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# Making use of genomics in beef cattle breeding

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# Introduction

In this session, we will look at genomics in the following areas:

- Markers & SNPs:
  - Breed composition
  - Reference populations
  - Trait prediction
- Genomic selection (incorporating genomics in genetic evaluation):
  - Blending
  - Single-Step model
  - Marker-effects model
- Benefits of genomics
- GeneProb: identification of genetic conditions



# The Bovine Genome

Genome = the genetic material (DNA) of an individual animal



Animal



Cell



Chromosome



DNA

*How many chromosomes in bovine genome?*



# What is a SNP?

**SNP** = **S**ingle **N**ucleotide **P**olymorphism



ATT**C**GGC**A**TGACGATGC



ATT**C**GGC**G**TGACGATGC





# What is a SNP?

Cattle, like humans, are diploid organisms – that is, they have two copies of each chromosome

**Animal 1**

**A/A**



ATTCGGC**A**TGACGATGC

ATTCGGC**A**TGACGATGC

**Animal 2**

**A/G**



ATTCGGC**A**TGACGATGC

ATTCGGC**G**TGACGATGC

**Animal 3**

**G/G**



ATTCGGC**G**TGACGATGC

ATTCGGC**G**TGACGATGC



Two possible alleles (di-allelic), giving 3 possible combinations



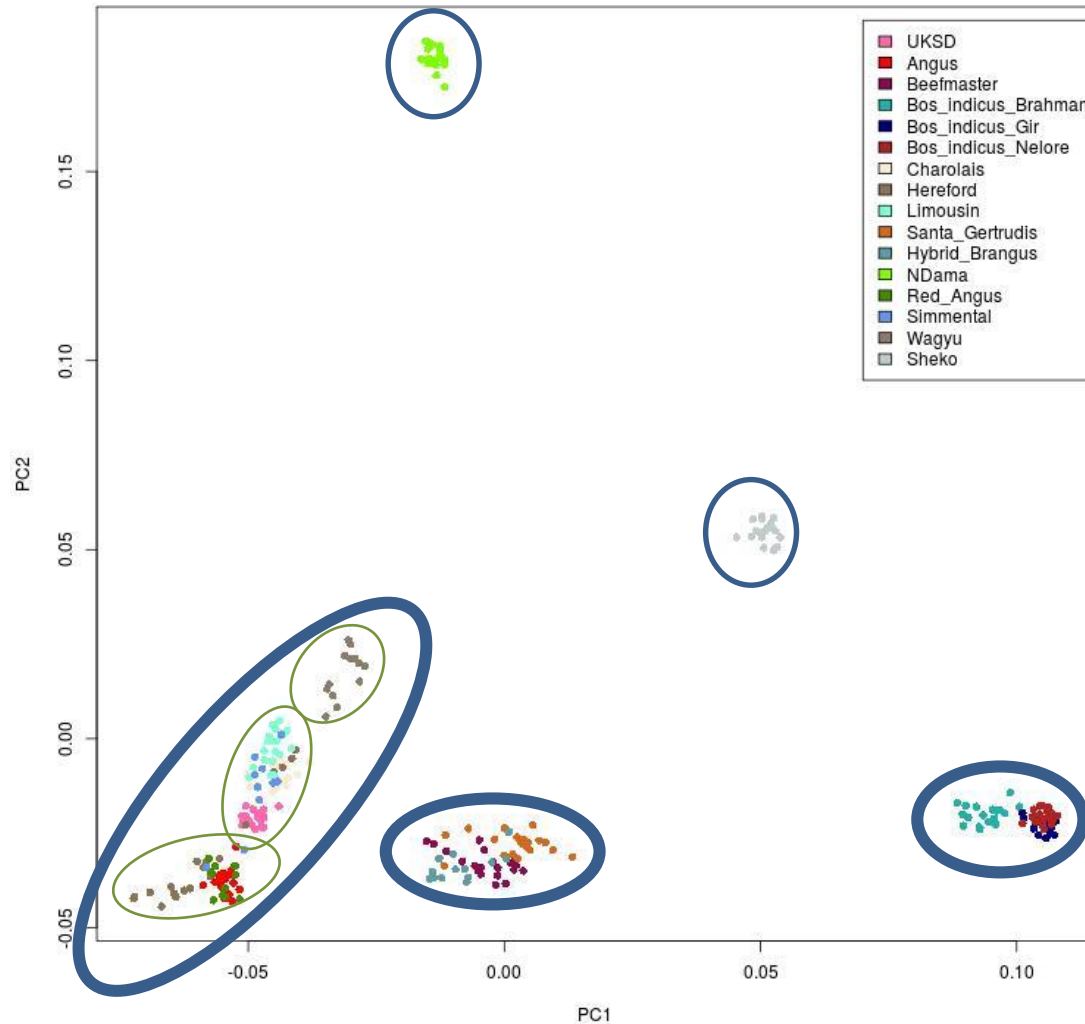
# Which is which?



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# Breed composition





# Which is which?

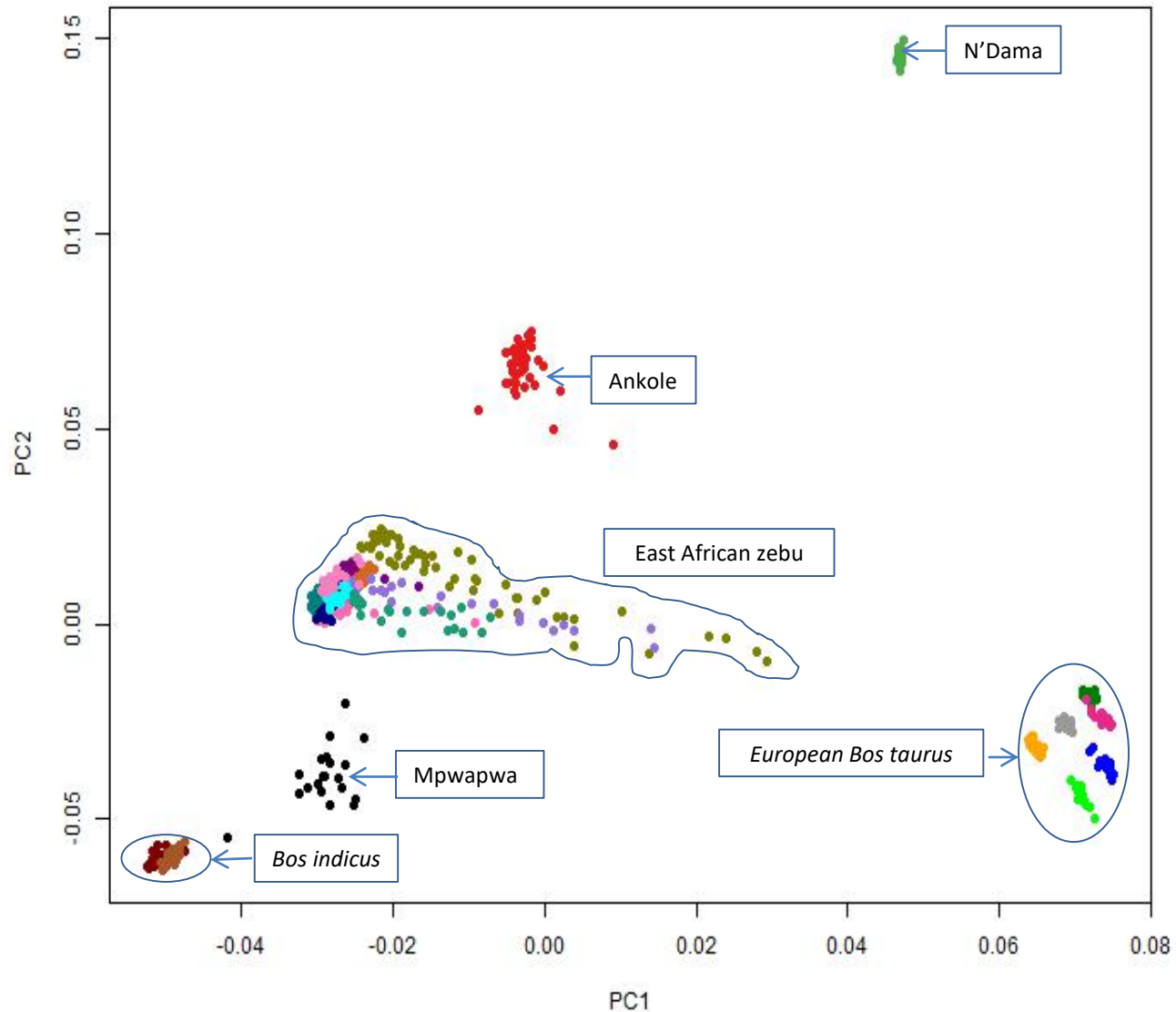


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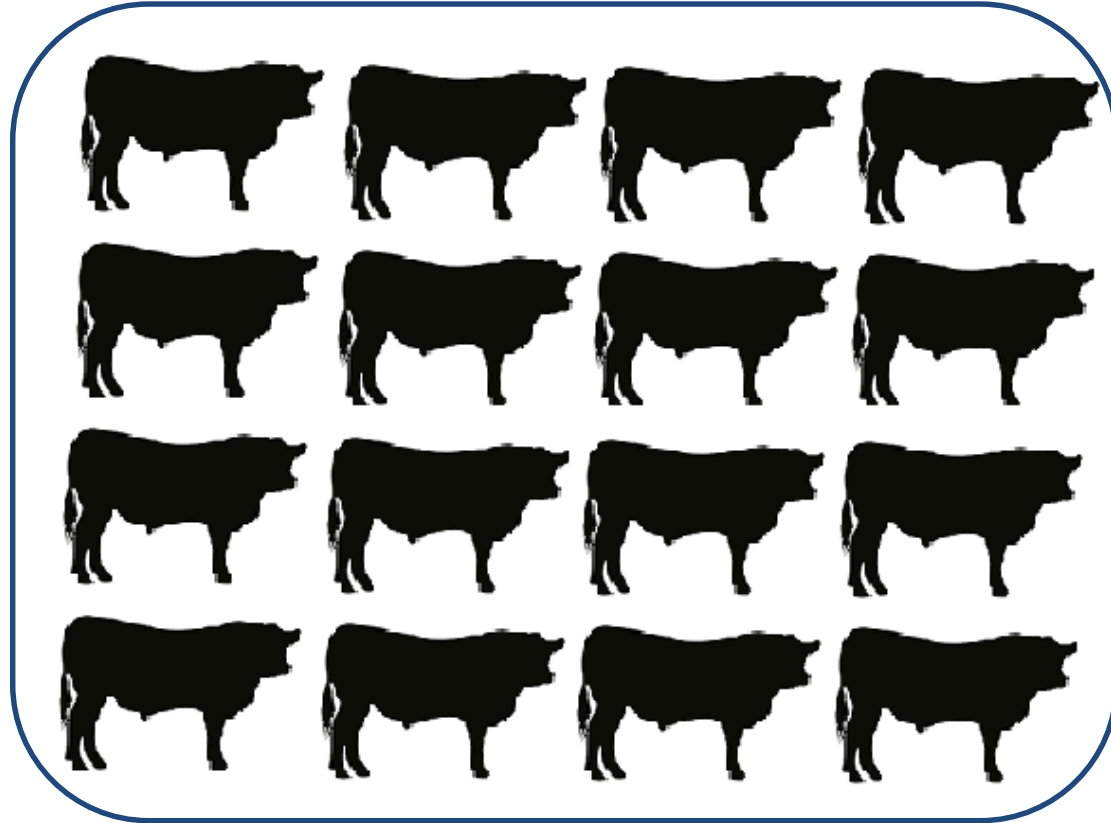


# Genetic diversity of East African Indigenous cattle



# REFERENCE POPULATIONS

are required for genomic data to be useful in trait prediction

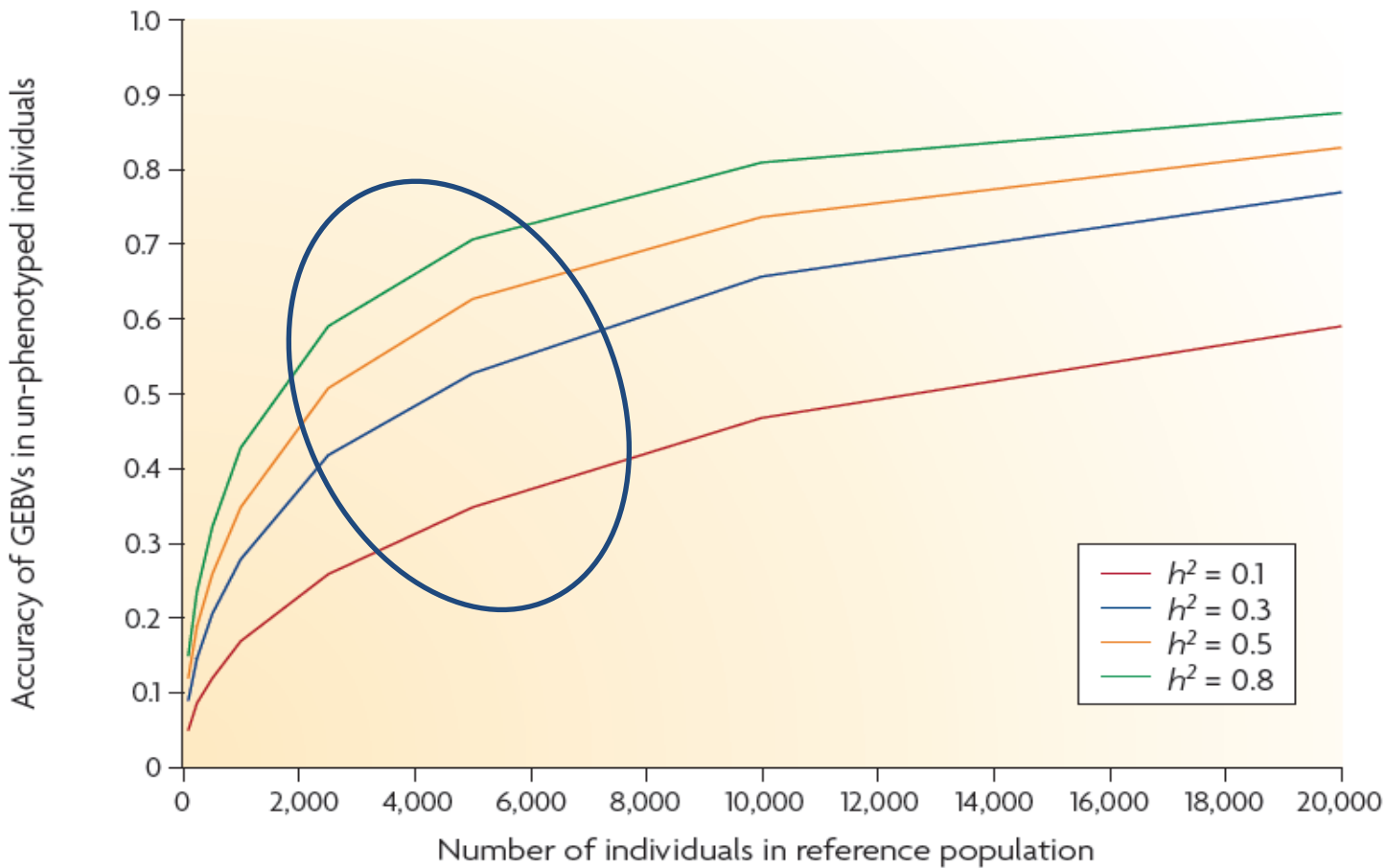


✓ Phenotypes

✓ Genotypes



## The reference population is critical for the successful use of genomic information in beef cattle breeding.

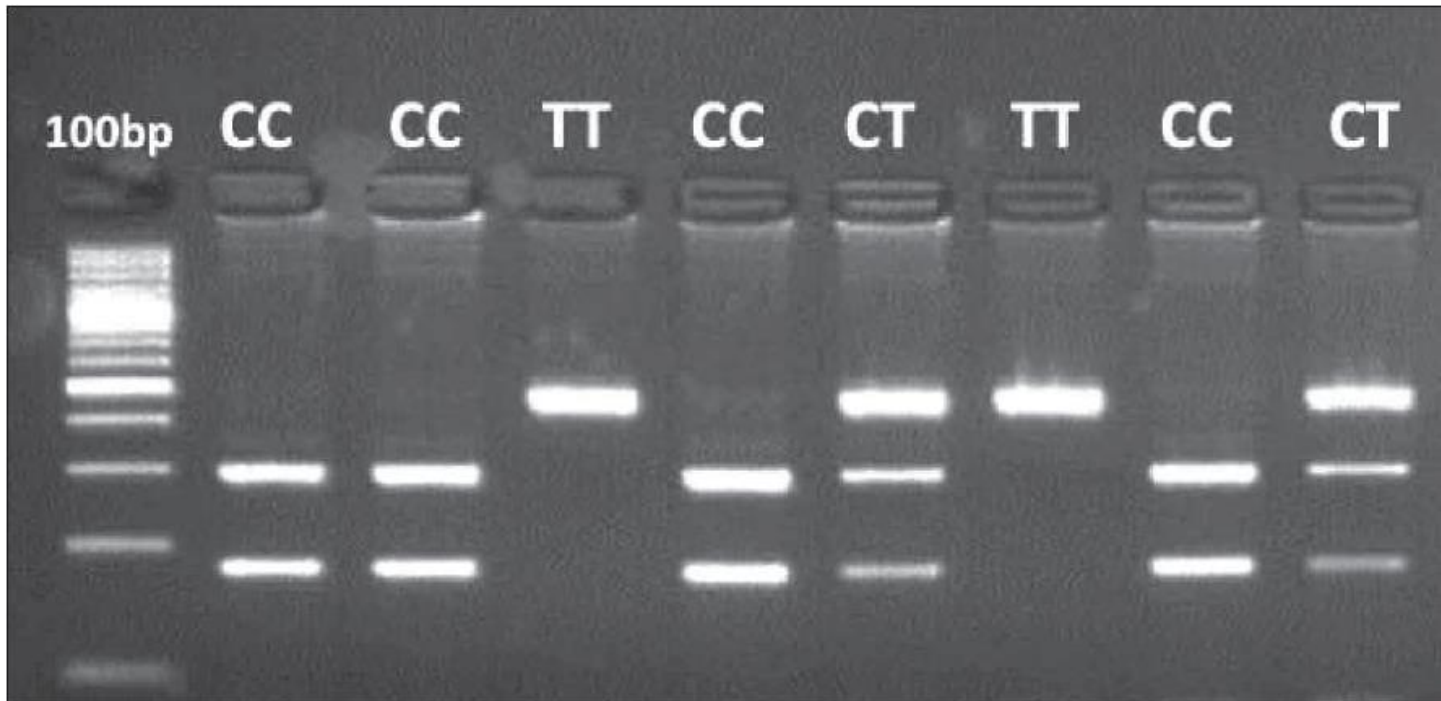


# Prediction of genetic merit & phenotype

**Goal:** Identify relationships between SNP markers & resulting phenotypes



TG5: alleles T or C, position 422 of X05380 → Thyroglobulin





# Prediction of genetic merit & phenotype

Goal: Identify relationships between SNP markers & resulting phenotypes



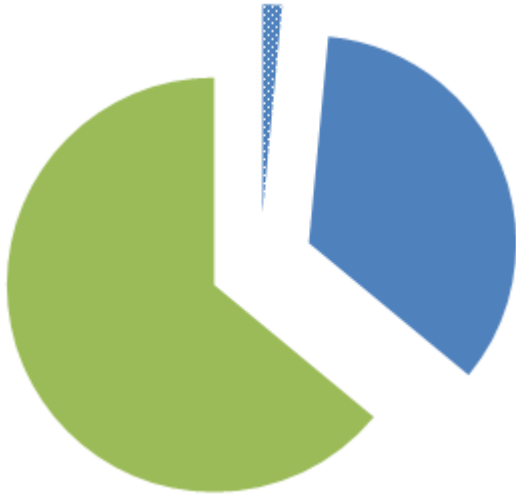
T



C



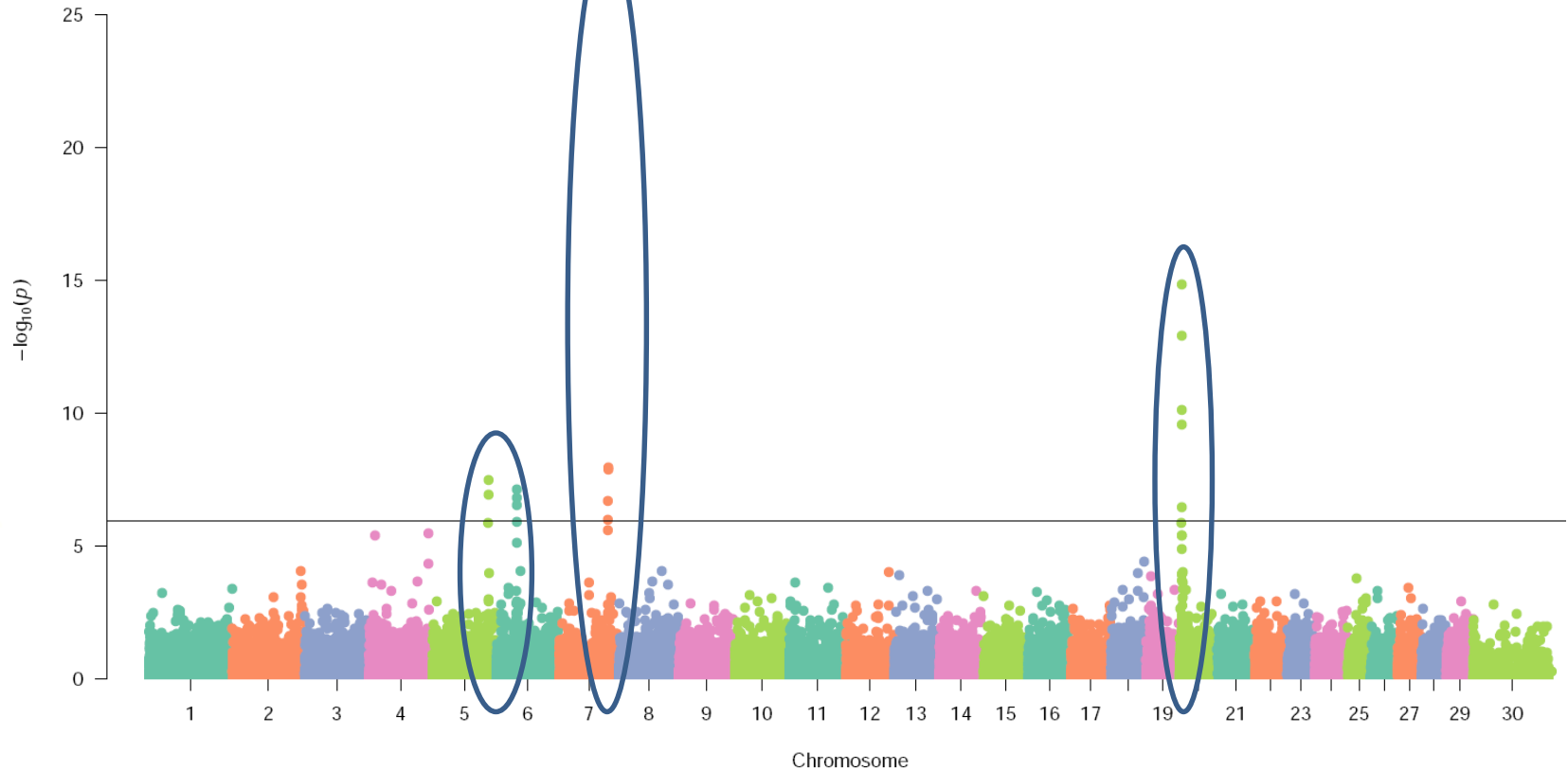
Wait!



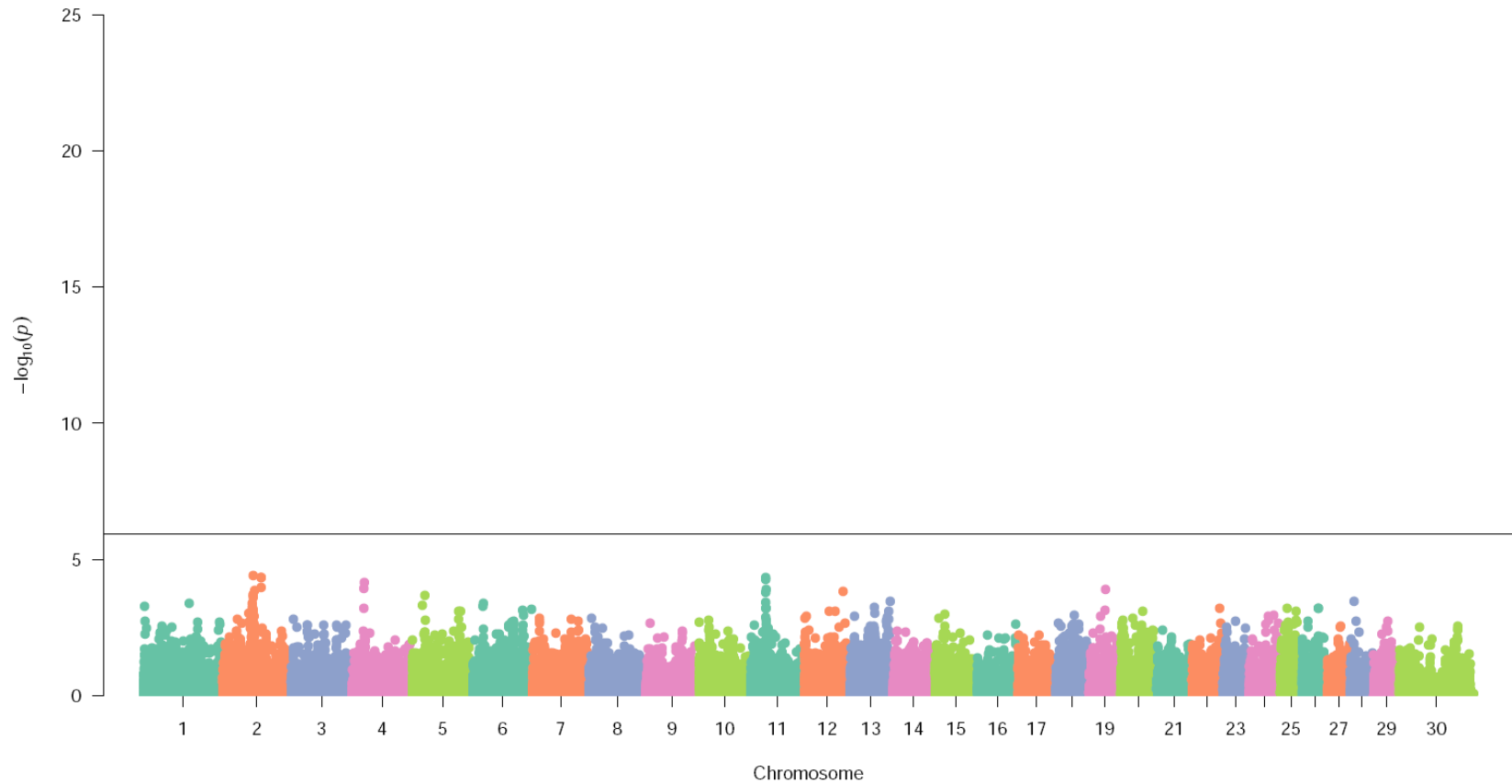
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# Birth weight (GWAS)

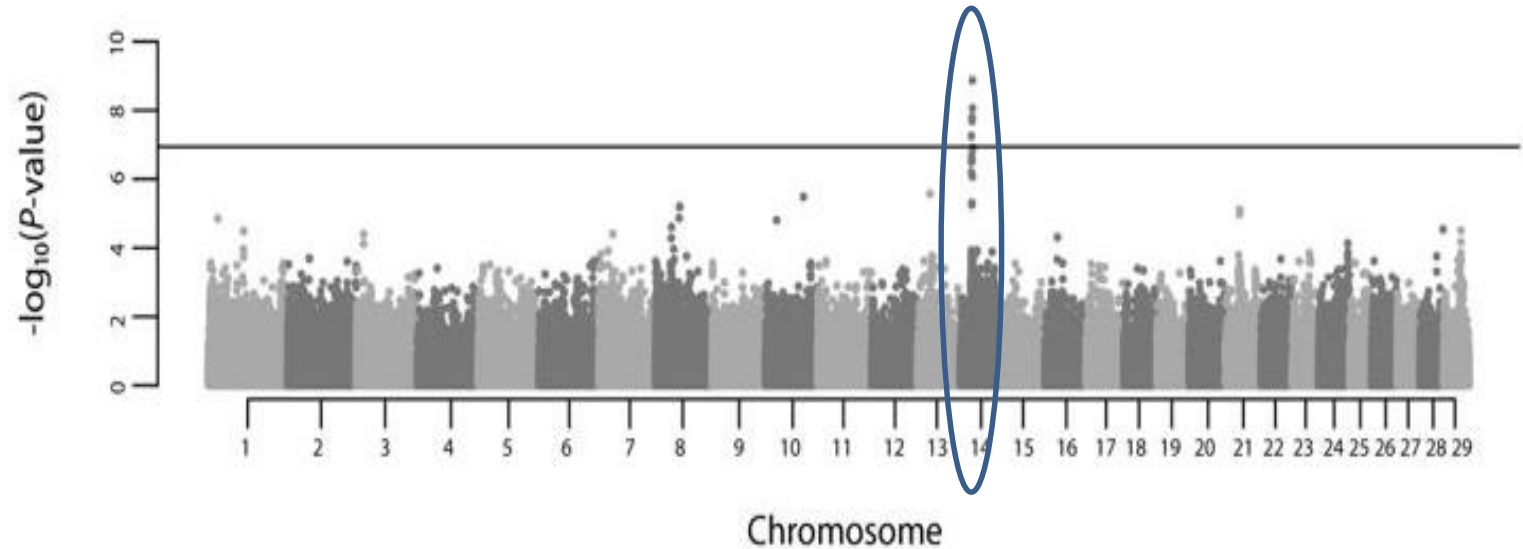


# Carcase Fat (GWAS)





# Birth weight (GWAS)



Manhattan plot of genome - wide -  $\log_{10}$  ( P-values ) for birth weight estimated breeding values in Nellore cattle. The horizontal line represents the Bonferroni significance threshold (Martínez *et al*, 2016).



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# Genomics 101

- May be a few SNPs of significant effect
- May be a few SNPs of lesser effect
- Many SNPs of minimal effect
- Most SNPs of no effect
- SNP effects vary by breed, trait and model



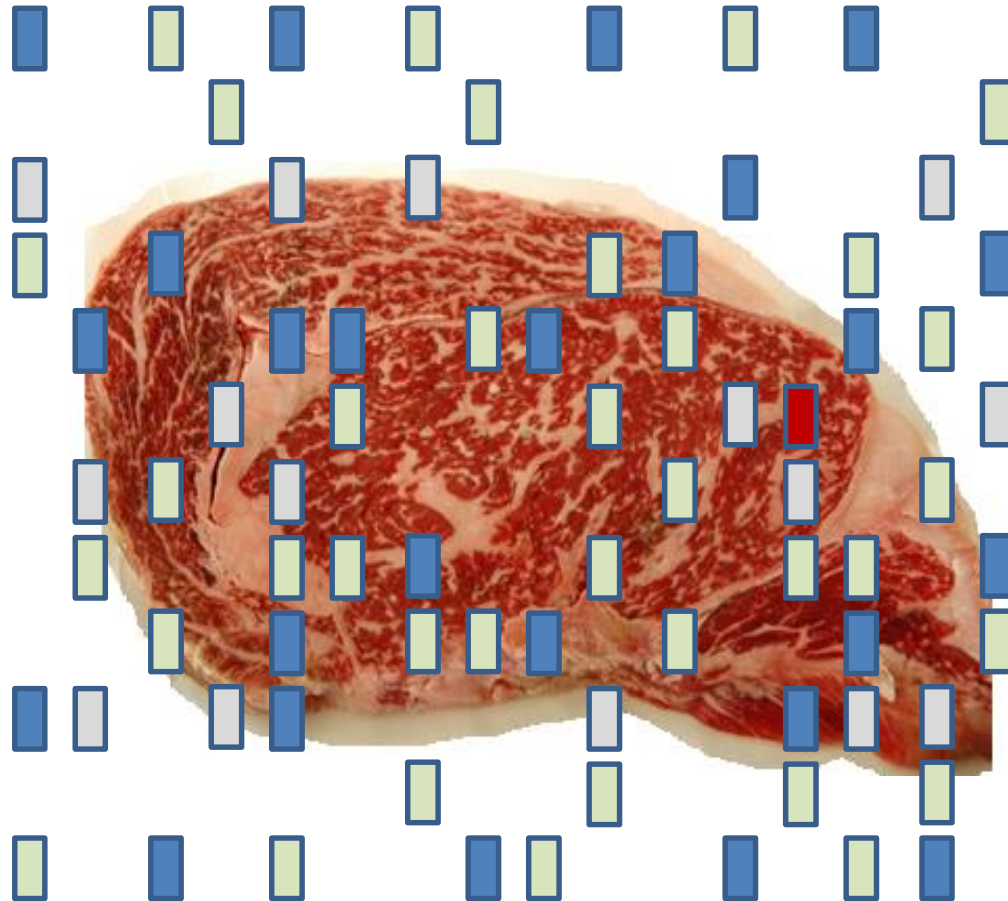
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# Genomic values

(density of genotype)



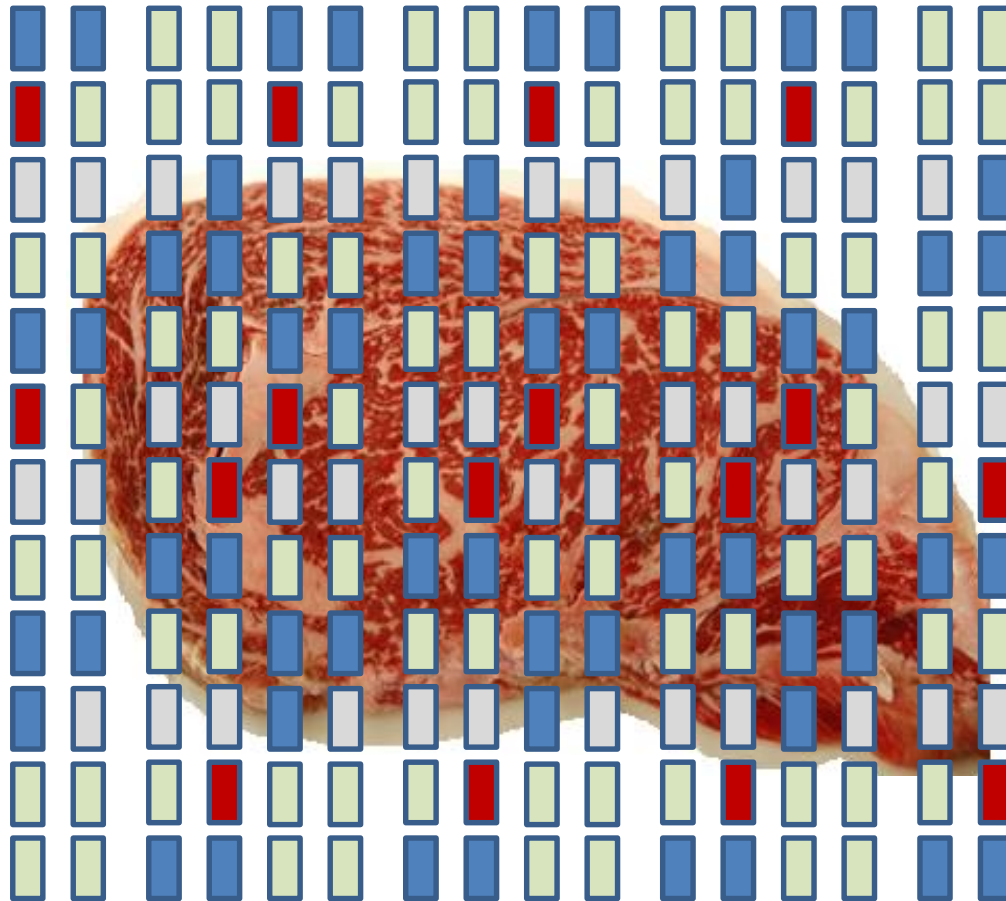
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# Genomic values

(density of genotype)



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Wait!



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# Genomics 101

- Higher density genotypes provide more information
  - But not all information is “informative”
- Genomic values provide information
  - But not all genomic values are “informative”
- Genomic values used in isolation have limited “benefit” in beef breeding and selection
  - Depends on breed and trait
  - Depends on reliability
  - Doesn't account for the remaining (majority) of genetic variation expressed in the population
- Depends on strength of relationship to reference population



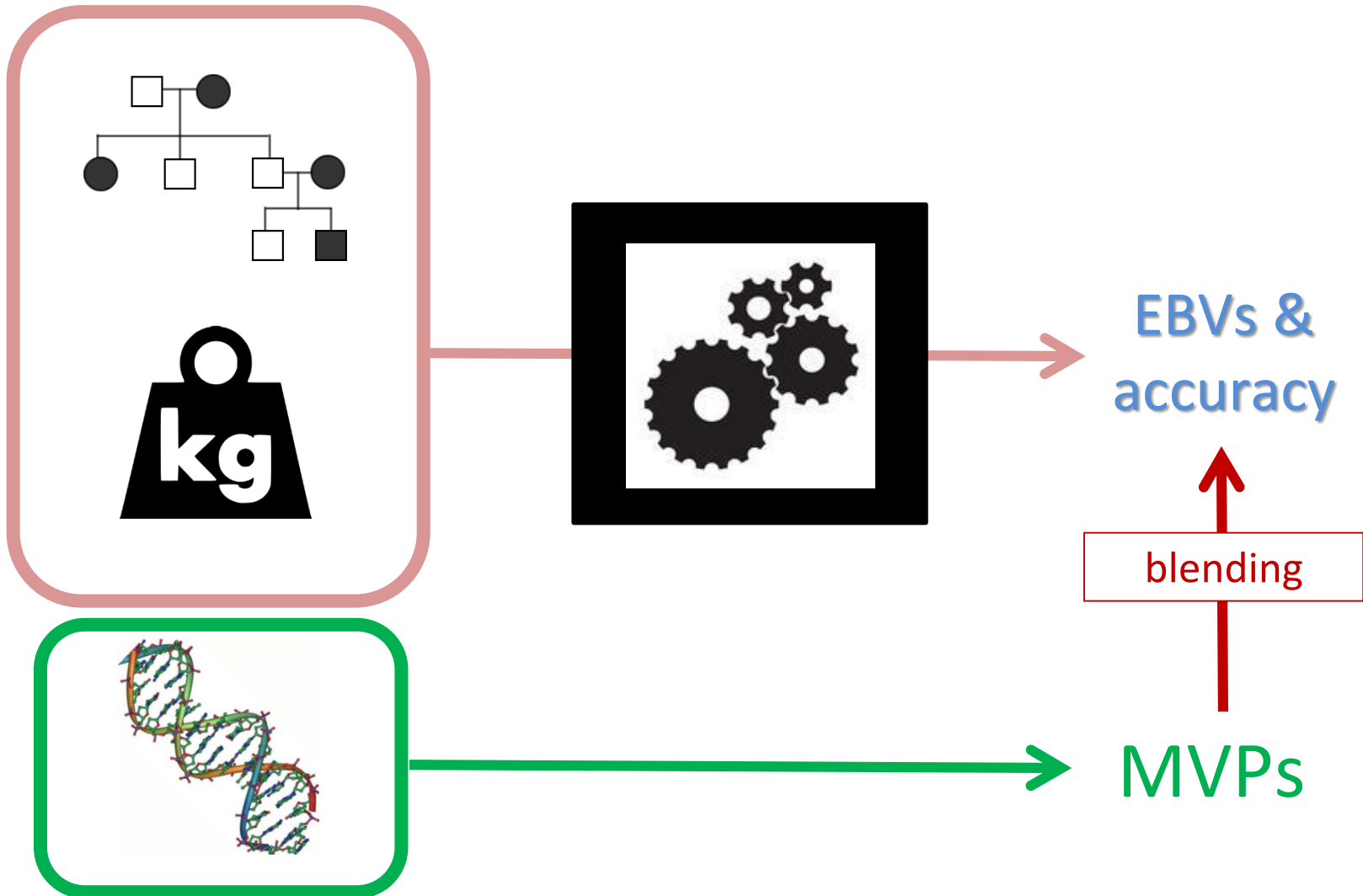
# Genomic relationship to reference population



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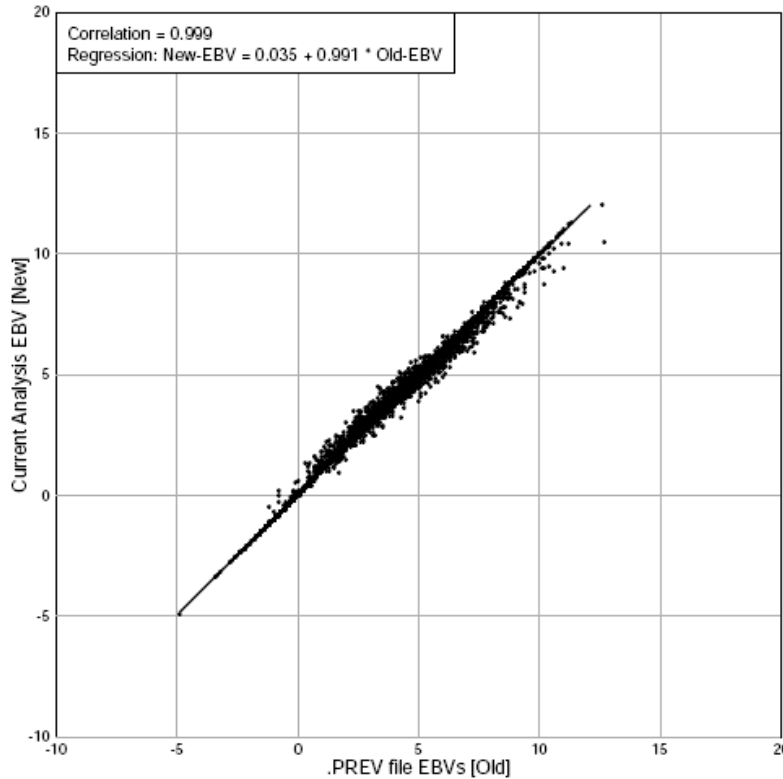
# Incorporating genomics in EBV calculations: (i) blending of genomic values



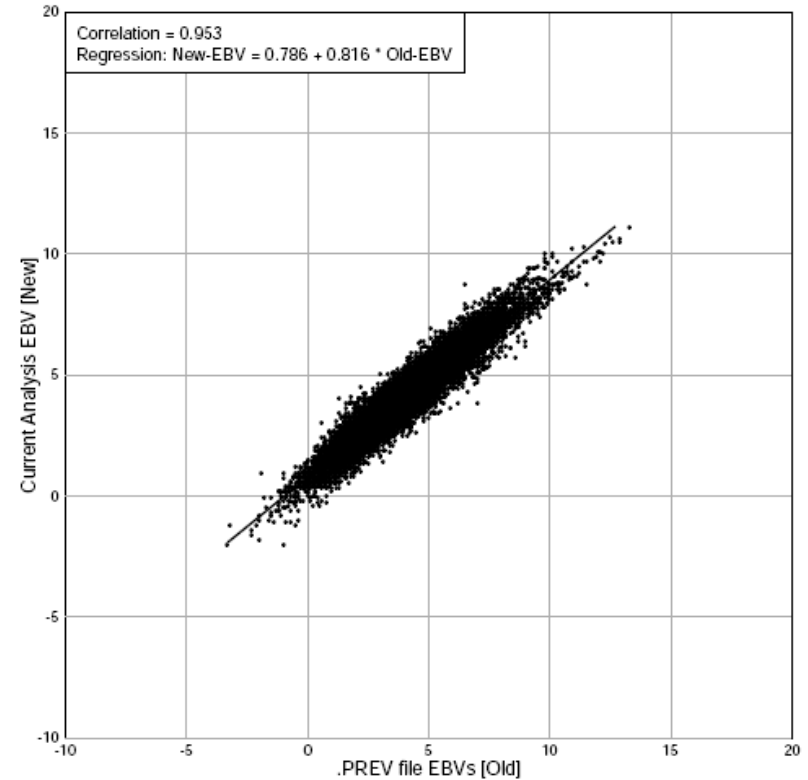


# Incorporating genomics in EBV calculations: (i) blending of genomic values

Sires (Acc >= 75%) - Birth Weight (kgs)



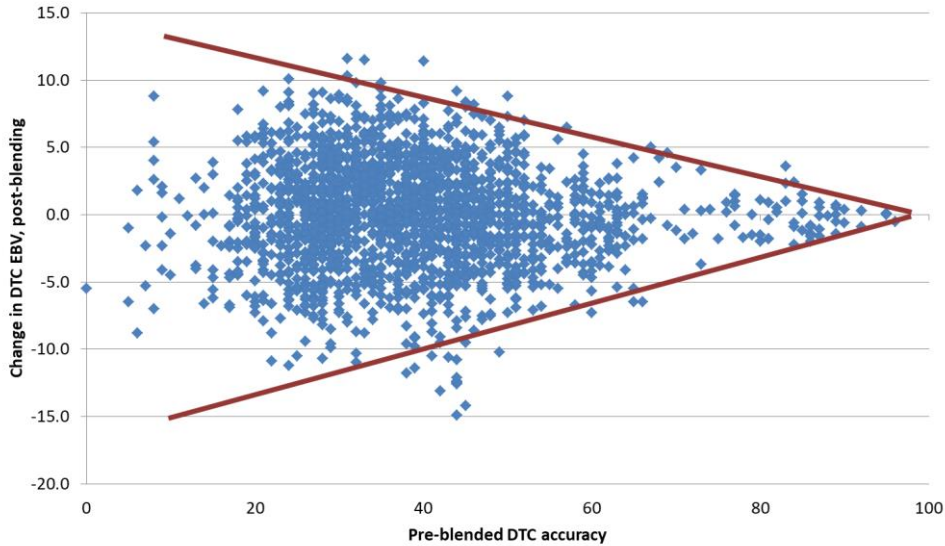
Calves with Genomics (Acc >= 50%) - Birth Weight (kgs)



- Blending only impacts on genotyped individual
  - no ongoing flow of influence to relatives

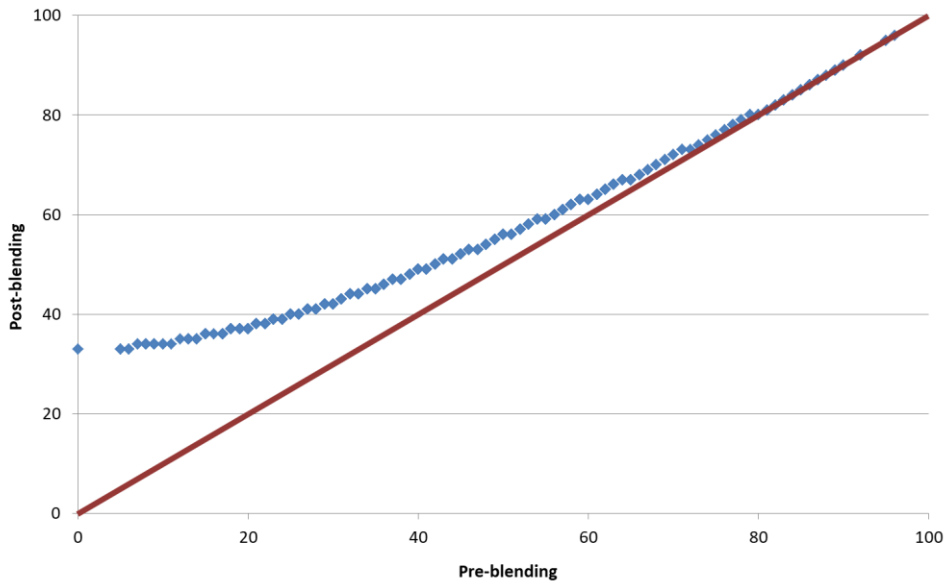


Figure 9 - Change in DTC EBV after blending of DGV\_FREP:  
influence of pre-blend accuracy

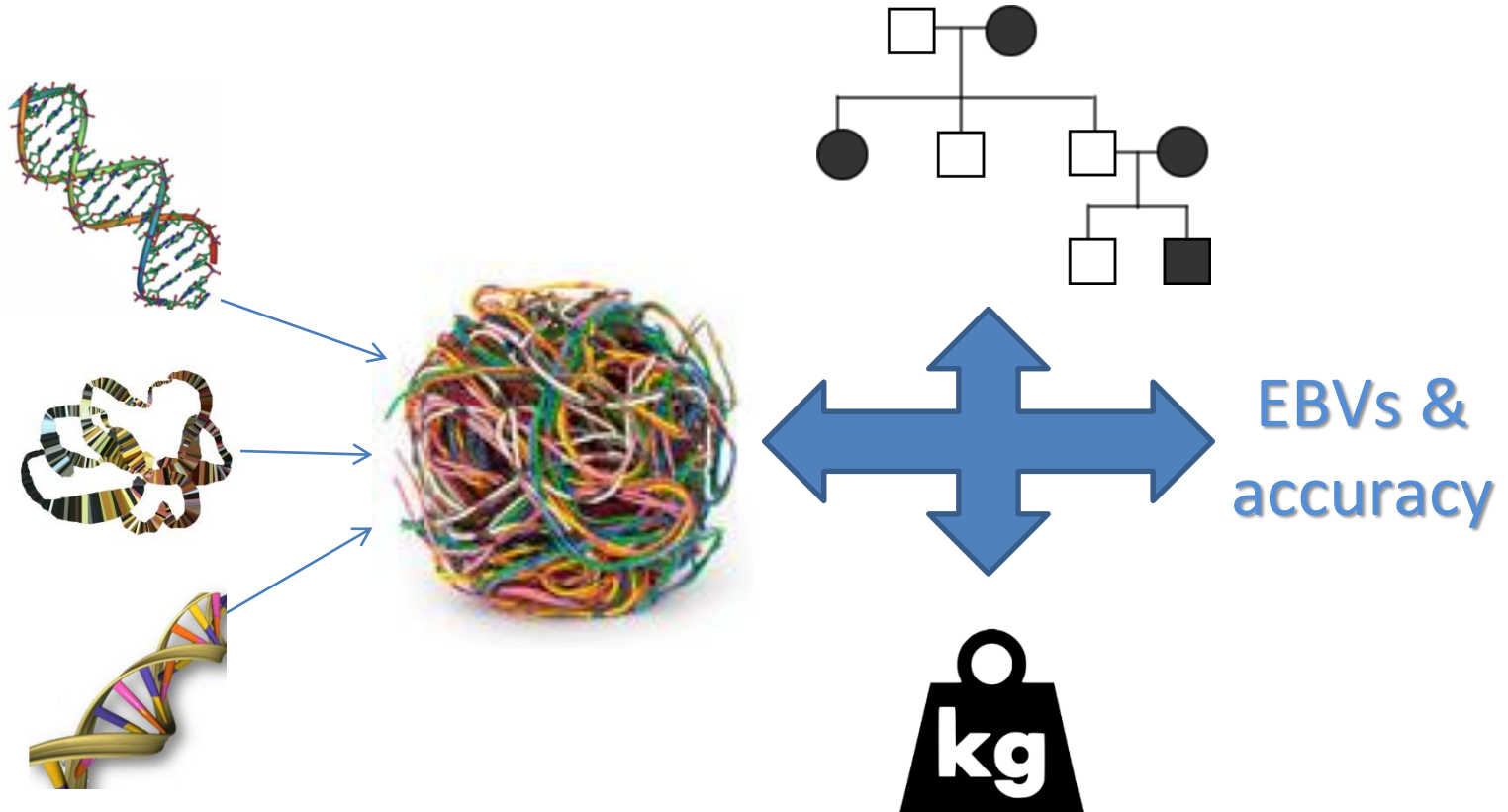


Impact of blending on  
EBV and accuracy  
**decreases**  
as pre-blend accuracy  
**increases**

Figure 8 - DTC EBV accuracy: pre- vs post-blending of DGV\_FREP



# Incorporating genomics in EBV calculations: (ii) single-step model



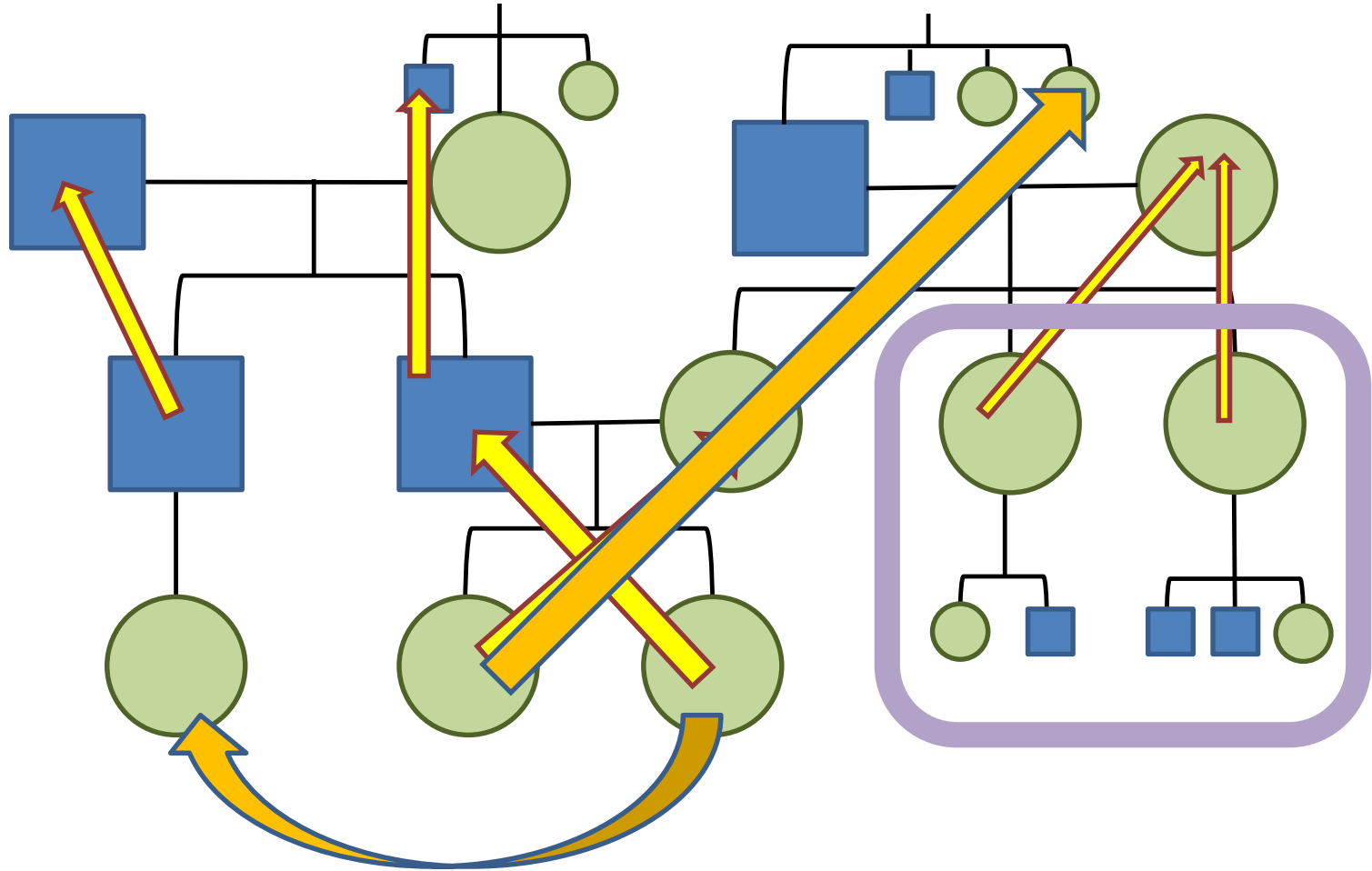
Individual animal  
genotypes

Genomic relationship  
matrix

EBVs &  
accuracy



# Genomic relationships

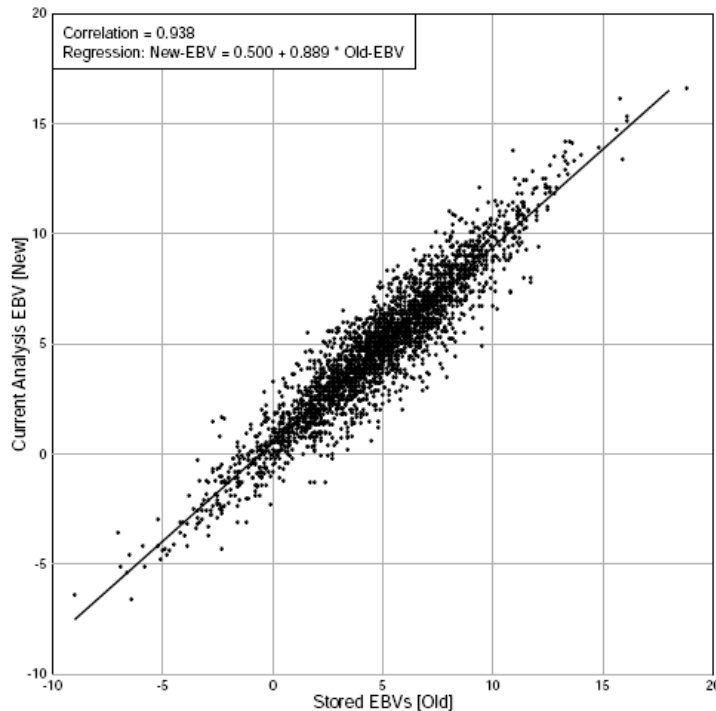


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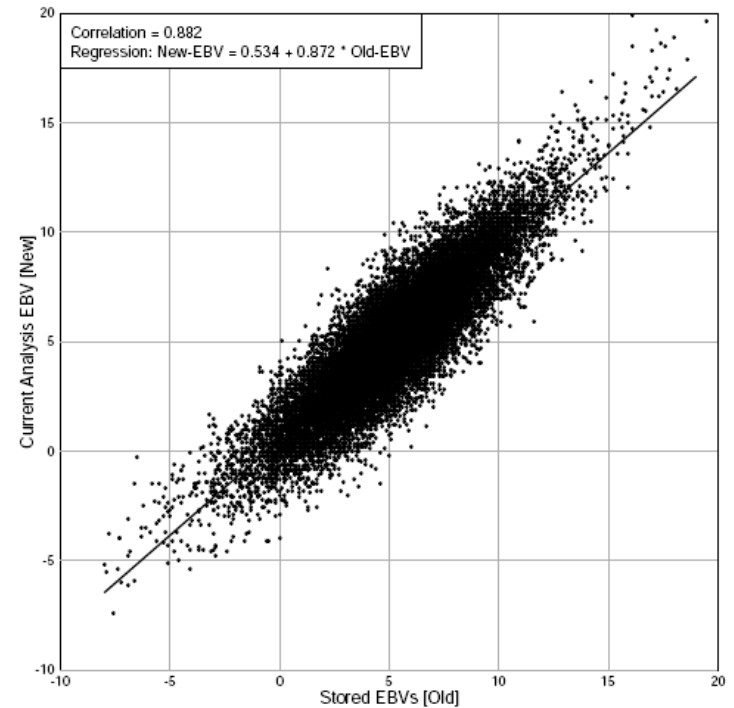


# Single-Step vs Blending (BREEDPLAN)

Sires with Genomics (Acc >= 50%) - Carc Eye Muscle Area (sq cm)



Calves with Genomics (Acc >= 30%) - Carc Eye Muscle Area (sq cm)



- Impact on accuracy as well
  - but accuracy might also DROP!
- SS models differences in genomic relationships
  - blending assumes there are no differences





## Brahmans first movers



The Brahman breed was **the first to adopt Single-Step Breedplan** in April 2017 after using a two-step blending approach since 2011. The current Brahman analysis includes about 13,500 genomic test results.

The biggest impact of utilising genomic prediction in the Brahman breed has been the significant increase in accuracy of the "Days to Calving" fertility EBVs in young bulls. This EBV is a prediction of the differences in the fertility of the future daughters of young bulls, so is a very economically important trait to the breed.

## Wagyu set to move to Single-Step BreedPlan analysis

by Genetics editor Alex McDonald, 03 April 2018



THE Wagyu breed is set to move to a Single-Step BreedPlan analysis for objective measurement, following in the footsteps of the Brahman, Hereford and Angus breeds.



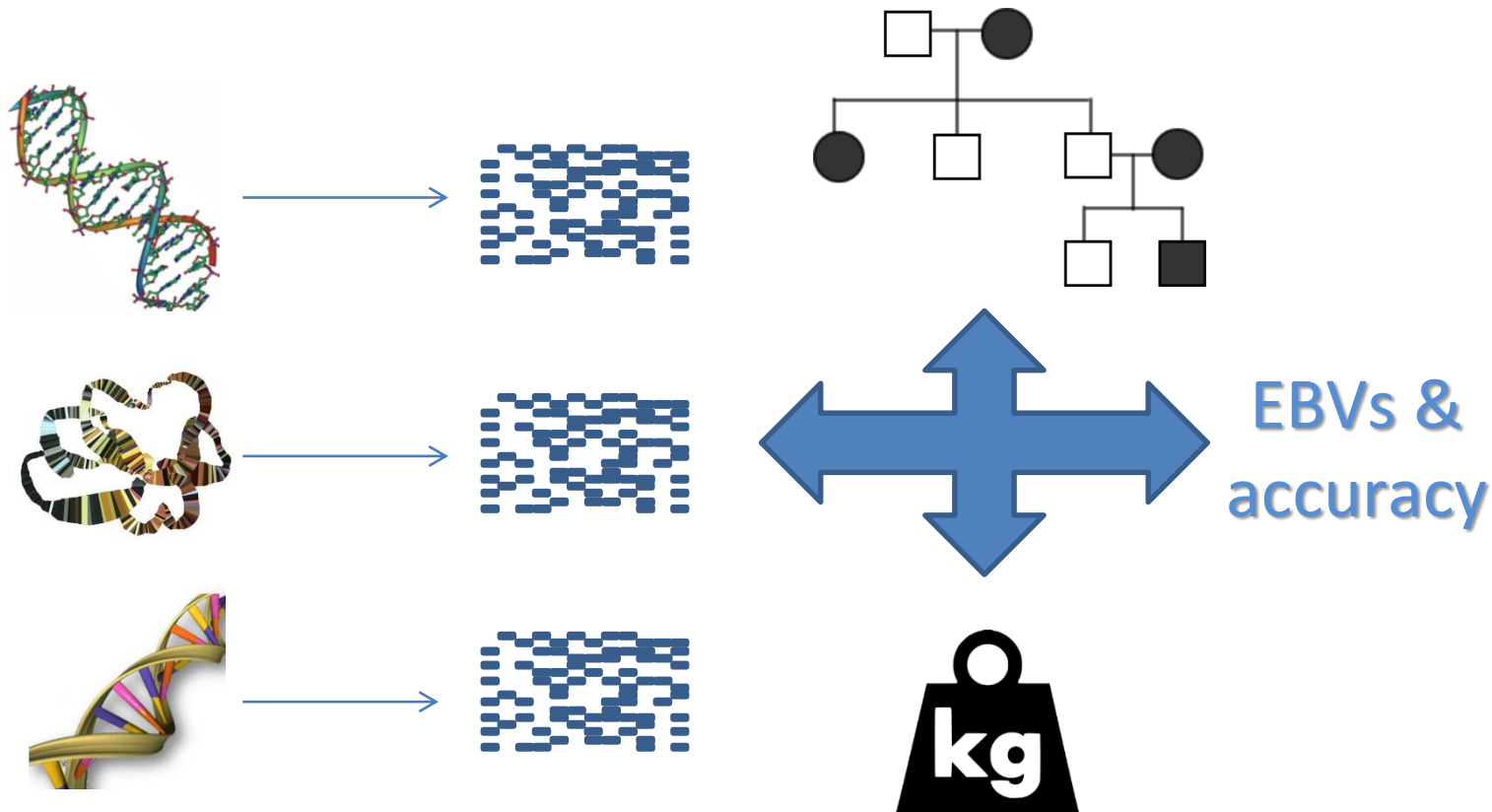
AGENDA > COMMENTARY

## 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.



# Incorporating genomics in EBV calculations: (iii) marker-effects model



Individual animal  
genotypes

Genomic marker  
subset

EBVs &  
accuracy



Saturday, 05 May 2018 10:58

# IGS Releases Multi-breed Genetic Evaluation powered by BOLT

| Written by IGS

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International Genetic Solutions (IGS) is an unprecedented collaboration between progressive breed associations fervently committed to enhancing commercial profitability. The collaboration has yielded the world's largest genetic evaluation of beef cattle with over 17 million animals and 120,000+ genotypes.

In keeping with our commitment to the cattle industry, IGS is pleased to announce the IGS Multi-breed Genetic Evaluation powered by BOLT. The new genetic evaluation provides more predictive EPDs, better use of genomics, more accurate accuracy reported with EPDs, all with weekly evaluations. The announcement ushers in a new era in genetic evaluation — an era made possible by a genetic evaluation system dubbed BOLT (Biometric Open Language Tools, owned by Theta Solutions, LLC).

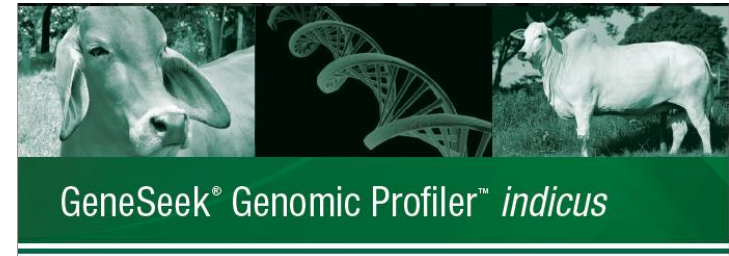


# Imputation





# Breed-specific options



Comparing the breed average minor allele frequency (MAF) of the GGP *indicus* chip and other commonly utilized arrays

Breed	GGP <i>Indicus</i>	GGP Bovine LD	GGP Bovine HDI	Illumina SNP50	Illumina BovineHD
Brahman	0.3603	0.2637	0.3168	0.1385	0.1899
Guzera	0.3291	0.222	0.2746	0.1151	0.1566
Gyr	0.3357	0.2311	0.285	0.1117	0.1595
Nelore	0.3527	0.2401	0.2969	0.1161	0.1638
Droughtmaster	0.3687	0.3062	0.329	0.2121	0.2643
Santa Gertrudis	0.32	0.2781	0.2712	0.2143	0.2467
Tropical Composite	0.3346	0.2958	0.2865	0.2251	0.2629
Other indicus	0.3545	0.2642	0.3186	0.1509	0.2055
Mean	0.3445	0.2626	0.2973	0.1604	0.2061

The highly optimized 35K SNP panel features:

- Average SNP spacing of 77kb across all autosomal chromosomes
- 19K backbone SNP targets, highly informative according to a weighted MAF
- 3K highly informative (breed-specific MAF > 0.40) SNPs for Brahman and Nelore, respectively
- 2K highly informative (breed-specific MAF > 0.40) SNPs for Guzera and Gyr, respectively
- 3K highly informative (breed-specific MAF > 0.40) SNPs for Droughtmaster, Santa Gertrudis and Tropical Composite, respectively
- An additional set of 1000 map-optimal SNPs (weighted MAF > 0)
- Imputation accuracy (to the Illumina Bovine HD) averages greater than 97% for all evaluated breeds



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# Questions



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# Benefits of Genomics

There will be two main benefits of incorporating genomic information into a genetic evaluation (such as a BREEDPLAN analysis):

## 1. EBVs can be generated for animals which do not have performance data

- animals too young to be measured → days to calving
- traits which are hard to measure → feed intake
- traits only measurable in one sex → scrotal circumference
- traits measured once animal is dead → shear force (tenderness)

## 2. More accurate EBVs can be generated for animals with limited performance information

- young bull with own observations but no observations on progeny



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# Benefits of Genomics

The actual improvement in EBV accuracy following a genomic test will vary depending on a number of factors:

- individual trait
- EBV accuracy before genotype is used
- genomic proximity to reference population
- size of reference population

Genomics allows identification of elite bulls and heifers at younger ages:

- shortens the generation interval
- **increases rate of genetic improvement**



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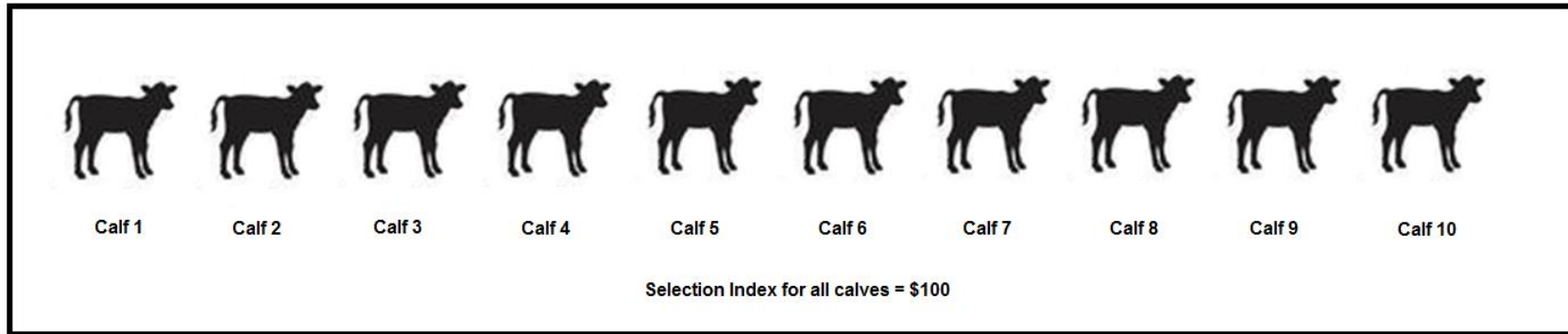
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# Practical Example

A breeder has implemented an ET program and has produced 10 full-sib bull calves



The breeder wishes to keep the top 6 bull calves - and steer the rest – by several months of age yet without any performance information on them.

Currently a difficult decision as all 10 calves only have mid-parent EBVs and Selection Indexes. Breeder cannot differentiate between them based on their genetic potential.

**Which are the best to keep as bulls?**



# Full ET Siblings

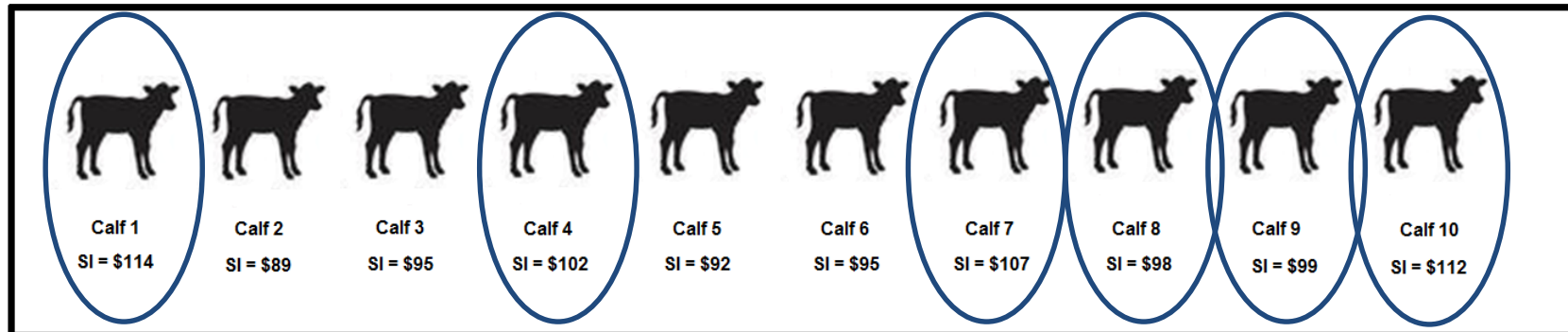
If genomics is incorporated into the BREEDPLAN analysis for this breed, then the breeder can:

- Take a hair sample for each calf
- Pay for a genetic test
- This information will then be incorporated into the BREEDPLAN analysis, and EBVs which include genomic information will be produced





# Full ET Siblings



The breeder can now differentiate between calves using their genetic potential

The breeder can identify which calves suit their particular breeding program, selecting those to keep as bulls and those to steer



**My breed is moving towards genomic selection, so I'm going to genotype my herd and get EBVs.**

**That means I can stop performance recording, right?**



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NO NO NO!  
NO NO NO!  
NO NO NO!



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# The Role of Performance Information in the Genomics Era

**“In the era of genomics,  
phenotype is king”**

Professor Mike Coffey  
Roslin Institute, UK



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# The Role of Performance Information in the Genomics Era

- A reference population is **VITAL** to the success of genomics
- Equally, genomic information is most useful when animals are closely related to the reference population
- Therefore, reference population needs to be updated over time
  - esp. if young animals are to be genotyped
- Animals with both **GENOTYPES** and **PHENOTYPES** are **ESSENTIAL**



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# The Role of Performance Information in the Genomics Era

When individual breeds move to genomics, EBVs will be calculated from:

- Pedigree information
- Individual performance information
- Progeny performance information

AND

- Genomic information

**Genomics is just another source of information**



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# One challenge....

- Markers



- Genomic values

		Molecular Value Prediction			
		FE	Marb	Tend	
Breed: Angus	Breed MVP Statistics:	Average	0.48	0.17	-0.17
		Min	-0.84	-0.30	-0.92
		Max	1.29	0.52	0.57
Herd MVP Statistics:	Average	0.53	0.19	-0.20	
	Min	-0.38	-0.25	-0.83	
	Max	1.21	0.52	0.57	
Herd Distribution of Animals Relative to Breed Quartiles:	Top 25% (76-100 quartile)	5%	52%	29%	
	51-75% (quartile)	21%	27%	25%	
	26-50% (quartile)	25%	18%	25%	
	Bottom 25% (1-25 quartile)	48%	4%	21%	
Herd Reliability Statistics:	Average	33.8%	21.8%	38.9%	
	Min	26.0%	15.8%	25.9%	
	Max	35.9%	22.9%	41.4%	

- Single-Step

- only “see” EBVs and accuracy
- won’t “see” if genotype is (un)favourable
- won’t “see” genomic relationships / contributions

Source: Pfizer technical summary, October 2013



# Questions



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# GeneProb



- Uses known DNA test results for a nominated gene and combines this with pedigree information stored on Breed Society Databases.
- Tracks recessive genetic conditions and genes of interest.
- Calculates and reports the probability of the animal being a carrier of the nominated gene.



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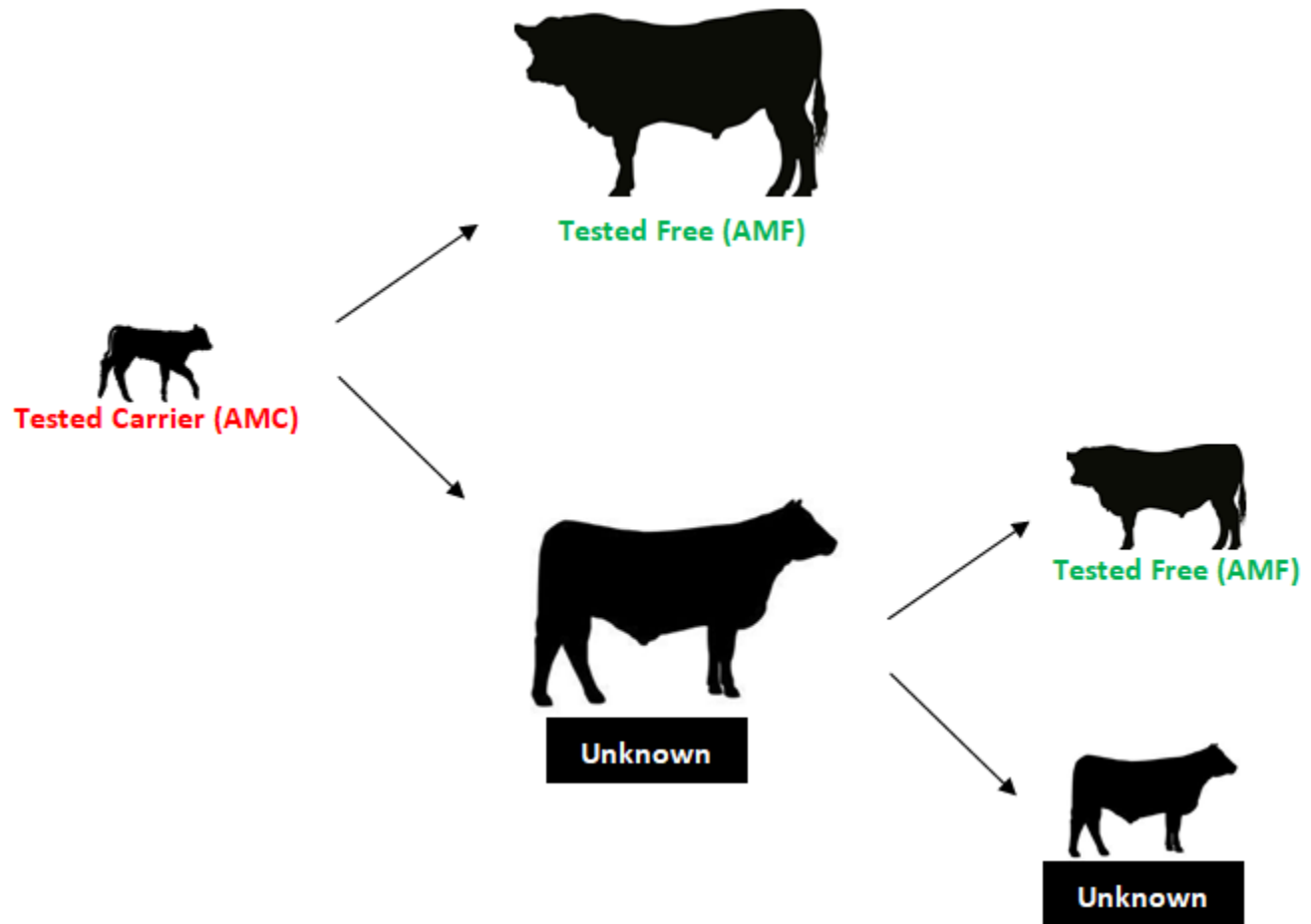


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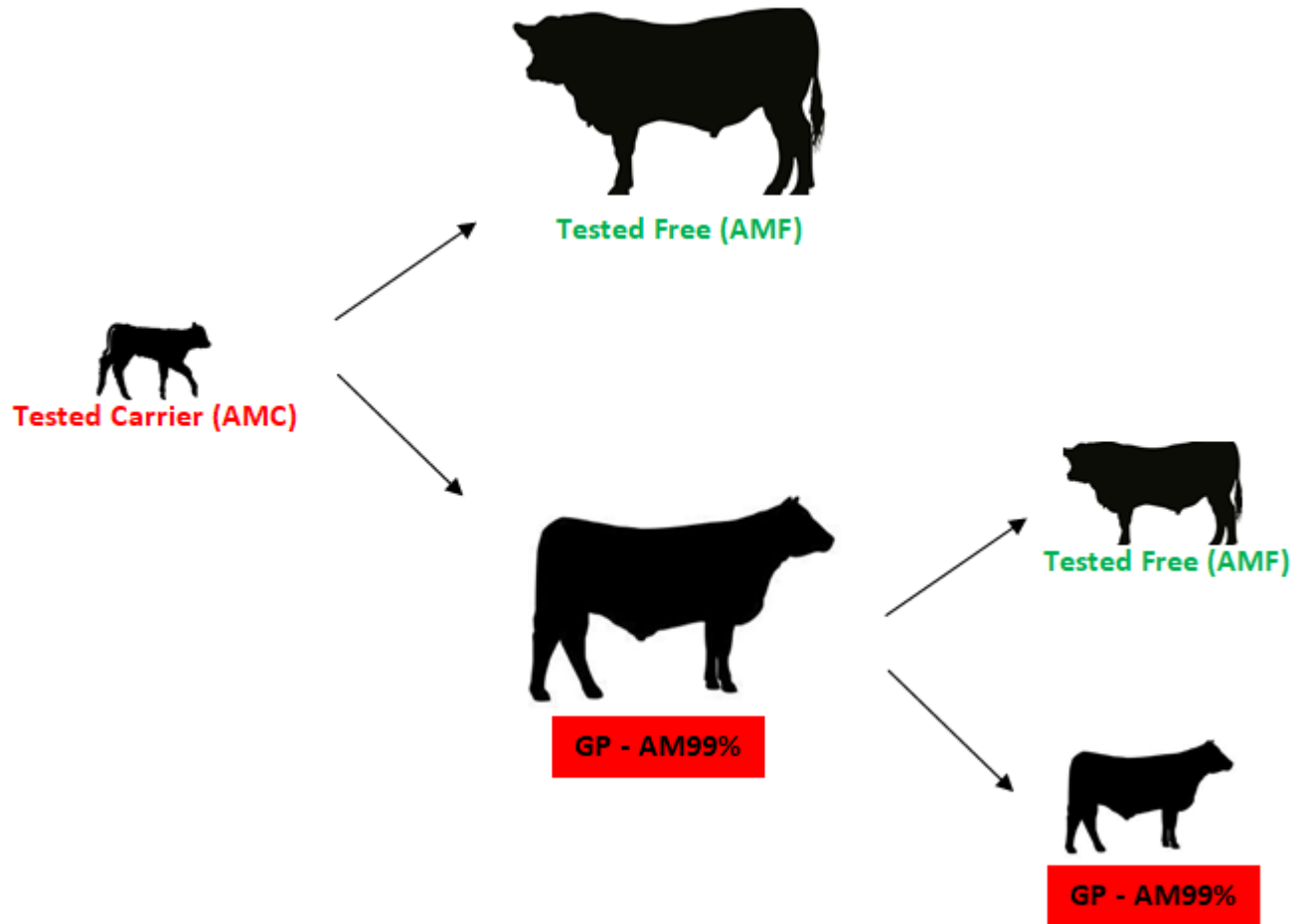


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# Example: Before Using GeneProb



# Example: After Using GeneProb



# Benefits of GeneProb

- Manages the spread of undesirable genes within each herd and the prevalence within the breed.
- Enables better identification of animals within each herd that need testing, rather than blindly testing all animals.
- Maximises the usefulness of the DNA test results stored on each breed society database.
- Identifies problematic animals that may have incorrect parentage. (pseudo parent verification test).





# Questions



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