Systematic Differences in the Response of Genetic Variation to Pedigree and Genome Based Selection

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For quality of life

HENDRIX GENETICS

Introduction

Traditional BLUP selection vs. Genomic selection

- **BLUP**: Predict breeding values (EBV) using phenotype & pedigree information
- **Genomic selection** (GS) $\xrightarrow{\textbf{Phenotypes \& genotypes}}$ GEBV
  (Meuwissen et al. 2001)
- Higher accuracy of GEBV vs. EBV $\longrightarrow$ higher genetic gain for GS than BLUP
- Most GS studies were on simulations
- Impact of different selection methods on genome diversity?

Introduction

- Selection impacts allelic diversity

- To assess the allelic diversity using population genetics statistics (Prasad et al. 2008)
    - Allele frequency
    - Linkage disequilibrium

- Frequency of favourable allele in population under selection increases (Kimura, 1989)

Objectives

- Compare selection methods for their impact on allelic diversity
- Identify signatures of selection

Materials & Methods

Data

- 60K SNP chip of 3 lines of layers: 2 Brown (B1 & B2) & 1 White (W)

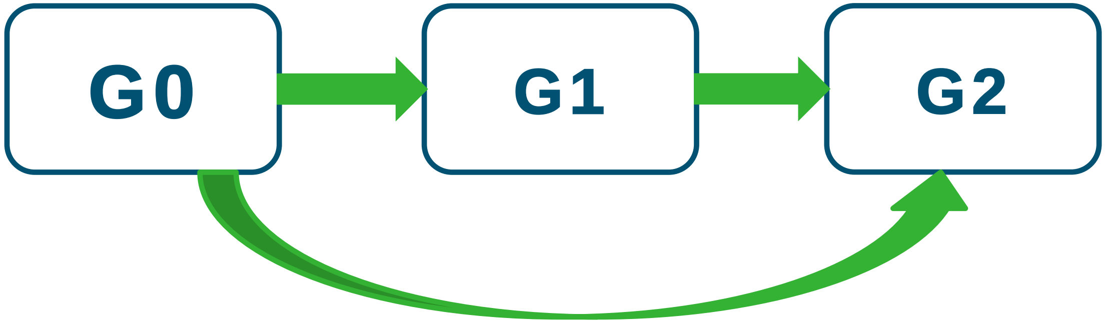
- 2 generations of selection (BLUP & GBLUP)
  - Selection on a commercial breeding program index

 # Animals selected based on GEBV & EBV

Line	Total	GEBV				EBV			
		G0-GBLUP		G2-GBLUP		G0-BLUP		G2-BLUP	
		Female	Male	Female	Male	Female	Male	Female	Male
B1	2252	238	128	0	130	0	953	0	110
B2	2334	248	126	0	130	248	1058	0	110
W	2176	230	141	0	150	230	1205	0	150

Materials & Methods

- Changes in allele frequency



G0

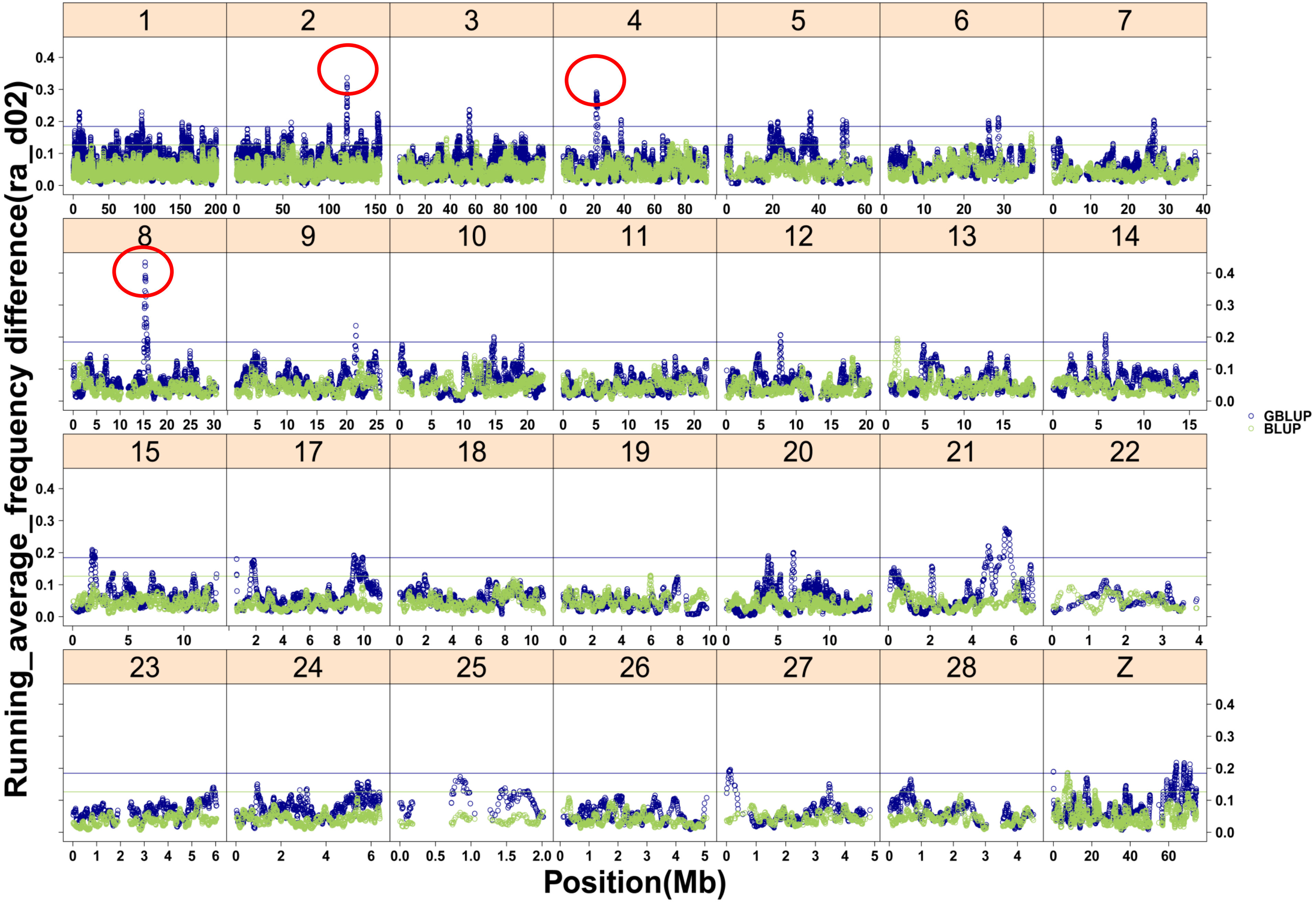
G1

G2

$$d_{02} = |f_2 - f_0|$$

  - Plot running average of 11 d_{02} values against the SNP locations

Comparison of GBLUP & BLUP changes in allele frequencies in Line B1



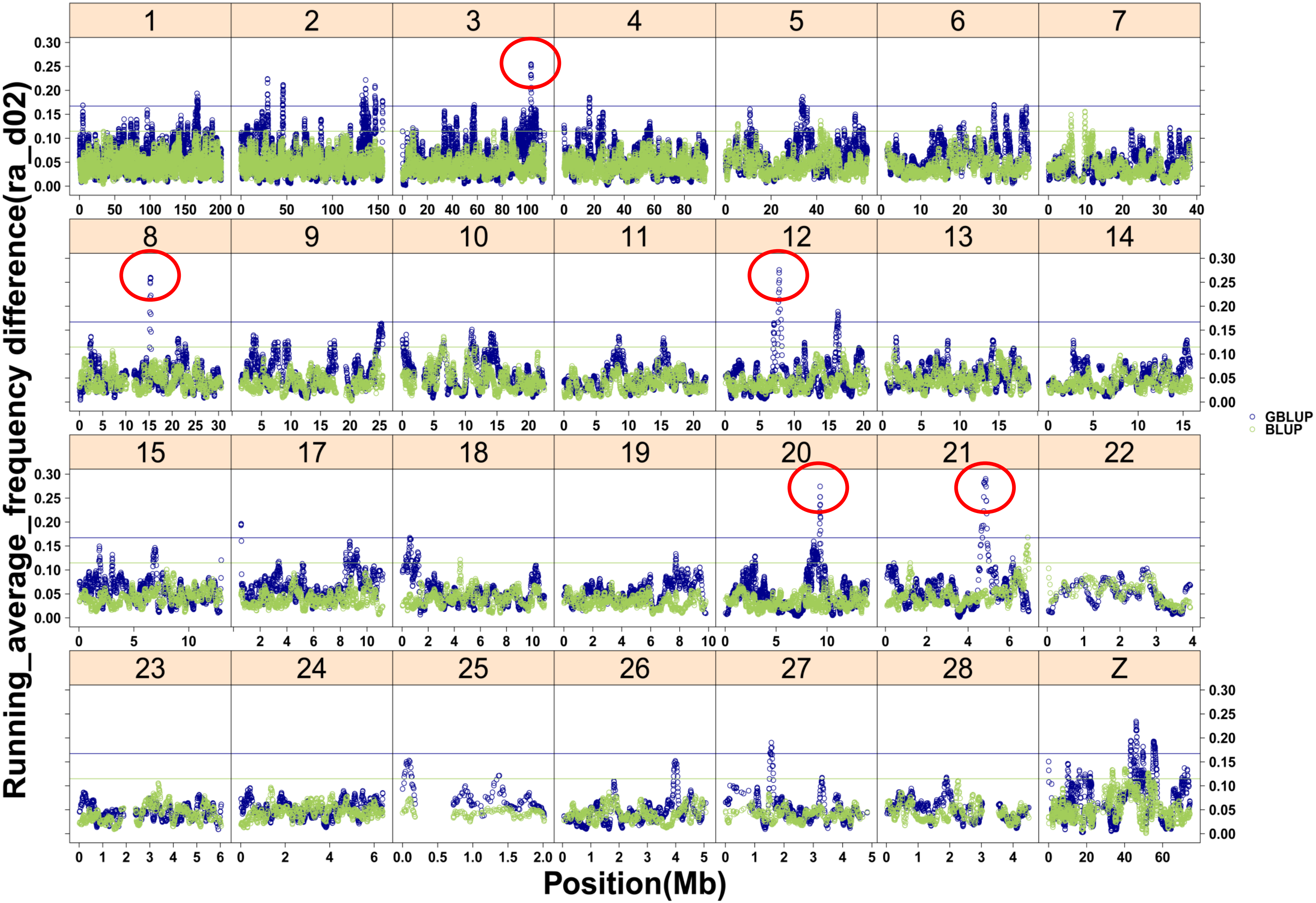
Estimation of significance threshold

To distinguish the real selection signal from genetic drift

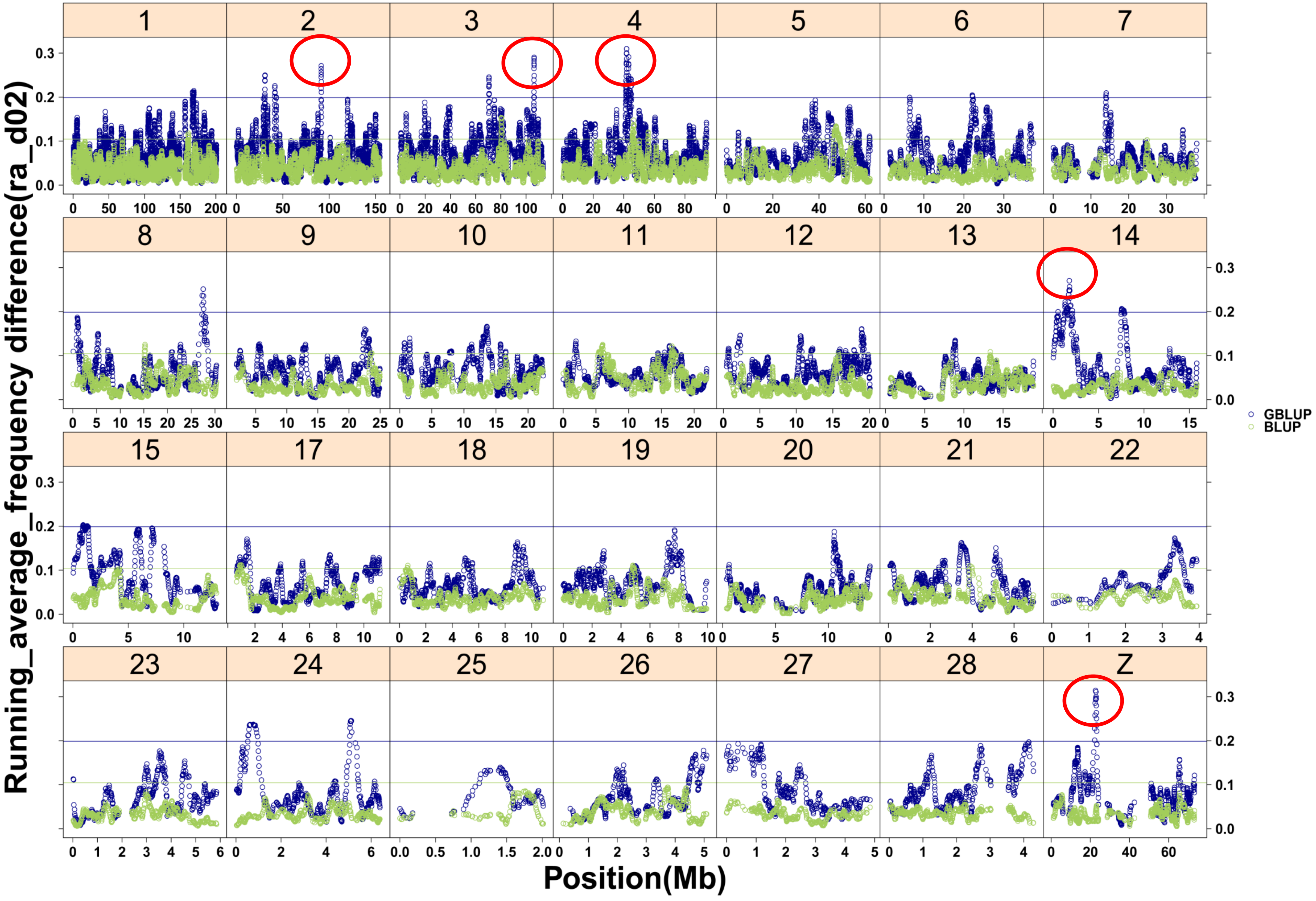
- **Gene dropping** (Maccluer et al. 1986)
  - Simulation along the existing pedigree
    - 1 Chromosome (1 Morgan) with 20 loci with starting frequency 0.5
    - 0 mutation rate
    - Haplotypes simulation for founder animals in pedigree
    - Mendelian transmission rule to drop alleles to offsprings
    - Allele frequency distribution in 1000 replications
    - Outliers beyond a 95% threshold as indicative of selection

Method	**Line**		
	B1 (Ne)	**B2(Ne)**	**W(Ne)**
GBLUP	0.184(**45**)	0.167(**46**)	0.198(**41**)
BLUP	0.126(**84**)	0.115(**86**)	0.105(**108**)

Comparison of GBLUP & BLUP changes in allele frequencies in Line B2



Comparison of GBLUP & BLUP changes in allele frequencies in Line W



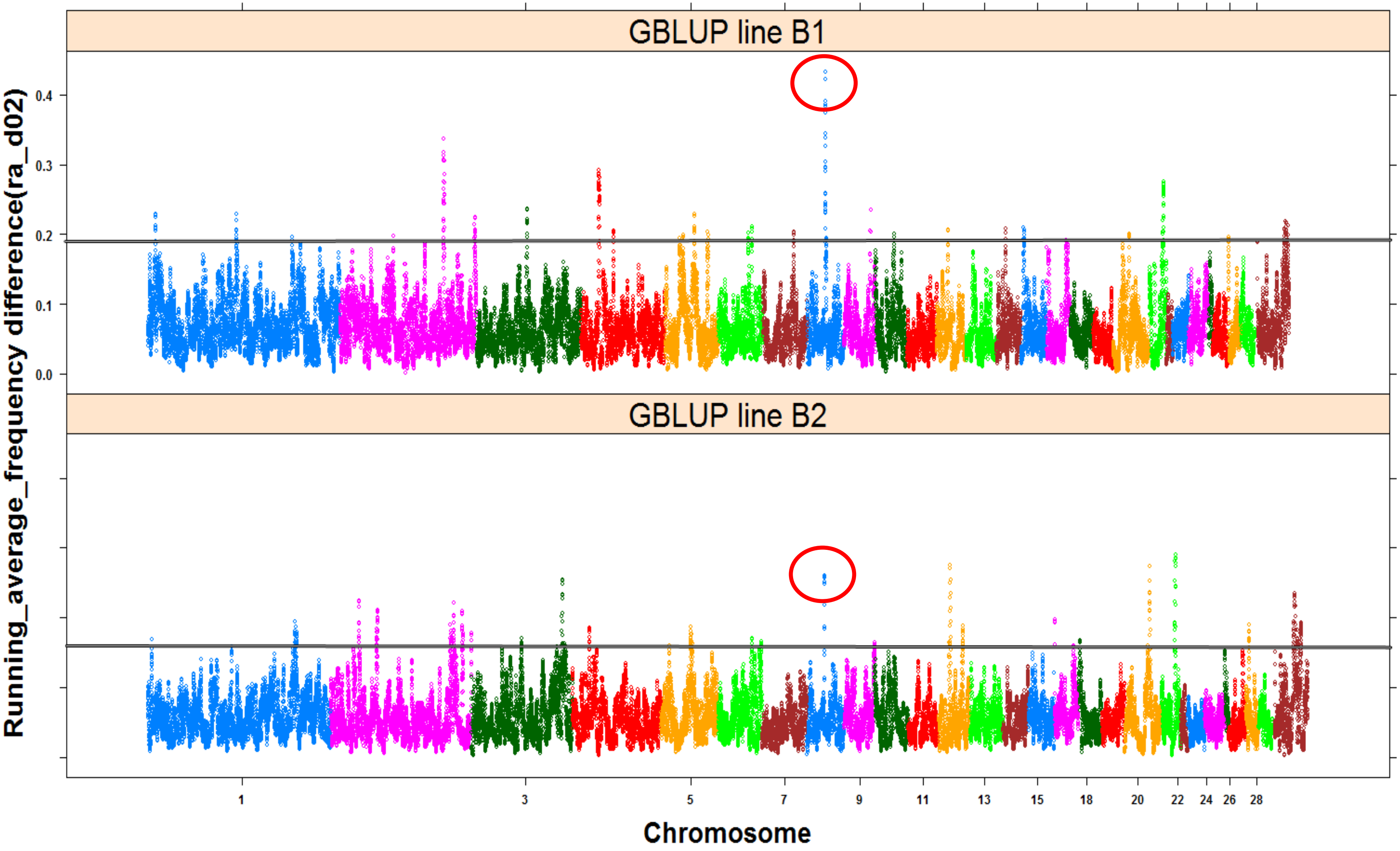
Results

- Average change in allele frequencies was ~ 51% larger in GBLUP than BLUP

Mean allele frequency difference (d_{02}) values

Method	Line		
	B1	**B2**	**W**
GBLUP	0.064	0.056	0.066
BLUP	0.045	0.044	0.036

Discussion


GBLUP line B1
GBLUP line B2
Running_average_frequency difference(ra_d02)
0.0
0.1
0.2
0.3
0.4
1
3
5
7
9
11
13
15
18
20
22
24
26
28
Chromosome

Conclusions

- Differences in effects of selection methods on genetic variation within and between lines
    - Larger number of selection signals & larger changes in allele frequencies with GS within lines
    - Locations of selection signals were different among lines

Thank you

Materials & Methods

Quality Control

- Remove SNPs with MAF = 0
- Remove 1144 unmapped SNPs
- Remove chromosomes 16,32, W (insufficient number of markers)

Number of SNPs after exclusions

Line	GBLUP	BLUP
B1	36582	36731
B2	37197	37254
W	26302	26337

Results

Number of selected parents and in different generations of GBLUP and BLUP

	GEBV						EBV				
	G0-GBLUP			G2-GBLUP			G0-BLUP		G2-BLUP		
Line	Female	Male	Ne	Female	Male	Ne	Female	Male	Female	Male	Ne
B1	54	15	47	46	15	45	-	-	95	27	84
B2	55	15	47	49	15	46	-	-	91	28	86
W	42	15	44	37	14	41	-	-	99	37	108

Mean difference in allele frequencies values within generations between lines

Method	G0			G2		
	B1 & W	B1 & B2	B2 & W	B1 & W	B1 & B2	B2 & W
GBLUP	0.419	0.209	0.416	0.424	0.222	0.421
BLUP	0.415	0.198	0.414	0.417	0.216	0.424