



# Improved Productivity Through Genomics: The USA Angus Experience

Oct 23, 2019 – Beef School– Bulawayo, Zimbabwe

**Stephen Miller, Genetic Research Director**

# Looking Ahead

- Genomic Adoption
- New Tools
- New Predictions





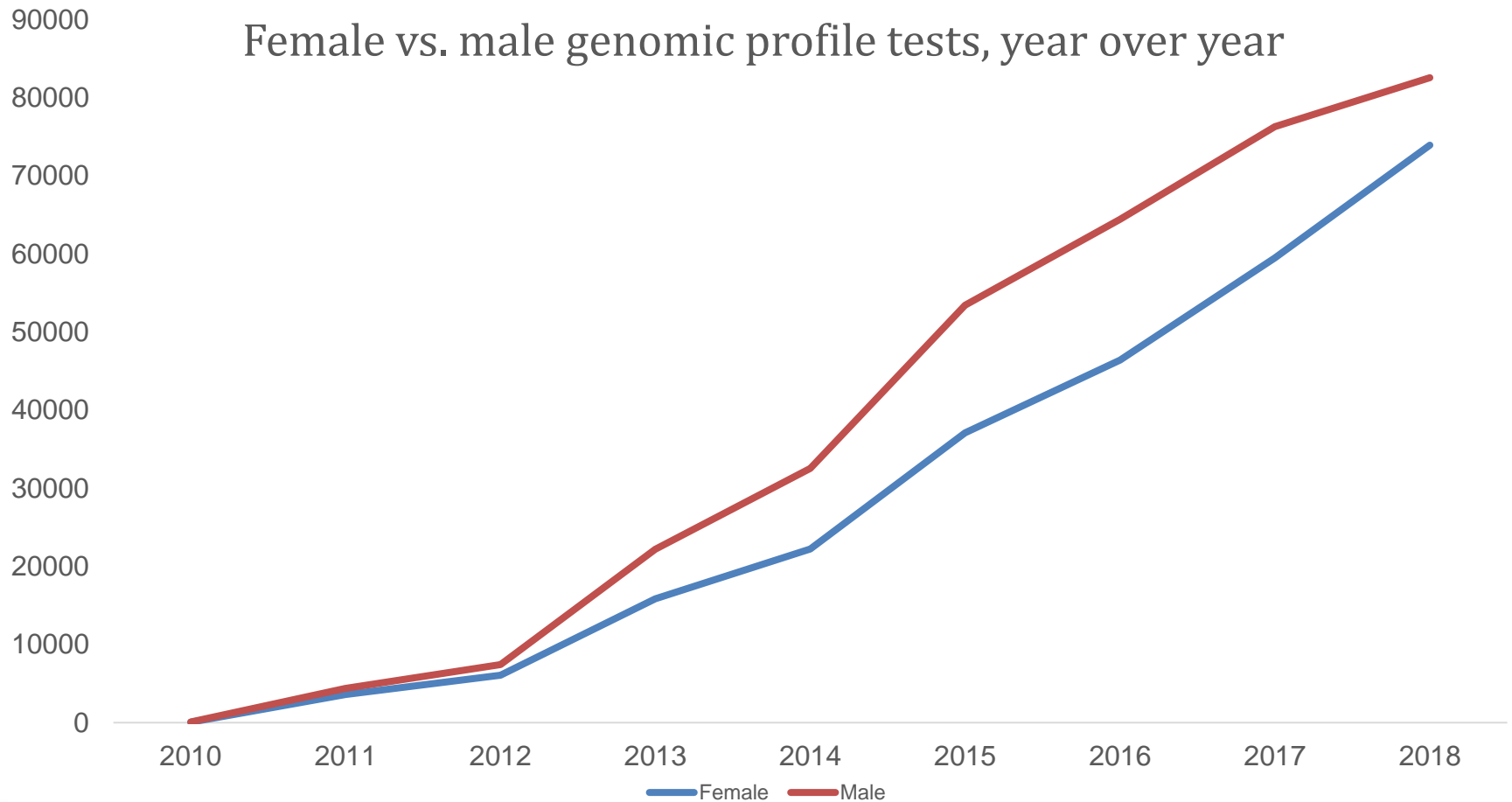
## Angus Genetic Evaluation Reaches Historic Milestone

Angus Genetics, Inc. collects 500,000 genotypes.

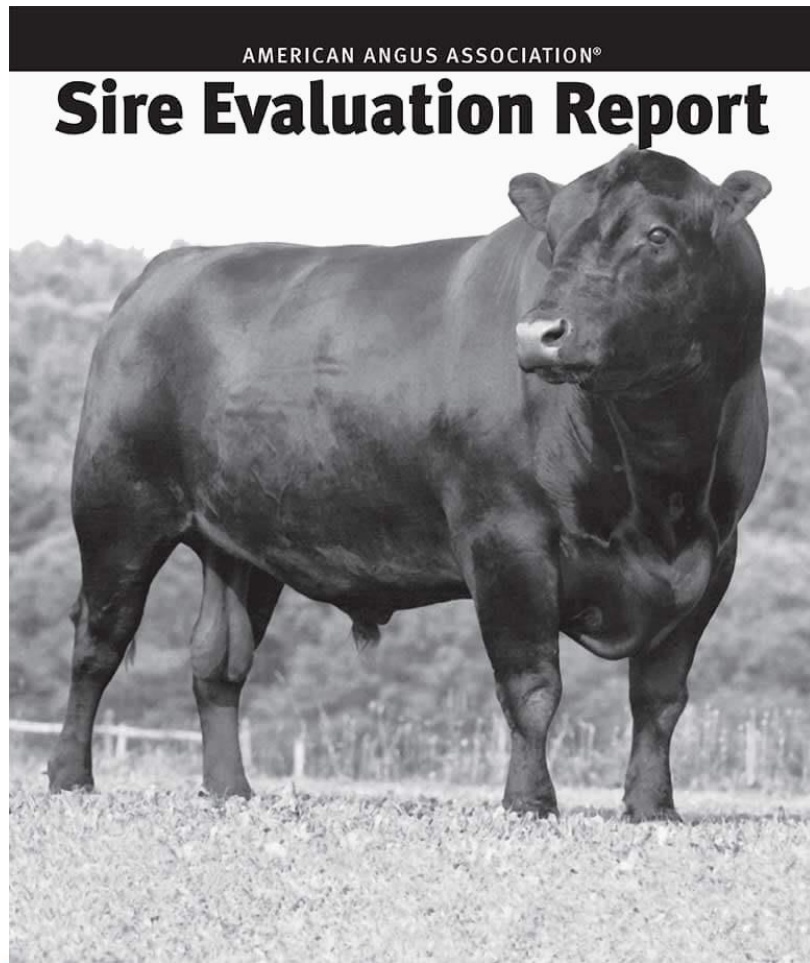
# Genotypes in Weekly Angus Genetic Evaluation

Date	Genotypes
Oct. 2012	11,000
Oct. 2013	42,000
Oct. 2014	89,000
Oct. 2015	159,000
Oct. 2016	262,000
Oct. 2017	383,000
Oct. 2018	556,710
Current (Sept 21 2019)	694,515

# Female testing increases with lower testing cost



# Details of Genetic Evaluation Published



## Calculators/Tables

Accuracy & Possible Change

Across-Breed EPDs

Adjusted Weight Averages

Age in Days

Breed Averages

Data Descriptions

Genetic Trend

Gestation

Heritabilities & Genetic Correlations

Optimal Milk Module

Percentile Breakdown

[angus.org/nce](http://angus.org/nce)

Joe Roybal



AGENDA > COMMENTARY

## Why the Angus Single Step evaluation is an industry game-changer

On July 7th, the American Angus Association unveiled a new genetic evaluation methodology that made big changes to its EPD system. As a result, seedstock and commercial producers have some readjusting to do as some bulls won, and some lost.

Troy Marshall | Jul 13, 2017

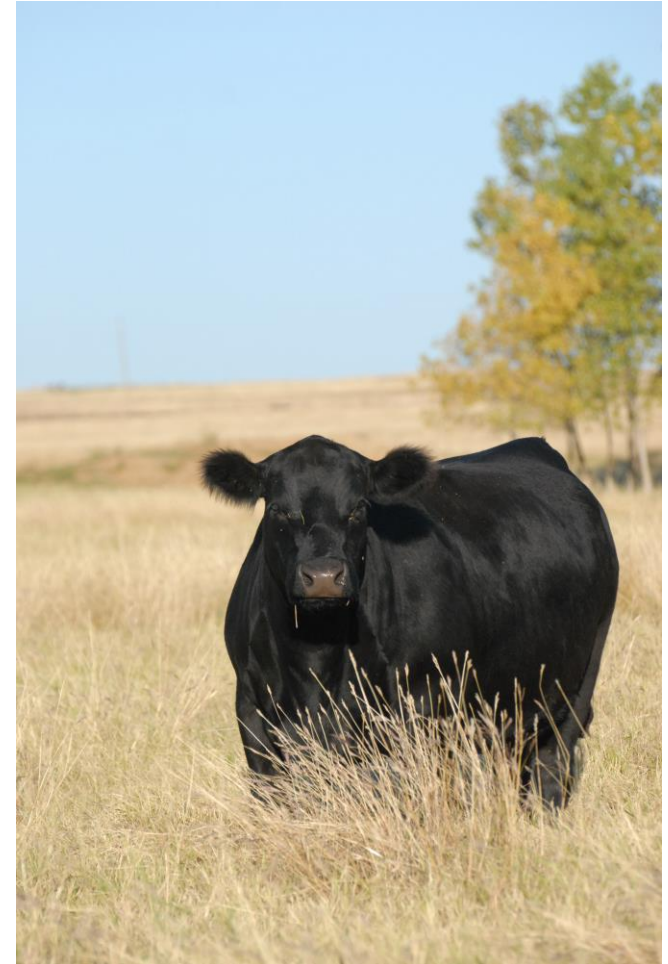
No looking back now.

# Data + DNA = Selection Tools that Work

- 8.7M birth weights
- 9.2M weaning weights
- 4.5M yearling weight records
- 1.7M heifer calving ease scores
- 124K carcass records
- 2.0M ultrasound records
- 26K individual intake records
- 305K docility scores
- 104K heifer pregnancy observations
- 223K mature cow weights
- 25K foot score
- 11K altitude tolerance
- **695K Genotypes**





As of 9/21/2019







# Genomic Testing Increases Accuracy of Prediction

	Birth Weight	Weaning Weight	Yearling Weight	Milk	Total Maternal	Scrotal Circ.	Calving Ease	Mat Calving Ease	Yield Grade	REA	Carcass Weight	Marbling	Fat
EPD	+1.7	+47	+84	+26	+50	+0.62	+4.0	+7.0	-	+0.43	+31	+0.82	+0.026
Acc	27	22	14	8	-	P	21	8	-	P	P	P	P
TOP %	40	30	25	7	10	55	45	50	-	30	40	2	80

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EPD	+1.7	+64	+116	+36	+68	+1.39	+5.0	+10.0	-	+0.61	+53	+0.42	-0.023
Acc	54	47	42	29	-	41	34	28	-	36	41	36	33
TOP %	40	3	1	1	1	4	35	15	-	10	3	25	4

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# Genomic Testing Increases Accuracy of Prediction

	Birth Weight	Weaning Weight	Yearling Weight	Total	Scrotal Gaining	Mat Gaining	Yield	Carass	Marbling	Fat			
EPD	+1.7	+4.2							+0.82	+0.026			
Acc	27	2							P	P			
TOP %	40	30	25	7	10	55	45	50	-	30	40	2	80

Birth Weight Accuracy of 0.27 = +/- 2.0 lb.  
 Confidence Range = -0.3 to 3.7

	Birth Weight	Weaning Weight	Yearling Weight	Total	Scrotal Gaining	Mat Gaining	Yield	Carass	Marbling	Fat			
EPD	+1.7	+4.4							+0.42	-0.023			
Acc	54	4							36	33			
TOP %	40	3	1	1	1	4	35	15	-	10	3	25	4

Birth Weight Accuracy of 0.54 = +/- 1.2 lb.  
 Confidence Range = 0.5 to 2.9



# Angus Progeny Equivalents with Genomic Testing

Genotyped non-parent animals (2014-2016 born).  
Average accuracy and number of progeny required to reach that accuracy.

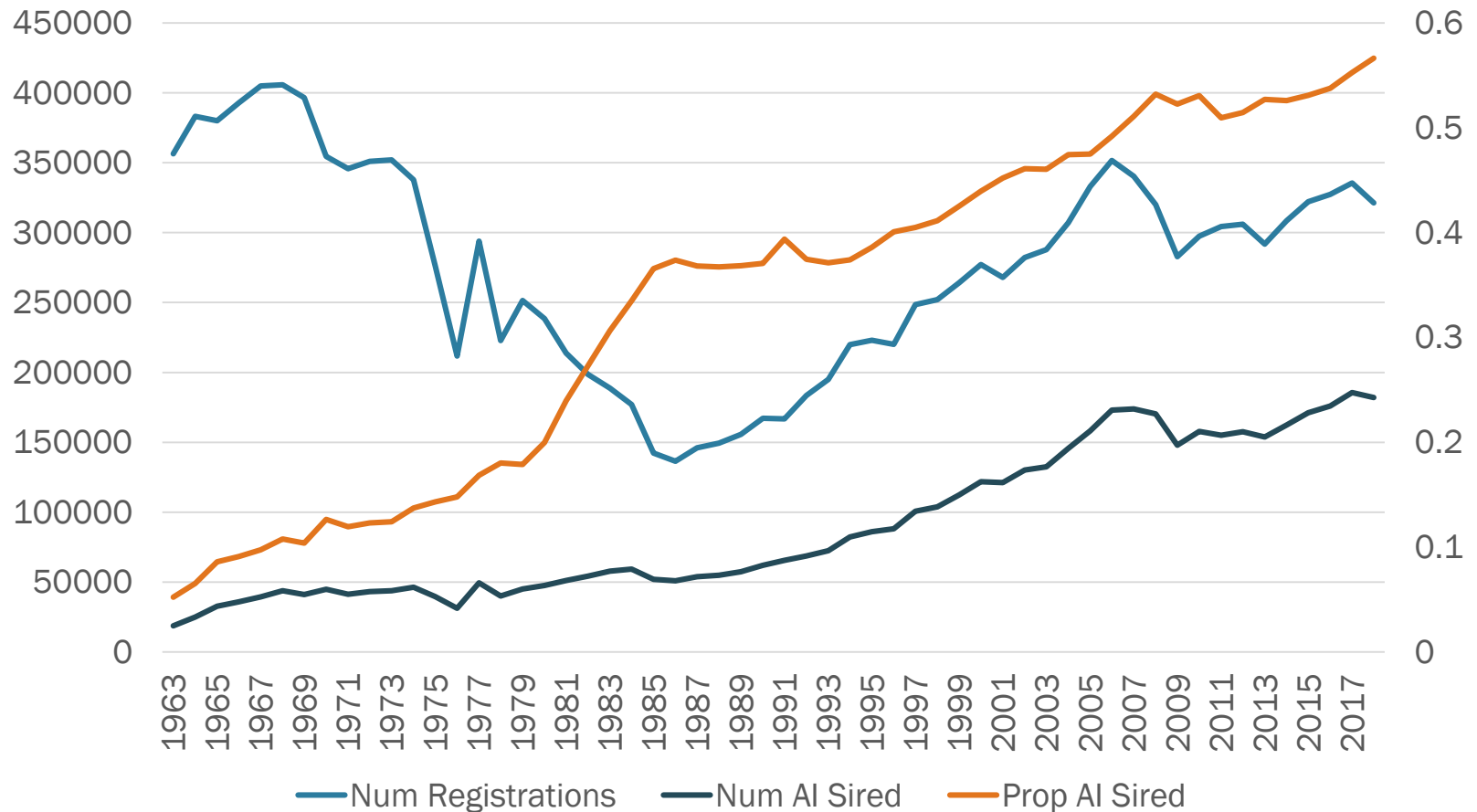


	$h^2$	Progeny Equiv	AverageAcc
CED	0.19	28	0.36
BW	0.46	21	0.48
WW	0.28	26	0.42
YW	0.27	21	0.38
Milk	0.12	33	0.30
SC	0.48	13	0.40
CWT	0.44	9	0.32
MARB	0.48	9	0.34
REA	0.32	12	0.30
Fat	0.33	10	0.29

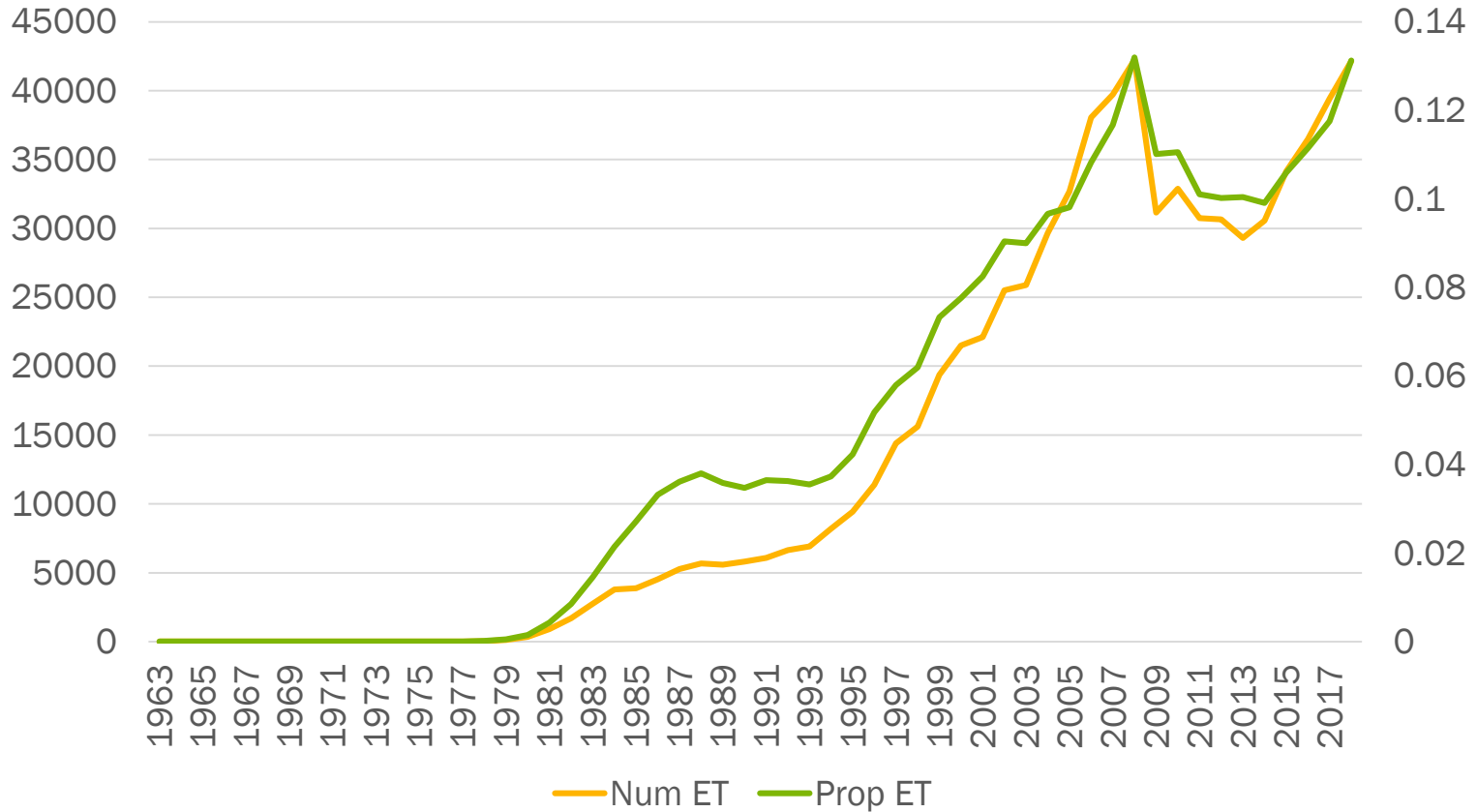
# Bottom Line: Genomics are a Risk Reduction Tool

- Genomic-tested animals have similar accuracies to older animals with **9** to **33** progeny born and measured, depending on the trait
  - Young bulls = higher accuracy
  - Females = greater EPD accuracy than with a lifetime of production records

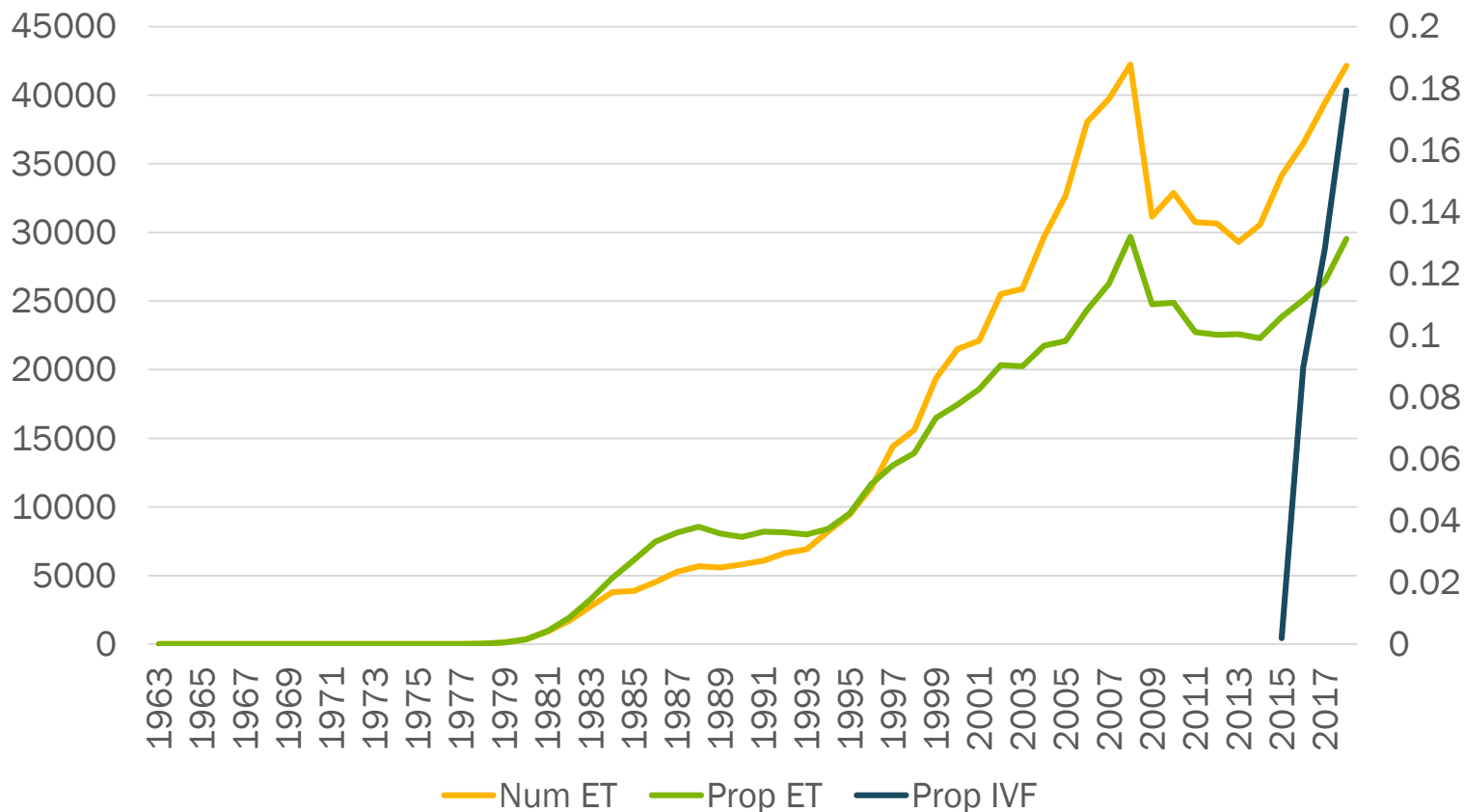
# AI in Angus has risen to over 55%



# ET in Angus is also rising Now 13% of registrations

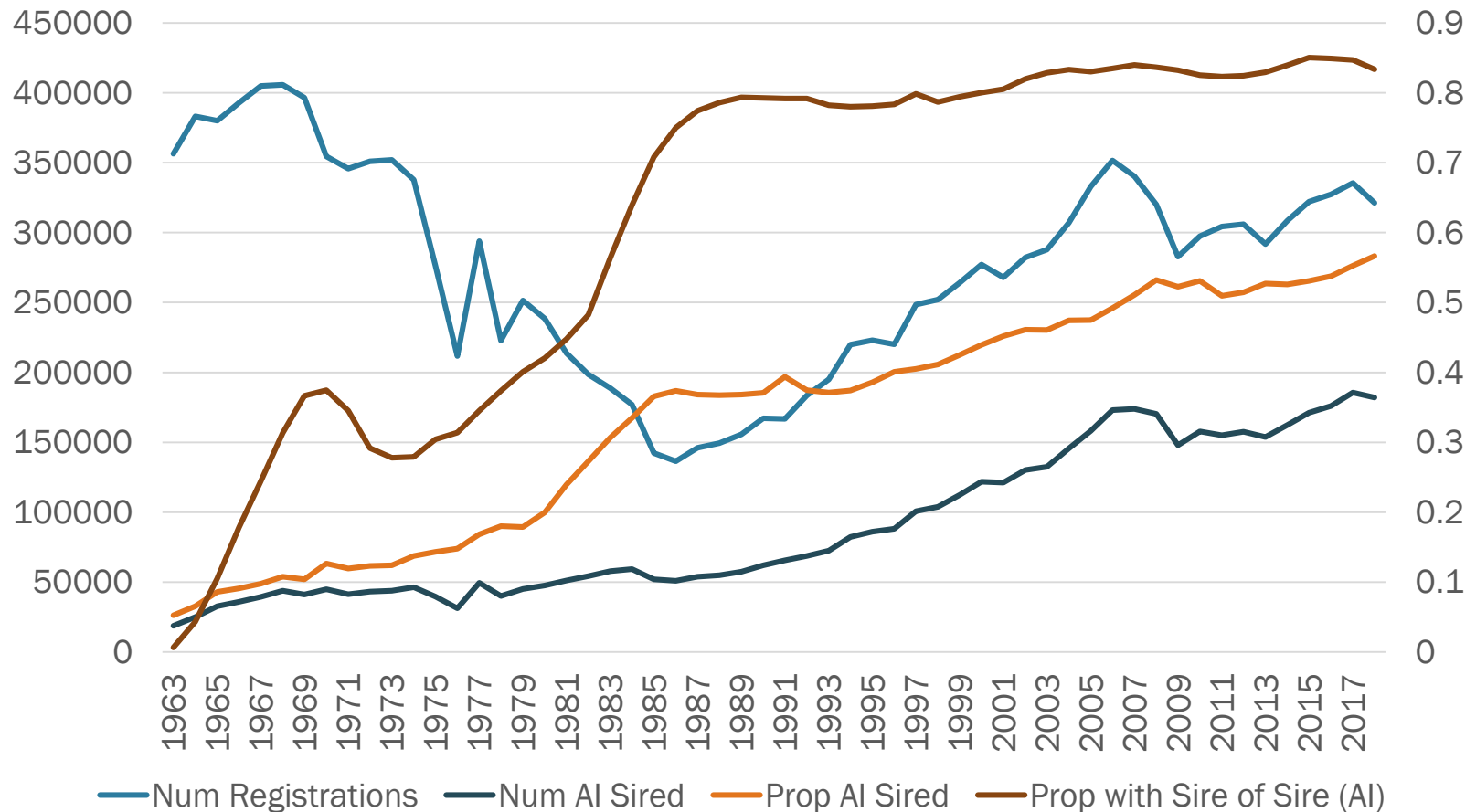


# Proportion of ET that are IVF in Angus is now approaching 20%

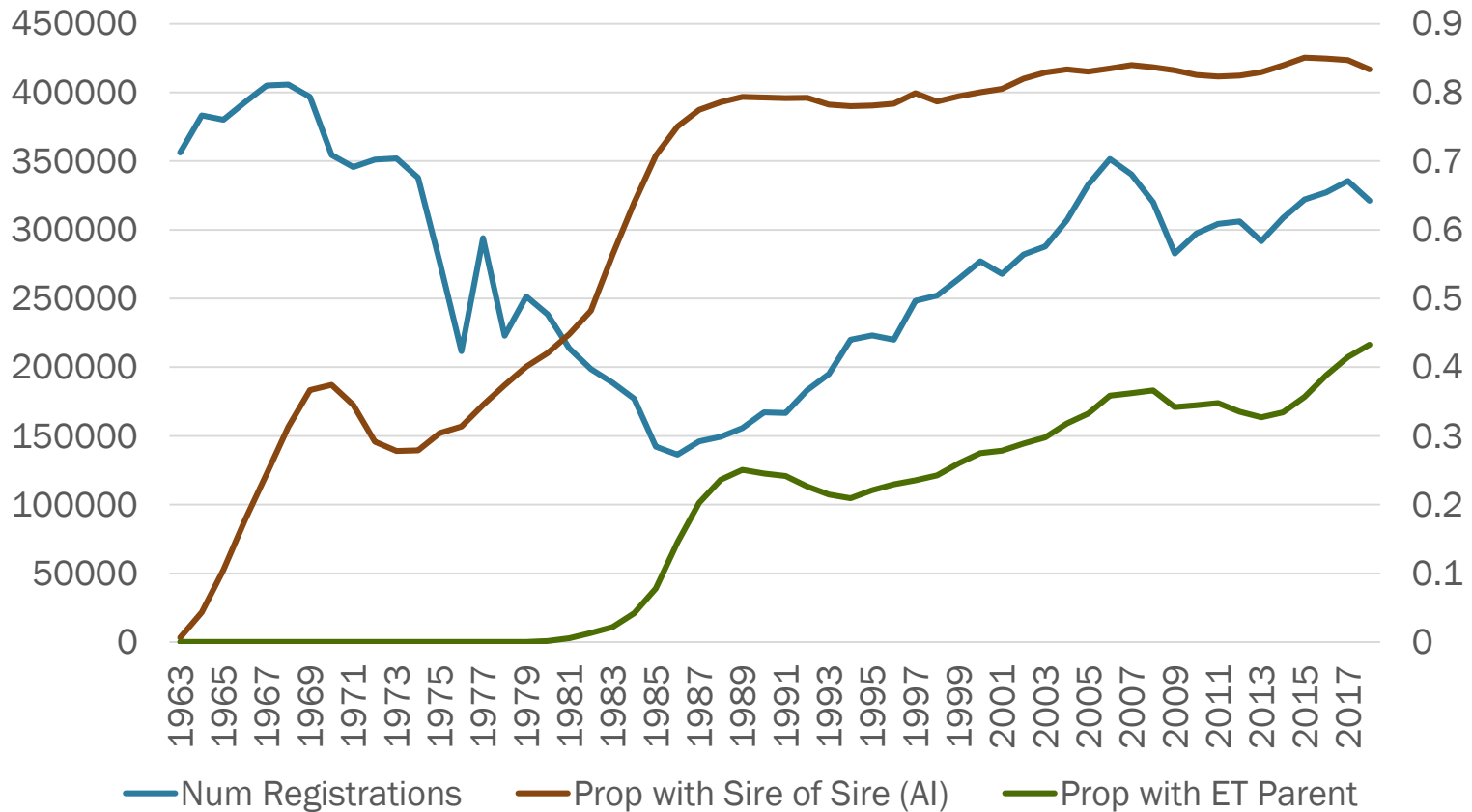




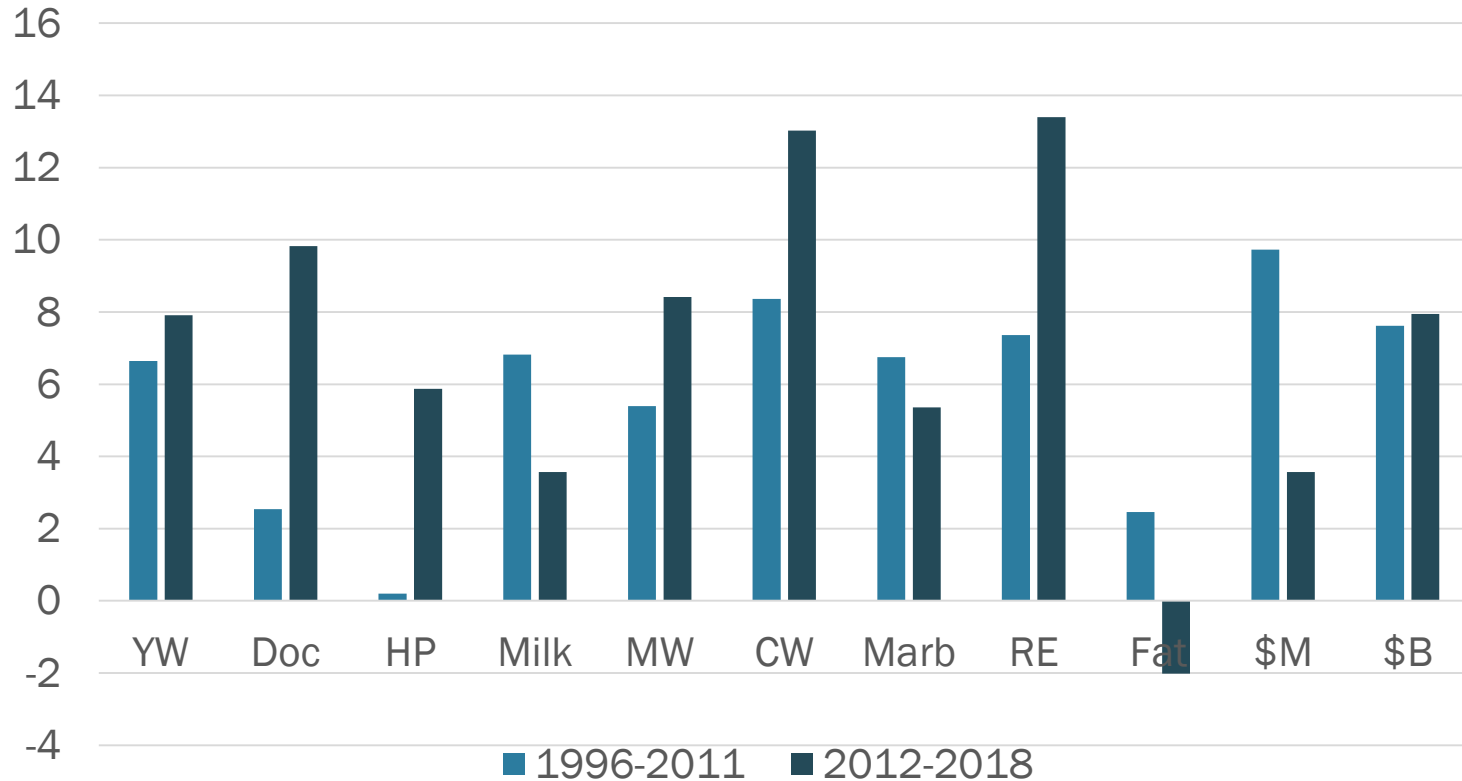
# Proportion of calves whose sire has an AI sire is over 80%



# Proportion of calves with an ET parent over 40%



# Generally more progress post genomics



Standardized units

# ANGUS. ONLY ANGUS.

There's only one DNA profile created specifically for Angus cattle.

Angus GS™ is the new standard in genetic testing for Angus cattle. Created by Angus Genetics, the profile is purely Angus DNA so it will have better predictability and deliver more power and accuracy than any previous generation genomic enhanced EPD, and at a much greater value. Visit [angus.org/agi](http://angus.org/agi) for the test that only Angus Genetics could create.

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Genomic Selection  
Parentage  
Conditions  
Traits  
Research

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THE BUSINESS BREED

**AGI**



# HiggsGene Solutions

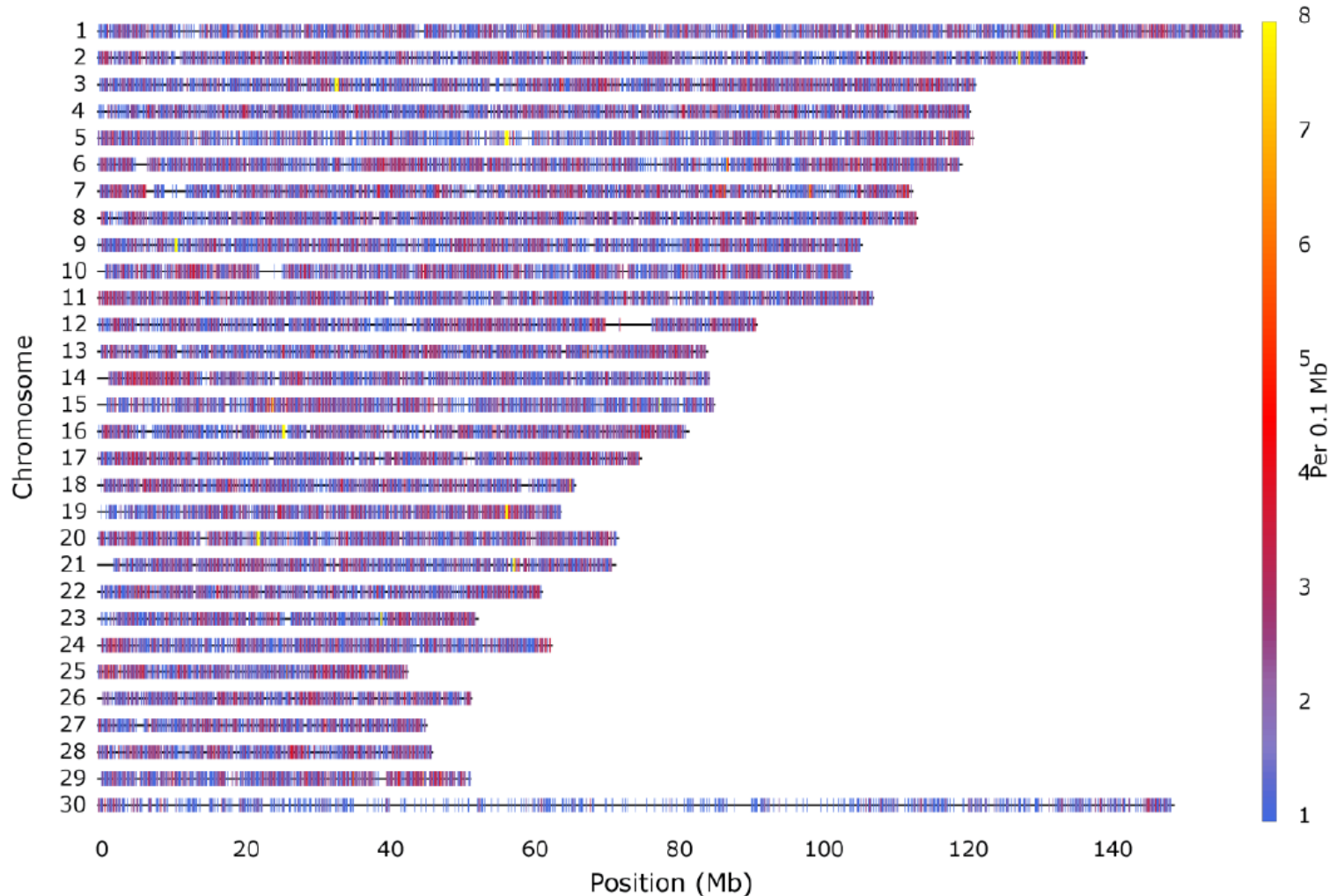
# More accuracy

- Imputation is accurate, but never as good as actual genotypes
- Single-Step uses a common ~40K SNP
  - This chip will provide these genotypes directly with minimal imputation



# The previous 40,000 SNP left gaps in Genome coverage

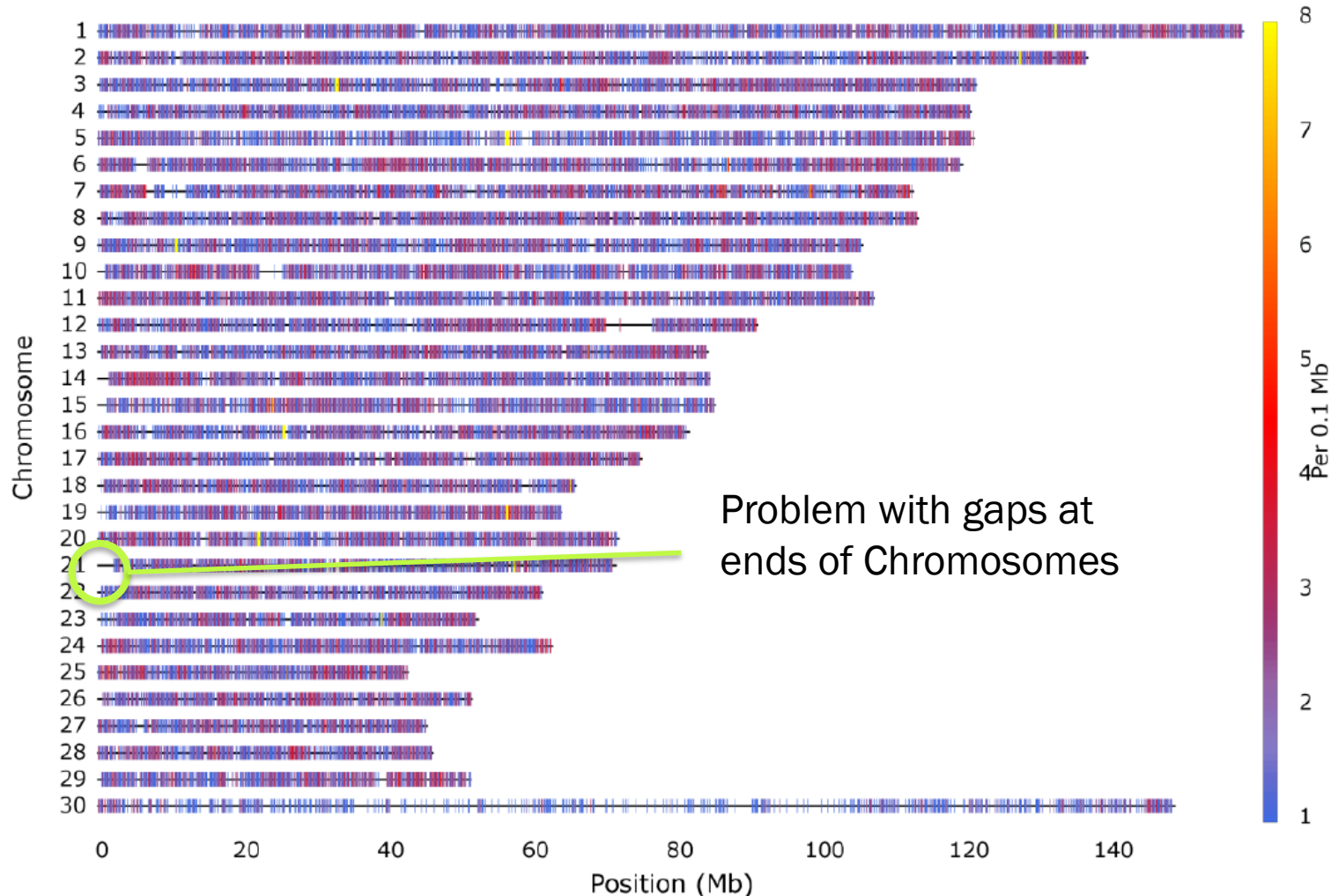
SNP density



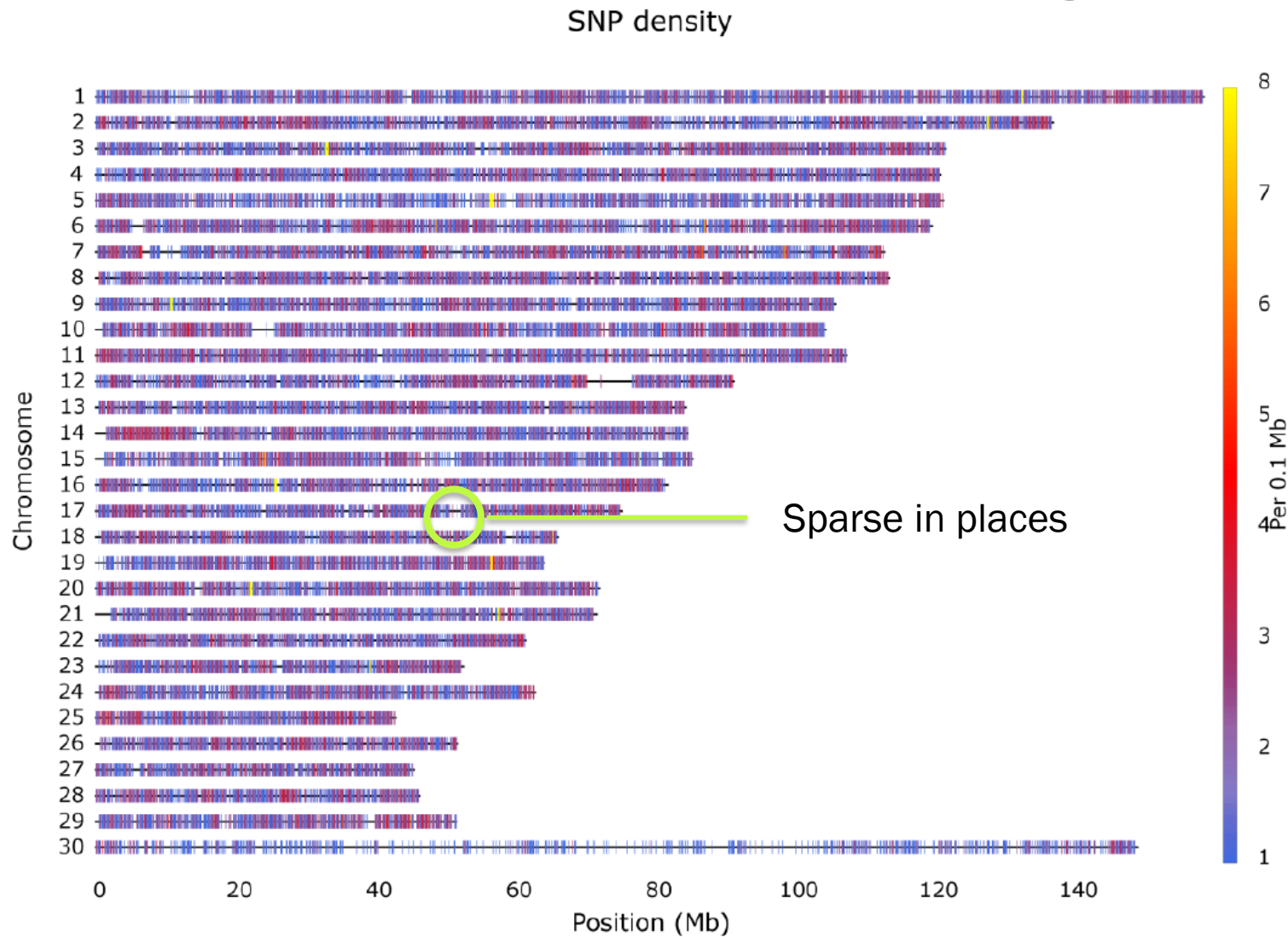


# The previous 40,000 SNP left gaps in Genome coverage

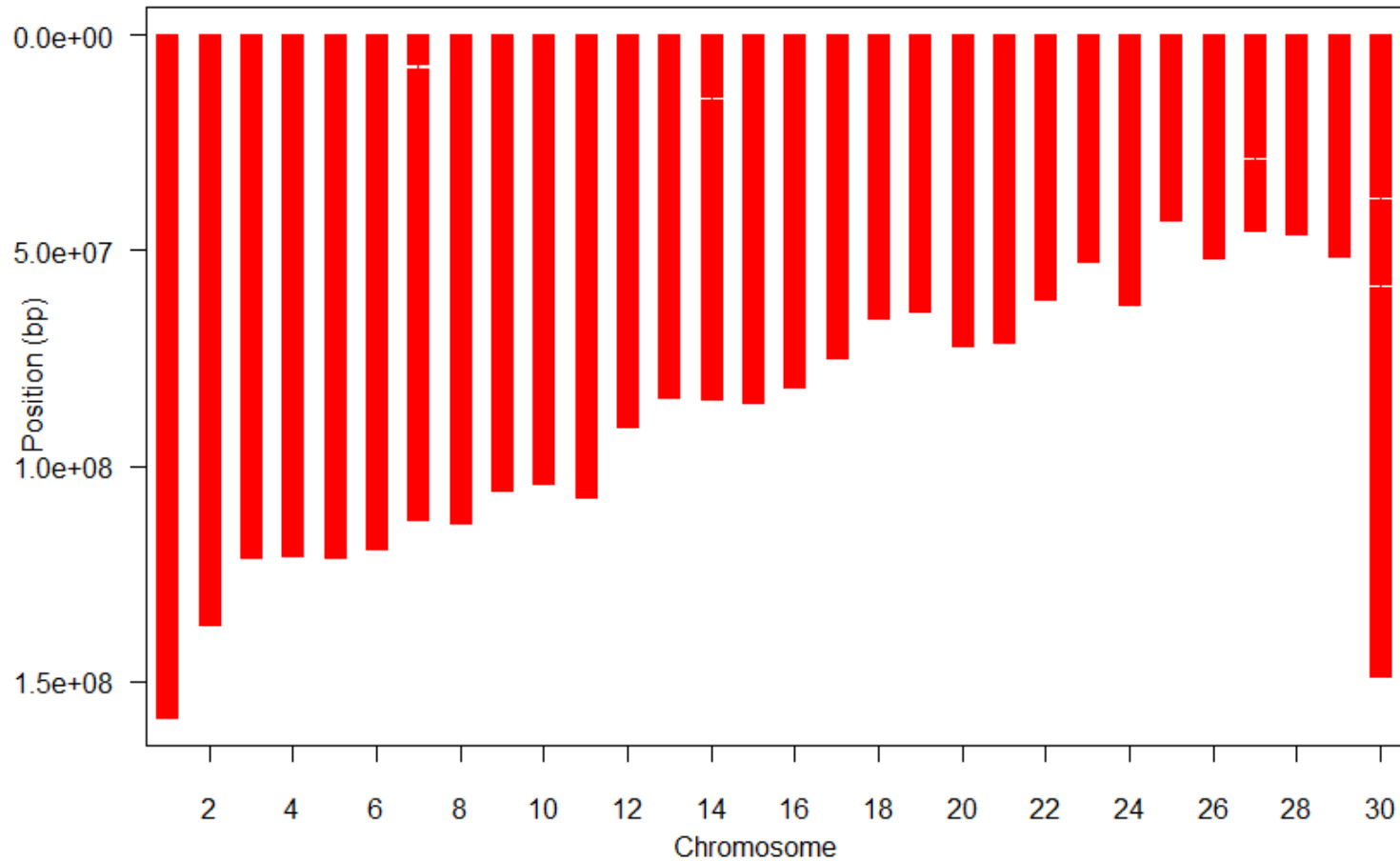
SNP density



# The previous 40,000 SNP left gaps in Genome coverage



# Genome Coverage of Angus GS



# AngusGS Content Summary

- 50,000 SNP for Angus
- Core SNP for Single-Step (~40K)
  - Parentage
  - Conditions
- Targeted Genes (>100)
  - Meat Quality, Carcass, Efficiency, Fertility, PAP, Fescue, Select F250 and more

# AngusGS Content Summary Cont ...

- Tenderness – 500 target SNP and Exclusive Calpastatin
- Angus Specific fertility haplotypes
  - 8,000 SNP added to track these regions influencing reproduction in Angus
- Coverage of entire genome – use for imputation to higher density in future
  - Example - Sequencing



328 Whole Genome Sequence, including many highly influential sires

Sequence from over 3,000 animals

20M Angus variants

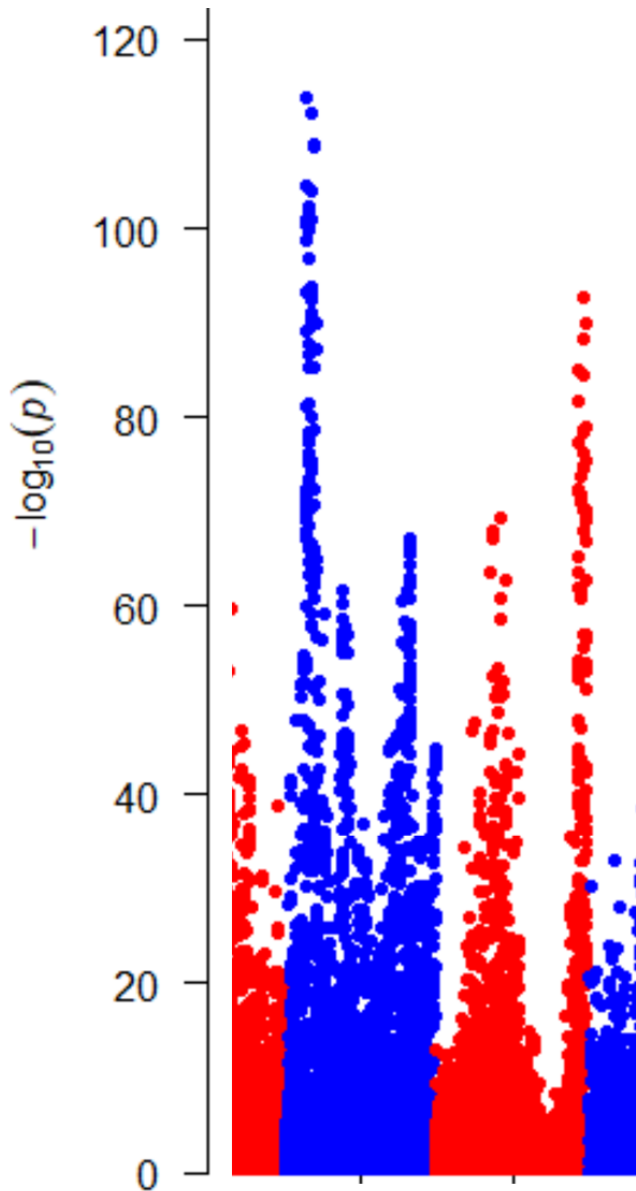
And we are just getting started ....



The **ANGUS** Genome Project

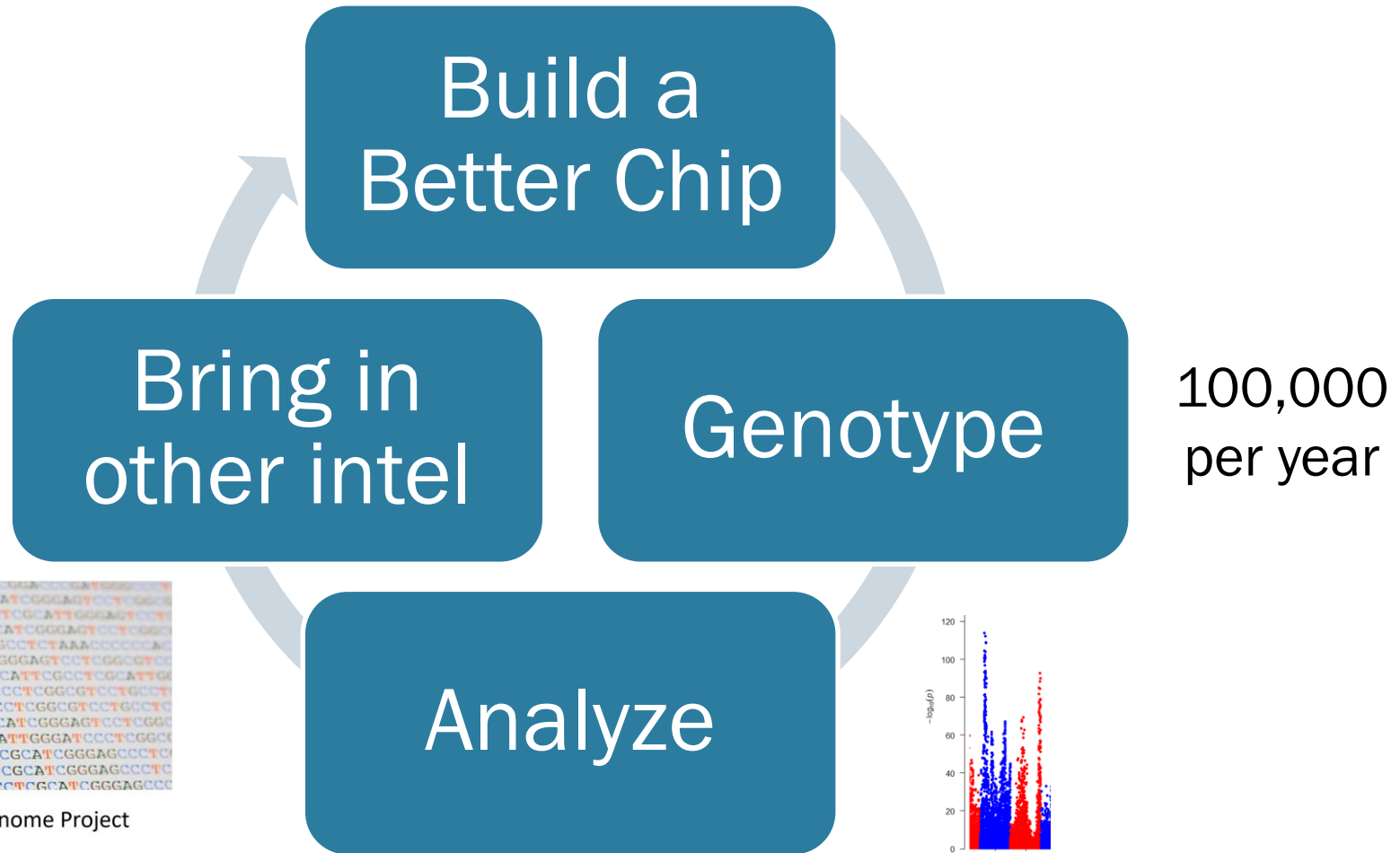


# Higher density genomic analyses narrows in on genomic regions



For important fertility traits like heifer pregnancy

# A Constant striving for better



```
...TAAACAGTCCGAACTGAGT...
FAGCATCAGCCTCGCATCGGAGT...
GCAGTAGCATTGGCCTCGCATTGGAGT...
TAGCATTTCGCCTCGCATCGGGAGT...
GTCCCTCGGGGTCTCTGCCTCTAAAC...
ATTCGCCTCGTATTGGGAGTCTCGG...
TCCTTTGGCCAGTAGCATTTCGCCT...
CTCGCATTTGGGATCCCTCGGGGT...
CTCGTATTGGGAGTCTCTCGGGGT...
TAGCATTTCGCCTCGCATCGGGAGT...
AGCATCAGCCTCGCATTTGGGATCC...
AGTAGCATCAGCCTCGCATCGGGAG...
AGTAGCATCAGCCTCGCATCGGGAG...
CGCATCAGCCTCGCATCGGGAGCC...
```

The **ANGUS** Genome Project



# Investigating Fertility Haplotypes

- Haplotype discovery and validation underway
- American Angus policy TBD
- We expect to be dealing with these within the next year
- Still a lot we don't know



# Fertility Haplotypes Track Embryonic Lethal Genes

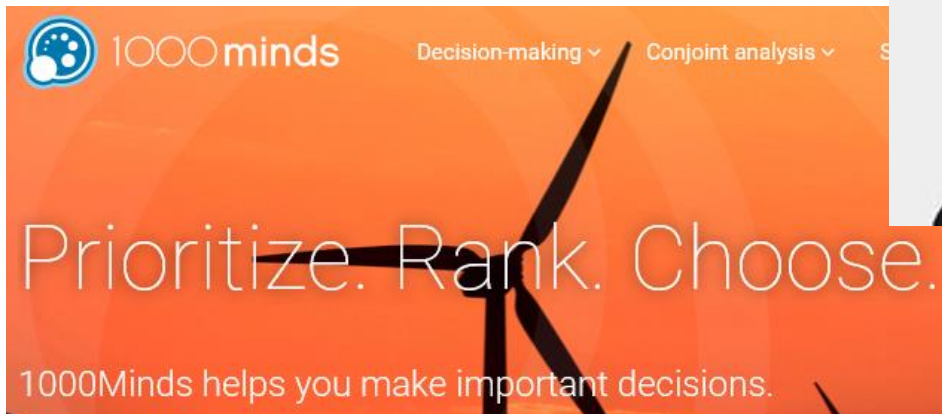
- Exist in all breeds and species
  - Detectable when genotypes are plentiful
- Detected and reported in dairy cattle since 2011
  - Holstein (5)
  - Jersey (1)
  - Ayrshire (2)
  - Brown Swiss (1)
- We expect to identify several in Angus using our genotypes and sequence information



# Engaging expertise to build the best \$ indexes



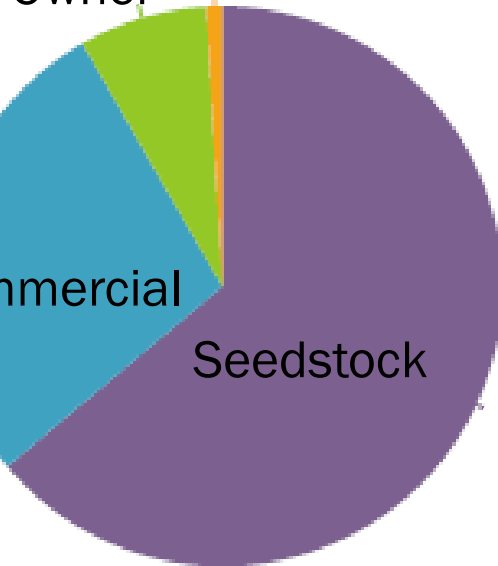
BRIDGING SCIENCE  
AND BUSINESS



Have experience developing indexes around the world in many species – eg Irish Beef

# Fertility is a High Priority Trait

Retained  
Owner



COMMERCIAL PRODUCERS,  
**WE WANT YOUR INPUT.**



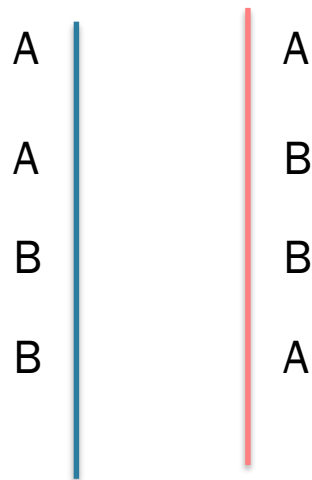
n	CLUSTER group	Weaning weight	Milk	Heifer pregnancy	Calving ease	Cow survival	Cow weight	Cow frame	BCS	Foot	Docility	Feedlot gain	Feedlot efficiency	Yield grade	Marbling grade
663	1 - Maternal	5.7	5.7	4.8	5.5	3.9	10.4	11.2	7.9	4.5	4.3	10.3	8.9	11.8	10.1
559	2 - Production	6.2	7.2	6.5	8.1	5.6	11.3	11.8	8.5	6.3	5.9	7.1	6.7	9.4	4.4
472	3 - Cow (hard)	8.5	11.9	5.6	6.6	3.8	7.1	8.4	5.7	5.8	5.6	9.8	7.4	10.6	8.2

# What is a Haplotype?

- Animals are Diploid
  - Chromosome pair (2) one from each parent
  - Genotypes then are in pairs AA, AB, BB
- 50,000 SNP Genotypes per animal
- Line SNPs up on a chromosome and zoom in on a region
  - Window of 72 consecutive SNPS
  - Lets keep it to 4 SNP for this example

# 4 SNP Haplotype example

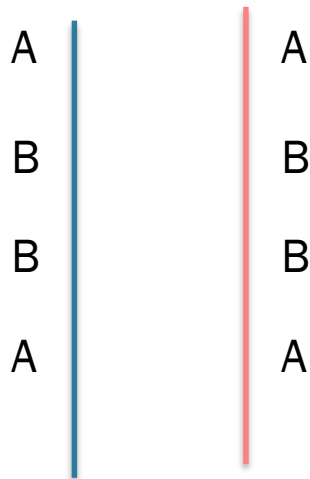
- 4 SNP Genotypes AA, AB, BB, AB
- What are the haplotypes?



This animal is heterozygous for this 4 SNP  
Haplotype ABBA

# Homozygous Example

- This animal is homozygous for the ABBA haplotype



Special Software is needed to convert genotypes to haplotypes

The haplotypes are tracking the underlying genetic variant causing the loss

# Searching for Haplotypes with reduced homozygosity

If we mate two carriers, we expect 25% of offspring to be homozygous

	$\frac{1}{2}$ H	$\frac{1}{2}$ h
$\frac{1}{2}$ H	$\frac{1}{4}$ HH	$\frac{1}{4}$ Hh
$\frac{1}{2}$ h	$\frac{1}{4}$ Hh	$\frac{1}{4}$ hh

What if hh does not exist, but there are lots of HhxHh matings?



# Example of Reduced Homozygosity

- 567,164 Genotypes
  - (316,910 Male and 250,254 Female)
- Genotyped Trios – 202,381
- Haplotype Frequency – 2%
- Heterozygotes – 21,979 (512 sires, including AI sires)
- Homozygotes (hh) = 0 Observed and 213 Expected
- 353 Hh x Hh matings with genotyped offspring

RESEARCH ARTICLE

Open Access



# Analysis of a large dataset reveals haplotypes carrying putatively recessive lethal and semi-lethal alleles with pleiotropic effects on economically important traits in beef cattle

Janez Jenko<sup>1</sup>, Matthew C. McClure<sup>2</sup>, Daragh Matthews<sup>2</sup>, Jennifer McClure<sup>2</sup>, Martin Johnsson<sup>1,3</sup>, Gregor Gorjanc<sup>1</sup> and John M. Hickey<sup>1\*</sup>

## Abstract

**Background:** In livestock, deleterious recessive alleles can result in reduced economic performance of homozygous individuals in multiple ways, e.g. early embryonic death, death soon after birth, or semi-lethality with incomplete penetrance causing reduced viability. While death is an easy phenotype to score, reduced viability is not as easy to identify. However, it can sometimes be observed as reduced conception rates, longer calving intervals, or lower survival for live born animals.

**Methods:** In this paper, we searched for haplotypes that carry putatively recessive lethal or semi-lethal alleles in 132,725 genotyped Irish beef cattle from five breeds: Aberdeen Angus, Charolais, Hereford, Limousin, and Simmental. We phased the genotypes in sliding windows along the genome and used five tests to identify haplotypes with

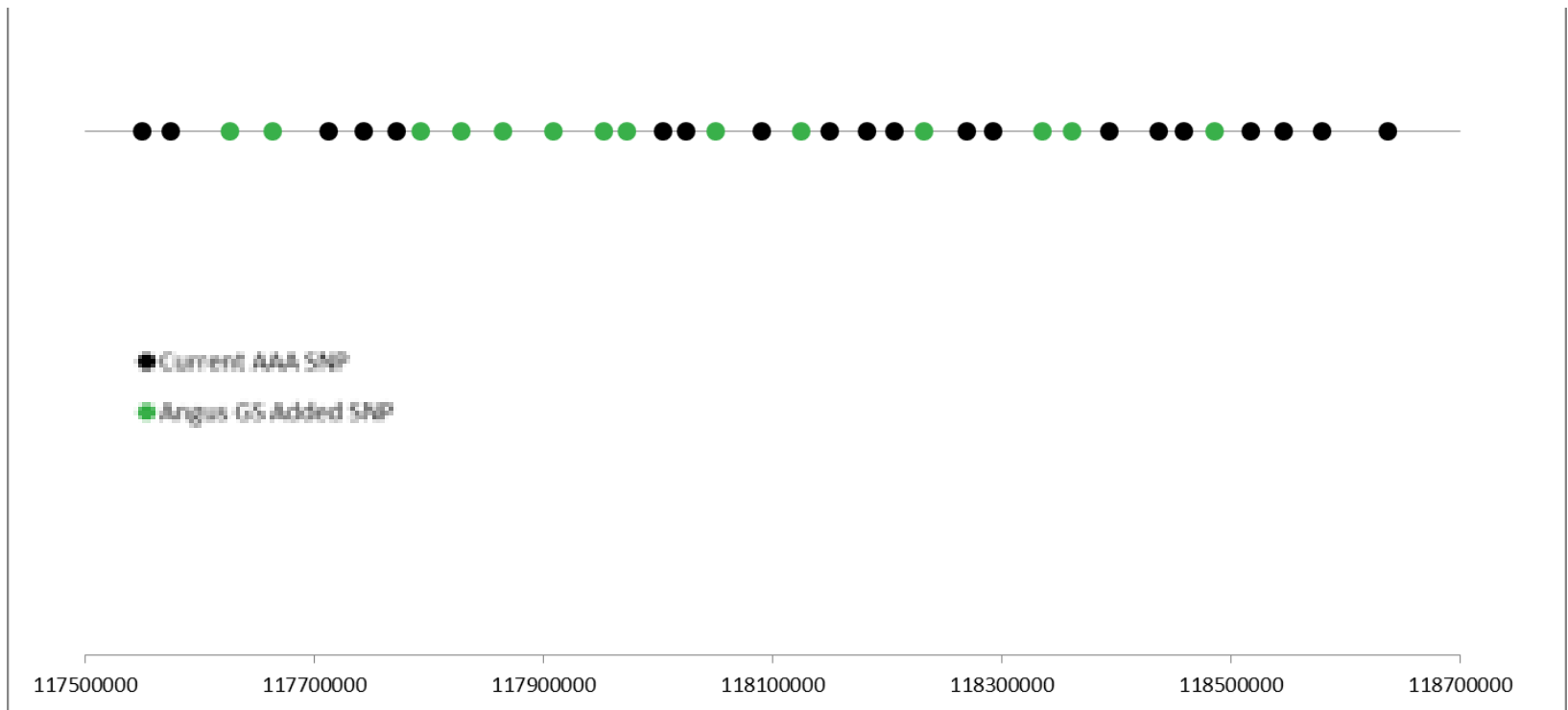
# Example of a semi-lethal allele

**Table 5 Statistics for the AA14H3, CH19H2, and SI16H5 haplotypes**

Haplotype	AA14H3
Genotyped animals	22,510
Frequency (%)	15.2
Recessive homozygotes	95
Expected recessive homozygotes	194.1
Sire-carrier x dam-carrier matings	220
Recessive homozygotes from sire-carrier x dam-carrier matings	2
Expected recessive homozygotes from sire-carrier x dam-carrier matings	55

Not everything discovered will follow the embryonic lethal model

# Increasing Density in Typical Fertility Haplotype Region

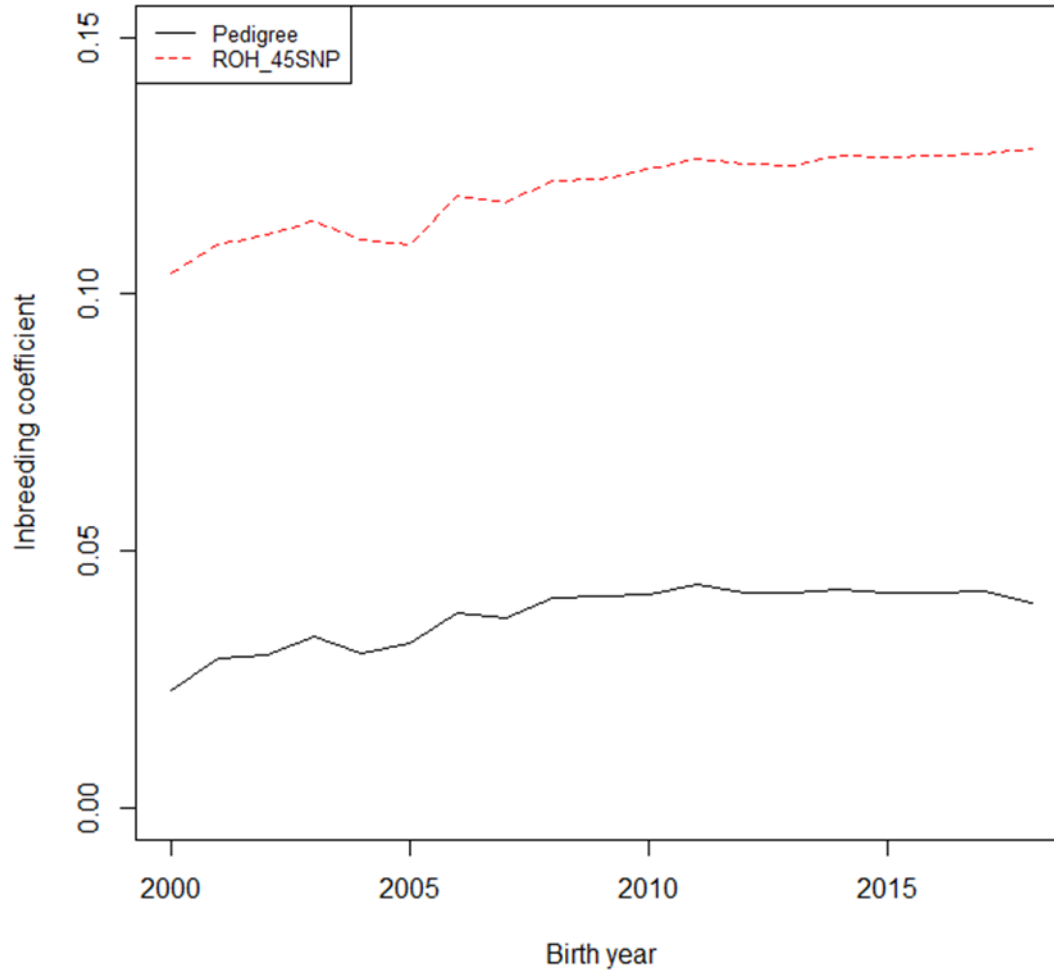


# Recessive management strategy will depend on a number of factors

- Frequency in population
- Effective population size
- Genetic merit of carrier animals and available alternates (Free)



# Inbreeding plays an important role



# Legacy Ancestors in Angus

**Table 1: Marginal contribution for the 30 most influential ancestors in order**

Name	Gender	Date of birth	Contribution	Cumulative	No. progeny	No. descendants
Q A S Traveler 23-4	Male	1978	9.92	9.92	30,201	7,899,413
N Bar Emulation EXT	Male	1986	7.21	17.12	66,738	4,836,852
Tehama Bando 155	Male	1980	6.66	23.78	16,435	5,611,927
P S Power Play	Male	1977	5.31	29.09	27,295	8,544,906
B/R New Design 036	Male	1990	4.57	33.66	27,120	2,756,022
Pine Drive Big Sky	Male	1980	3.75	37.42	47,656	8,208,623
R R Rito 707	Male	1967	3.72	41.13	1,804	9,838,304
Schearbrook Shoshone	Male	1971	3.40	44.54	15,113	9,028,430
Candolier Forever 376	Male	1972	3.23	47.77	798	7,847,354
Bemindful Maid D H D 0807	Female	1980	2.07	49.84	33	4,223,308
Hanton	Male	1852	1.84	51.68	21	20,680,632
Sitz Traveler 8180	Male	1990	1.71	53.39	12,694	1,946,153



# Management of lethal recessive alleles in beef cattle through the use of mate selection software

Lindsay R. Upperman<sup>1,5</sup>, Brian P. Kinghorn<sup>2</sup>, Michael D. MacNeil<sup>3,4</sup> and Alison L. Van Eenennaam<sup>1\*</sup> 

## Abstract

**Background:** Recessive loss-of-function (LOF) alleles at genes which are essential for life, can result in early embryonic mortality. Cattle producers can use the LOF carrier status of individual animals to make selection and mate allocation decisions.

**Methods:** Two beef cattle breeding strategies i.e. (1) selection against LOF carriers as parents and (2) simultaneous selection and mate allocation to avoid the occurrence of homozygous offspring in three scenarios, which differed in number and frequency of LOF alleles were evaluated using the mate selection program, MateSel. Scenarios included (a) seven loci with high-frequency LOF alleles, (b) 76 loci with low-frequency LOF alleles, and (c) 50 loci with random high- and low-frequency LOF alleles. In addition, any savings resulting from the information obtained by varying the percentage (0–100%) of the herd genotyped, together with segregation analysis to cover ungenotyped animals, were calculated to determine (1) which percentage optimized net profit for a fixed cost of genotyping (\$30/test), and (2) the breakeven cost for genotyping.

**Results:** With full knowledge of the LOF alleles carried by selection candidates, the most profitable breeding strategy was always simultaneous selection and mate allocation to avoid homozygous affected offspring (*aa*) as compared to indiscriminate selection against carrier parents (*Aa*). The breakeven value of genotyping depended on the number of loci modeled, the LOF allele frequencies, and the mating/selection strategies used. Genotyping was most valuable when it was used to avoid otherwise high levels of embryonic mortalities. As the number of essential loci with LOF



**Genomics has been widely adopted  
in American Angus and the impact  
will continue to grow**





# Questions/Discussion

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