Genomics-What else can we gleam from this technology?

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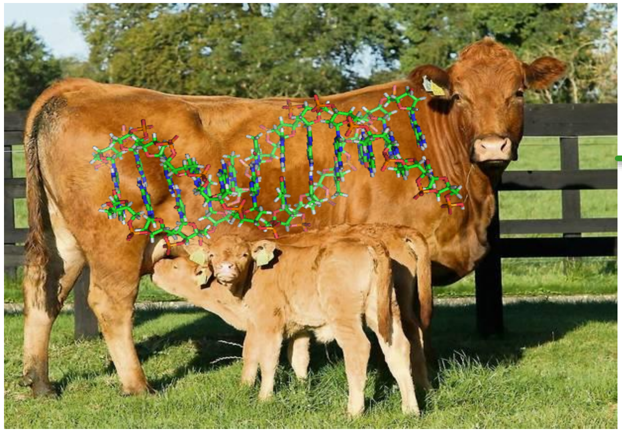
Bovine Genome



Over 3 Billion Nucleotides

↓

Share 80% of DNA with humans

↓

30 Chromosomes

↓

22,000 Genes

↓

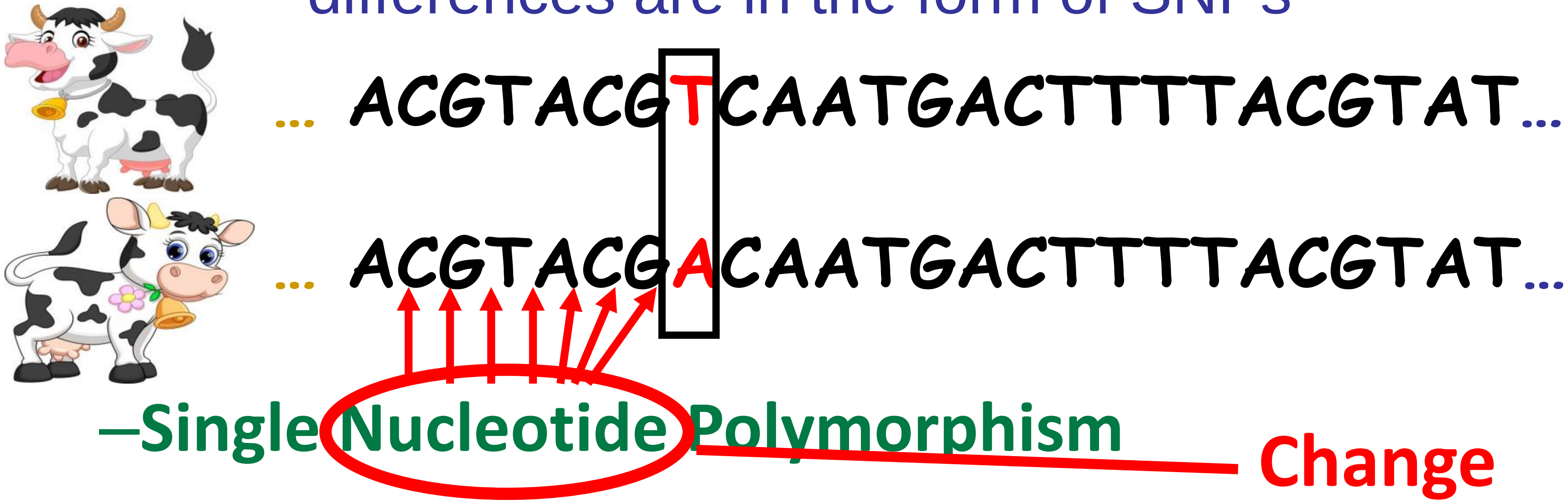
Several types of mutations

↓

Single Nucleotide Polymorphisms

What is a SNP?

- 99.9% of bovine DNA is identical – most of the differences are in the form of SNPs



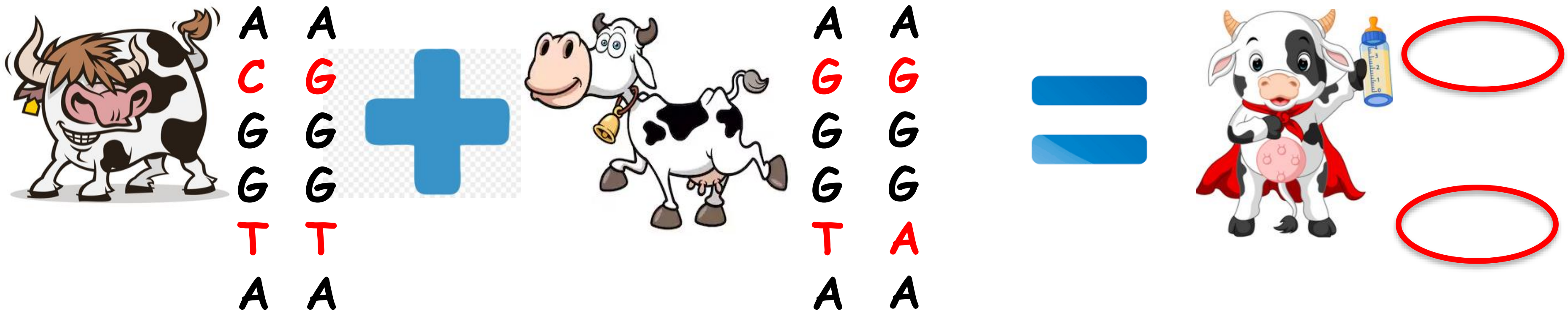
… ACGTACGTCAATGACTTTTACGTAT…

… ACGTACGACAATGACTTTTACGTAT…

– **Single Nucleotide Polymorphism**

Change

Genotypes are the pair of SNPs inherited at a given position



A	A	A	A
C	G	G	G
G	G	G	G
G	G	G	G
T	T	T	A
A	A	A	A

How do SNPs relate to performance?

- The cattle genome has ~ **3 billion nucleotides**
- Scientists have discovered ~ **40 million SNPs**

At a SNP location different nucleotides are present

Each nucleotide may **affect performance** differently

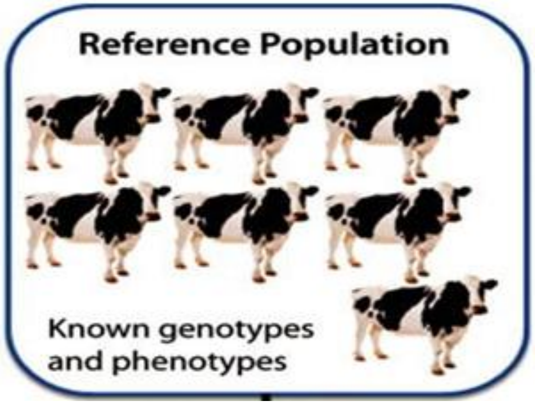
SNP1A

SNP1G

How SNP chips work

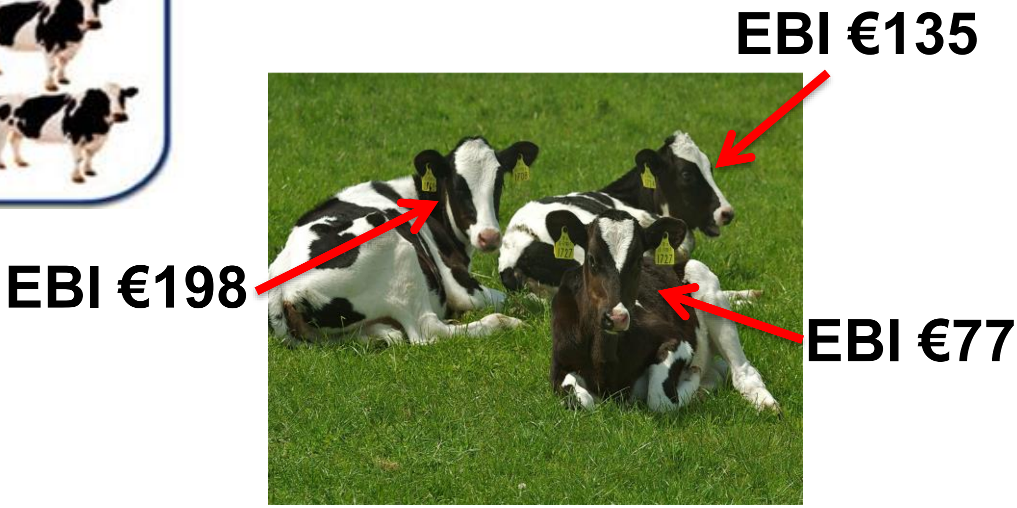
SNP	Var	Milk	Beef
1	A	+20	-0.6
1	G	+5	-0.4
2	A	12.3	-0.6
2	T	-14.46	+20.2
⋮	⋮	⋮	⋮
n	A	+25	+5.2

x ~50,000
on a SNP chip



Reference Population

Known genotypes
and phenotypes



What are we getting from genotypes?

Parentage assignment

Increase accuracy of genetic evaluations

Traceability

Breed composition

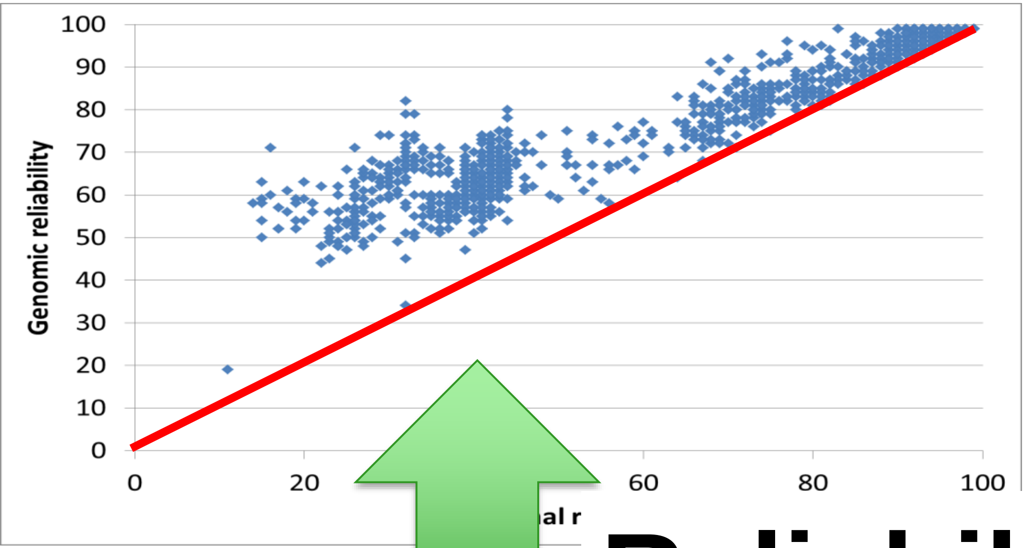
Mating advice

Monitoring lethal genes

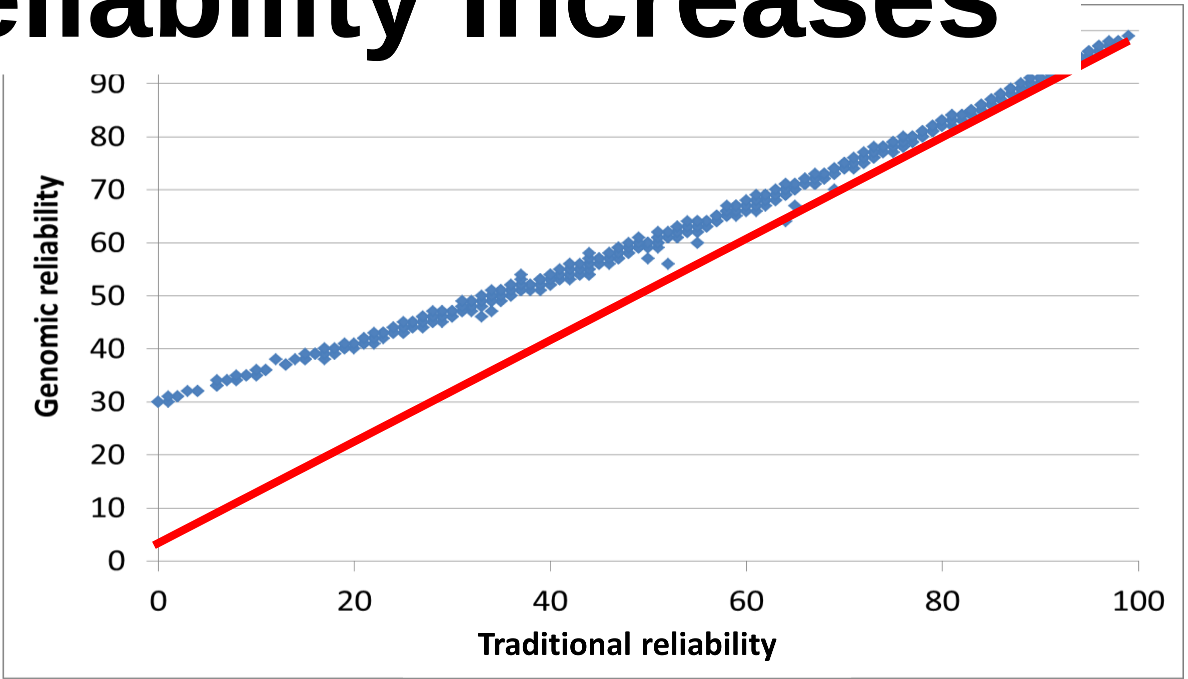
Inbreeding

Monitoring major genes

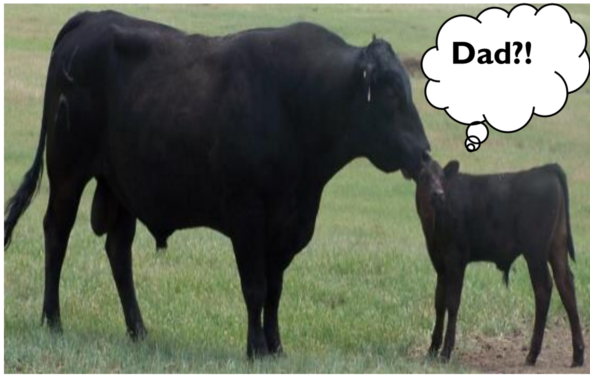
Select Candidates



Reliability Increases

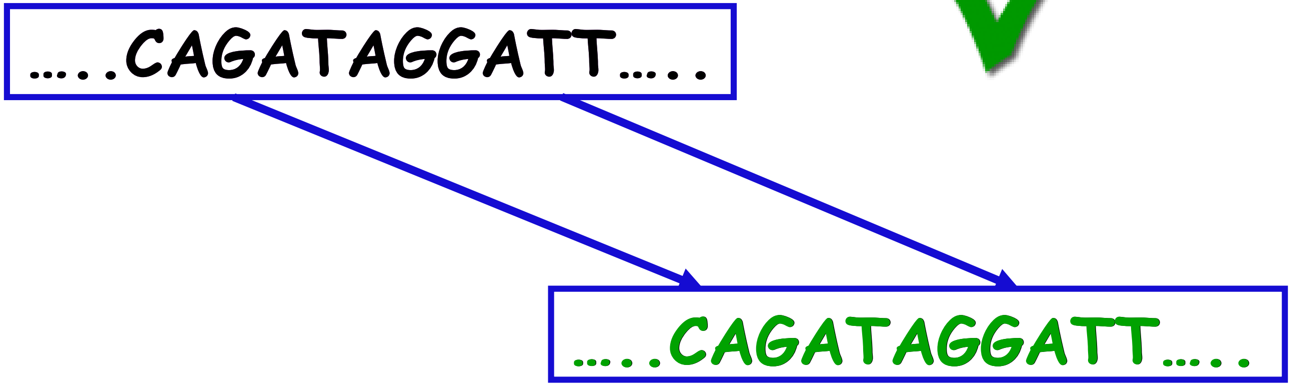


Determining Parentage



Sire

…..TCACCGCTGAG…..



…..CAGATAGGATT…..

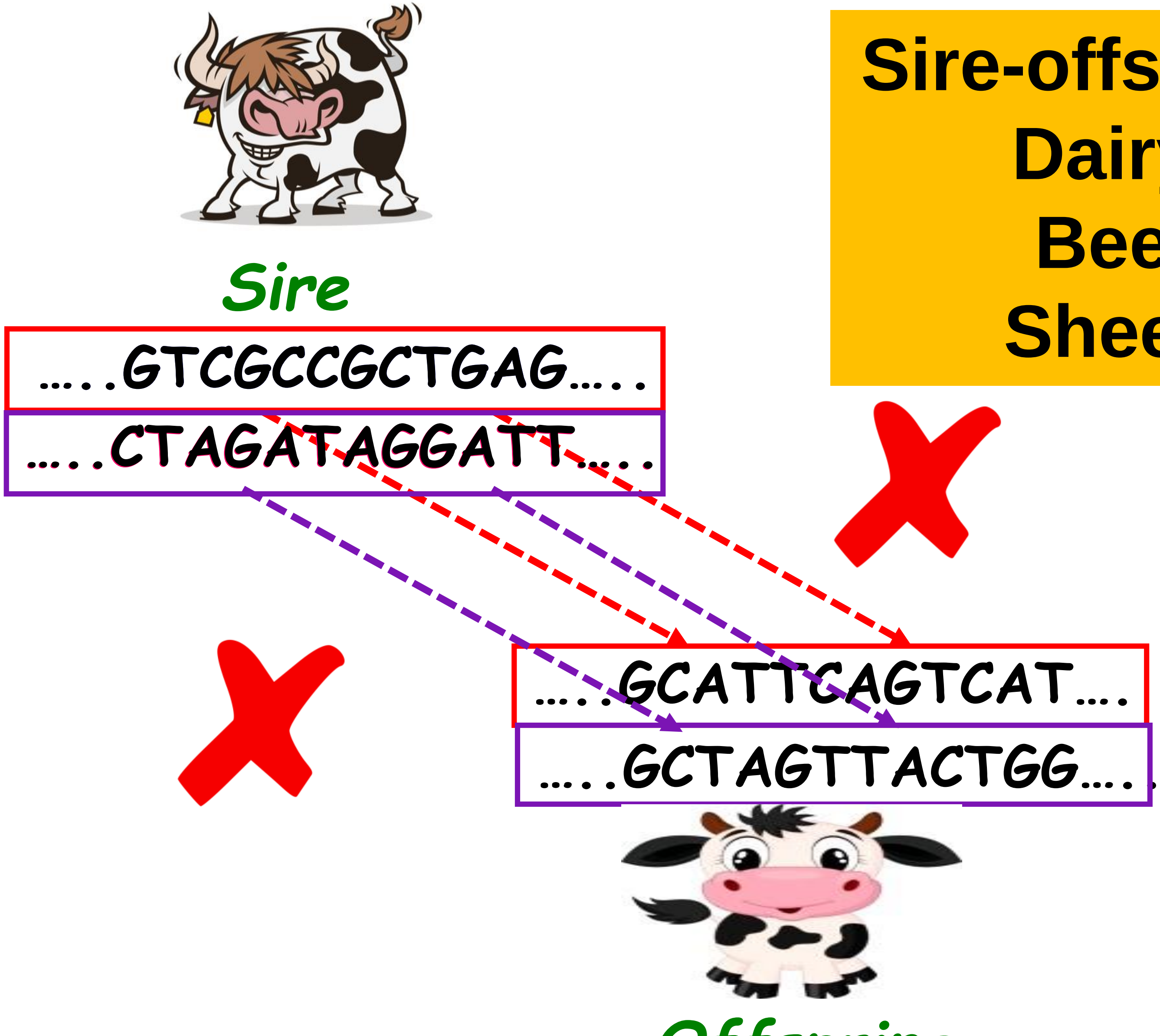
✓

…..CAGATAGGATT…..

…..GTTAGCCTGTCA …..

Offspring

Determining Parentage



Sire

…..GTCGCCGCTGAG…..

…..CTAGATAGGATT…..

…..GCATTCAGTCAT….

…..GCTAGTTACTGG….

Offspring

Sire-offspring errors

Dairy ~7.5%

Beef ~14%

Sheep ~13%

Parentage resolution

Database

“Sire 1” …..ATTCGGGCTGTG…..

“Sire 2” …..CAGATAGGATTC…..

“Sire 3“ …..GTCACCGCTGAG…

“Sire 4” …..GCATTCAGTCAT…..

…..GCATTCAGTCAT….

✓

…..GCTAGTTACTGG…..

Offspring

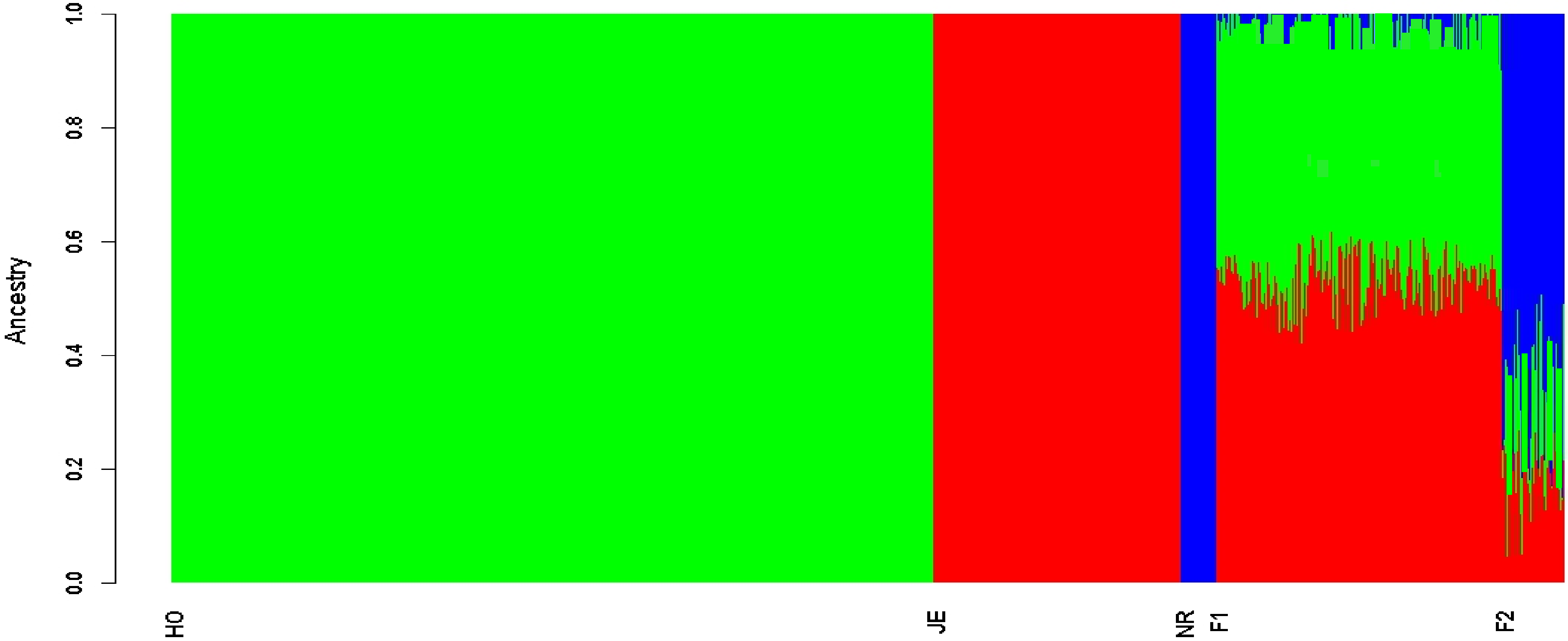
By checking against the genotypes of all sires we can correct 80% of parentage errors

Breed Composition

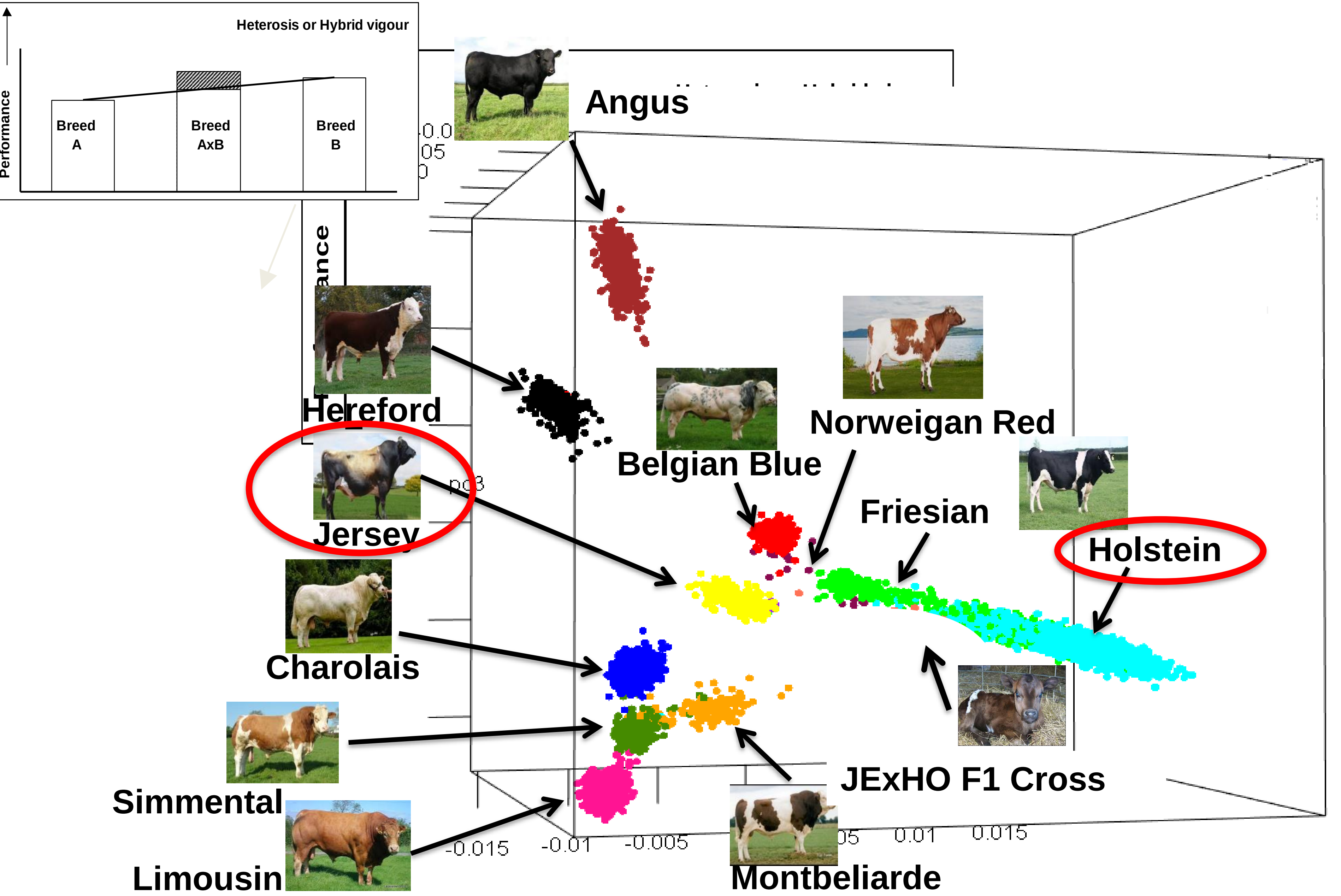
50% JE : 50% HF
(assuming parents
are pure)

50% NR : 25% HF : 25% JE
50% NR : 50% HF : 0% JE
50% NR : 0% HF : 50% JE

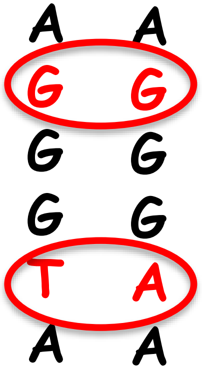
F2 crosses in reality



Breed composition for crossbreeding

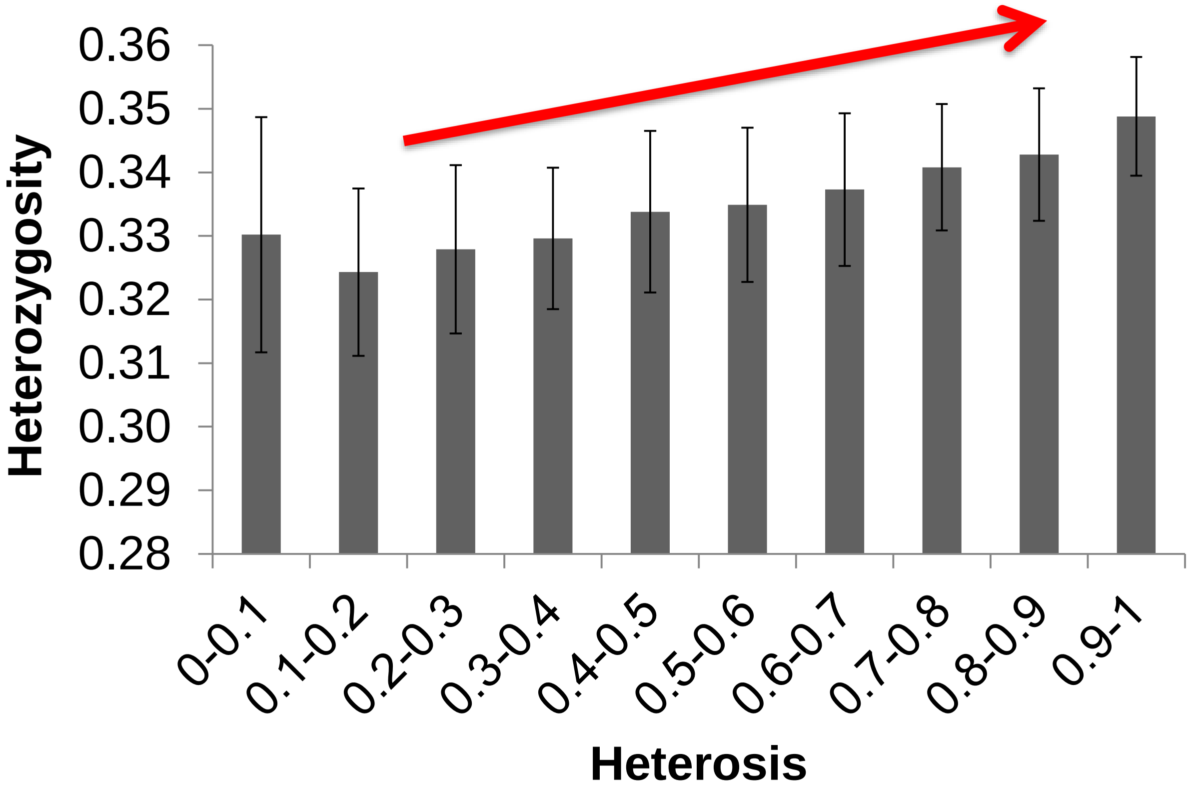


Breed composition for crossbreeding



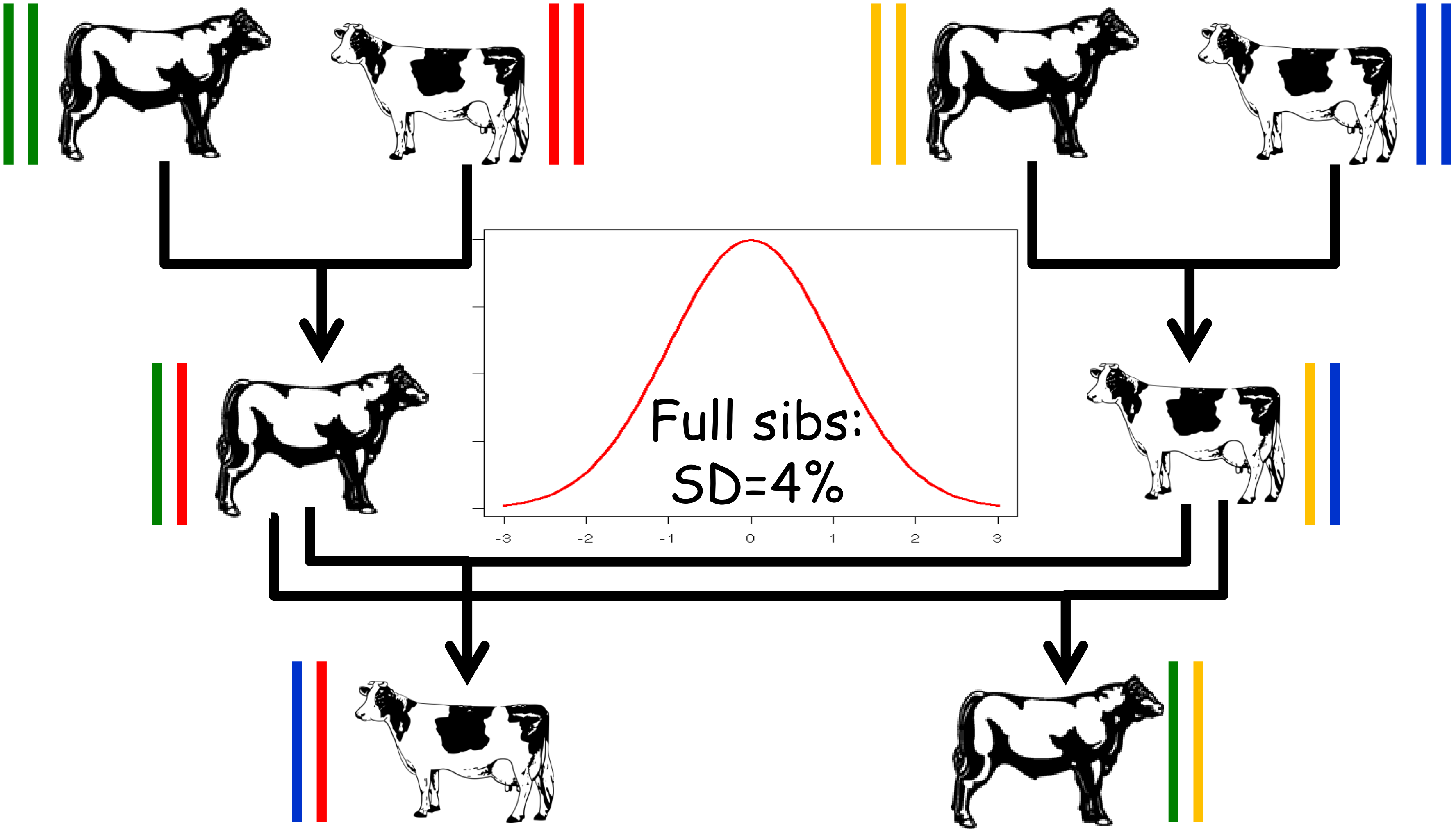
Double copy genotype

Heterozygote genotype



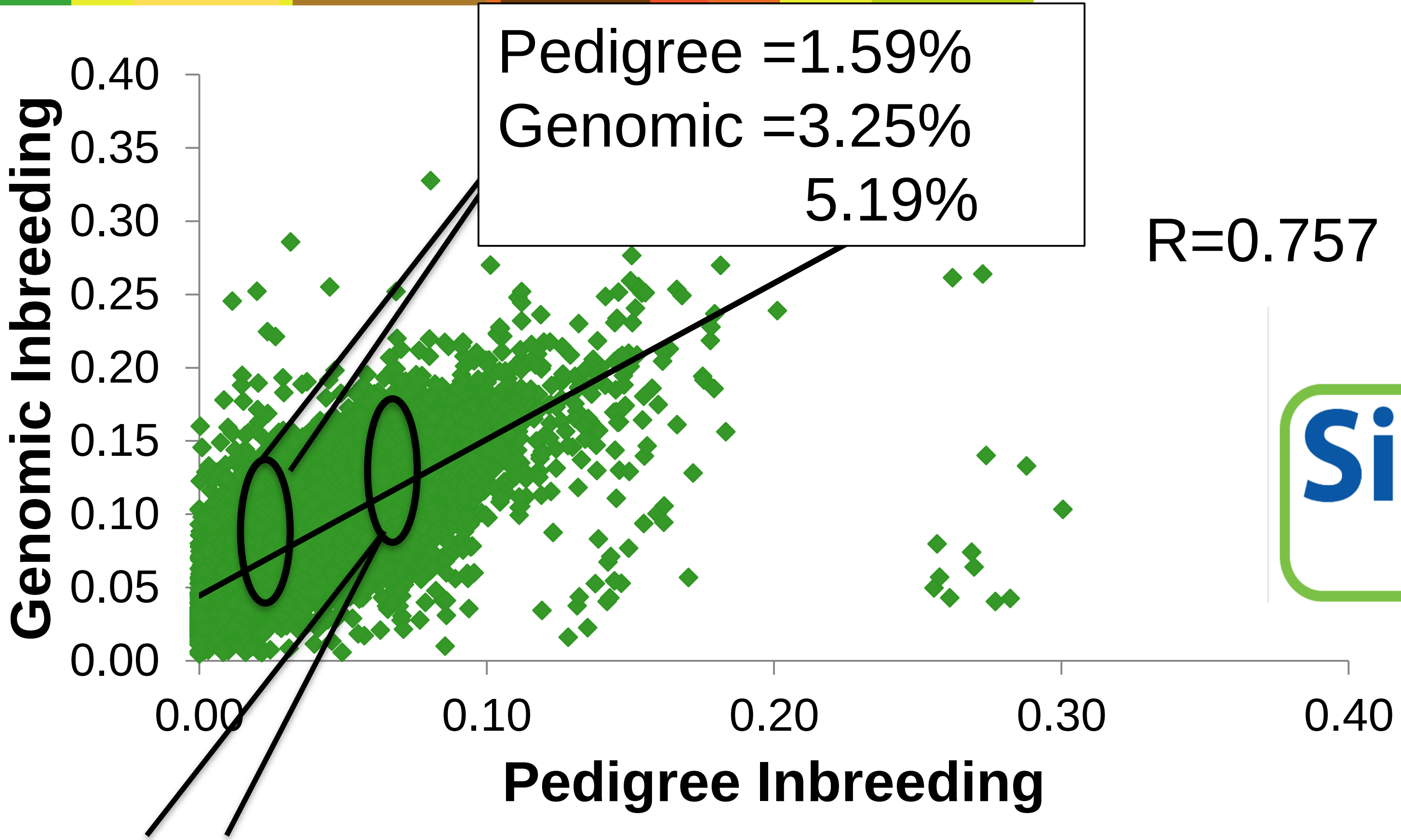
	Mean Het	Min	Max
AA	**0.29**	**0.24**	**0.32**
CH	**0.3**	**0.27**	**0.32**
HF	**0.31**	**0.24**	**0.33**
JE	**0.26**	**0.2**	**0.32**
F1	**0.34**	**0.32**	**0.35**

Genomic Precision Matings



Full sibs:
SD=4%

Genomic Vs Pedigree Inbreeding



Pedigree =1.59%
Genomic =3.25%
5.19%

R=0.757

Sire Advice

3 Progeny
All Full Sibs

Progeny Pedigree Inbreeding
Coefficient = 7.79%

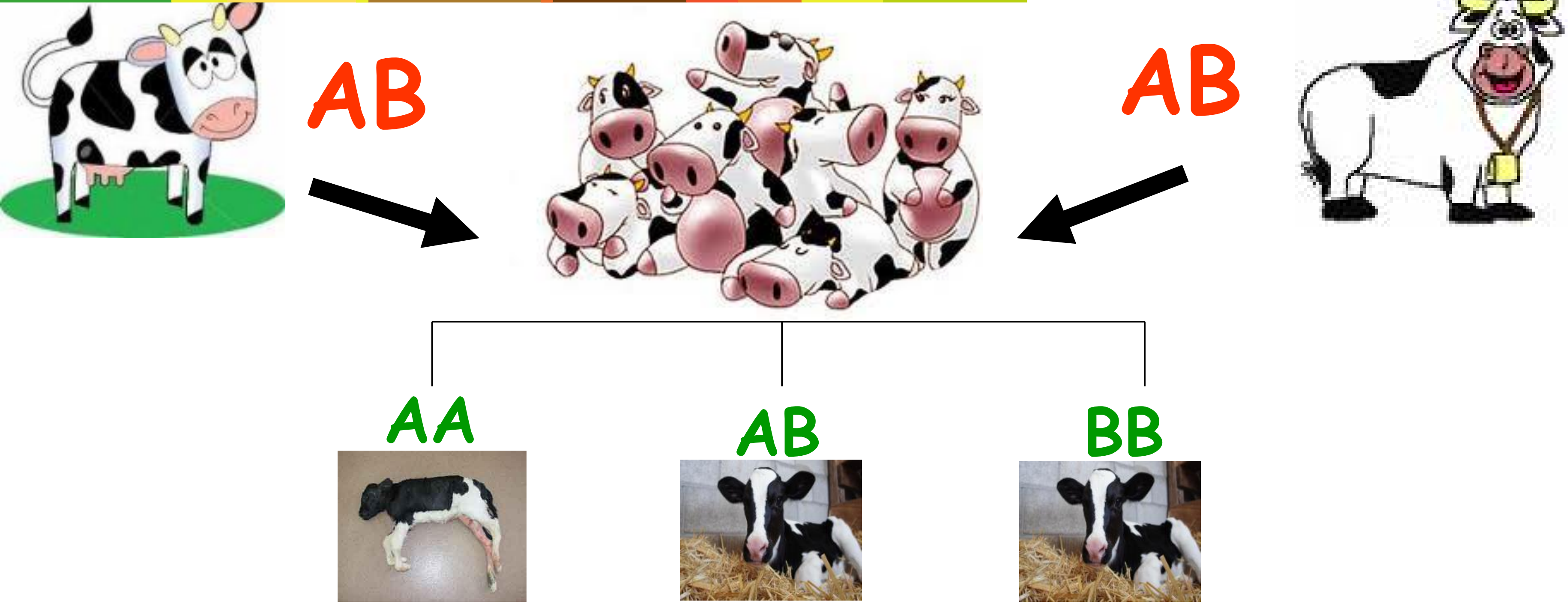
18.18%

17.61%

7.52%

Genomic Inbreeding

Tracking Lethal Recessives



AB

AB

AA

AB

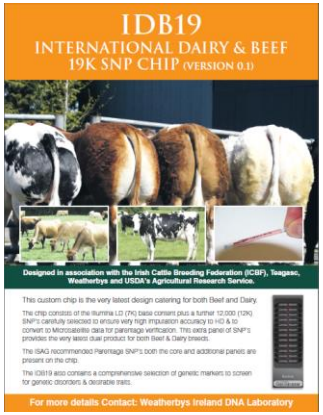
BB

25%
Has CVM

50%
Carries CVM

25%
No CVM

- **Identify carriers using IDB chip**
- **Choose NOT to mate 2 carriers of CVM**
- **4 lethal recessives and 291 major genes on IDB**



IDB19
INTERNATIONAL DAIRY & BEEF
19K SNP CHIP (VERSION 0.1)

Designed in association with the Irish Cattle Breeding Federation (ICBF), Teagasc, Weatherbys and USDA's Agricultural Research Service.

This custom chip is the very latest design catering for both Beef and Dairy.

The chip consists of the Illumina LD (7K) base content plus a further 12,000 (12K) SNP's carefully selected to ensure very high imputation accuracy to HD & to convert to Microsatellite data for parentage verification. This extra panel of SNP's provides the very latest dual product for both Beef & Dairy breeds.

The ISAG recommended Parentage SNP's both the core and additional panels are present on the chip.

The IDB19 also contains a comprehensive selection of genetic markers to screen for genetic disorders & desirable traits.

For more details Contact: Weatherbys Ireland DNA Laboratory

Identifying Major Genes

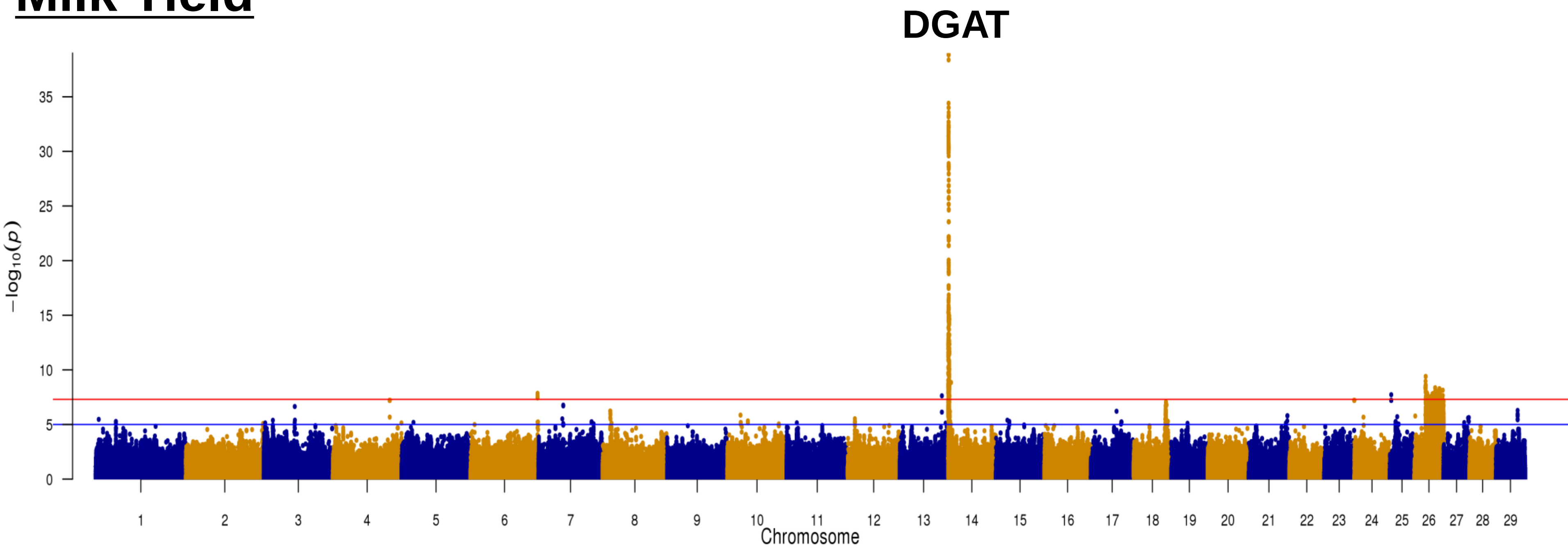
- Members of the **1000 Bull Genomes Project**

635,000 cattle to 40 million SNPS

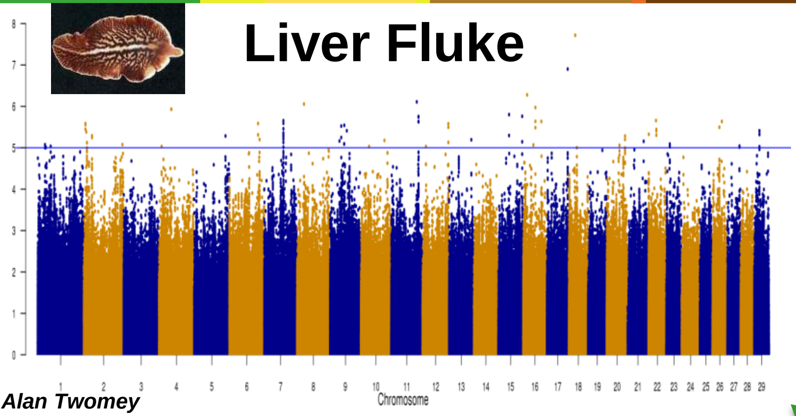
25,400,000,000,000,000 genotypes

Purpose: To identify DNA variants affecting performance and improve genomic predictions

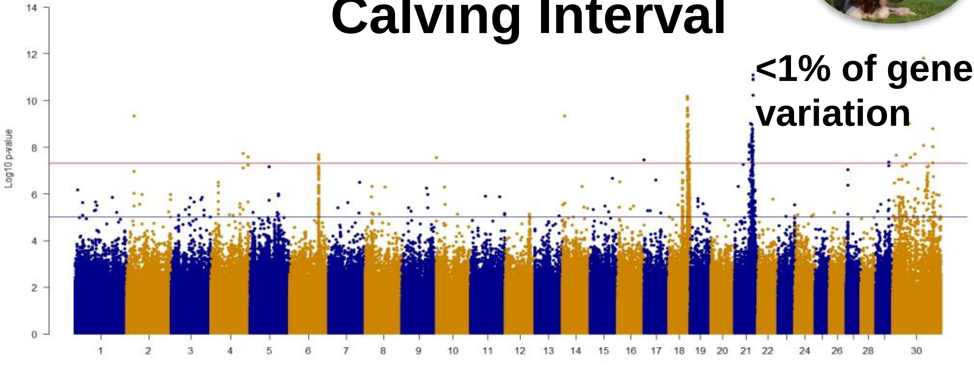
Milk Yield



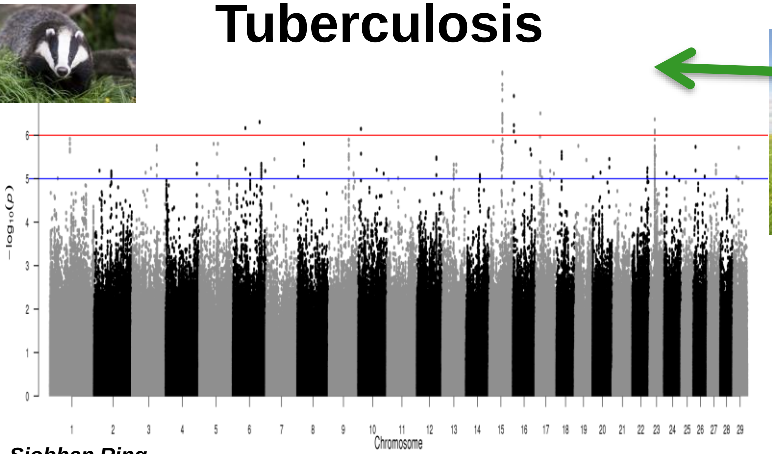
Most often no "Major Genes"



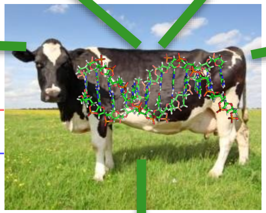
Alan Twomey

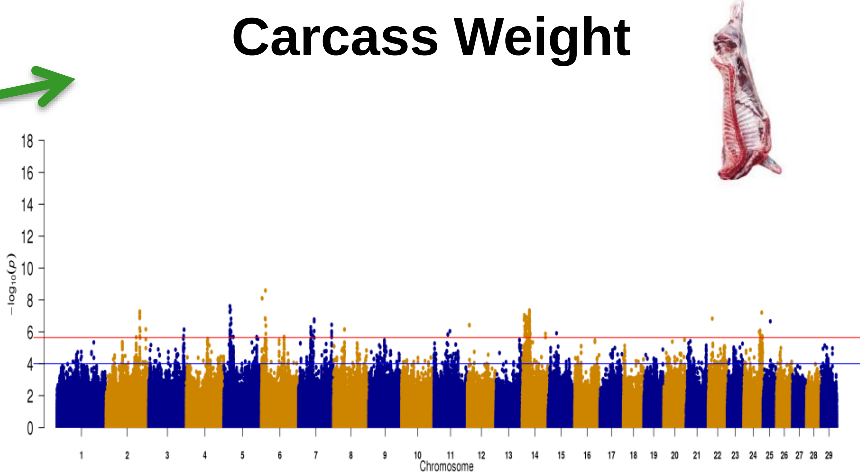


<1% of genetic variation

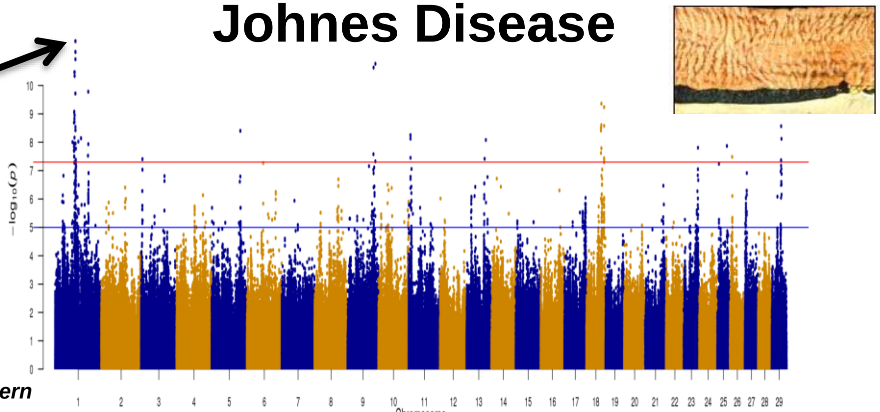


Siobhan Ring





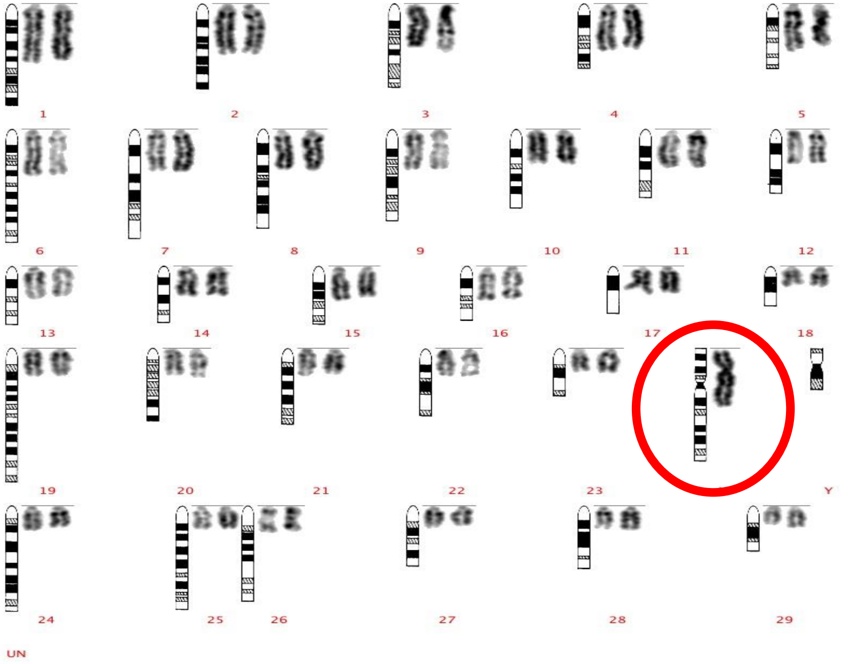
~1% of genetic variation



Shaileen McGovern

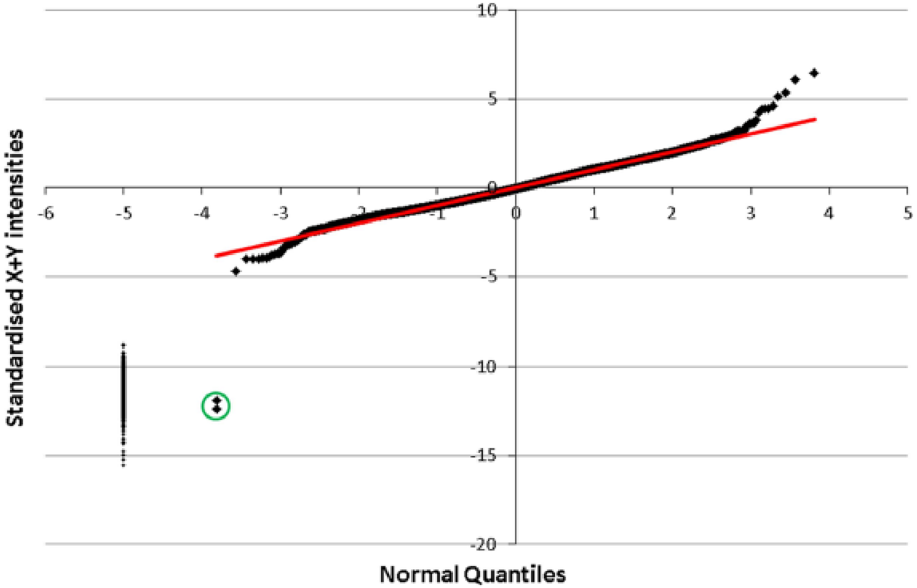
All completed using 18 million DNA variants

Chromosome abnormalities



- Turner syndrome
- Single X chromosome
- **Will NEVER be fertile!**

Detectable using readily available information from genotype file



Conclusions

- Inclusion of genomic information into evaluations clearly **beneficial**
  - Ongoing research for better, more efficient methods
  - Constantly evolving -> new traits
  - **Profit orientated**

- Many benefits of genotyping
  - Increased genomic prediction accuracy, parentage, breed prediction, inbreeding measures, mating advice, track lethal/major genes
  - Increased **Genetic Gain**

- **Custom genotyping panel** very beneficial