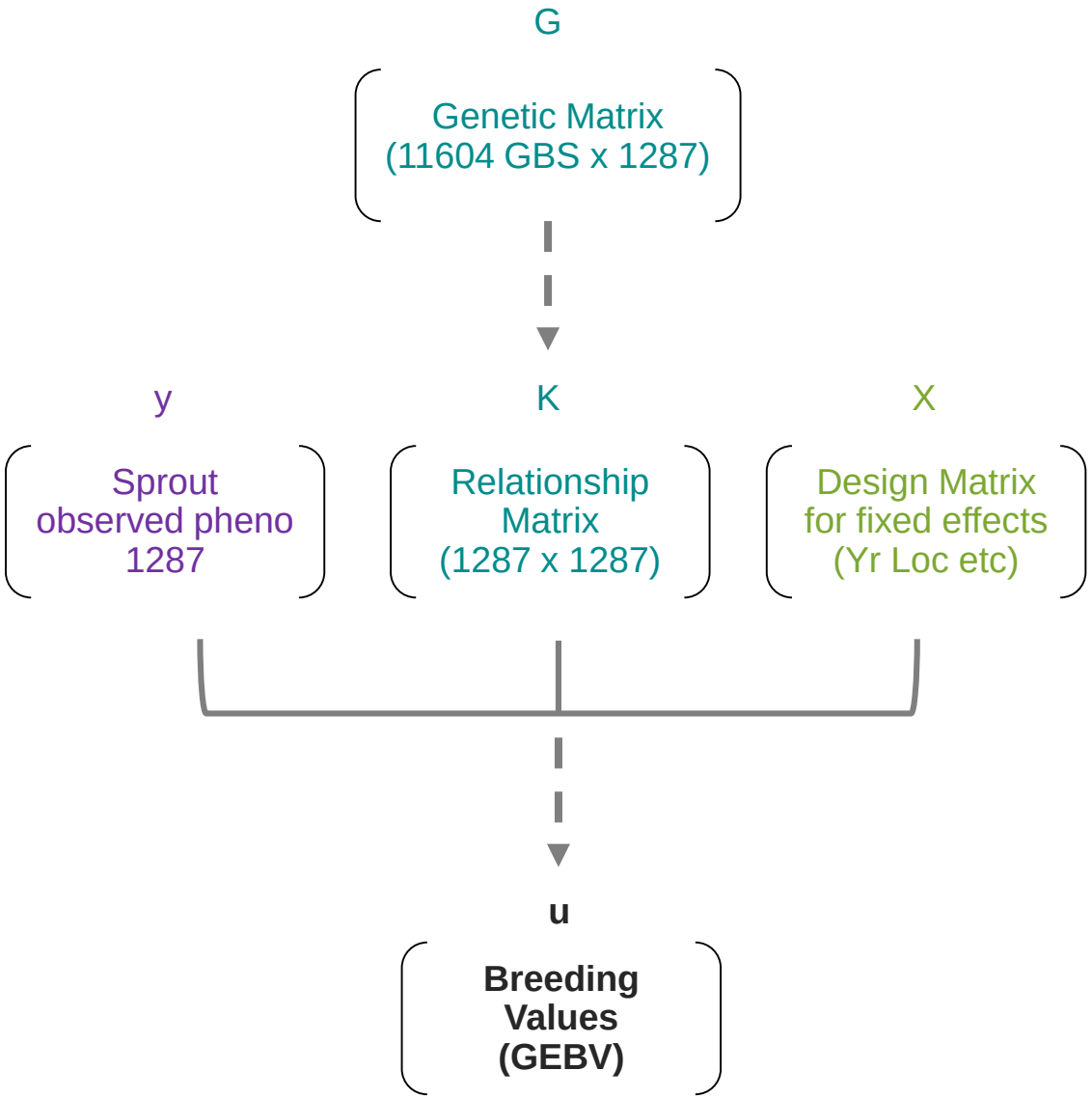
KC group
sig. marker position



Not found in the Both dataset…
Could the R genes be masking a 4A QTL when red and white kernels are analyzed together?


White KC
Red KC
Both
GWAS: Year
QPhs.cnl-2D?
R-B1
DOG1
MKK3
QPhs.cnl-6A?
QPhs.cnl-5A?
QPhs.cnl-7A?
QPhs.cnl-2A?
QPhs.cnl-2B.3?
Qsd1
QPhs.cnl-2B
R-A1
R-D1
-log10(p-value)
0
2
4
6
1A
1B
1D
2A
2B
2D
3A
3B
3D
4A
4B
4D
5A
5B
5D
6A
6B
6D
7A
7B
7D
Chrm Pos
2008
2009
2010
2011
2012
2013
2014
2015
2016

Genomic Prediction: Another Tool in the Toolbox

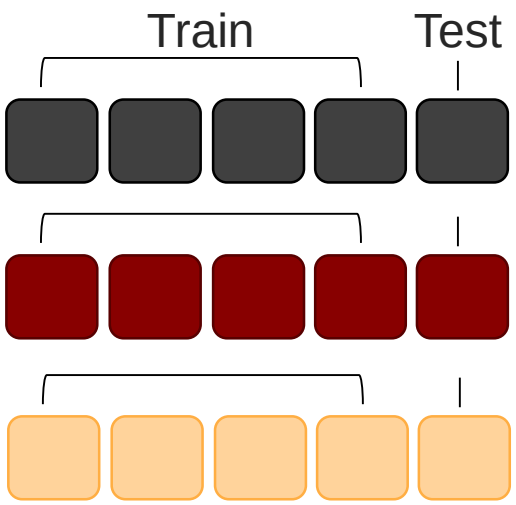


Genomic Prediction

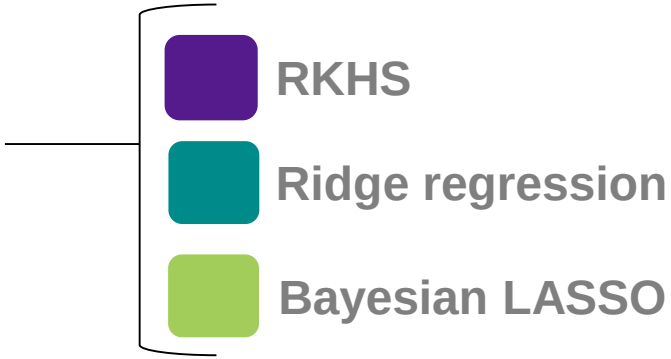
All Env

	total n
Both	1287
Red	369
White	904

Five-fold CV



Prediction Model



Prediction Accuracy (PA)

$cor\ (\ Pheno_{obs}\ ,\ GEBVs_{model})$

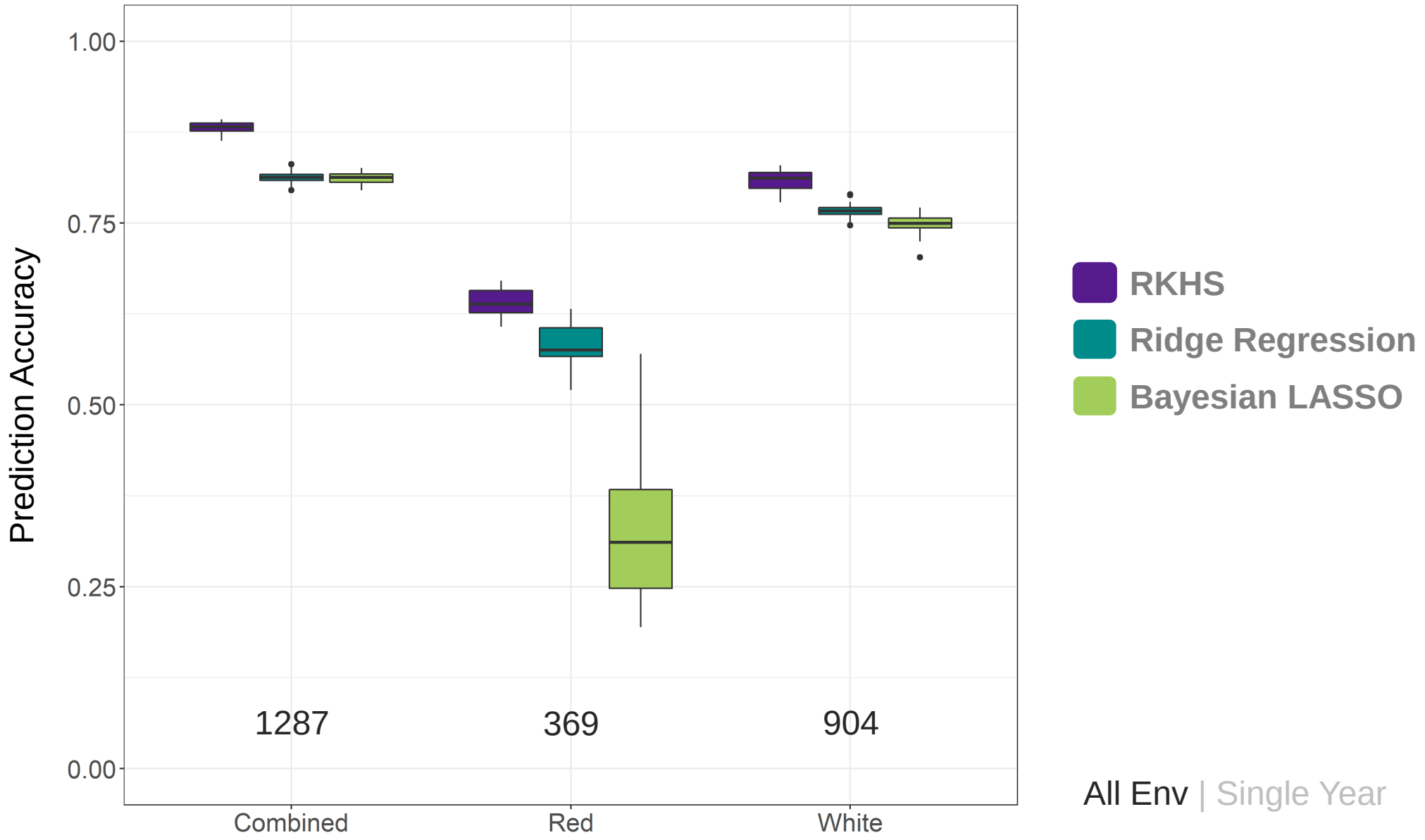
$cor\ (\ y_{test}\ ,\ GEBVs_{train})$

1.0 Perfect Prediction

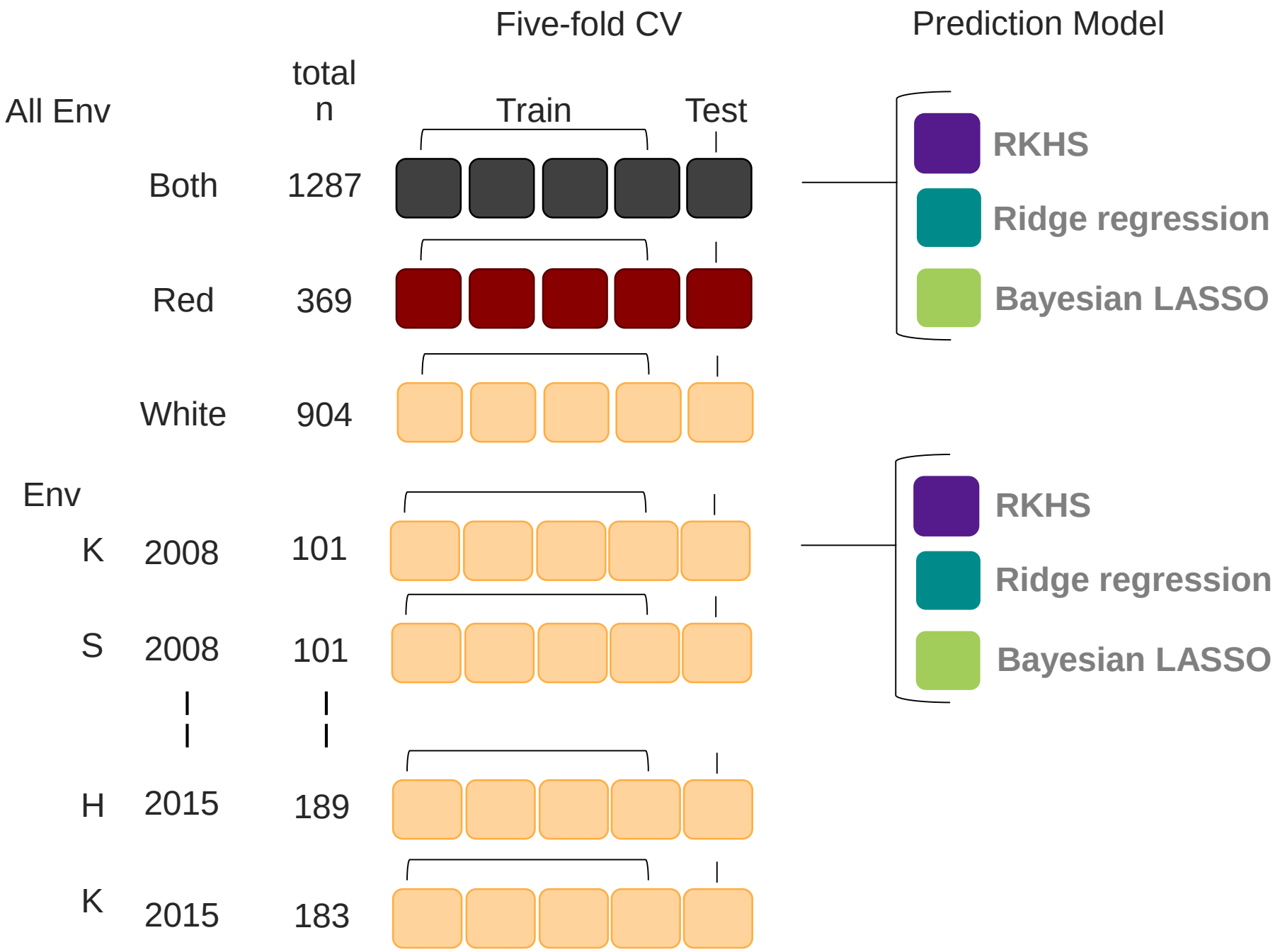
0.0 Inaccurate

All Env | Single Env

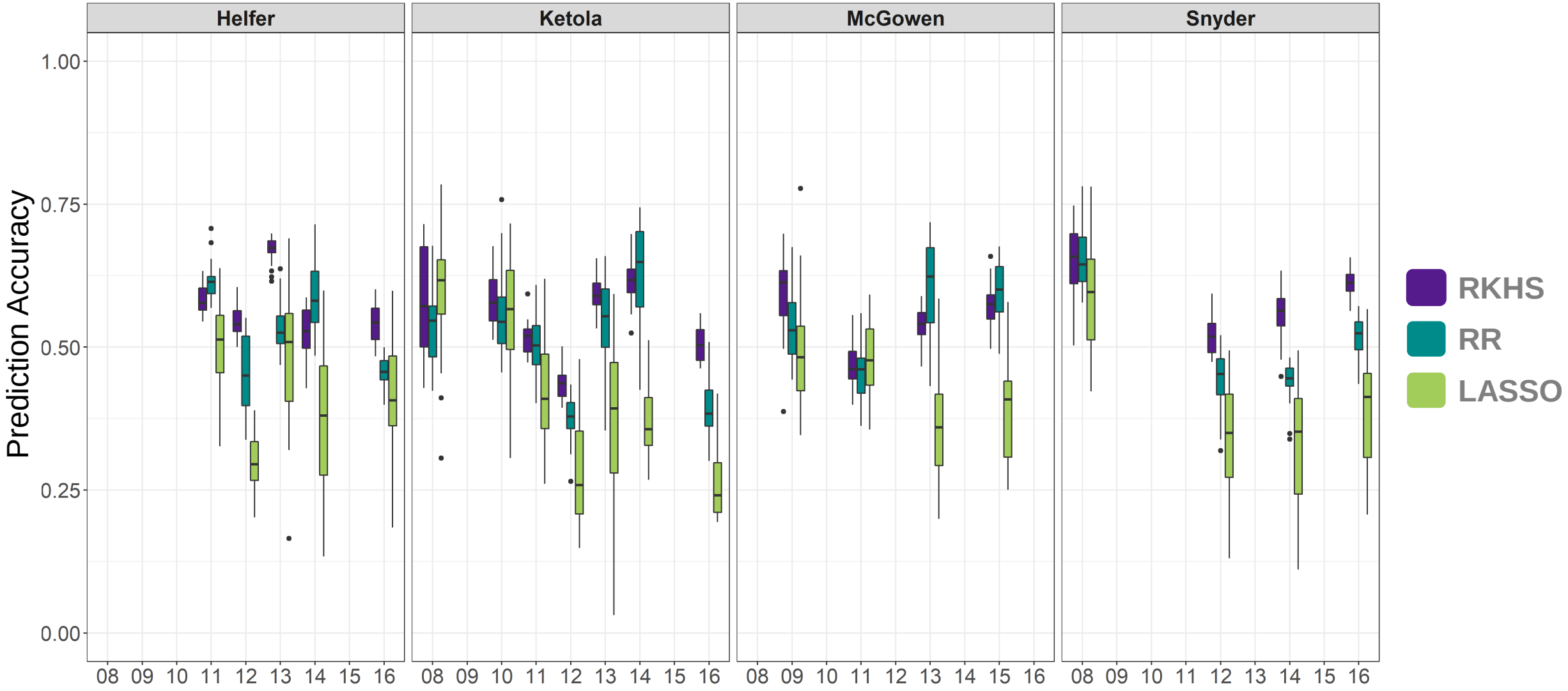
The RKHS Model Appears to Predict Better



All Env | Single Year

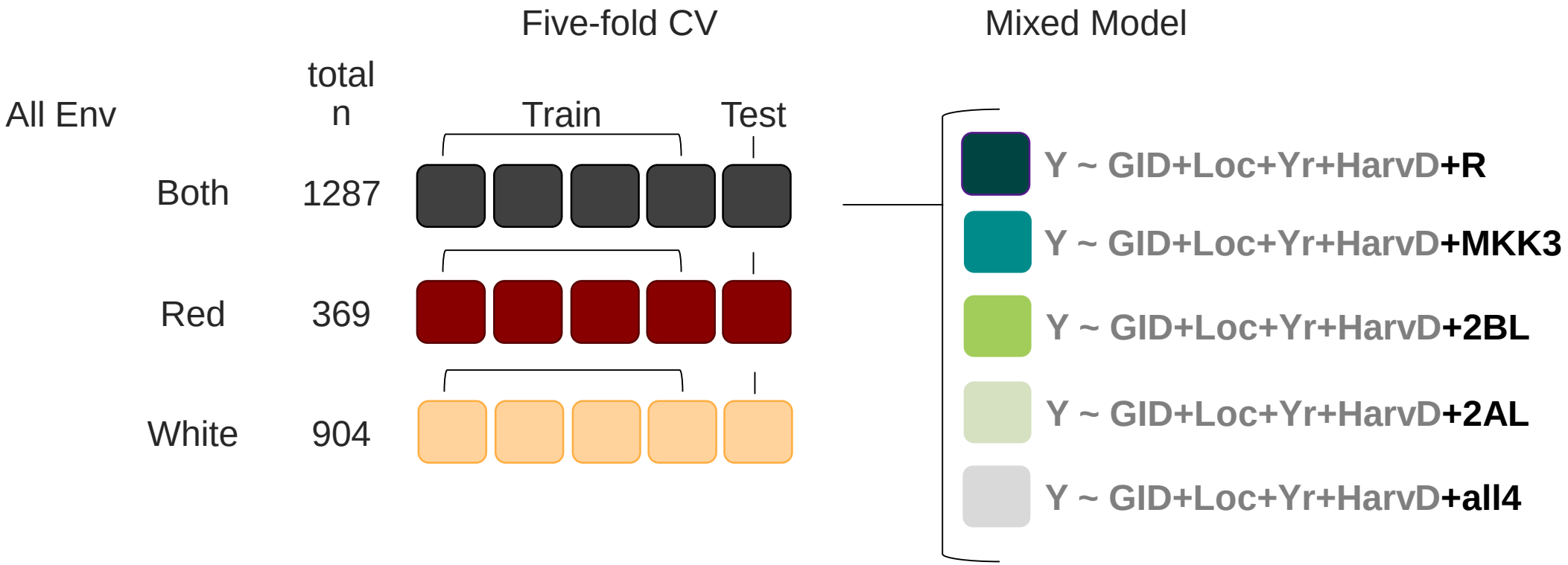

Five-fold CV
Prediction Model
All Env
total n
Train
Test
Both
1287
Red
369
White
904
RKHS
Ridge regression
Bayesian LASSO
Env
K
2008
101
S
2008
101
H
2015
189
K
2015
183
RKHS
Ridge regression
Bayesian LASSO

It's Not as Obvious: "The RKHS Model Appears to Predict Better"



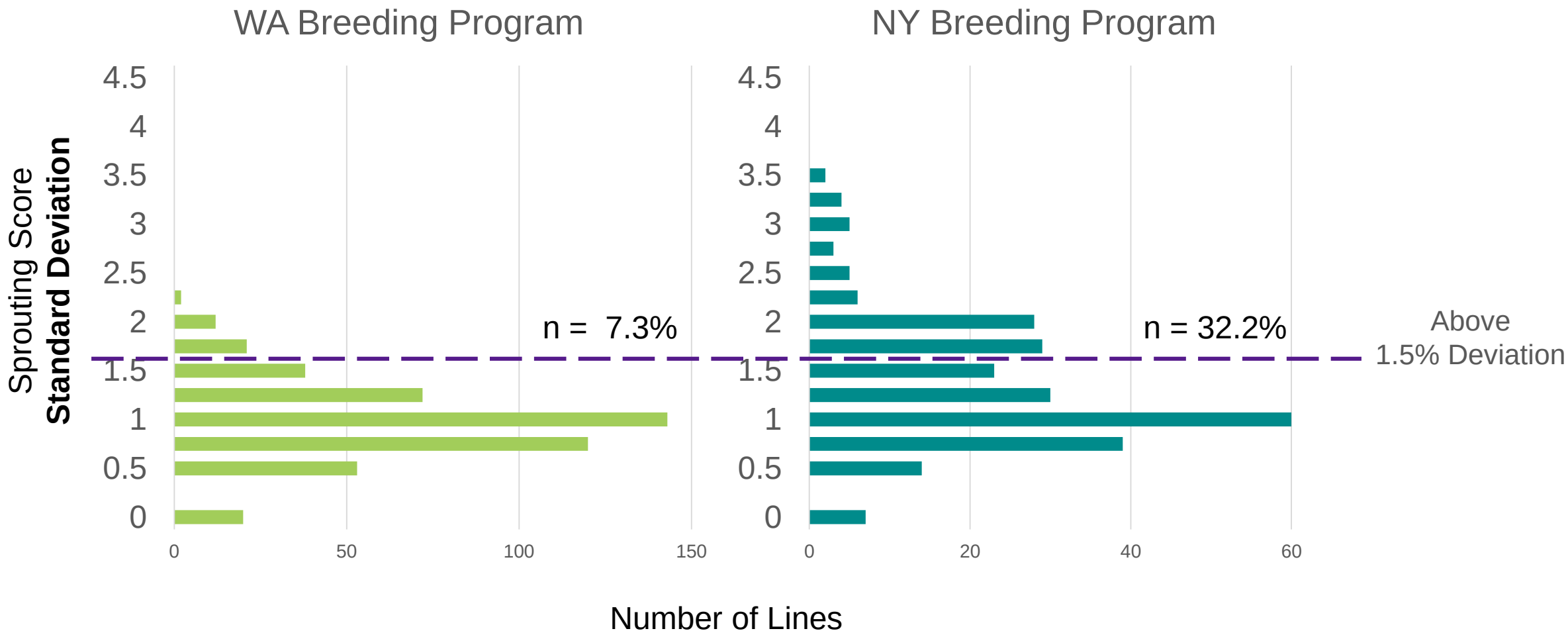
All Env | Single Env

Next Steps: Will Known Genes Improve Prediction?

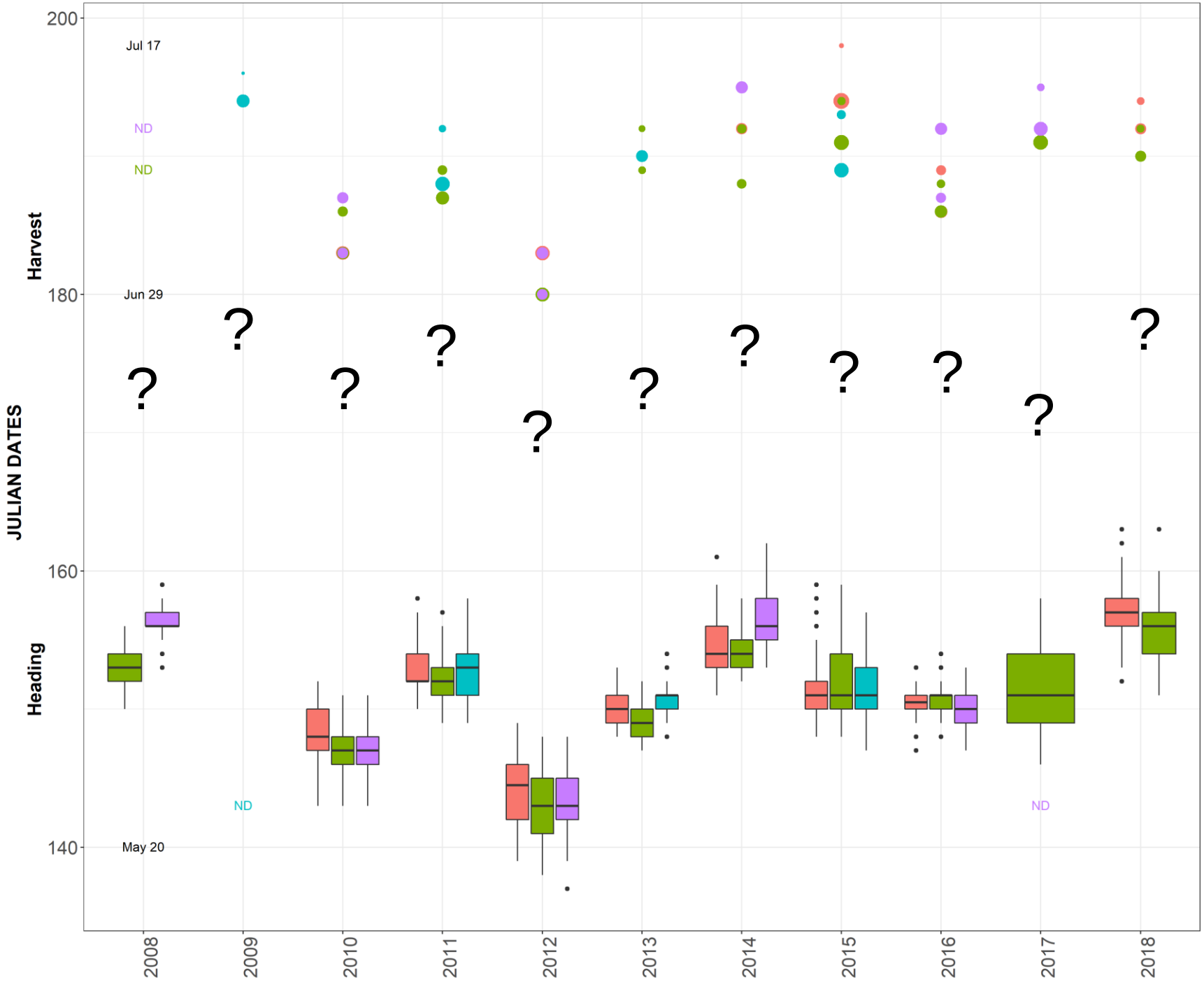


Fixed Marker Effects

When Implementing Spike-Wetting Tests in a Breeding Program: The Germplasm / Environment Could Affect the Variance



Grain Development



$Temp_{high}$

$Temp_{low}$

Humidity

…

Genomic Prediction: Why

What is the best model Mark Sorrells (et al) can use to
predict sprouting susceptibility and tolerance
if he only had the resources to genotype a line(s)
and no spike wetting test

Early generations prediction?:
sprouting response to a 50%-75% accuracy

Breeding for PHS

MAS known PHS genes, (MKK3, MFT, etc)

2018: 828 wheat and 414 barley plots
S.Martinez & D.Sweeney PHS genomic prediction

D.Sweeney is on track to release CNL Barley

Fine mapping Cayuga's 2B dormancy gene

shantel-martinez.github.io

Identifying Loci and Genomic Prediction Models for PHS Tolerance in Northeast Soft Wheat Breeding Programs

Shantel A. Martinez

Mark E. Sorrells

Cornell University

Soft Wheat Quality Meeting

April 23rd, 2019