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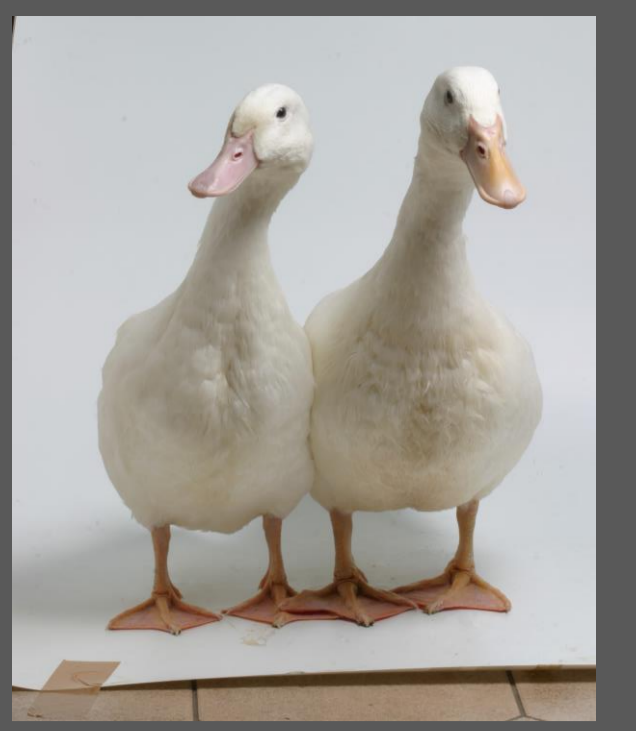
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Genome-wide association analysis (GWAS) and accuracy of genomic selection on growth traits in two duck lines using imputed genotypes

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Justification

- The Pekin duck is well characterised for its fast growth and meat qualities
- Traditional breeding rely on laborious and costly pedigree gathering usually through trap nests
- Change to open pen-mating system with many drakes and hens in a single pen:
 - First we used a low density SNP array to reconstruct parentage
 - Subsequently, we imputed to the 60k Duck SNP array



Summary

- Good quality imputed genotypes with MAF well distributed between 0.01 and 0.5
- High imputation accuracies ~ 0.93
- All traits were heritable with estimates from G-Matrix always lower than those from A matrix
- GWAS found evidence of genome-wide significant ($p < 0.05$) QTL in both lines
- Higher genomic accuracies with G matrix compared to A matrix
- Lower bias with G matrix than with A Matrix



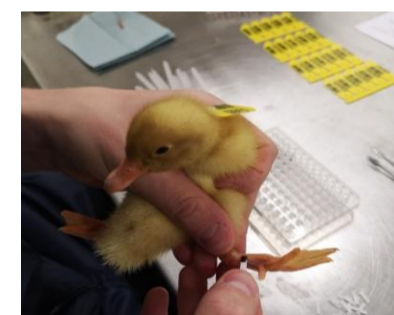
Objectives

Estimate variance components and genomic accuracies using both marker and pedigree data and carry on GWAS in two commercial duck lines.



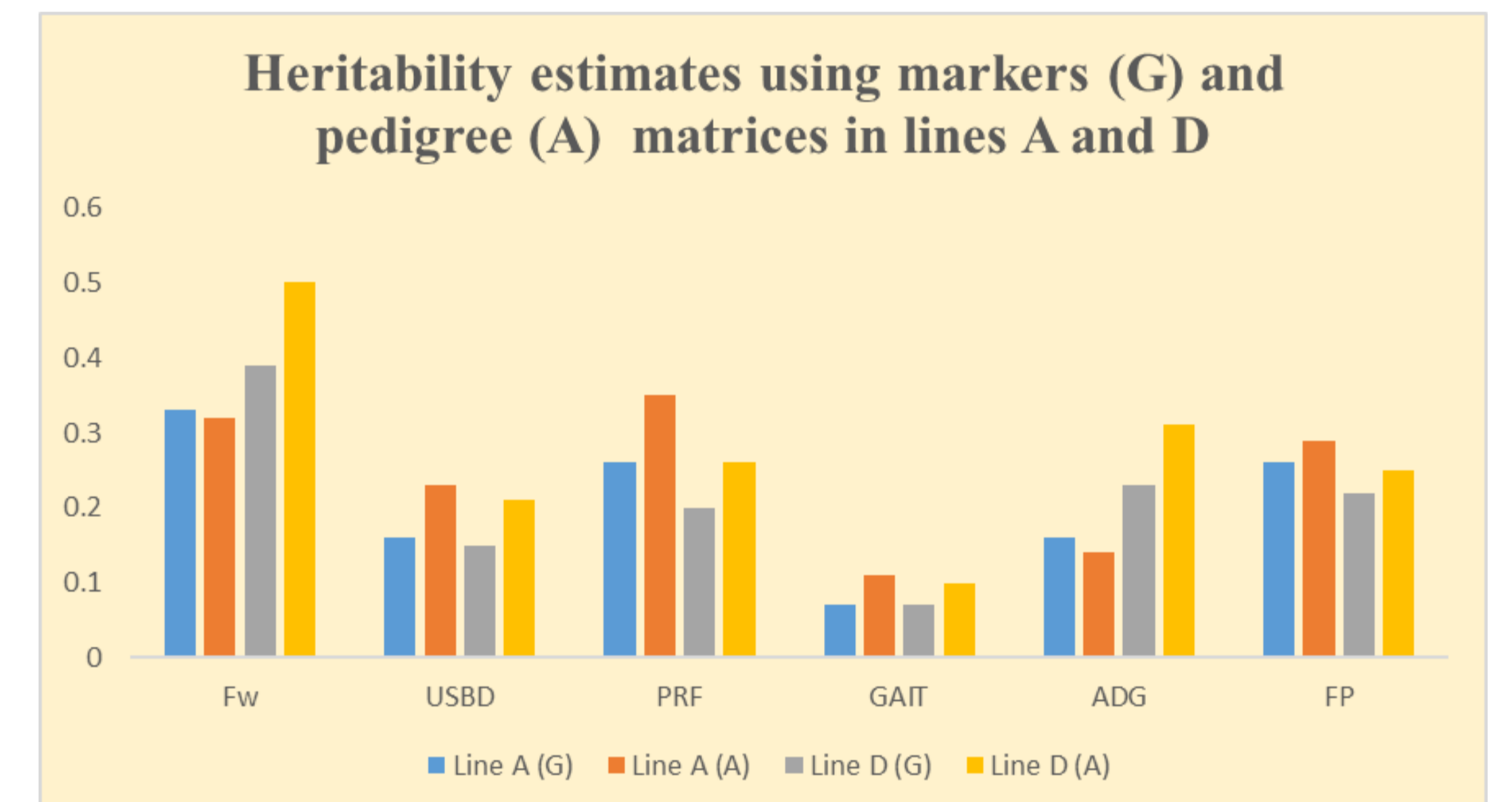
Data

- About 13k ducks per line genotyped with parentage panel → **training set**
- Approx. 1500 ducks per line genotyped with the 60K Duck SNP array → **reference panel**
- Imputation from **training set** to **reference panel** with AlphaImpute¹ software:
 - accuracy of 0.93 and 0.92 for lines A and D
 - SNPs after QC 47156 and 46297 for lines A and D



What was measured

- Finish weight (FW), Breast Depth (USBD), primary feather length (PRF), Gait score (GS), Average daily gain (ADG) and Foot pad score (FP)



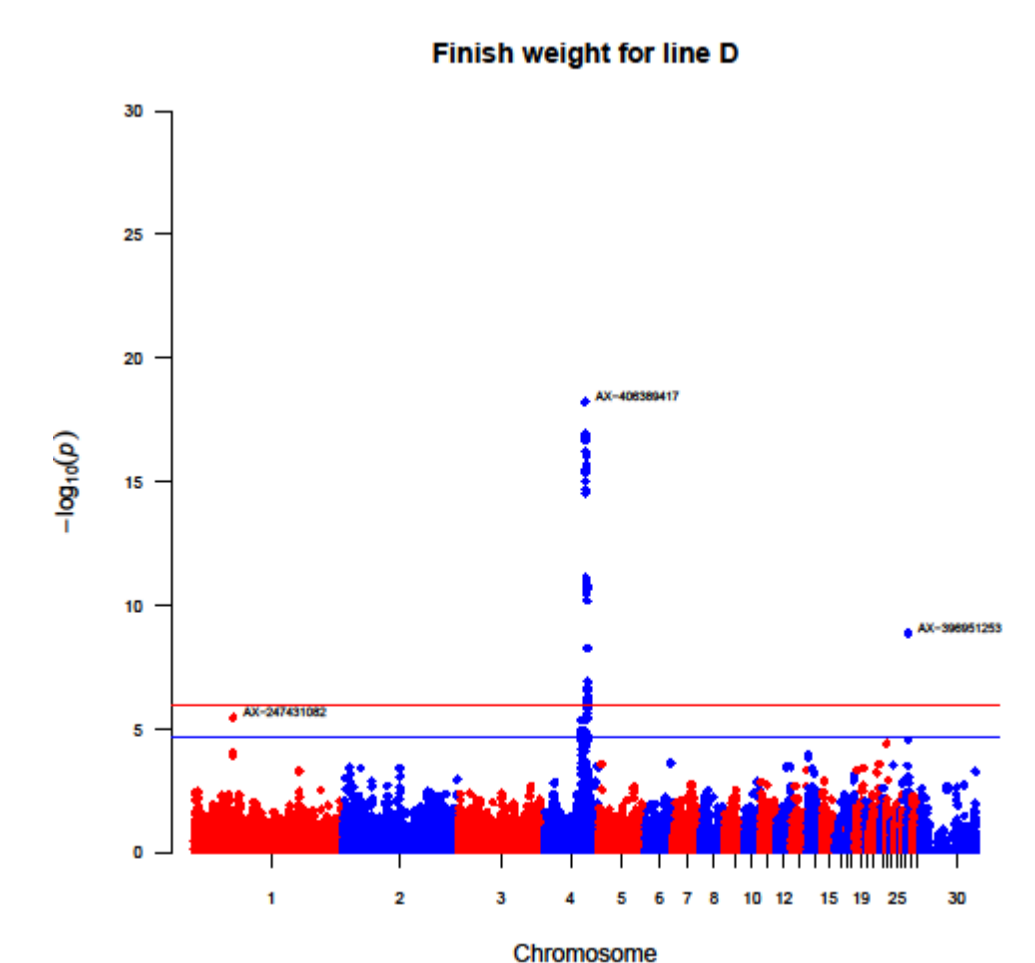
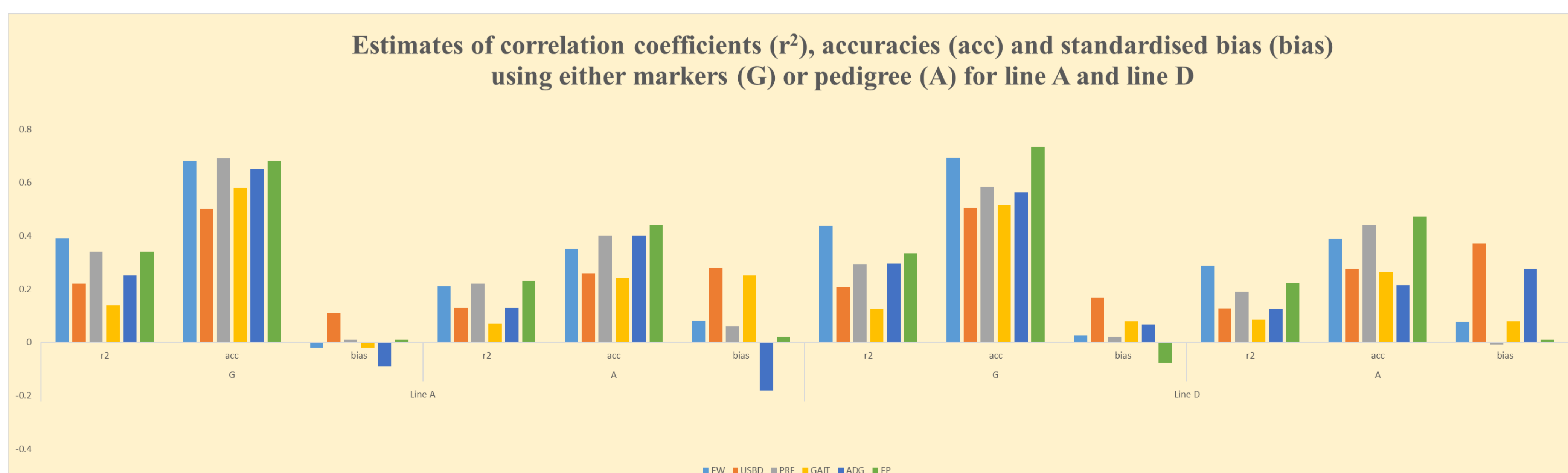
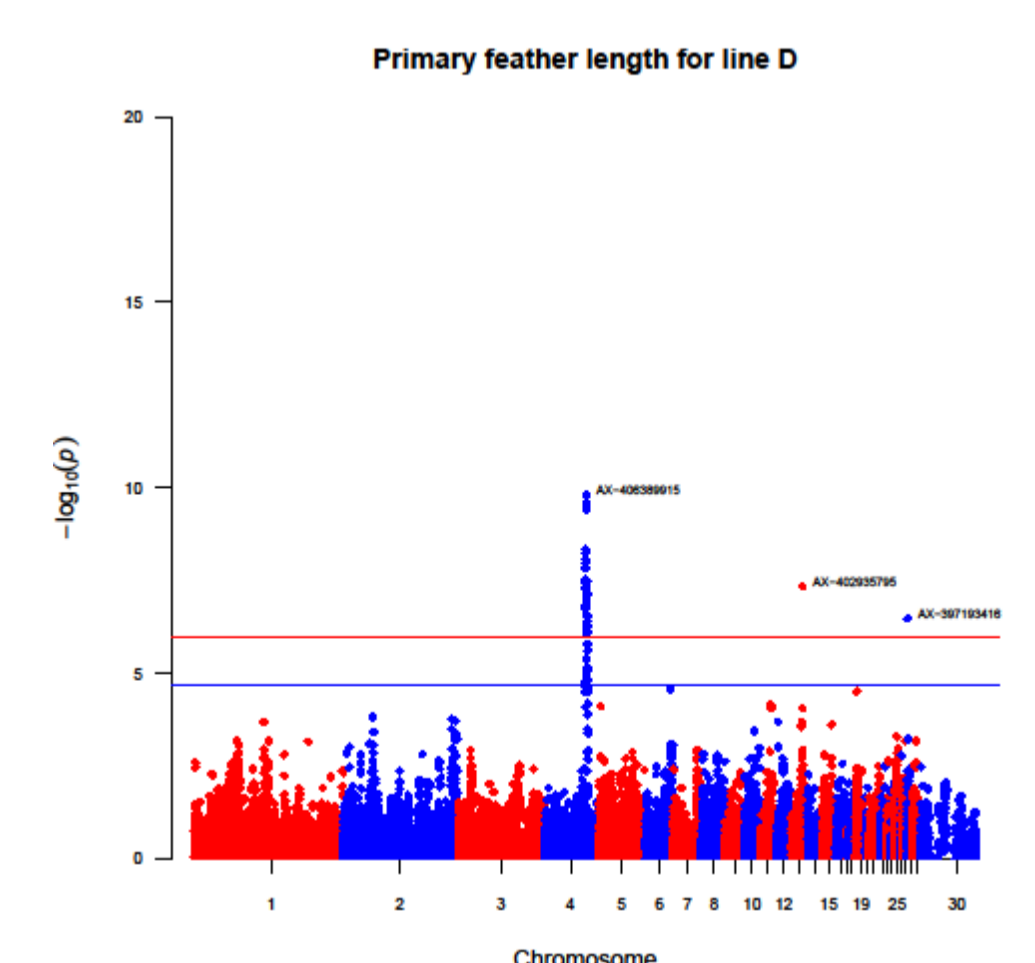
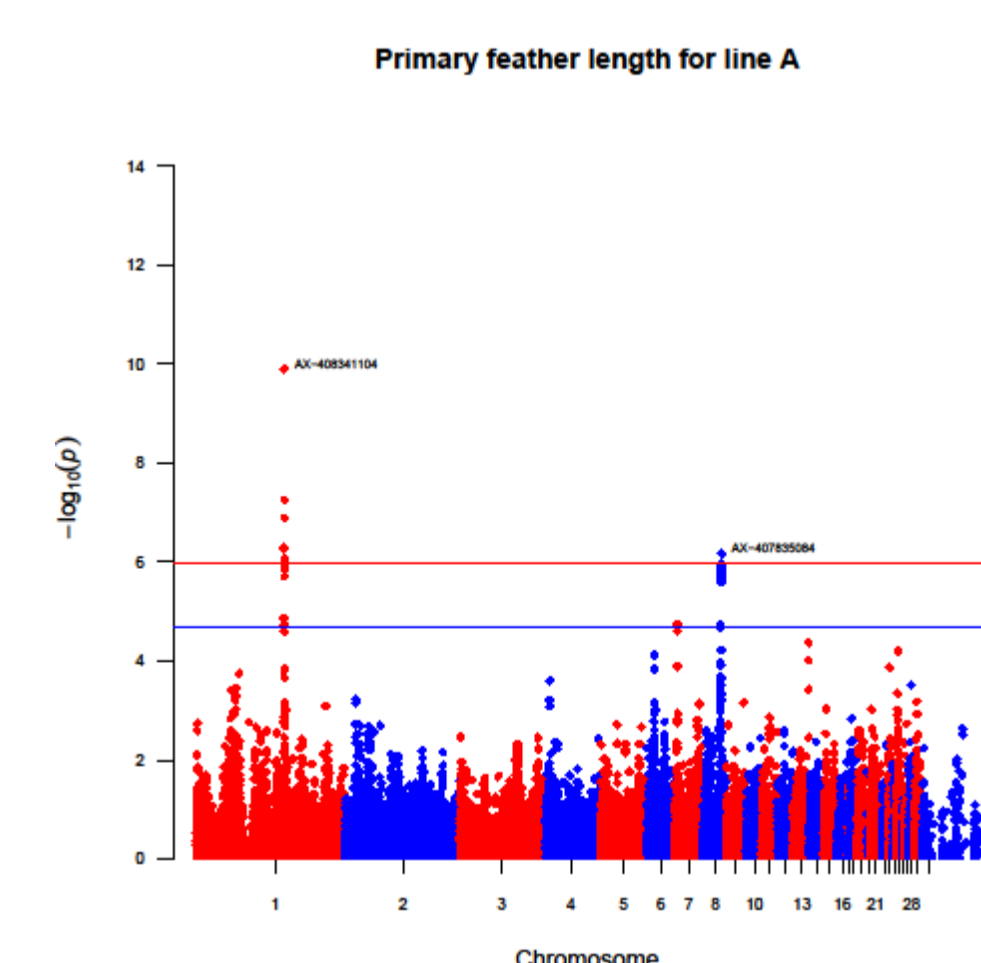
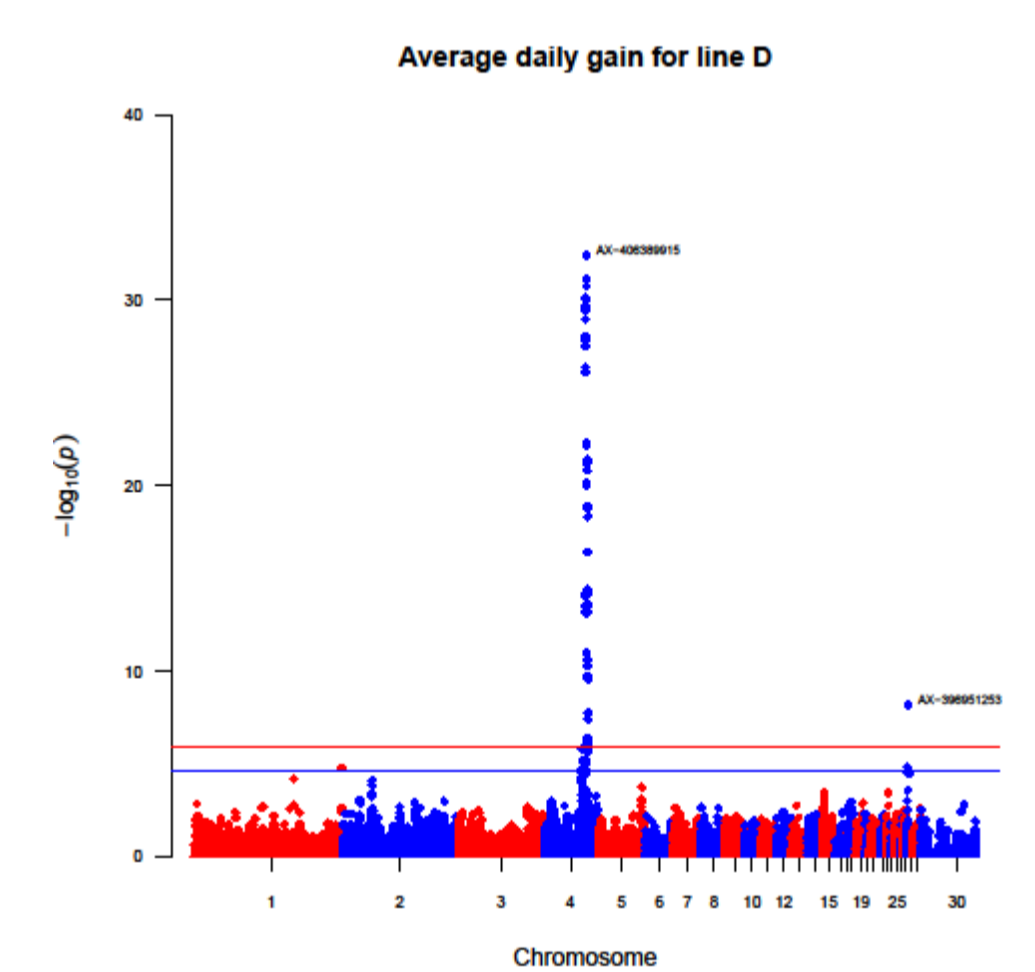
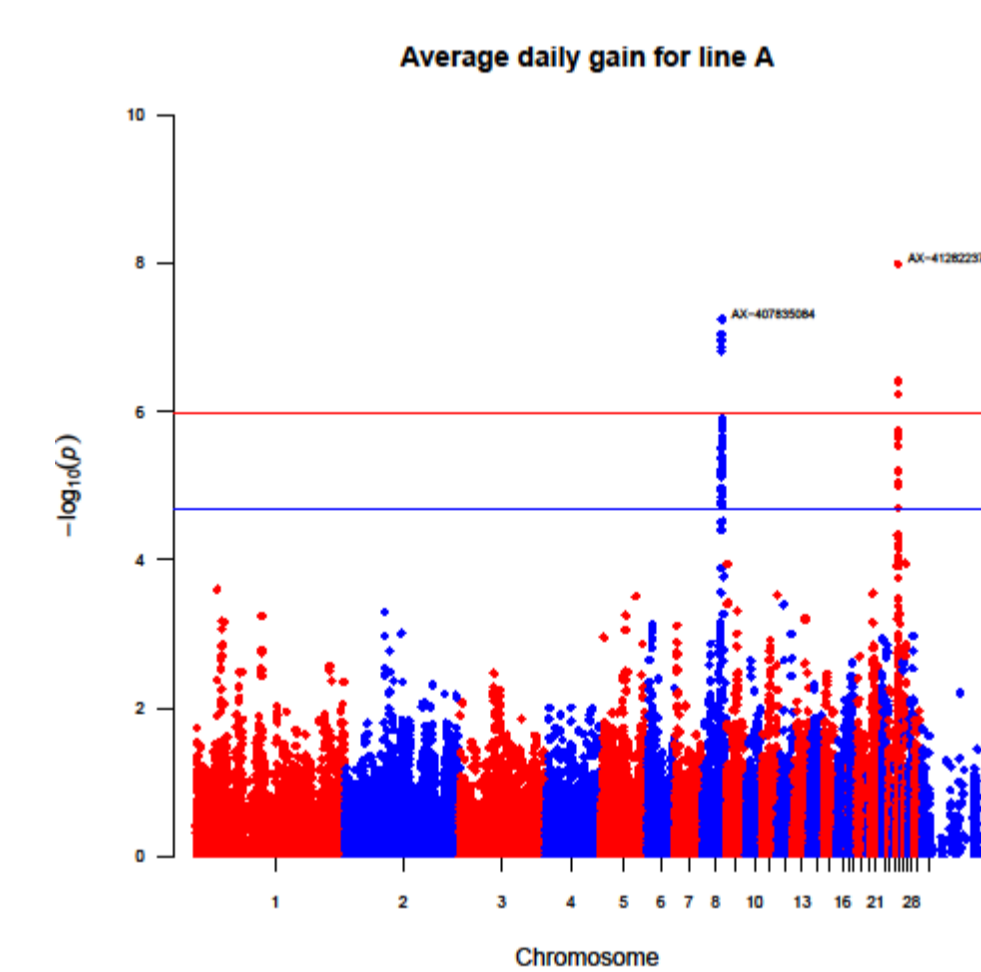
Statistical analysis

- Genetic parameters estimated in ASReml² using either pedigree (A) or markers (G) relationship matrix
- GWAS performed with GEMMA³
- Genomic selection accuracies estimated with ASReml² using either pedigree (A) or markers (G) relationship matrix
 - in line A, 9579 ducks in generation 1 to 5, were used to predict 4066 ducks in generation 6
 - in line D, 8134 ducks from generation 1 to 4, were used to predict 4885 in generation 5
 - the non-masked phenotypes in the reference population were then analysed to predict the breeding values (either genomic or with pedigree) of the masked-phenotype individuals
 - bias (b) is given by regression of “True” EBV (estimated with phenotype) on Predicted EBV (phenotype masked)^{4,5}

$$b = \text{reg.coef}(\text{EBV}, \text{TBV})$$

$$\text{Accuracy} = \frac{r_{gy}}{\sqrt{h_y^2}}$$

$$\text{Std bias} = \begin{cases} 1 - b & b < 1 \\ \frac{1}{b} - 1 & b > 1 \end{cases}$$



- ¹Whalen and Hickey (2020). *bioRxiv*, <https://doi.org/10.1101/2020.09.16.299677>
- ²Gilmour *et al.* (2015). ASReml User Guide Release 4.1 VSN International Ltd, Hemel Hempstead, HP1 1E, UK.
- ³Zhou and Stephens (2012). *Nature Genetics* 44:821–824.
- ⁴Legarra *et al.* (2008). *Genetics*, 180:611–618.
- ⁵Zefreh *et al.* (2023). *Frontiers in Genetics*, 14:1127530.