

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:** caused by consumption of fescue forage infected with the endophytic funugs *Neotyphodium coenophialum*. The fungus makes fescue more hardy but causes adverse side effects in livestock.
- Susceptibility to heat stress and fescue toxicosis can be quantified via 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 progeny¹. **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

GWAA
Univariate linear mixed model for each year implemented in GEMMA².

$$y = u + \text{sex} + \text{SDD} + \text{age} + \text{MYT} + \text{SNP} + Z_u + e$$

Where:

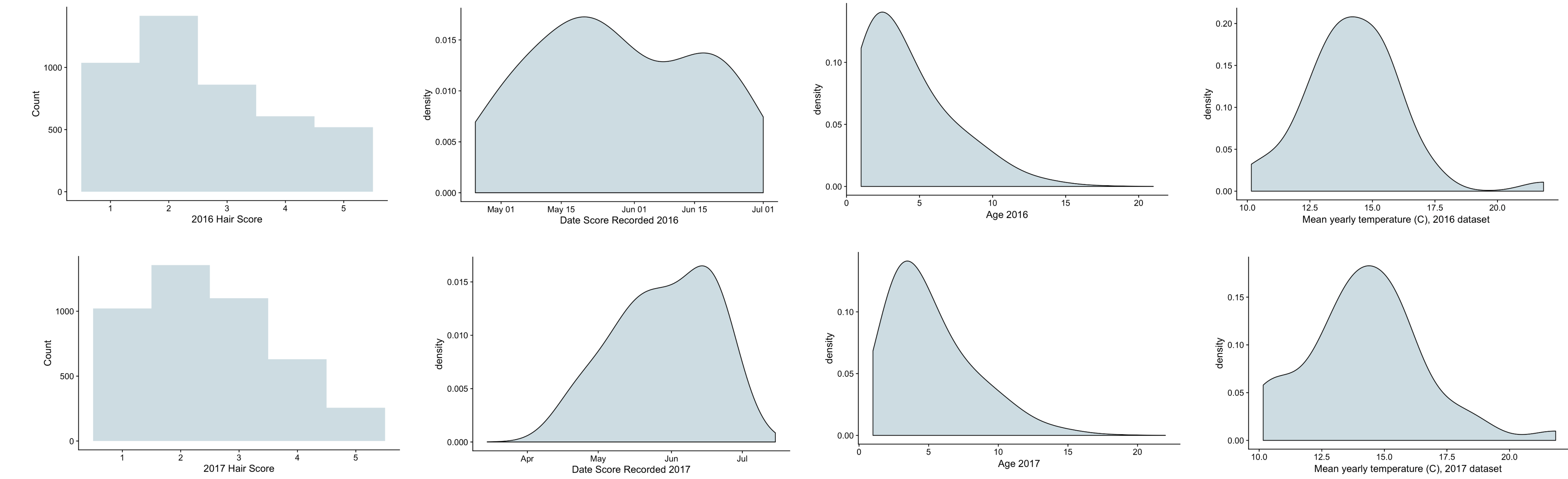
- u is the mean
- Sex: M, F, U (unknown)
- SDD is the deviation of the scoring date from May 1
 - Missing date deviations mean imputed
 - 2016: 27 days
 - 2017: 29 days
- Age is the animal's age at time of scoring in years
 - Missing ages mean imputed
 - 2016: 3
 - 2017: 4
- MYT is the 30-year mean yearly temperature from the PRISM database for the zip code where the animal was located.
- SNP is the SNP effect
- u is the random animal effect fit using the genomic relationship matrix.

Future directions

- Data sharing agreements with breed associations
 - Obtaining genotypes of animals assayed through breed association outside of the project
- Work in cooperation with breed associations
 - Further recruitment, especially in currently under-sampled regions
 - Addition of several un-sampled breeds, including those with *Bos indicus* (zebu) ancestry
- Genotype imputation
 - MU Animal Genomics imputation pipeline
 - ~500 enrolled animals with lower density genotypes on hand
- More sophisticated modelling of genotype-by-environment interaction
- Multivariate model using repeated measures
- Herd adjustment

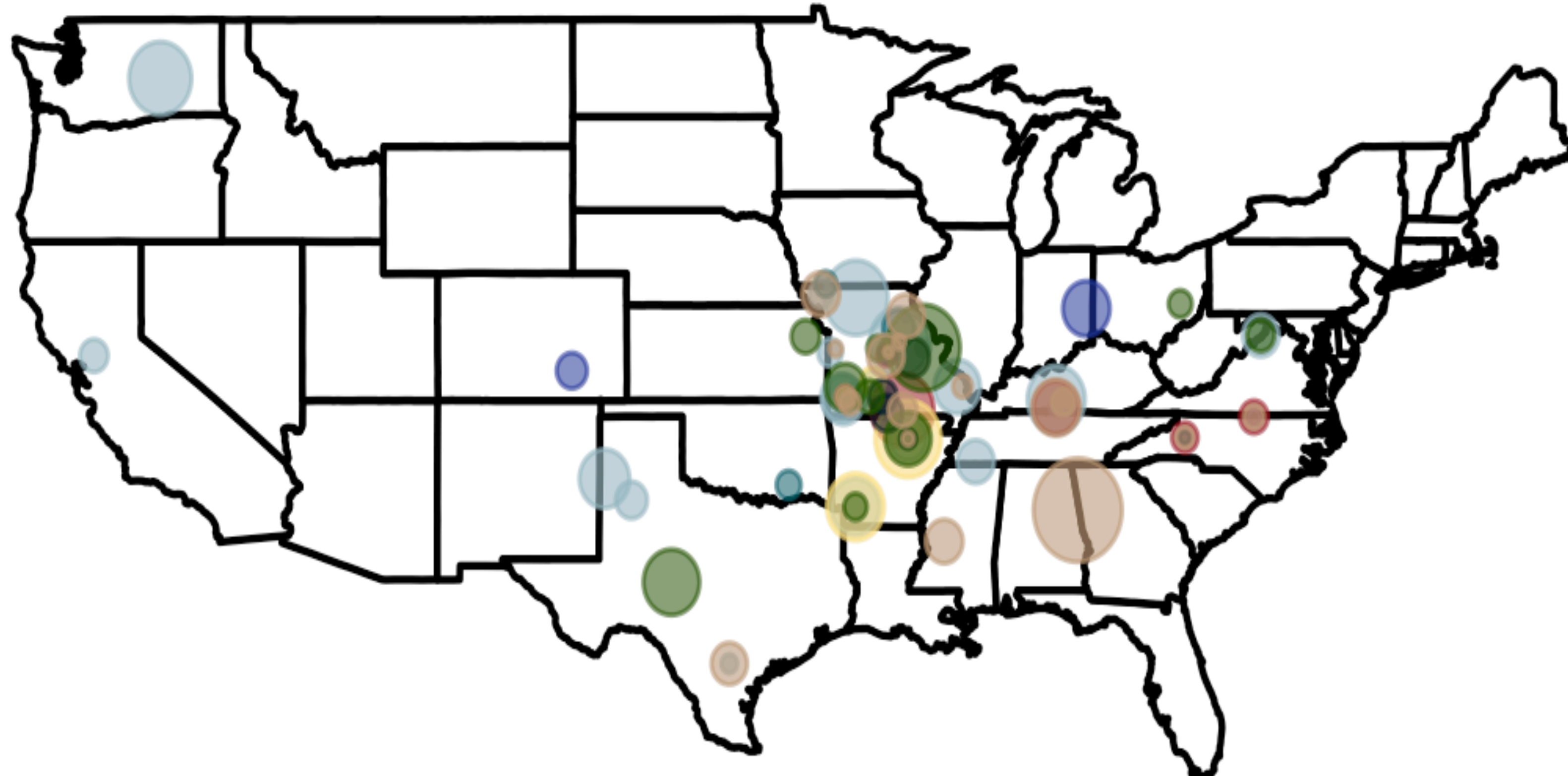


Reduced datasets		
Breed	2016 (n)	2017 (n)
Angus (AN)	1,467	1,677
Red Angus (ANR)	301	217
Charolais (CHA)	234	192
Chianina (CHI)	1	1
Cross-bred (CROS)	217	85
Gelbvieh (GEL)	252	126
Hereford (HFD)	459	608
Maine-Anjou (MAAN)	1	1
Shorthorn (SH)	171	46
Simmental (SIM)	1,336	1,411
TOTAL:	4,439	4,364



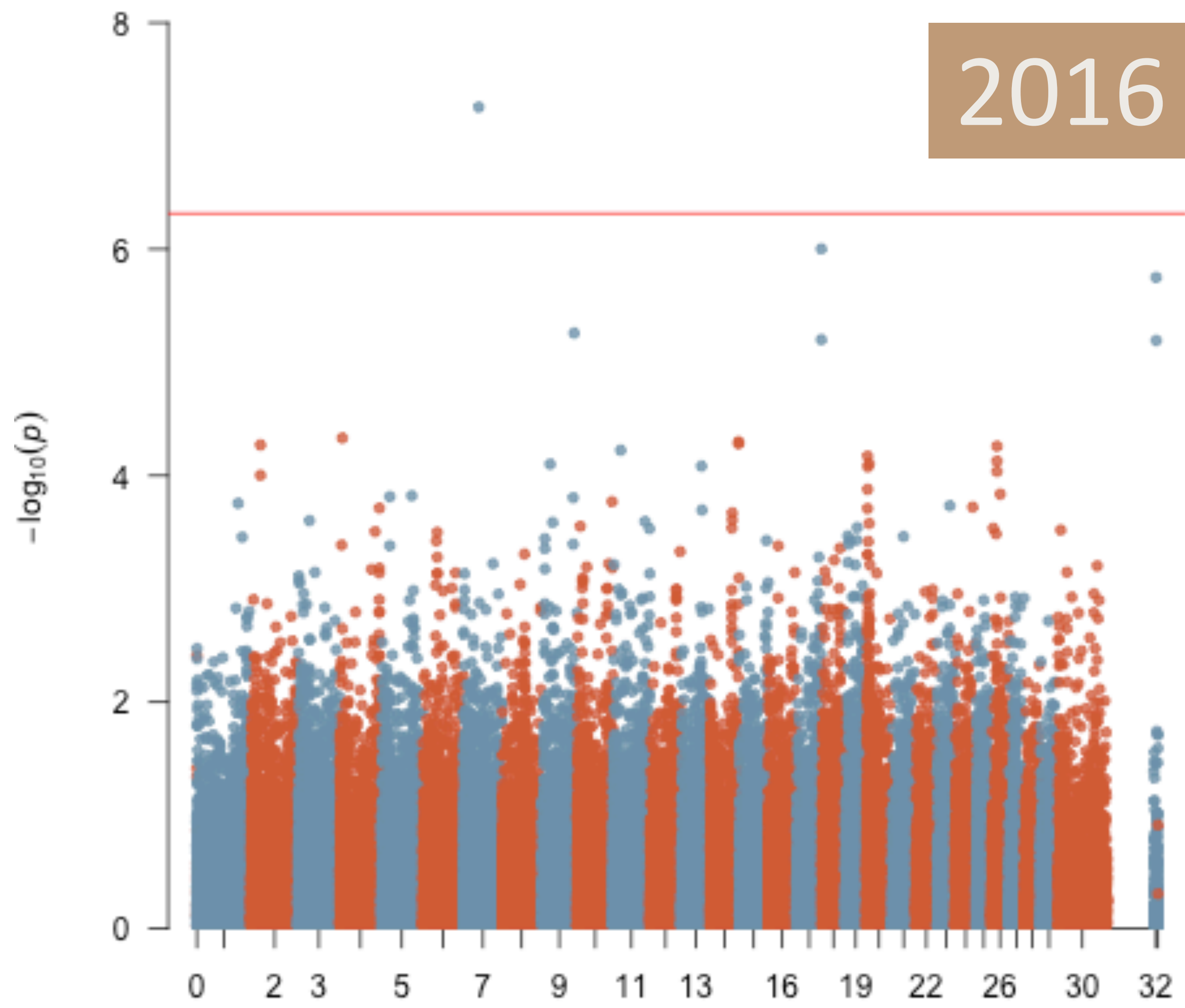
Gene ontology enrichment top hits (2016)	
Term	Bonferroni corrected p-value
Canalicular bile acid transport	8.96e-04
Canalicular bile acid transmembrane transporter activity	2.73e-04
Intercellular canaliculus	0.002601
Mitotic cytokinesis checkpoint	0.005372
Flemming body	0.006127
Abscission	0.018796
Ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway	0.018796
Bile acid secretion	0.025058
Negative regulation of cytokinesis	0.032214
Bile acid transmembrane transporter activity	0.037051

Geographic distribution of samples: full dataset

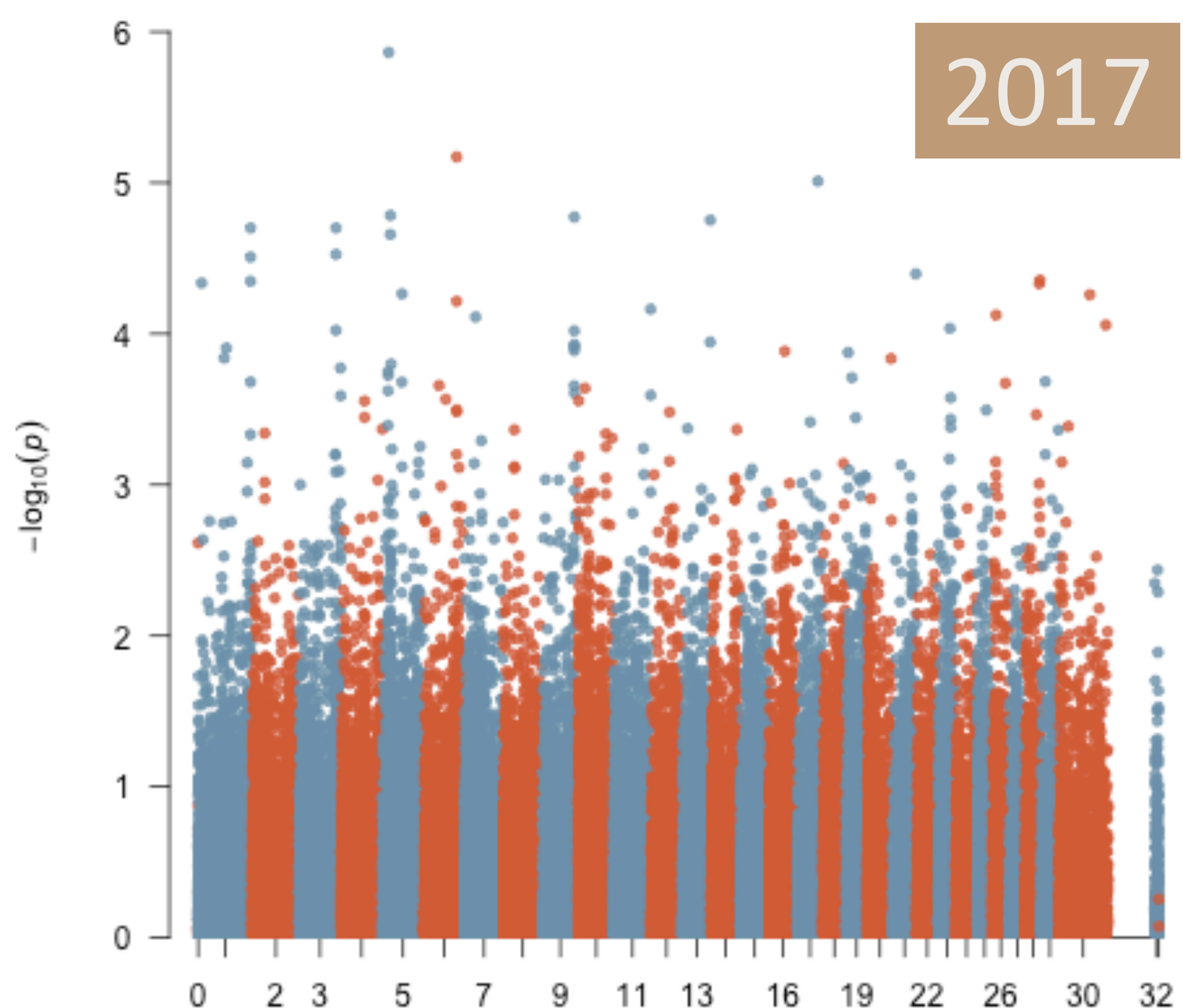


Breed

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



Visualization of 2016 univariate GWAA results using 4,439 observations and 104,890 SNPs. Red line represents Bonferroni corrected significance threshold. A heritability of 0.482 was estimated by the model.



Visualization of 2017 univariate GWAA results using 4,364 observations and 104,890 SNPs. No SNPs exceed Bonferroni corrected significance threshold. A heritability of 0.527 was estimated by the model.

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