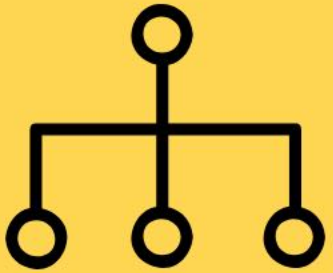

Genotype-by-environment interactions across discrete climate regions in U.S. beef cattle

Harly Durbin

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Intern, Angus Genetics, Inc.

@harlyjaned

Phenotype

=

Genotype

+

Nutrition & management

Weather & climate

Environment

Phenotype

=

Genotype

+

Nutrition & management

Weather & climate

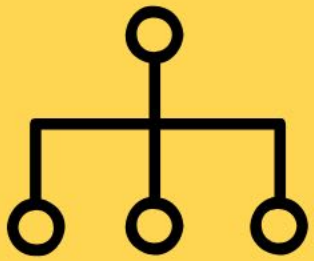
Environment

+

Genotype*Environment

- Beef cattle spend most of life on pasture in a wide range of environments, management strategies

- Genetic evaluations conducted at the **national level** – estimate of average performance of progeny across all environments



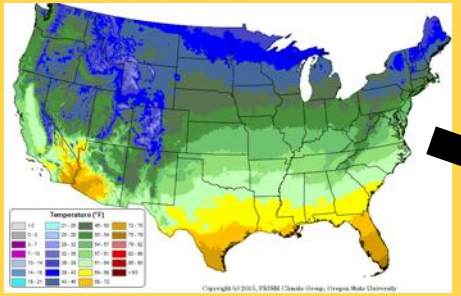
- **P:** How much does cattle growth differ between environmental regions?
- **E:** How much of the difference is due to management & environment vs. genotype?
- **G x E:** How much re-ranking of genotypes across regions? What variants significantly interact with the environment?

Predicting genetic merit for weaning weaning weight

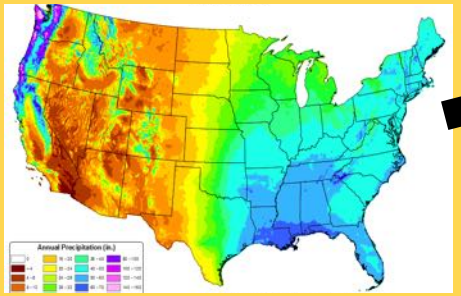
$$y = Xb + Z_1u + Z_2m + Z_3p + e$$

- y = weaning weight at ~7 months of age adjusted to 205 days
- b = fixed contemporary group effect (environment)
- u = random genetic effect of calf (direct)
- m = random genetic effect of dam (maternal)
- p = random maternal permanent environment effect

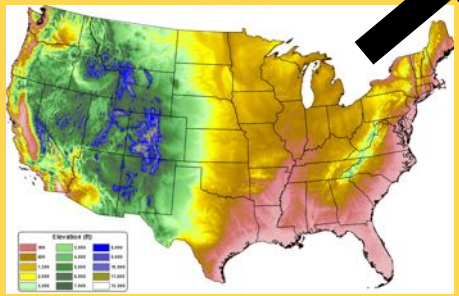
Continuous climate variables → **K-means clustering** → **Discrete environmental regions**



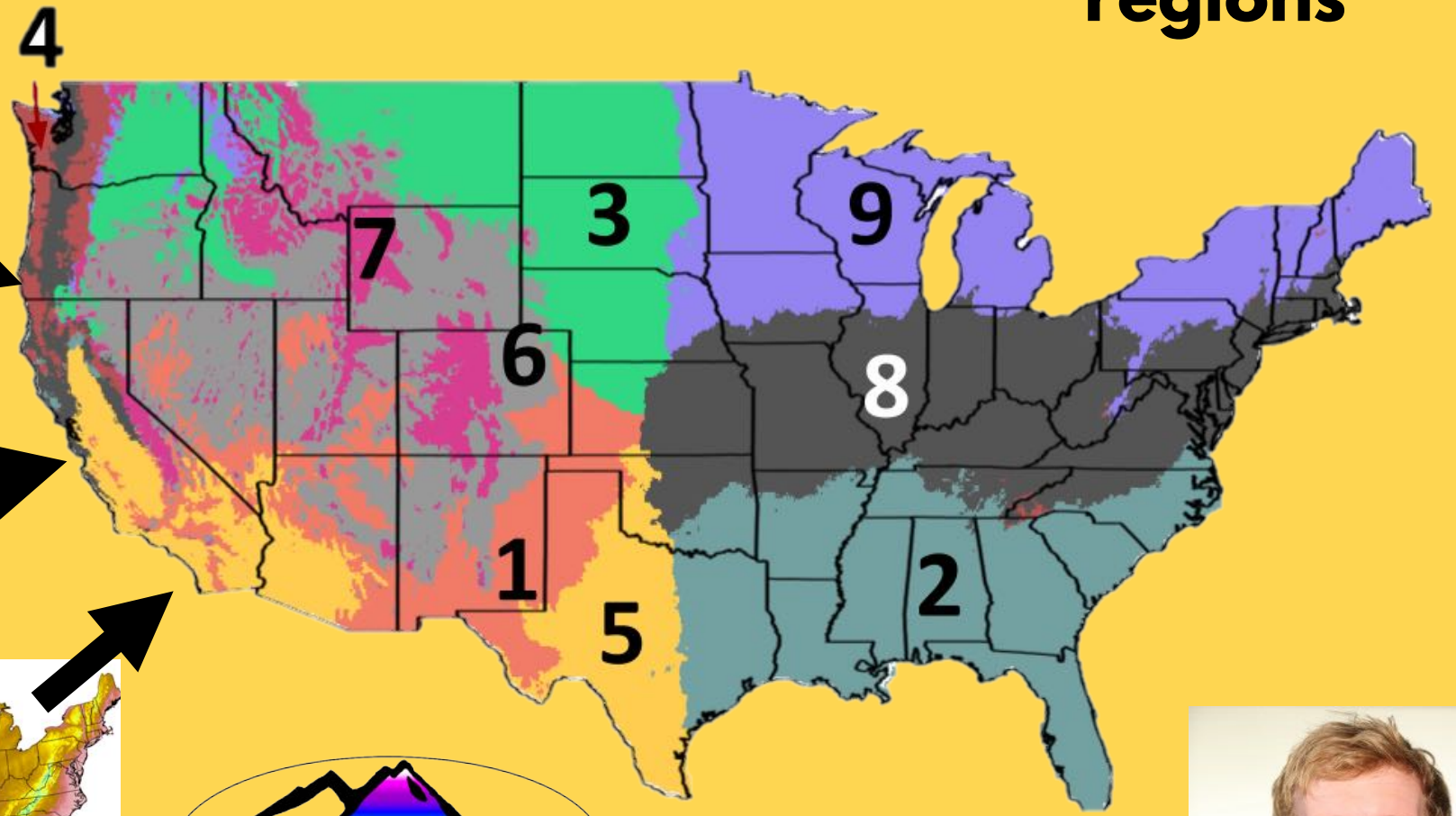
Temperature



Precipitation



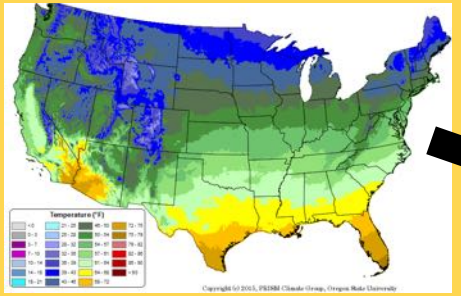
Elevation



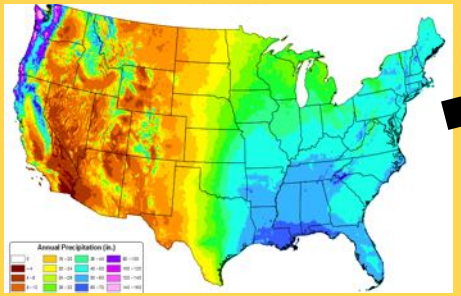
PRISM GROUP

Troy Rowan

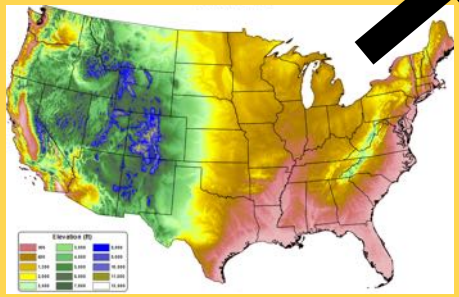
Continuous climate variables → **K-means clustering** → **Discrete environmental regions**



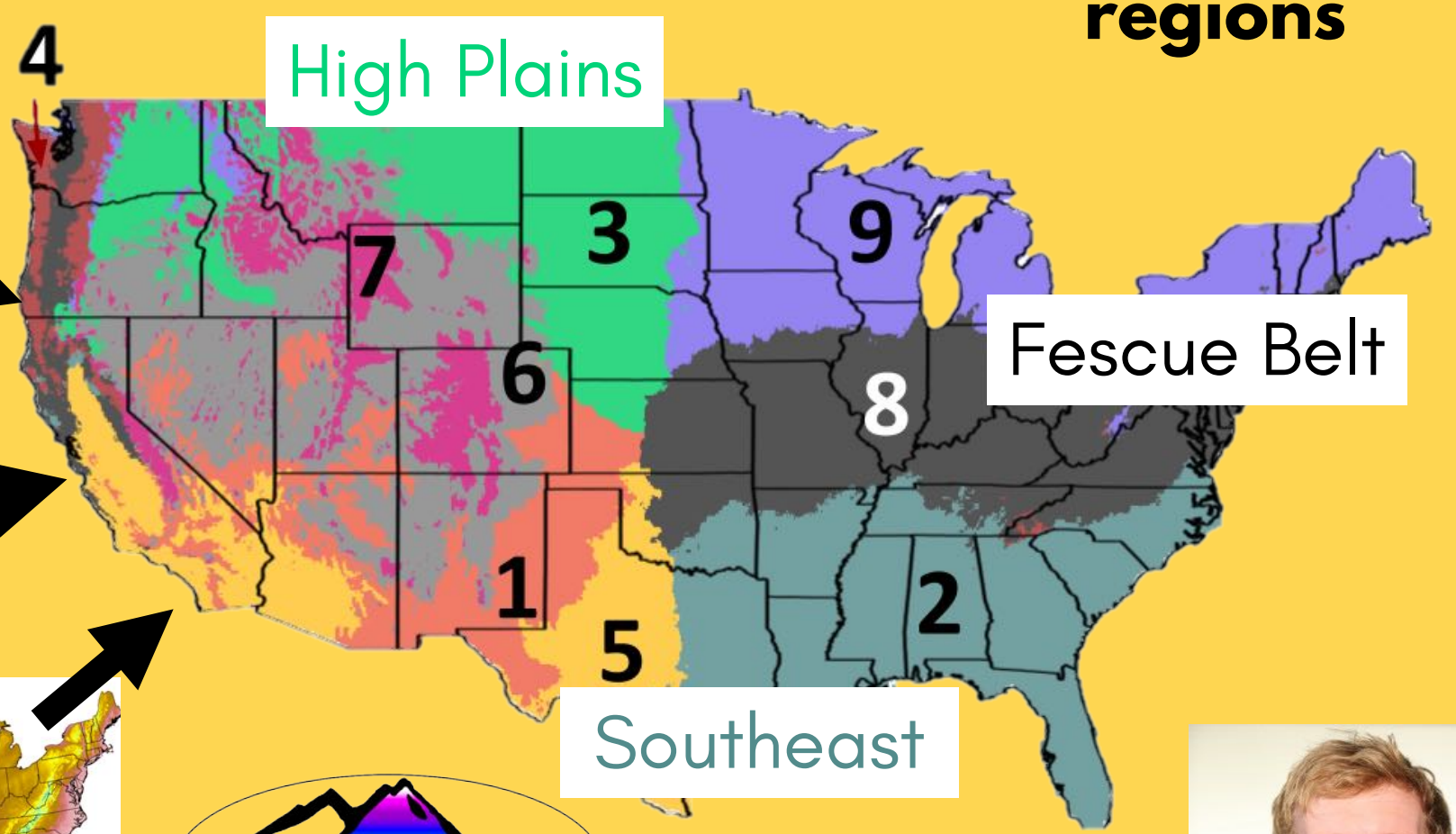
Temperature



Precipitation



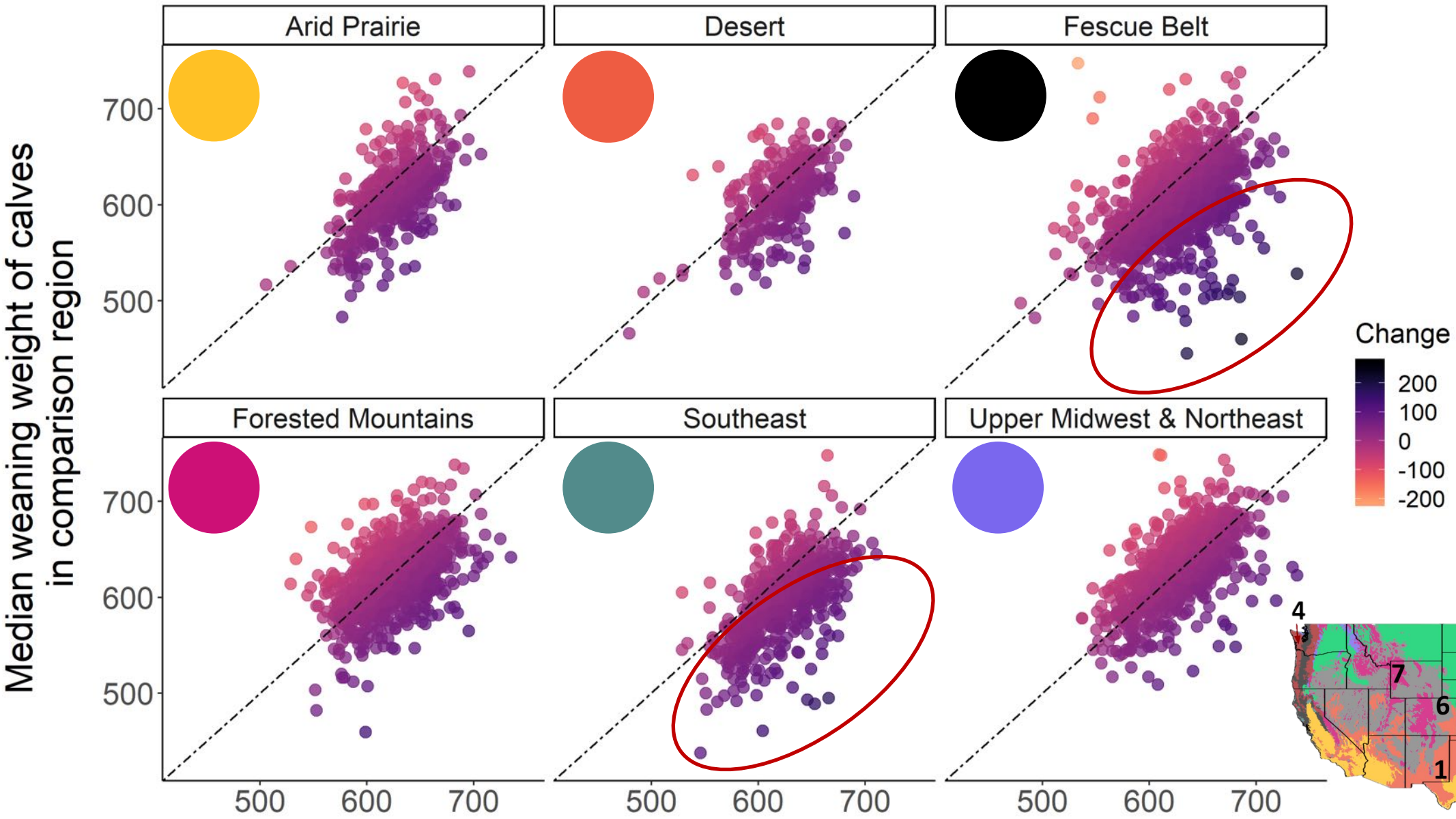
Elevation

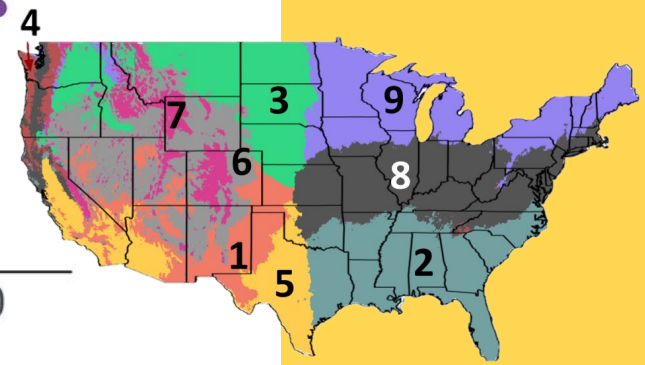


PRISM GROUP

Troy Rowan

Many AI sires perform inconsistently across regions





P = G + E + G*E

Estimating the effect of environment: contemporary groups

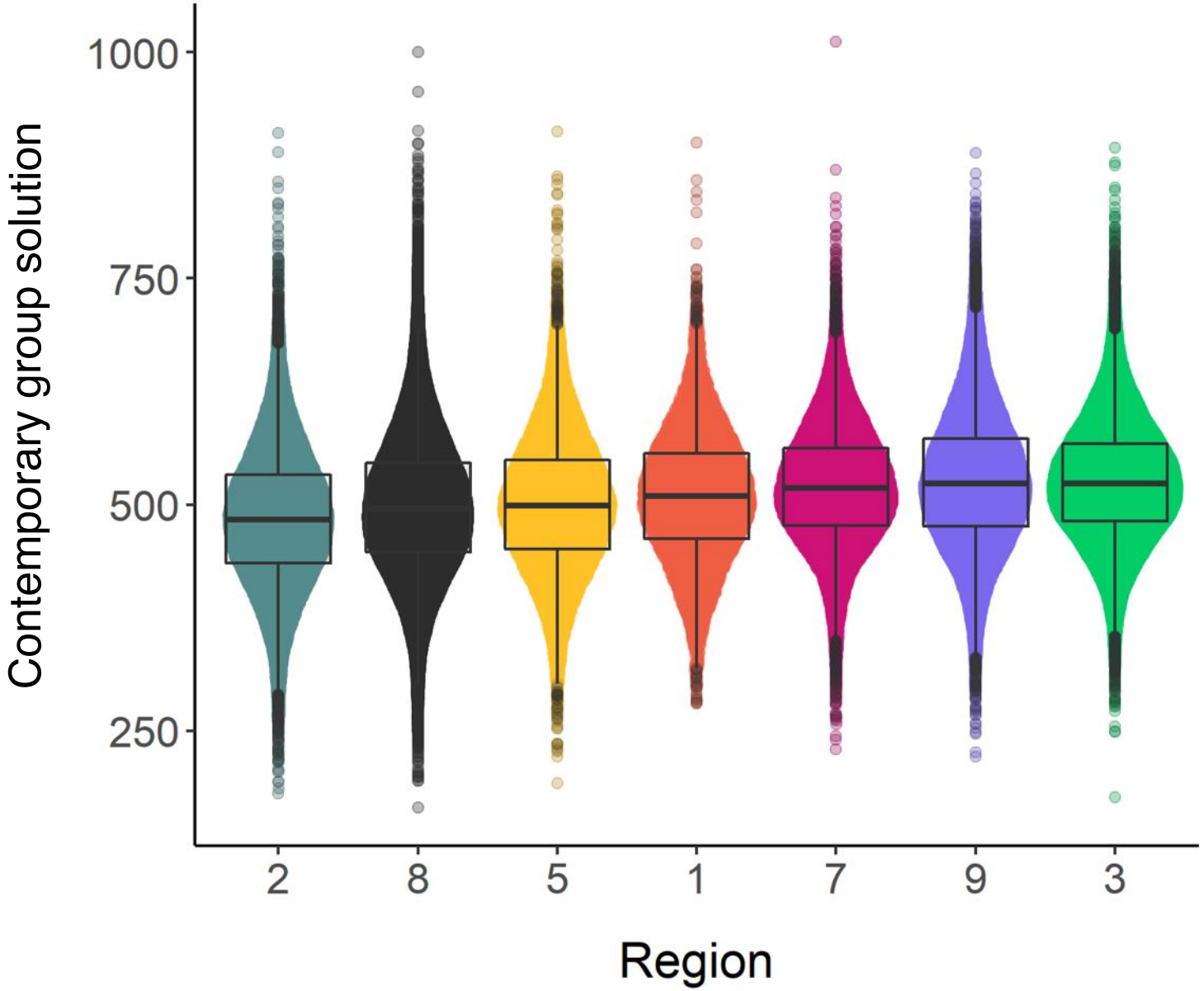
Set of animals who had equal opportunity to perform:

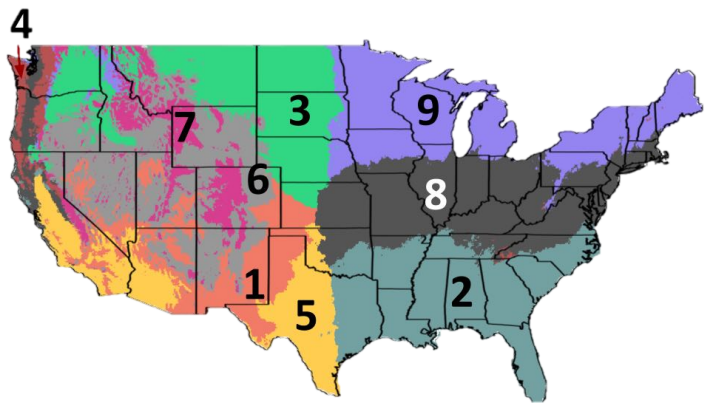
- Managed alike at same farm
- Same sex, close in age
- Exposed to the same environmental conditions & feed resources

$$y = X\mathbf{b} + Z_1u + Z_2m + Z_3p + e$$

Contemporary group solution

Weaning weight contemporary group solutions (1990-present)





- 2: Southeast
- 8: Fescue Belt
- 5: Arid Prairie
- 1: Desert
- 7: Forested Mountains
- 9: Upper Midwest & Northeast
- 3: High Plains

P = G + E + G* E

Estimating the extent of G x E interaction

Random regression (reaction norm) models

- Genotypes regressed on continuous variable (i.e., temperature, disease incidence, etc.)
  - Each genotype has a unique curve
- Difficult to capture stressors that aren't explicitly measured

P = G + E + G*E

Multivariate models

- Observations on the same variable made under different conditions treated as separate **(potentially correlated)** traits
- Genetic correlation (r_g) interpreted as degree of re-ranking across environments
  - 0.8 threshold (Falconer, 1952)
- **May be better for capturing local stressors & interactions**

Multivariate model data & methods

- Keep:
  - Records after 1990
  - Contemporary groups with at least 15 animals
  - Zip codes with at least 10 years of data (maternal effect calculation)
- Within High Plains and comparison region, sample zip codes up to ~100,000 total records
- Calculate variance components & genetic correlations using AIREMLF90
  - 10 bootstrapped iterations with re-sampling

P = G + E + G*E

Minimal G x E in weaning weight direct

Region	N records	Min. r_g	Mean r_g	Max. r_g	SD r_g
1: Desert	113,834	0.805	0.860	0.914	0.039
2: Southeast	259,394	0.757	0.867	0.921	0.050
3: High Plains	1,659,770	-	-	-	-
5: Arid Prairie	129,173	0.802	0.867	0.916	0.038
7: Forested Mountains	549,759	0.752	0.859	0.892	0.048
8: Fescue Belt	831,581	0.819	0.868	0.961	0.050
9: Upper Midwest & Northeast	416,763	0.848	0.893	0.953	0.043

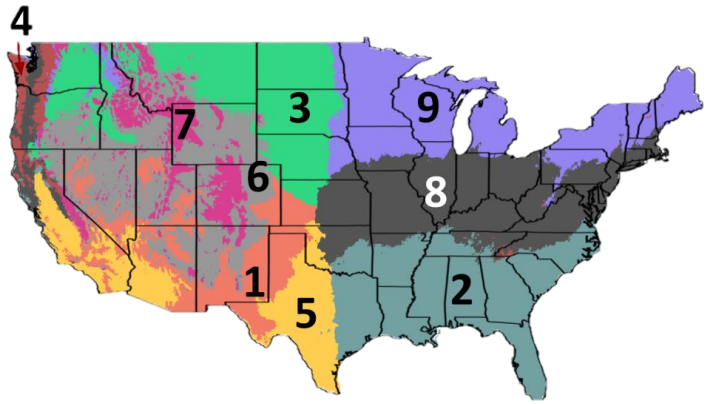
P = G + E + G*E

Possible G x E in weaning weight maternal

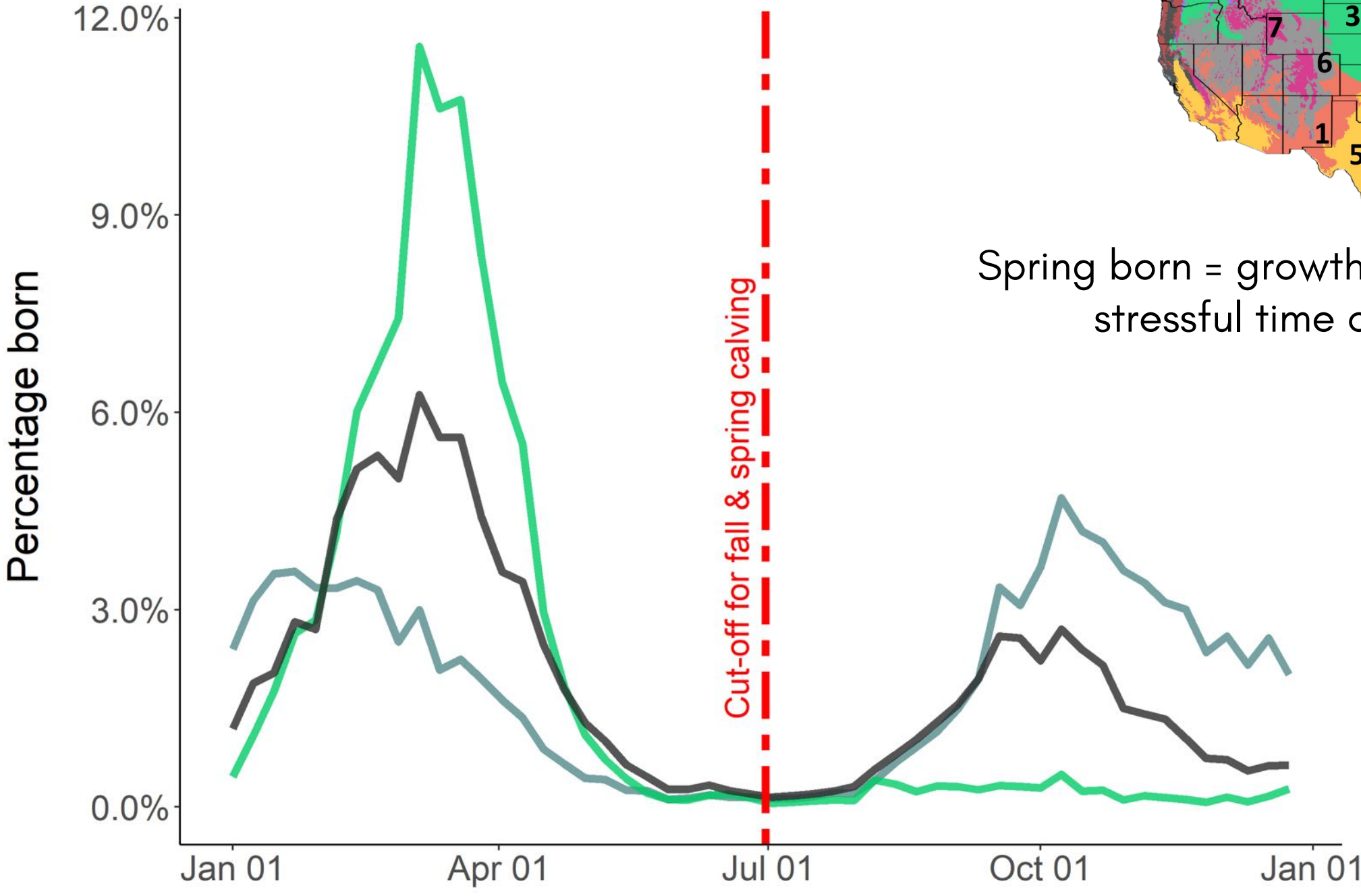
Region	N records	Min. r_g	Mean r_g	Max. r_g	SD r_g
1: Desert	113,834	0.800	0.861	0.945	0.055
2: Southeast	259,394	0.672	0.772	0.892	0.068
3: High Plains	1,659,770	-	-	-	-
5: Arid Prairie	129,173	0.783	0.867	0.915	0.050
7: Forested Mountains	549,759	0.778	0.847	0.904	0.047
8: Fescue Belt	831,581	0.665	0.815	0.950	0.087
9: Upper Midwest & Northeast	416,763	0.794	0.854	0.950	0.052

$$P = G + E + G*E$$

Calving season distribution by region



Spring born = growth during most stressful time of year

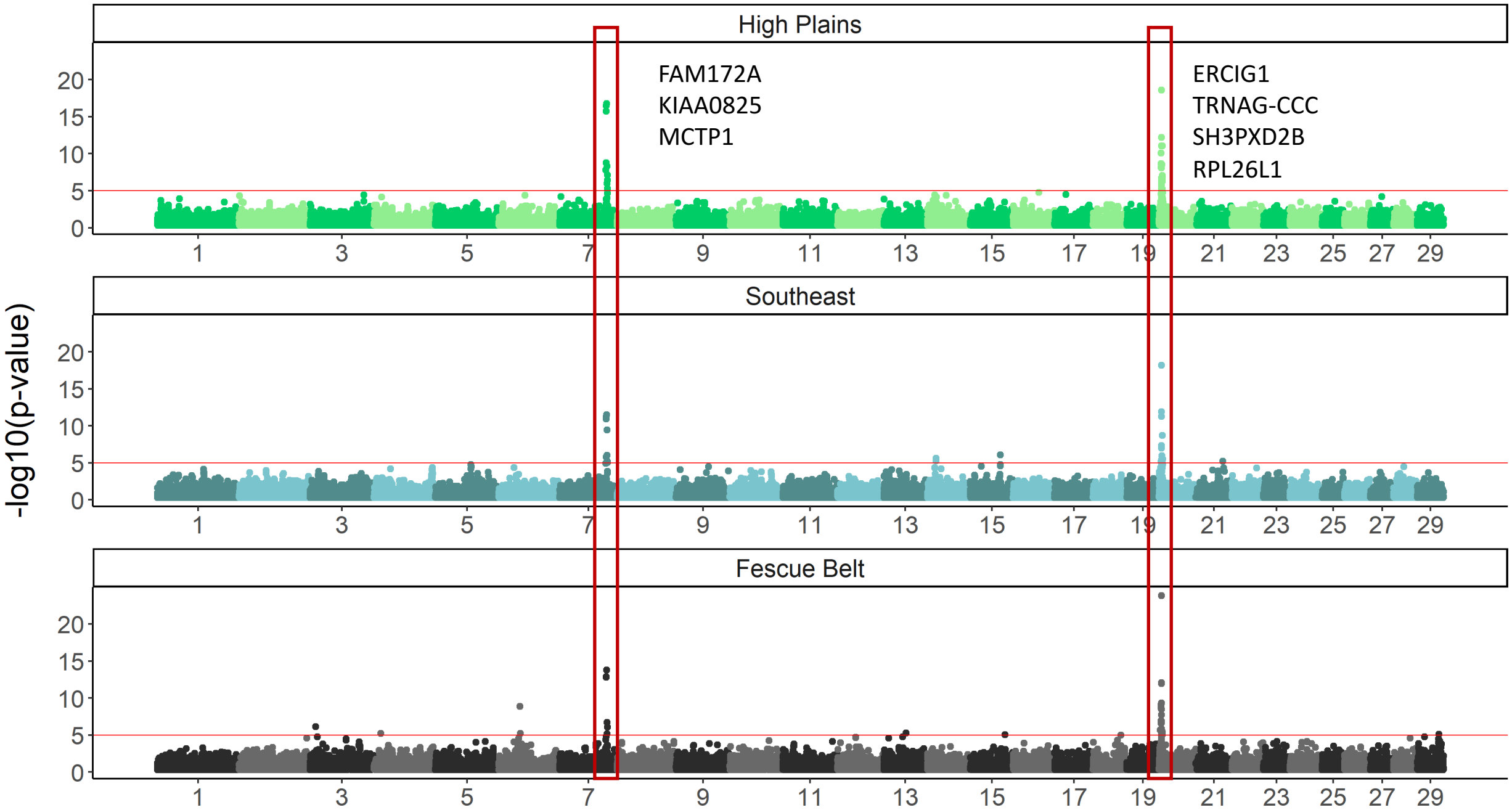


Single-step GWAS

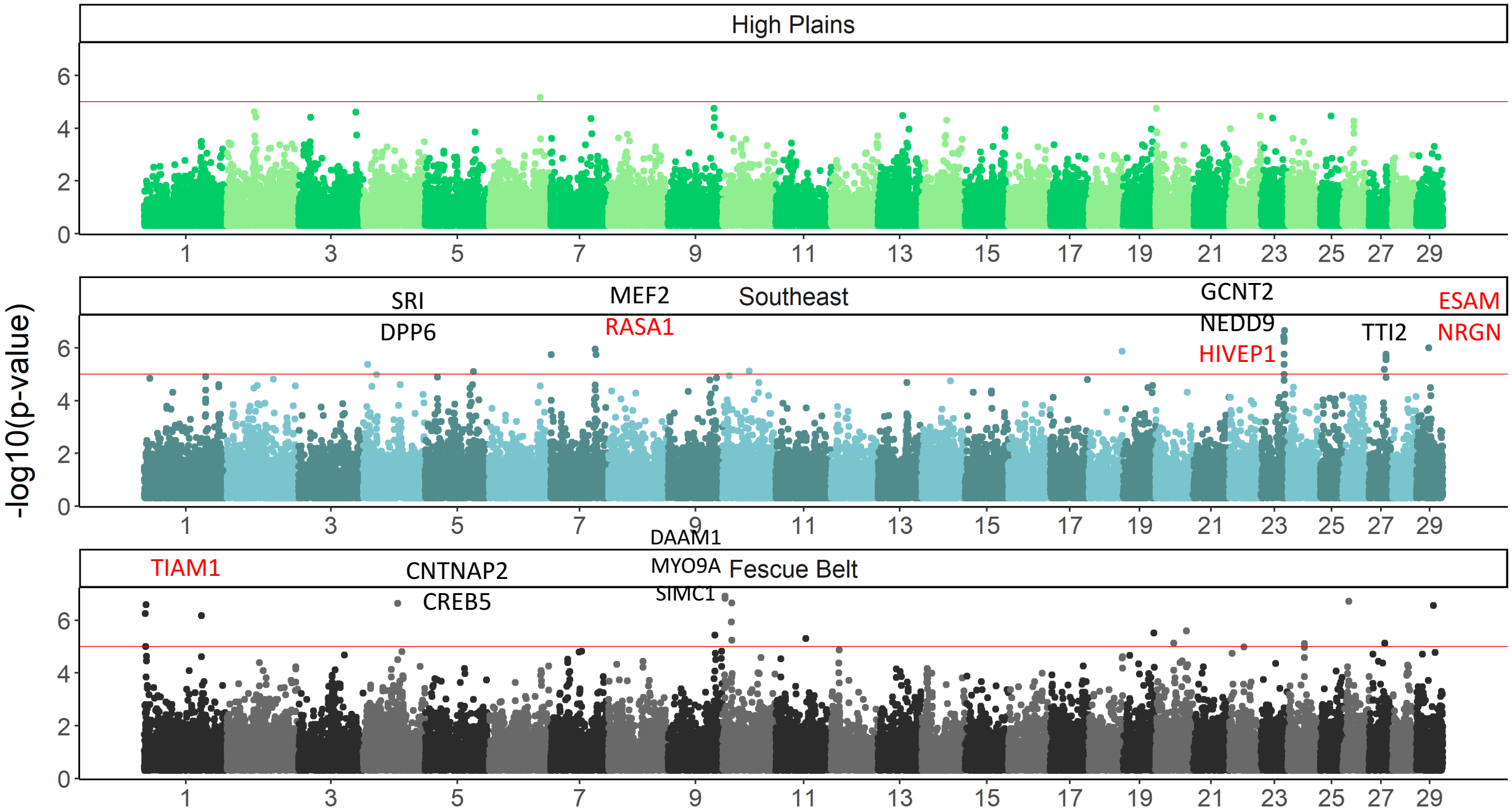
- Combines genotyped and non-genotyped pedigreed animals using BLUPF90 (Aguilar et al., 2019)
  - Genotypes "projected" onto non-genotyped animals
  - Calculate p-values using PVE

- Animals genotyped 18K - ~50K commercial assays, imputed to 54K
  - 168,980 phenotyped/10,472 genotyped animals in High Plains
  - 137,901 phenotyped/10,407 genotyped animals in Southeast
  - 123,461 phenotyped/10,429 genotyped animals in Fescue Belt

Weaning weight (direct effect)



Weaning weight (maternal effect)



Conclusions

- Little evidence for G x E in weaning weight direct
- Possible G x E in maternal effect of weaning weight
- Calving season

Future directions

- Yearling weight & birth weight
- Robustness: genotypes that show consistent performance across environmental regions
- Genotype imputation to higher density

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ANGUS GENETICS

Data provided by the American Angus Association

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MU Animal Genomics is recruiting Ph.D. students & post-docs!!!!

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@pop_gen_JED on Twitter

Bob Schnabel
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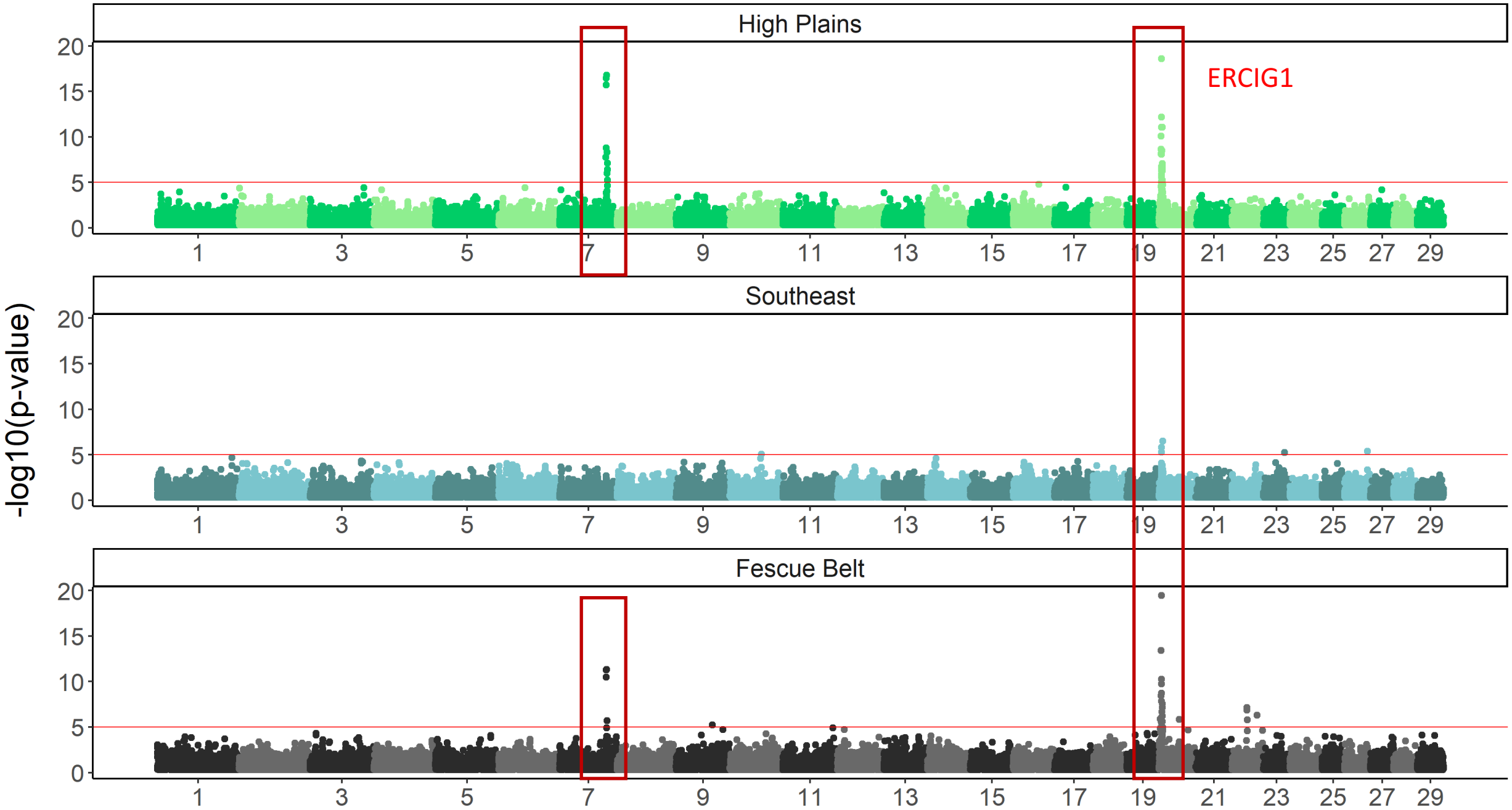
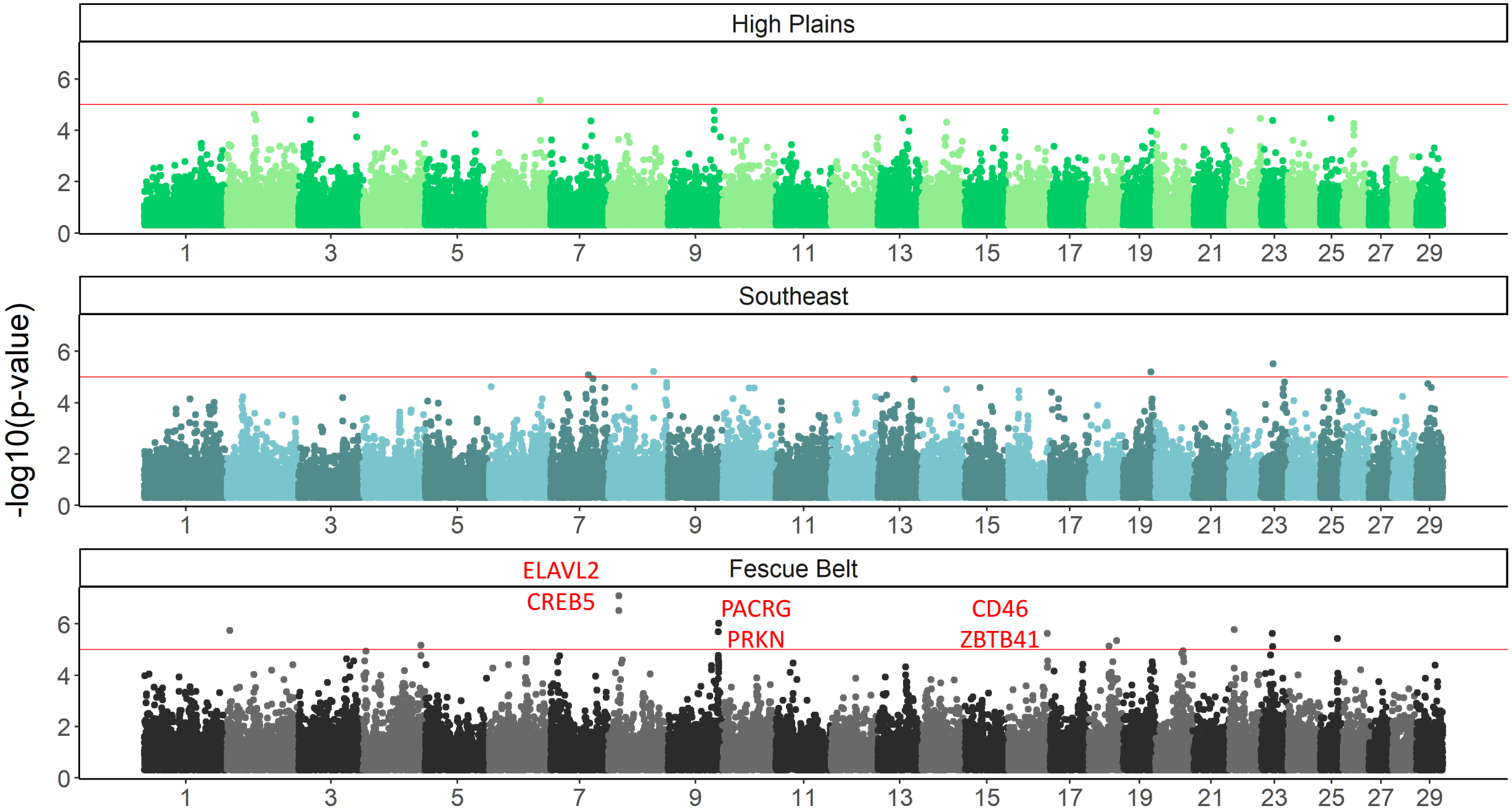
"Yes ... I believe there's a question in the back."

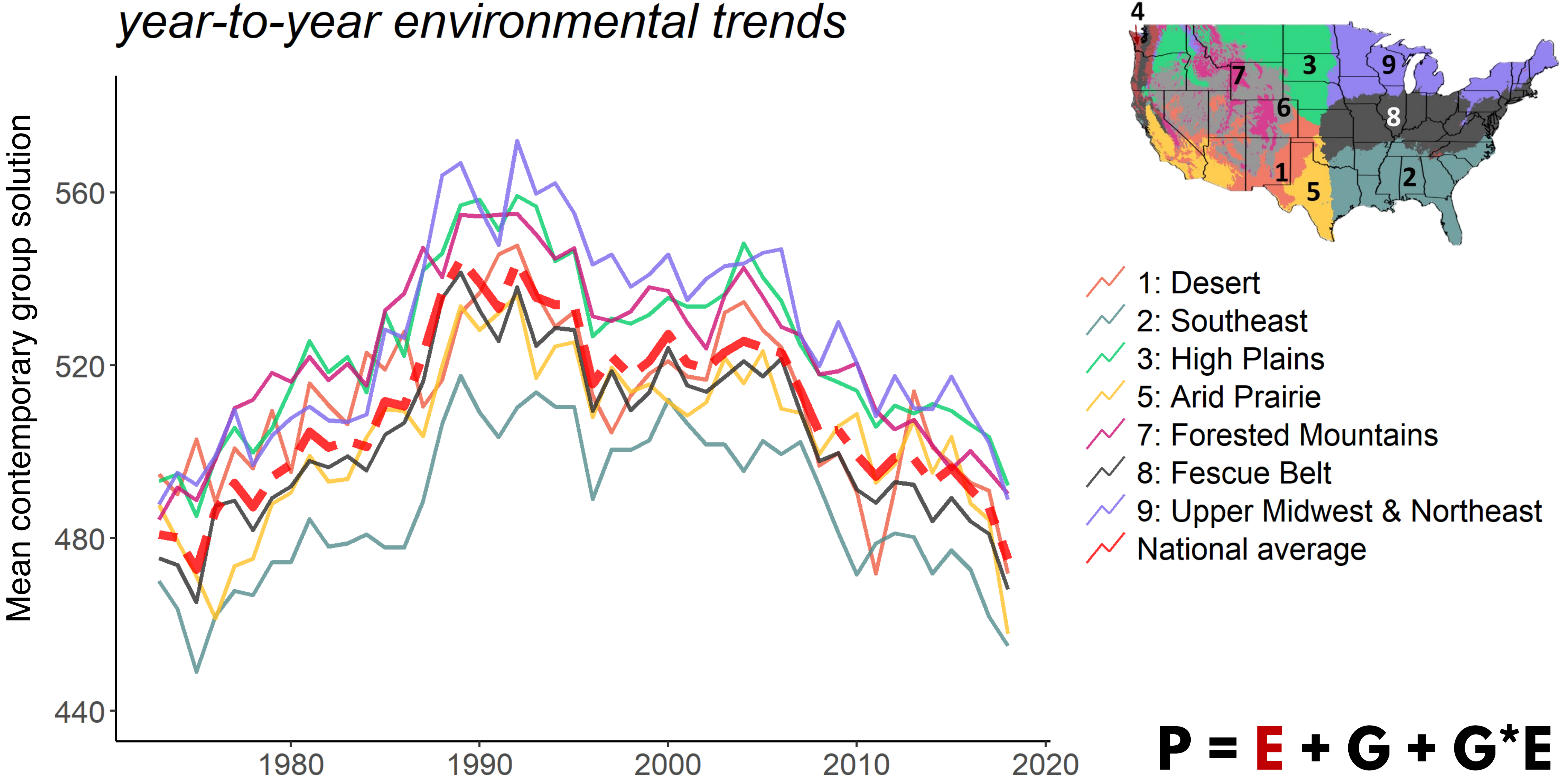
Weaning weight direct (spring calving)



Weaning weight maternal (spring calving)



Weaning weight contemporary group solutions reflect year-to-year environmental trends



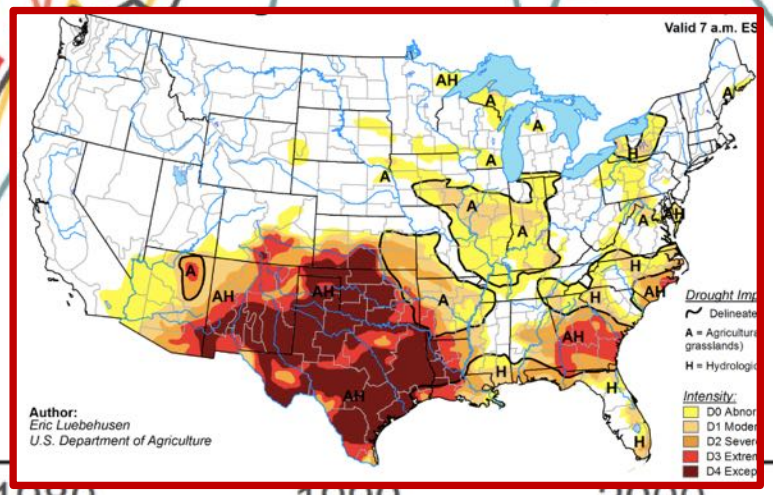
P = E + G + G*E

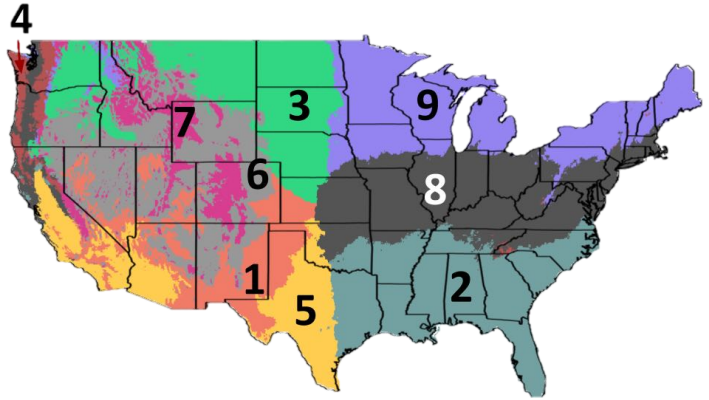
Weaning weight contemporary group solutions reflect year-to-year environmental trends

Mean contemporary group solution

560
520
480
440

1980
1990
2000
2010
2020





1: Desert
2: Southeast
3: High Plains
5: Arid Prairie
7: Forested Mountains
8: Fescue Belt
9: Upper Midwest & Northeast
National average

$$P = E + G + G*E$$