

# Changes in the genome due to genomic selection in two pig populations



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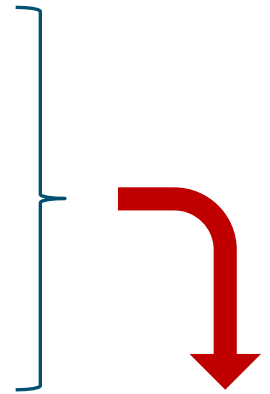
# Genomic selection



**Genetic gain: ↑**

**Genomic changes in simulation: ↑**

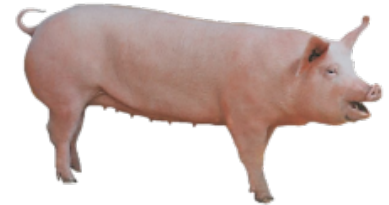
- Allele frequency
- More fixation of loci: Favorable and unfavorable
- Effect size of loci
- ...



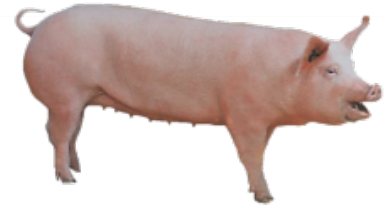
**Future genetic variance  
& Genetic gain**

# Objective

Investigate impact of **genomic selection**  
on **allele frequency** change  
and **GWAS** results  
in pigs



# Data: two sow lines



	Line A	Line B
2015	3,505	921
2016	5,826	3,670
2017	6,586	3,886
2018	7,361	4,995
2019	6,492	4,165
2020	7,689	4,140
2021	2,616	1,710
<i>Total</i>	<b>40,000</b>	<b>23,000</b>

- 44k SNP genotypes
- Pedigrees
- 8 phenotypes
  - 7 selected traits
  - the selection index

# Methods

## **Allele frequency**

- Absolute change 2015 - 2021

## **GWAS**

- Missing SNPs imputed (Beagle)
- Single SNP regression (SNP Snappy in Wombat)
- G-matrix (including all SNPs) to account for relationships

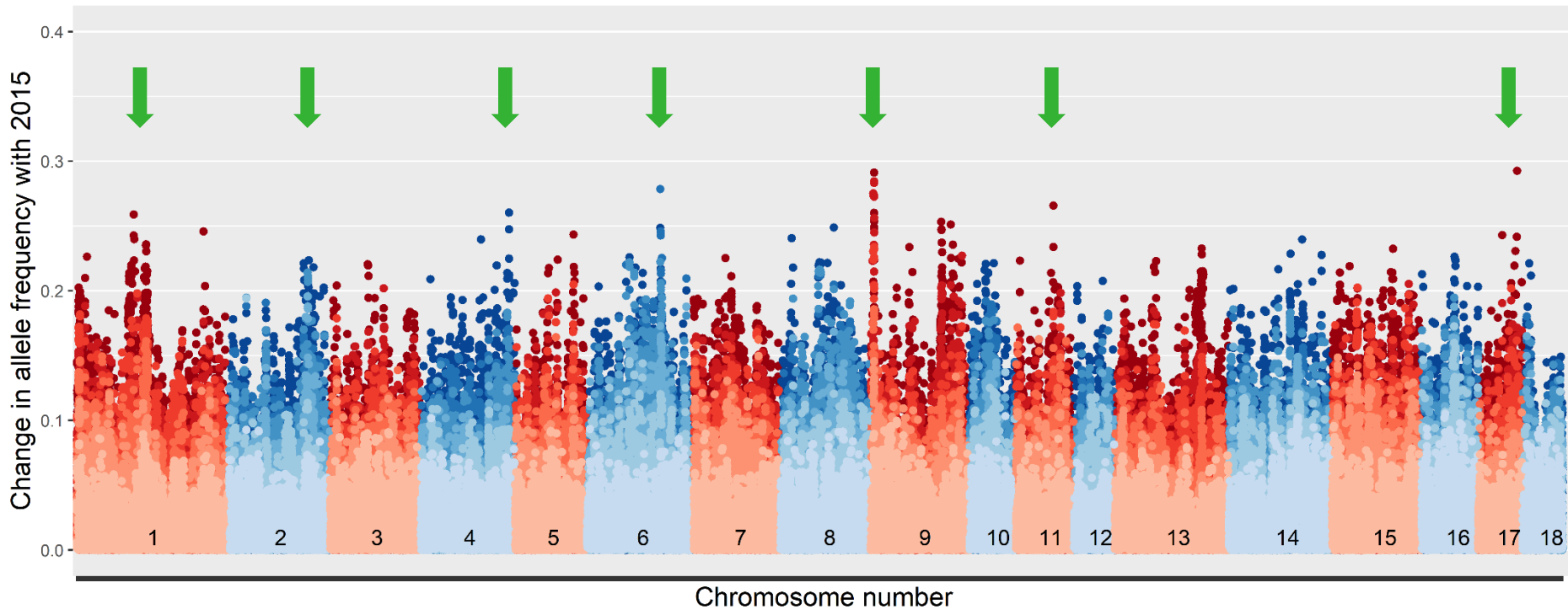
## **Gene dropping**

- Founders: Allele frequencies [0.01, 0.02, 0.03, ..., 0.50]
- 1000 replicates per allele frequency
- Complete pedigree

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# Results

# Change in allele frequency – Line A

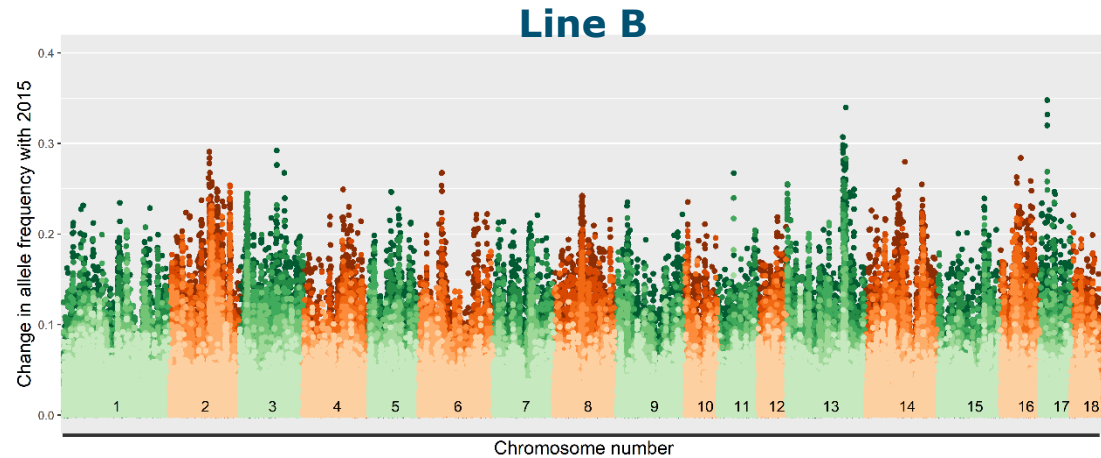
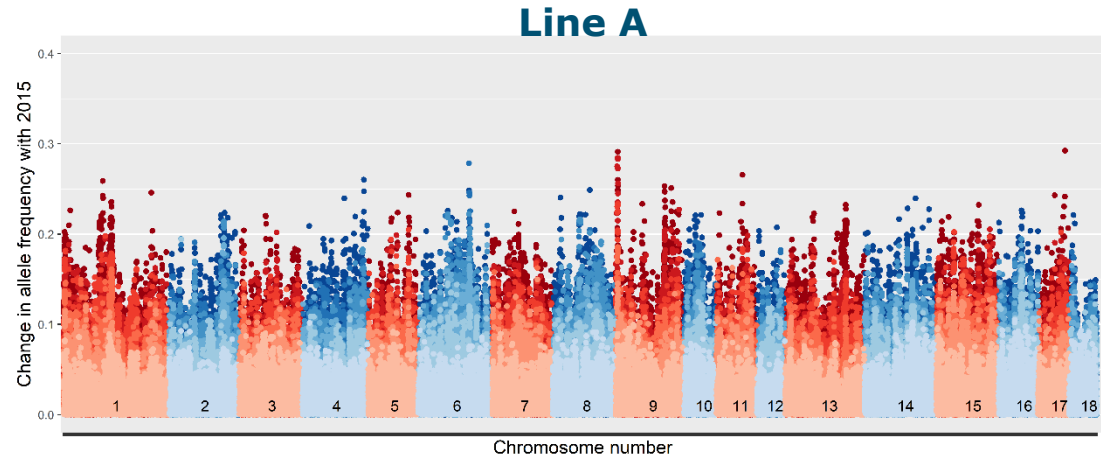


Year

2016	2017	2018	2019	2020	2021
2016	2017	2018	2019	2020	2021

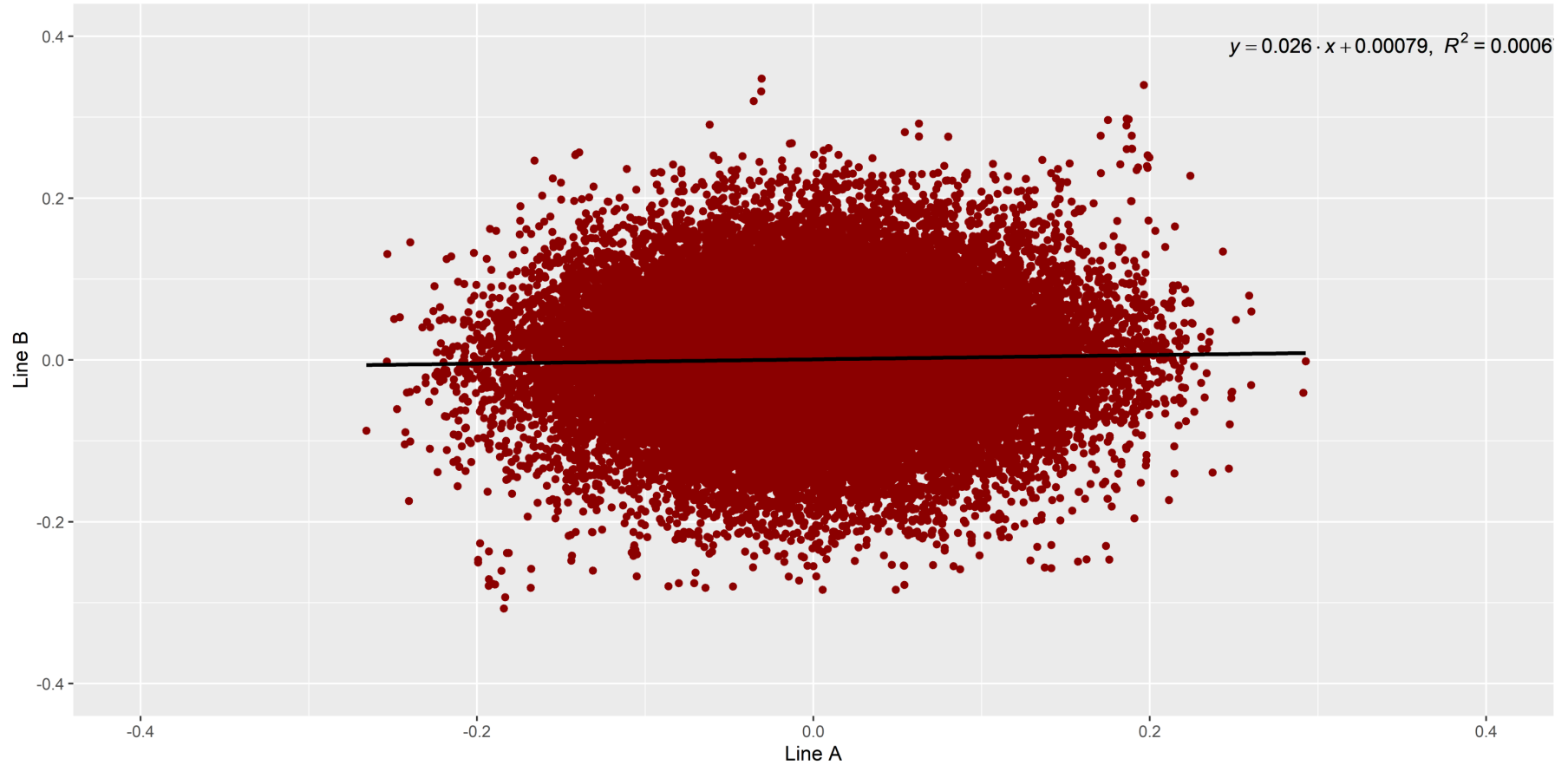
# Change in allele frequencies – Line A vs Line B

Peaks do not overlap





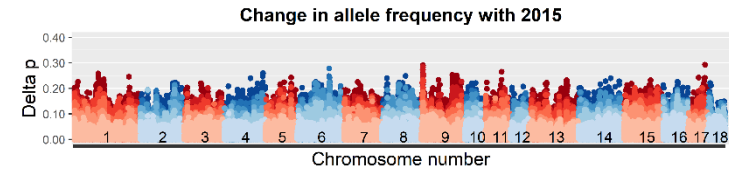
# Change in allele frequency – Line A vs Line B



# Allele frequency change vs GWAS

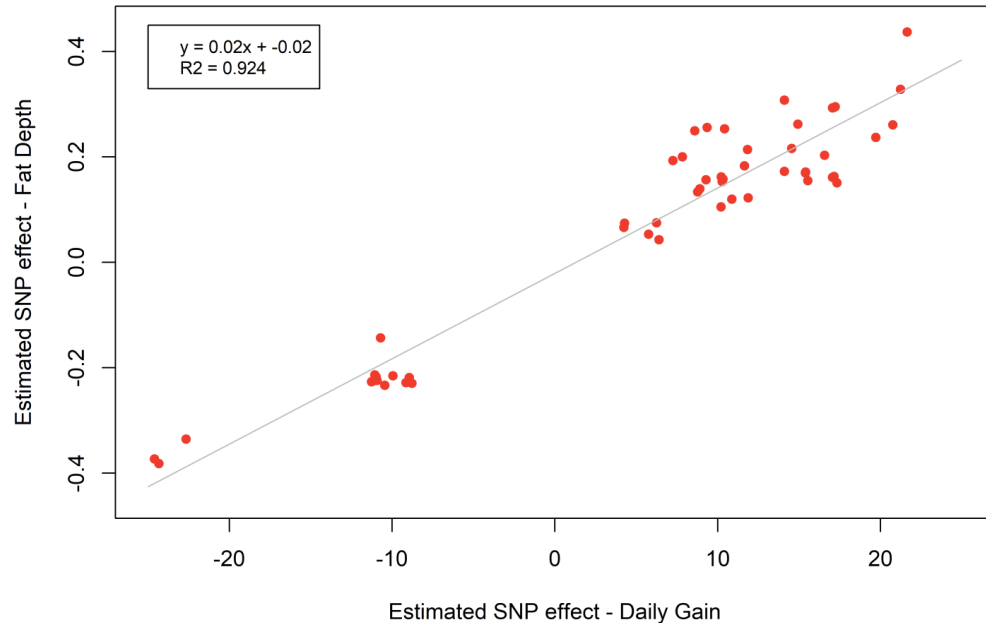
## Line A - Yield traits

- Clear peaks in allele frequency change
- GWAS:
  - Clear and known peaks for traits
  - Not for the index
  - Antagonistic pleiotropy



# Antagonistic pleiotropy

SNP effects Daily Gain – Fat Depth (Top Chr. 1)



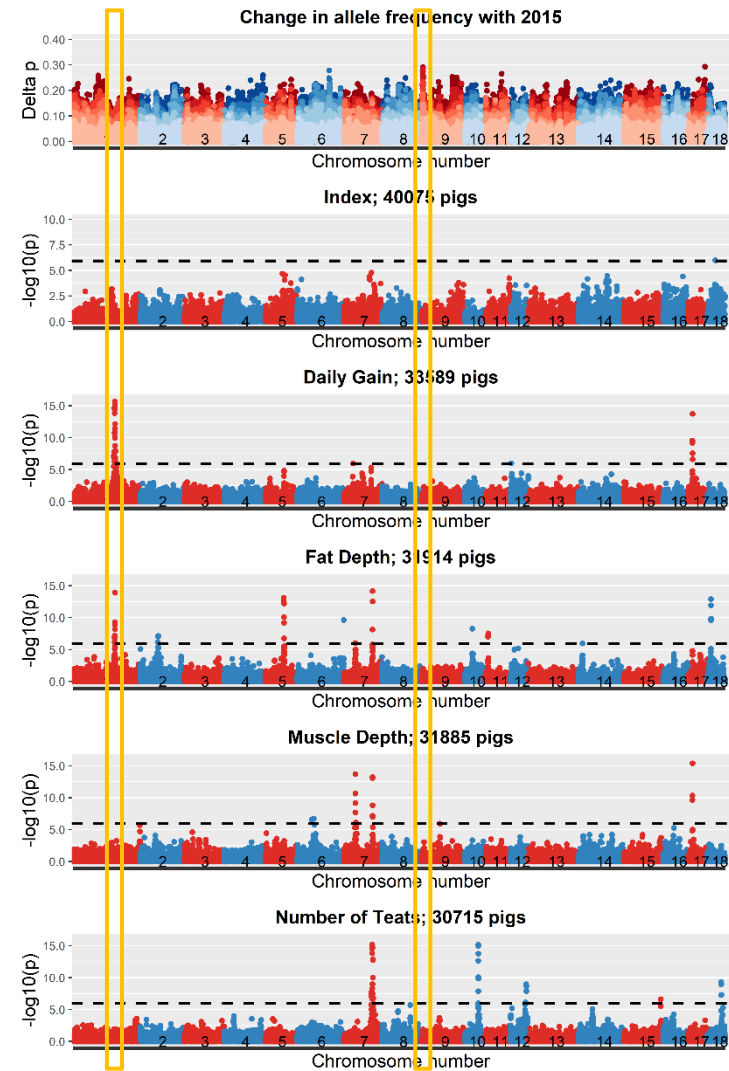
SNP in MC4R Gene

**Suggests pleiotropy**

# Allele frequency change vs GWAS

## Line A - Yield traits

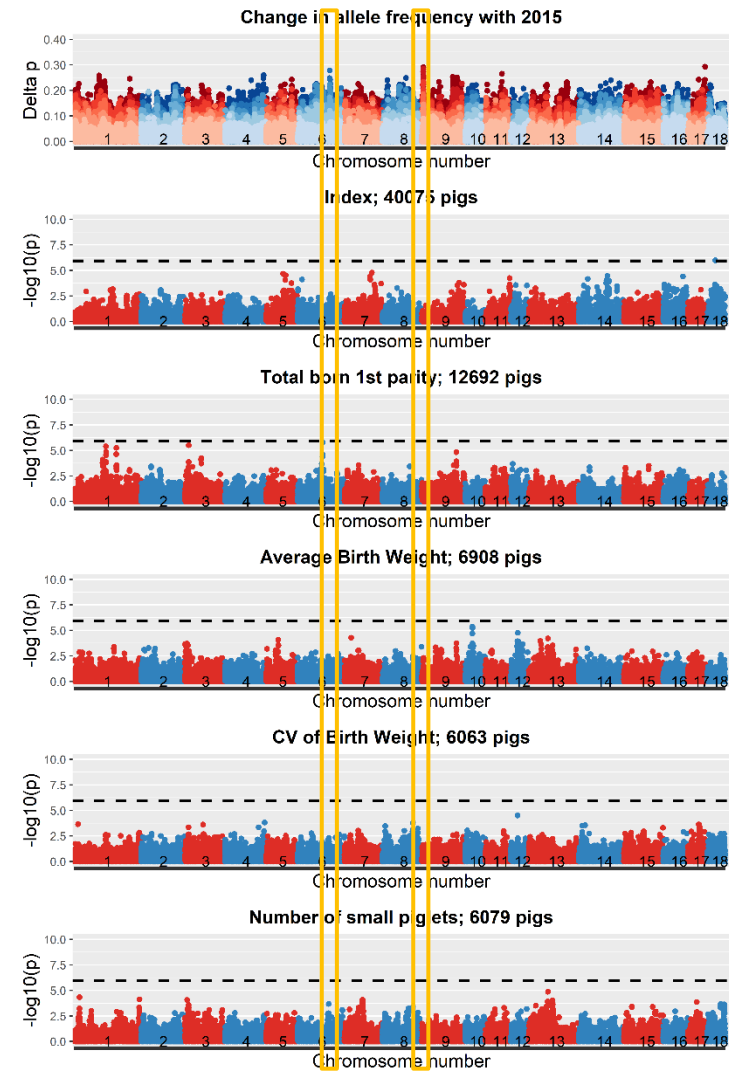
- Clear peaks in allele frequency change
- GWAS:
  - Clear and known peaks for traits
  - Not for the index
  - Antagonistic pleiotropy
- No overlap peaks allele frequency change and GWAS
  - Also not for the index



# Allele frequency change vs GWAS

Line A - **Reproduction traits**

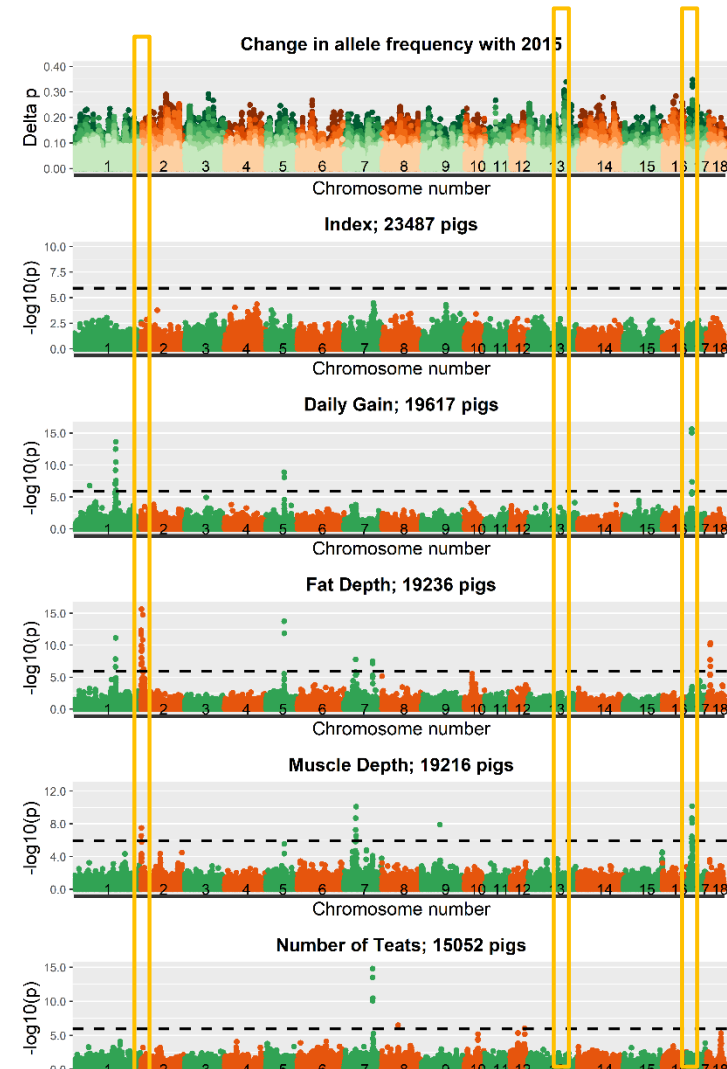
- Clear peaks in allele frequency change
- GWAS
  - Lower peaks
  - Fewer phenotyped animals
- No overlap



# Allele frequency change vs GWAS

## Line B - Yield traits

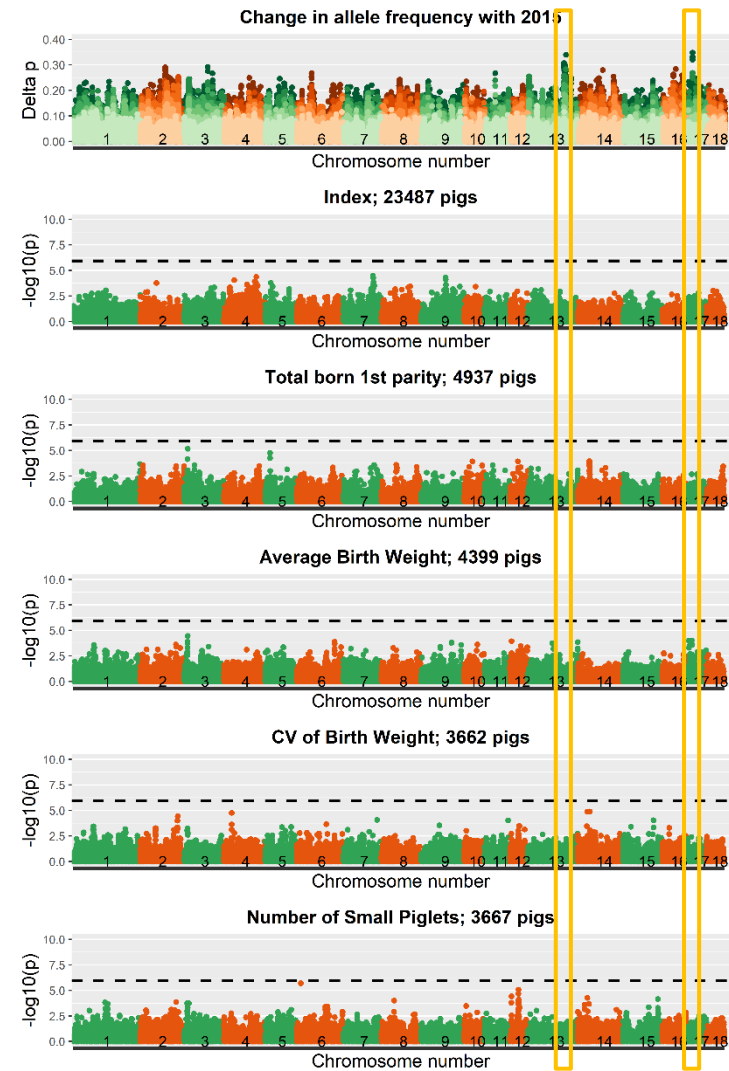
- Clear peaks in allele frequency change
- GWAS:
  - Clear and known peaks for traits
  - Not for the index
  - Antagonistic pleiotropy
- No overlap



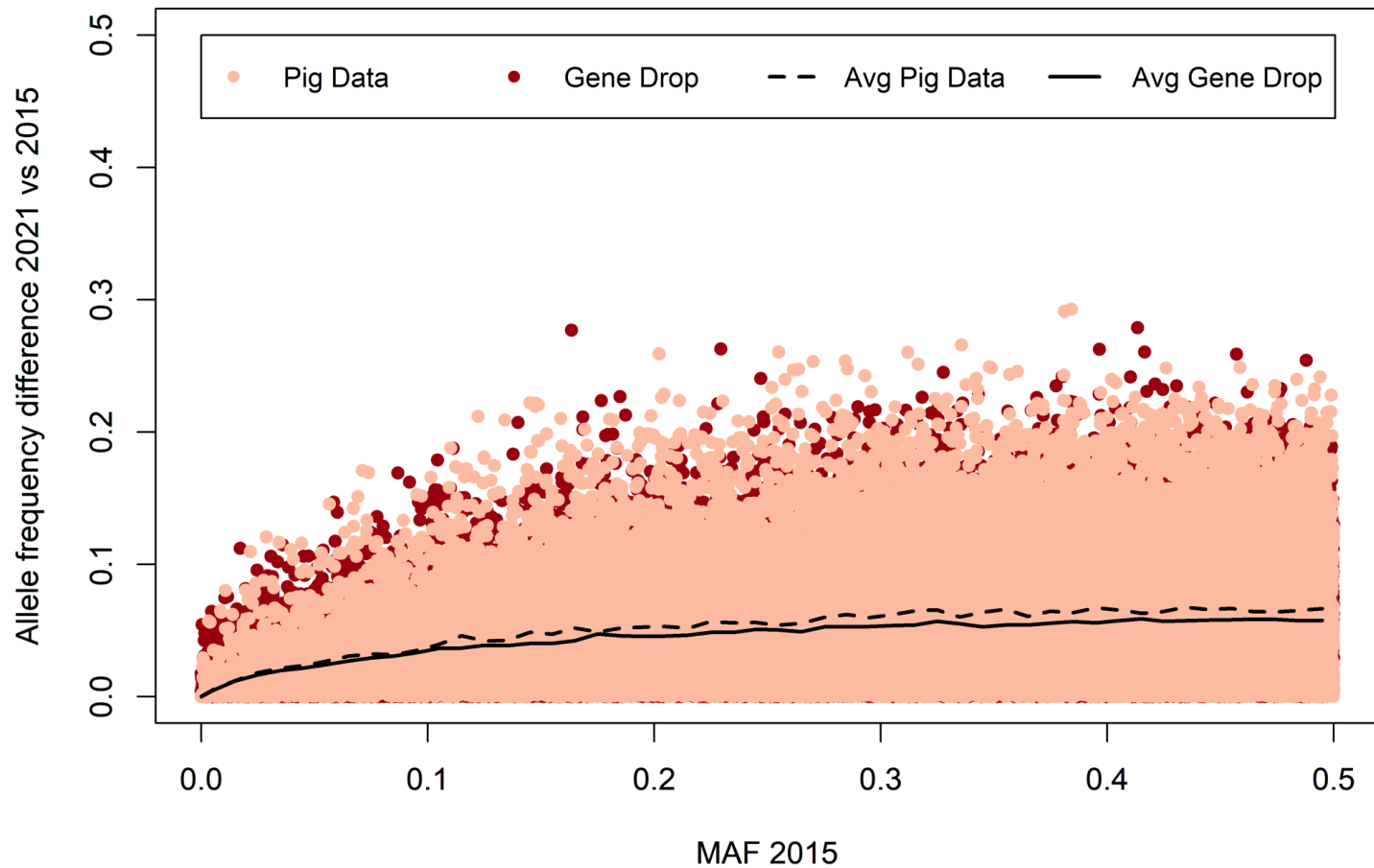
# Allele frequency change vs GWAS

## Line B - Reproduction traits

- Clear peaks in allele frequency change
- No significant GWAS results
- No overlap

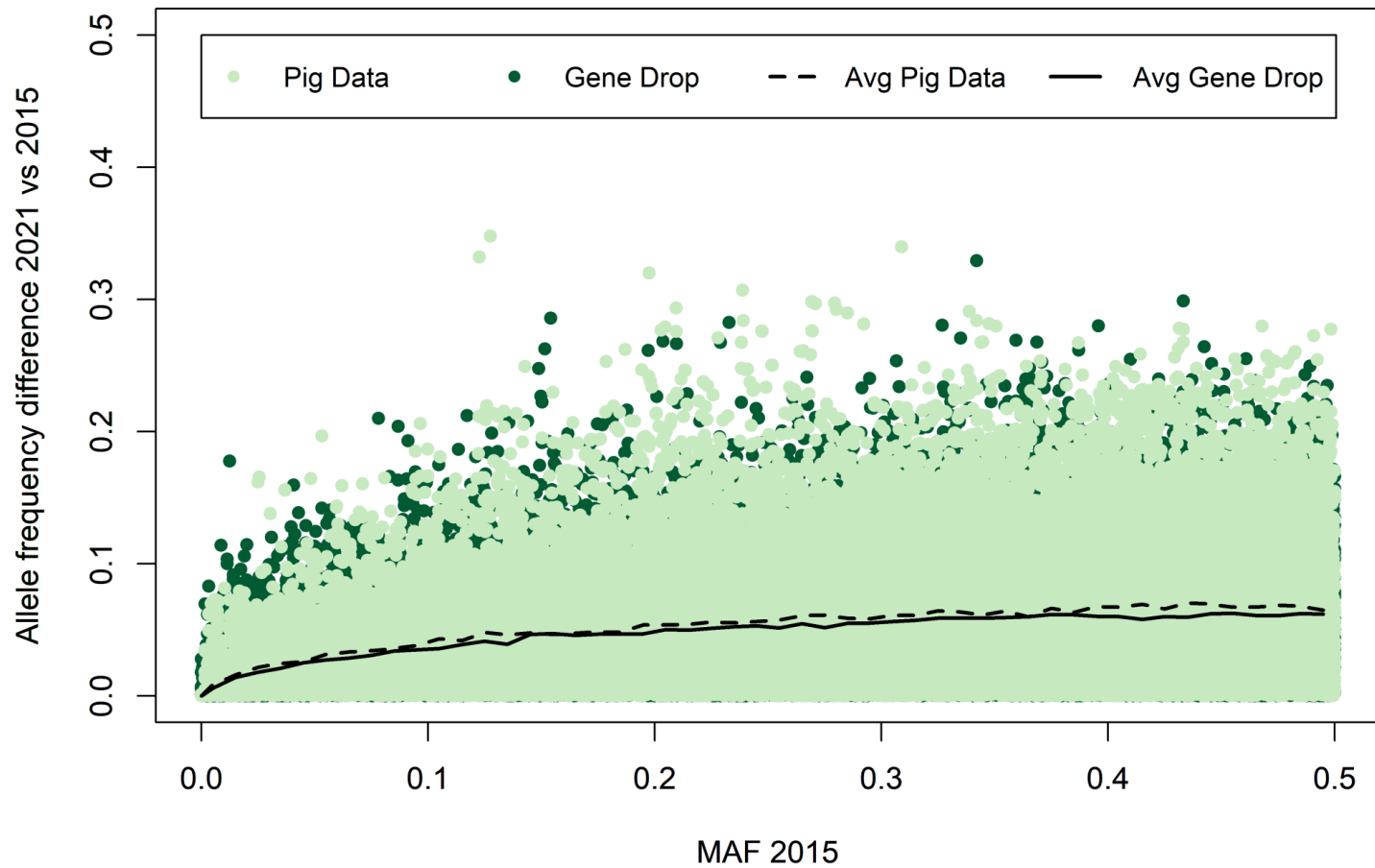


# Drift *versus* selection – Line A

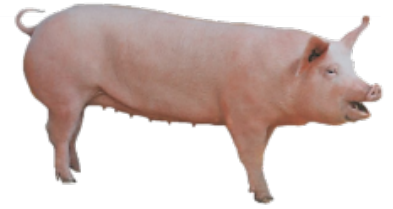




# Drift *versus* selection – Line B



# Conclusion



## Allele frequencies do change due to selection

- On average more than due to drift
- Largest changes not larger than expected under drift

## Allele frequency changes unrelated to GWAS for traits & index

- Peaks in GWAS are pleiotropic?
  - Reason why they are still segregating
- Many small effect QTL are underlying the index

**Genetic gain is a result of many small changes  
in allele frequency**

