

# Impact of early summer hair shedding on susceptibility to fescue toxicosis and heat stress in taurine cattle

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## Background

- Two key abiotic stressors (heat stress and fescue toxicosis) cost the beef industry > \$1 billion a year
  - Heat stress**
  - Fescue toxicosis** results from consumption of fescue forage infected with the endophytic fungus *Neotyphodium coenophialum*. The fungus makes fescue more hardy but causes adverse side effects in livestock. Fescue makes up the majority of available forage in the Midwest and Southeast.
- Susceptibility to heat stress and fescue toxicosis can be quantified via the animal's ability to **adaptively shed** their winter coat at the beginning of the summer
- Adaptive hair shedding is also correlated with cow performance, particularly day 205 weaning weight of progeny<sup>1</sup>. **Less stress = higher productivity.**

## Methods

### Data generation

- Enrolled cattle are **hair shedding scored** between May 1 and June 30 in 2016, 2017, and 2018 by beef producers
- Genotyped** via GGP F250 SNP panel developed by the University of Missouri and Neogen GeneSeek
  - ~170,000 candidate functional variants
  - ~25,000 variants in common with industry standard genotyping assays
- Genotypes **imputed**<sup>2,3</sup> to ~856,000 SNPs
- Quality control**
  - Missing SNPs > 0.1
  - Missing individuals > 0.1
  - HWE p-values < 1e-20

### Phenotype pre-adjustment

Hair shedding scores were pre-adjusted for sex, age, SDD, farm, calving season, and animal effect in sommer<sup>4</sup>.

Where:

- Sex** is male, female, or U (unknown)
- Age** is age in years at time of scoring
- SDD** is the deviation of the scoring date from May 1
- Farm** is the herd contemporary group
- Calving season** is spring (January 1-June 30) or fall (July 1-December 31)
- Animal effect** is random animal effect of genomic fit using using genomic relationship matrix calculated in GEMMA<sup>5</sup>

In the model using 2016 and 2017 data together, hair shedding scores were additionally pre-adjusted for year effect and repeatability.

### Multi-year GWAA

A multi-year univariate linear mixed model was fit in GEMMA<sup>5</sup> using BLUP breeding values obtained via pre-adjustment in sommer<sup>4</sup> as the response term.

$$y = u + \text{SNP} + e$$

Where:

- u** is the mean
- SNP** is the SNP effect

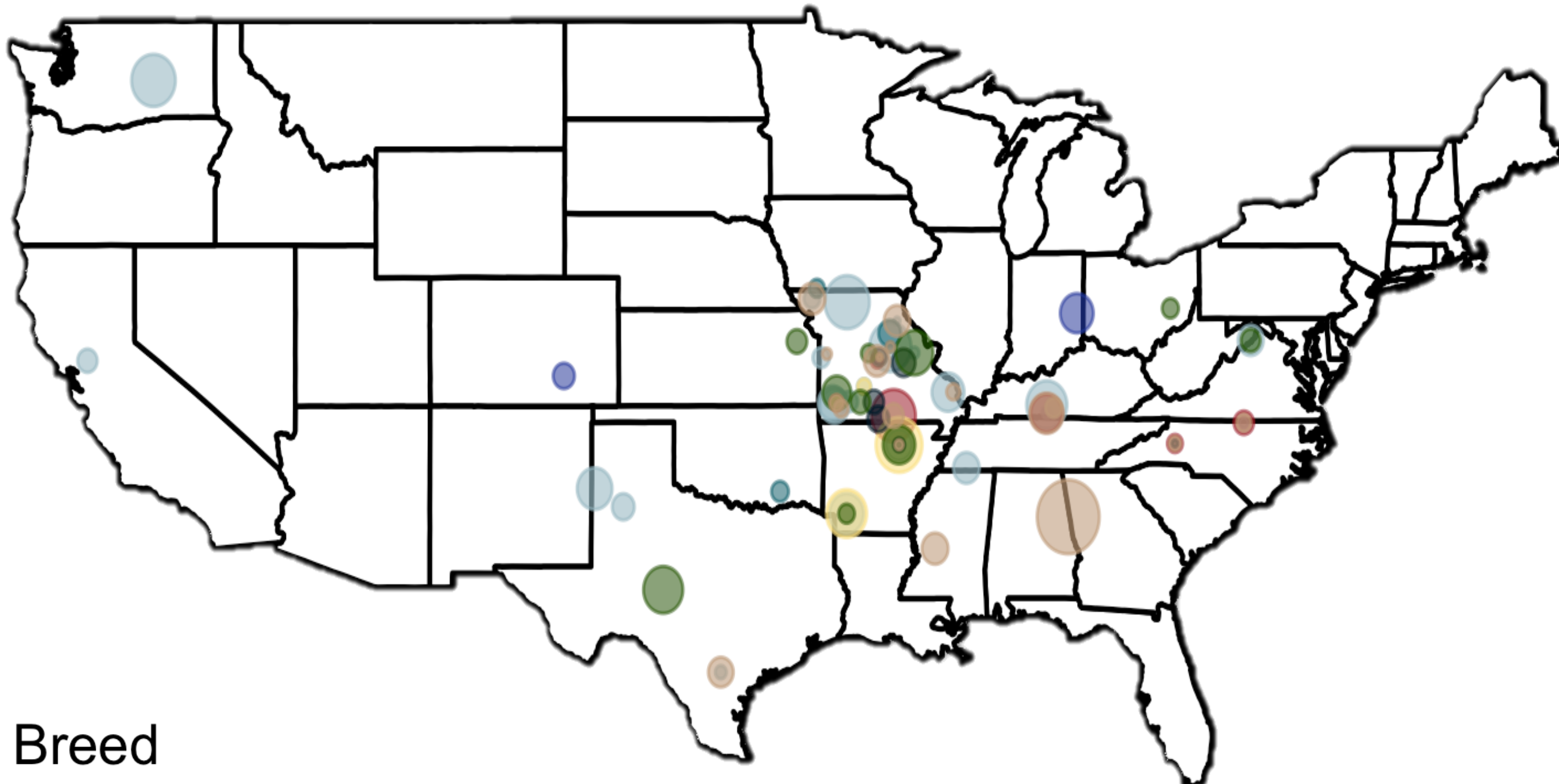
### G x E GWAA

A univariate linear mixed was fit for each 2016 and 2017 in GEMMA<sup>5</sup> using the residual environmental value obtained via sommer<sup>4</sup> pre-adjustment as the response term. Both included a genotype-by-environment covariate term.

$$y = u + \text{SNP} + 60\text{d average} + \text{SNPxE interaction} + e$$

Where:

- SNP** is the SNP effect
- 60d average** is the average temperature for the zip code in which the animal was scored during the 60 days prior to scoring



- Breed
- AN: 2,935
  - ANR: 708
  - CHA: 285
  - CROS: 439
  - GEL: 282
  - HFD: 1,273
  - SH: 276
  - SIM: 1,831

Figure 1. Location and breed type of the 6,041 individuals analyzed in the project.

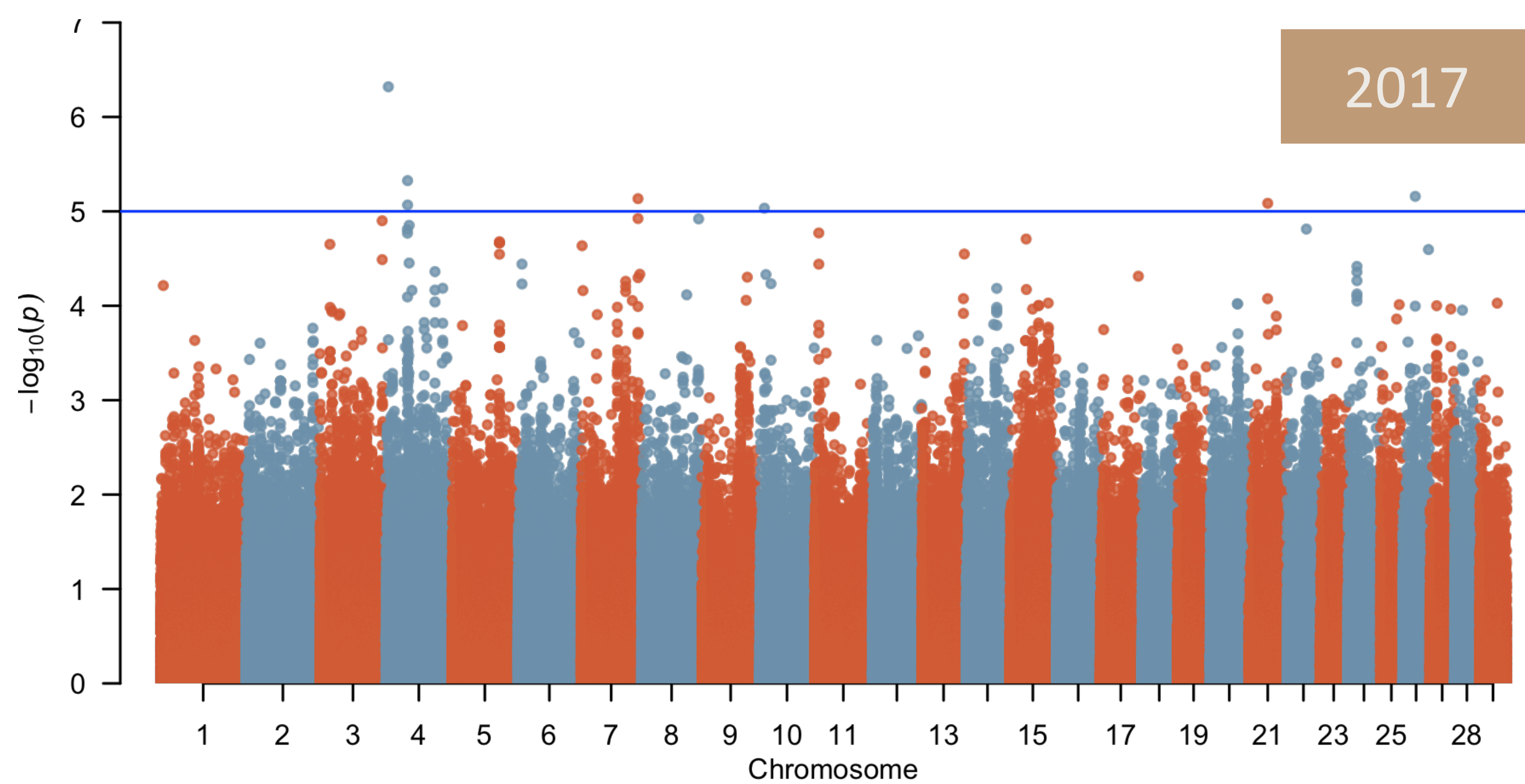


Figure 2. Visualization of 2017 GxE GWAA. P-values represent the interaction term between genotype and 60-day-average temperature. Red line represents Bonferroni corrected p-value. Heritability estimates were 0.44 and 0.49 for 2016 and 2017 respectively.

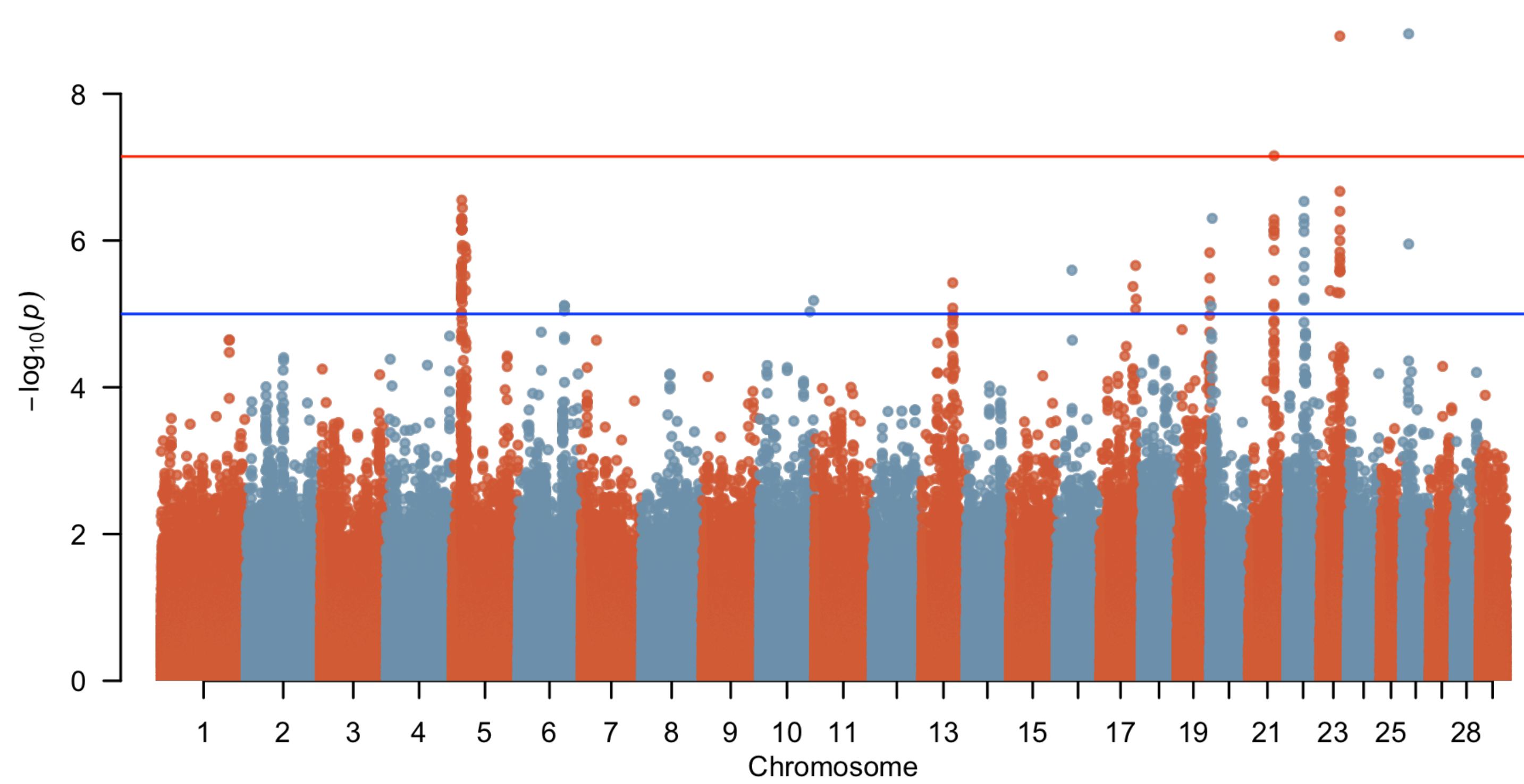


Figure 3. Visualization of multi-year GWAA model results (6,041 individuals; 9,692 total observations). Red line represents Bonferroni corrected p-value. A heritability of 0.37 was estimated by the pre-adjustment model.

Figure 4. BLUP breeding values for hair shedding score after pre-adjustment via sommer<sup>4</sup>. Outliers appear to be skewed towards higher breeding values (i.e., higher hair shedding scores, later shedding)

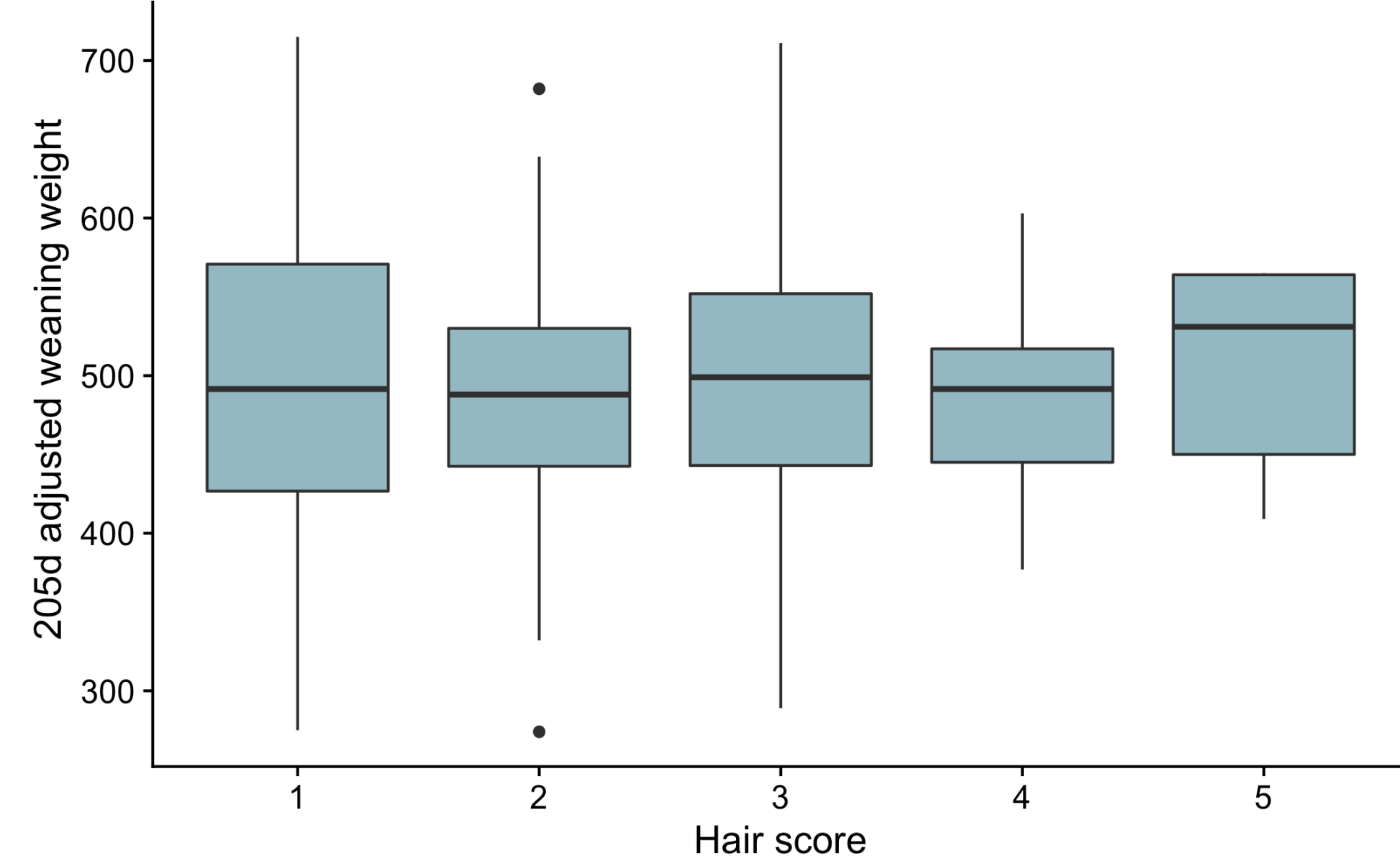
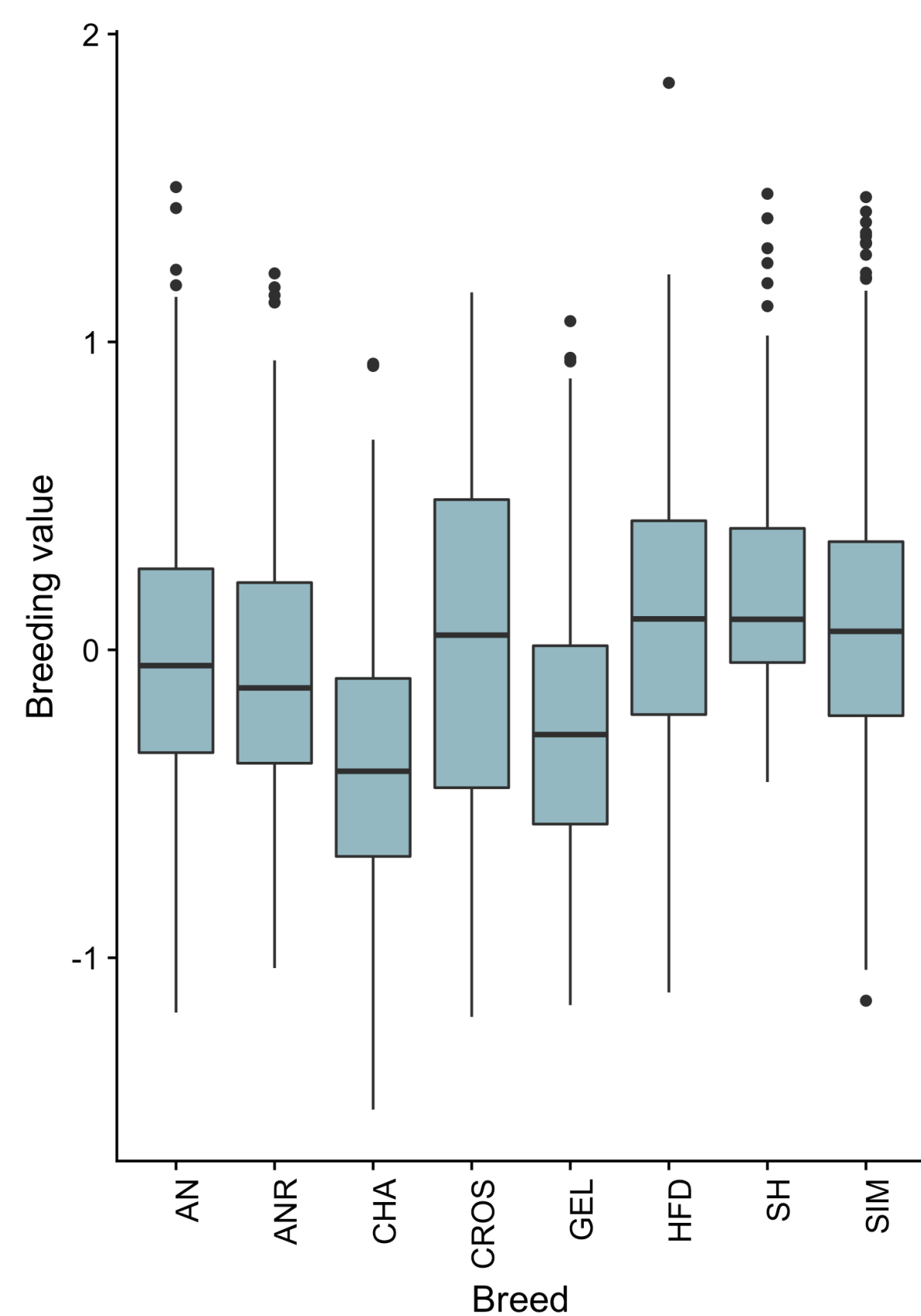


Figure 5. After adjusting calf weaning weight for the effect of farm, birth date, sex and adjusting hair shedding score for score date deviation, decreasing hair score by 1 unit results in an increased weaning weight of 12.6036 lbs (p = 0.056)

## Future Directions

### Environmental variables

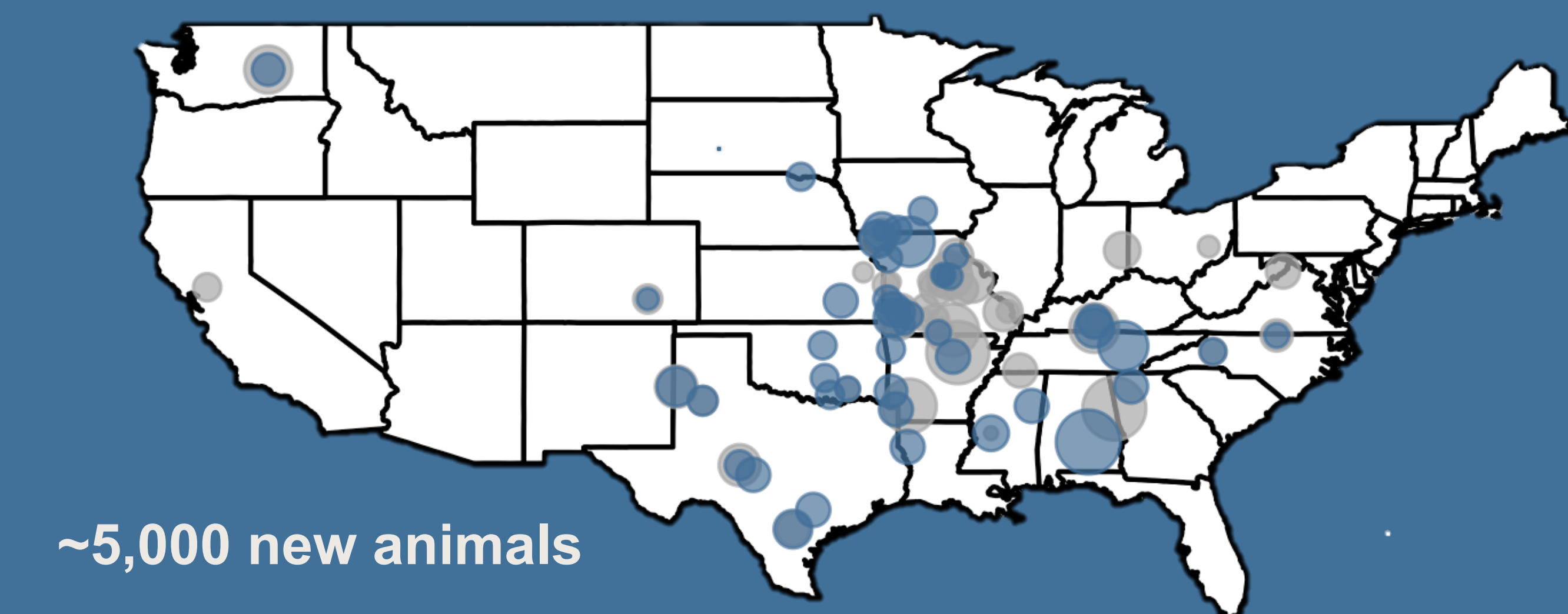
- Is weather (60 day average) or climate (30 year average) a better predictor of hair shedding?
- Heat index
- Fescue G x E GWAA

### Breed

- Ancestry assignment using MU animal genomics breed analysis pipeline
- Do estimates of hair shedding heritability vary between breed?

### New enrollment

In exchange for continuing to score currently enrolled animals in 2019 and 2020, producers received the opportunity to enroll new animals. Enrollment was also opened up to new herds, including those with zebu or indicine (*Bos indicus*) ancestry.



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