

# **THE APPLICATION OF GENOMIC SELECTION IN SOUTH AFRICA: IMPLEMENTATION, ADAPTATION, CHALLENGES AND FUTURE PROSPECTS**

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# Implementation

Implementation of Genomic Selection in SA had a slow start:

- Initially no public funds & currently very limited
- Lack of local laboratory capacity
- Weak local economy
- Weak currency

Bonsmara Breeders' Society started with investing by genotyping first 650 Bonmara cattle (2013-2015)

During 2016 the Beef Genomic Program, funded by TIA

2016 to 2020, 9 880 beef cattle from 9 breeds genotyped

After BGP, SA Stud Book established Genomic Reference populations for 3 beef breeds (BON, BMA and DRB)

Implemented a Single Step G-BLUP using MIX99

- In-house genomic pipelines developed and set-up
- Parent verification and discovery using Fimpute2 and in-house software
- Breed fractions estimated using a SNP-BLUP approach using MIX99, 2018 (thanks to Dr D. Barry)

\*\* Ryan *et.al* 2023. Front. Genet., Vol.14

Unfortunately, during the BGP period, no single gene traits were made available to participants

# Implementation

Post BGP: Own private genotyping by SA Beef breeders, mainly for single gene trait information like myostatin and polled genes

Currently, Stud Book run Genomic SS-GBLUP for 7 Beef Breeds. (17 764 genotypes of 17 breeds)

1<sup>st</sup> Dairy genotypes were obtained through research projects with Teagasc – sharing 286 HOL genotypes

Dairy Genomics 3-year Program, funded by TIA commenced in 2017

Uptake of dairy genotyping is very slow with 4 799 dairy animals currently genotyped – SS-GBLUP implemented for 3 dairy breeds in 2020

# Implementation

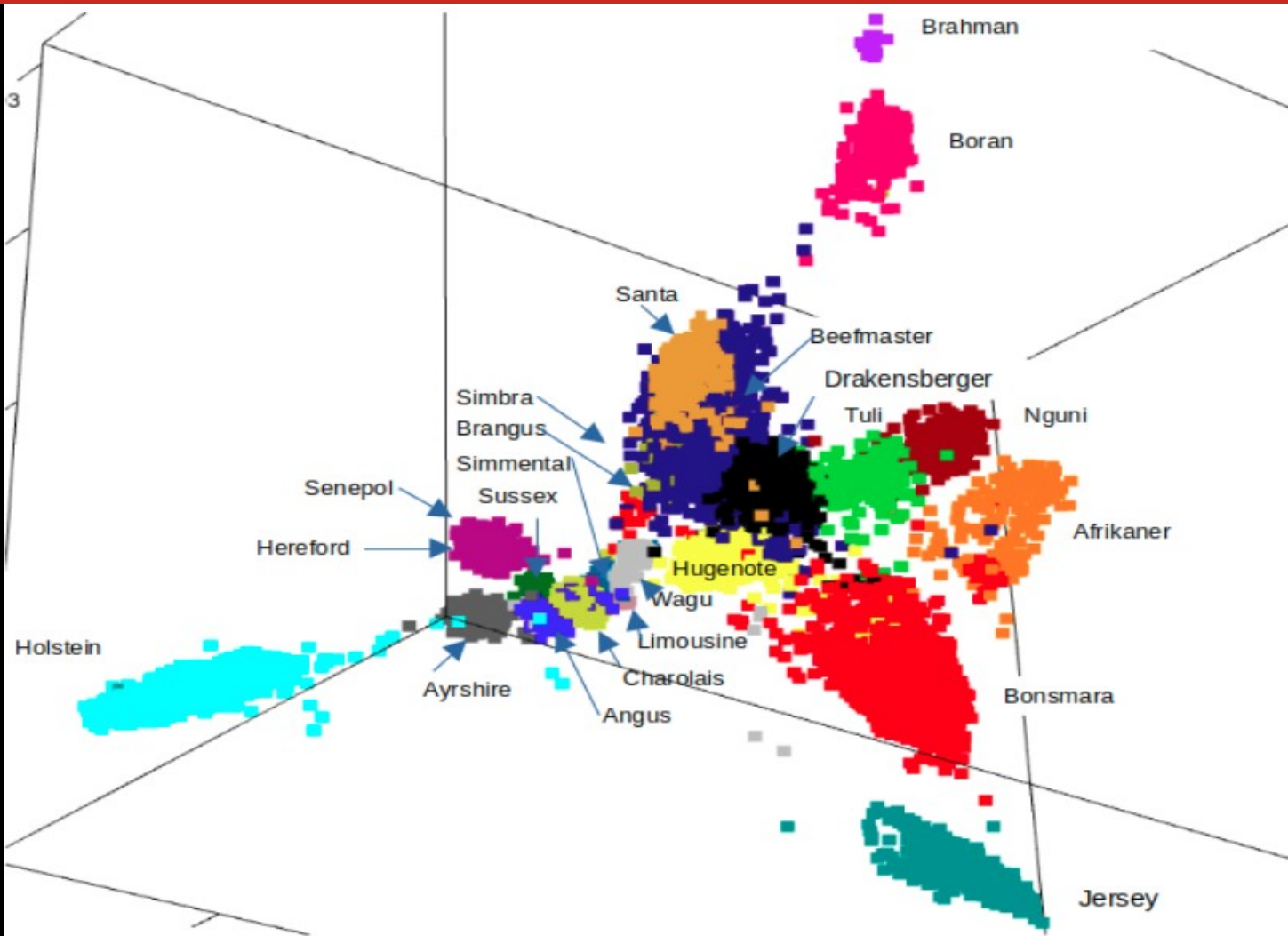
Genotyping for Small Stock has just commenced for only the **Merino** breed (2 344 genotypes running a SS-GBLUP (MIX99))

Initial genotypes were mainly obtained through collaboration between Stud Book and Grootfontein Agricultural Development Institute (GADI)

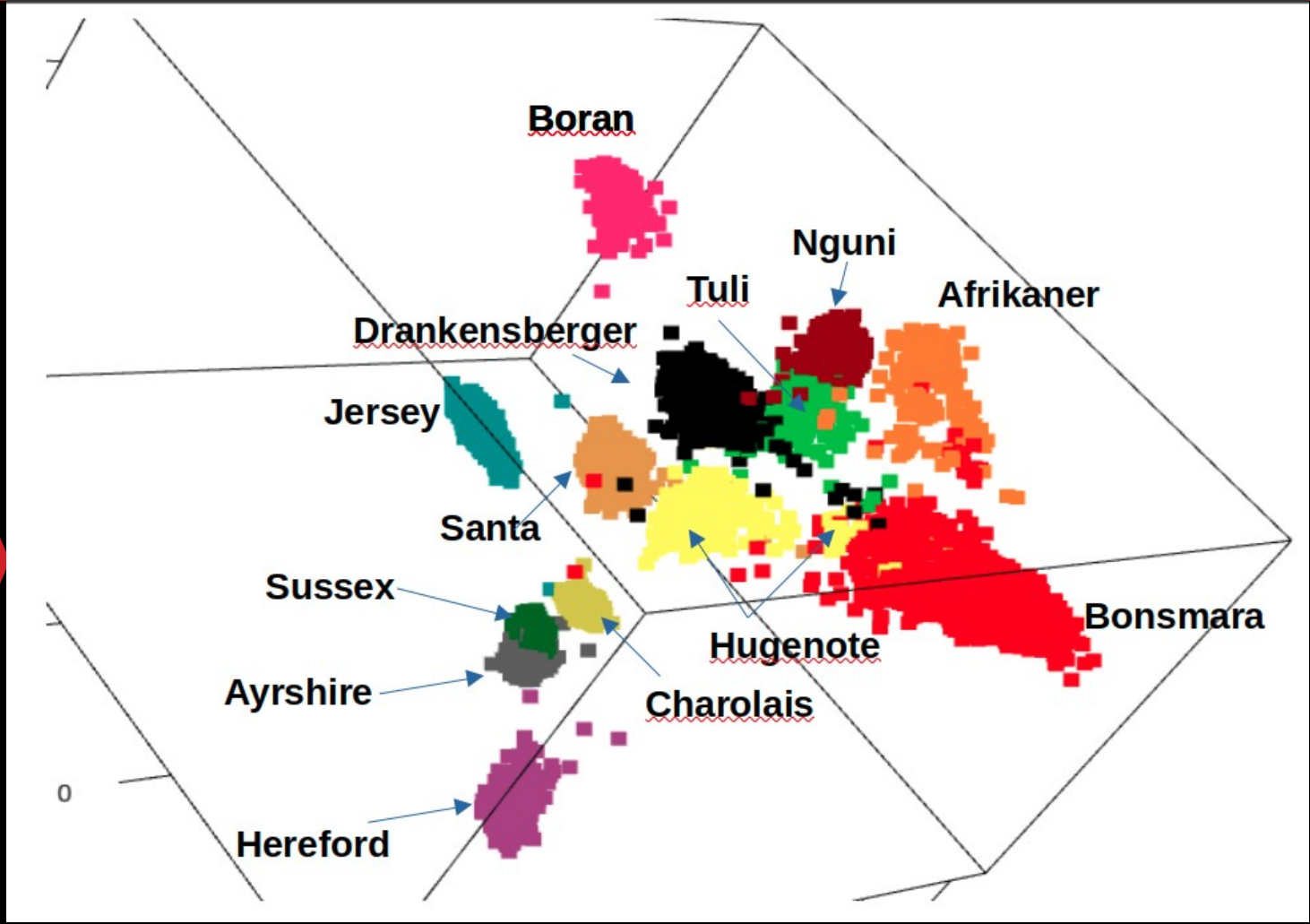
Majority of genotypes from high genetic impact animals in research and commercial herds

Currently, 2 413 sheep genotypes from 6 breeds

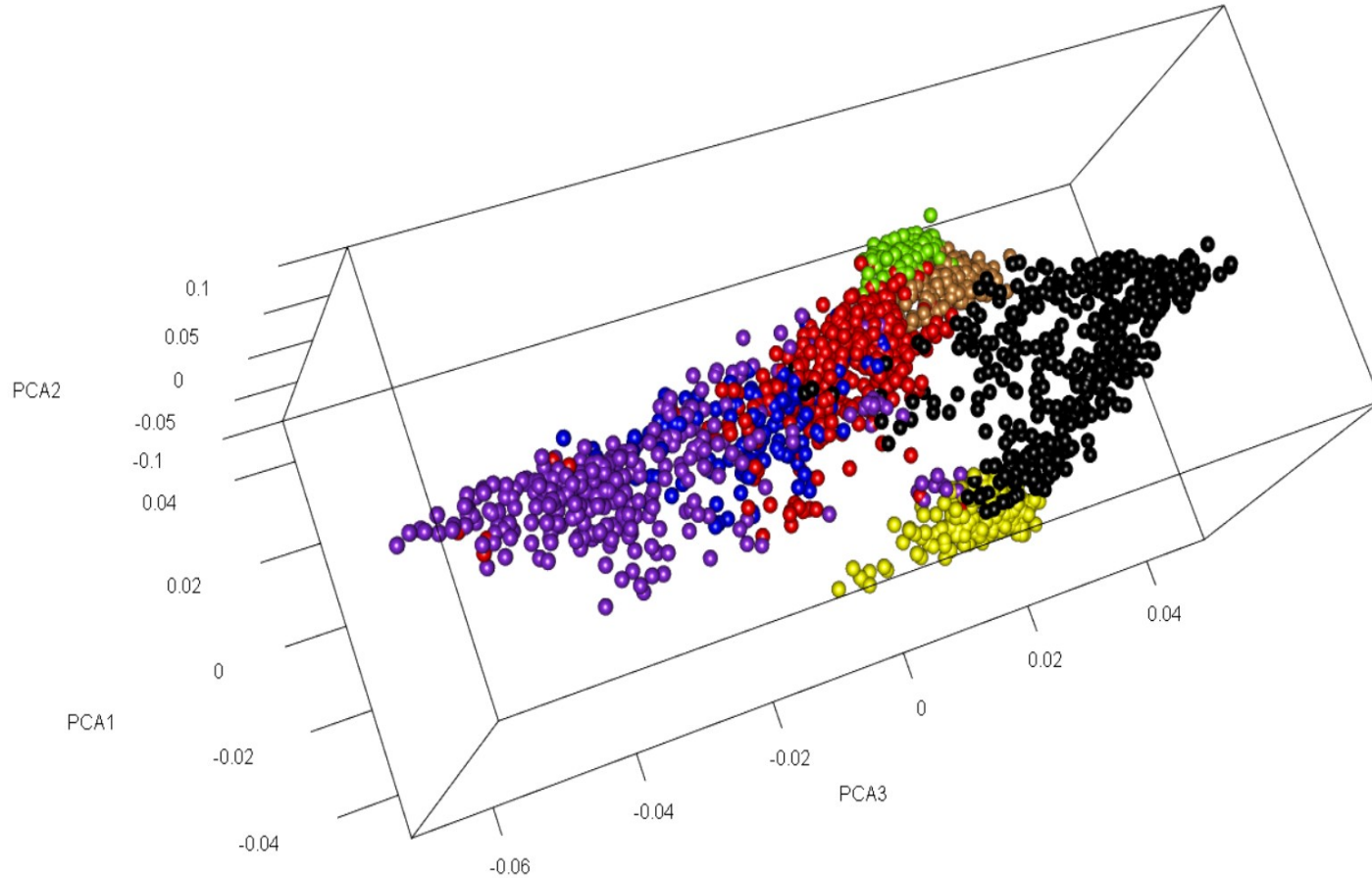
# Results - Bovine PCA



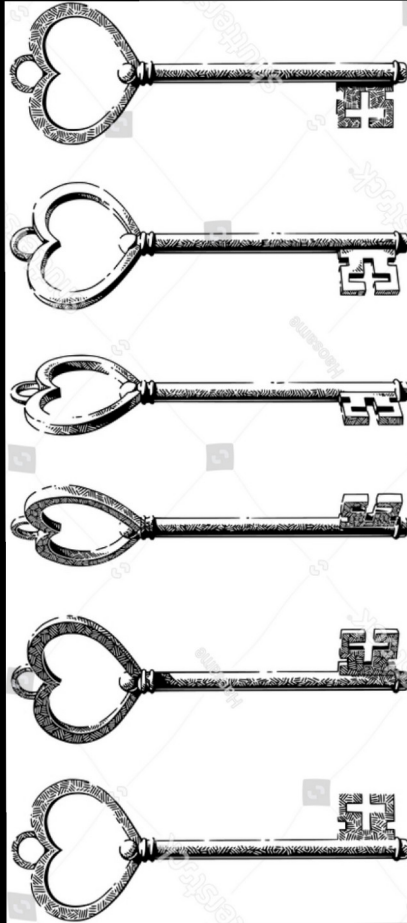
# Results – Bovine PCA



# Results - Merino PCA







# The Key?

# BREED KEYS!!

# Results - Breed Keys



snp_name	bma	bon	bor	chl	hfd	drb	ngi	tul
ARS-BFGL-NGS-65067	0,001332	0,000205	0,000111	0,000048	-0,000396	0,000014	-0,000828	-0,000255
ARS-BFGL-BAC-34682	-0,000209	-0,000979	-0,000065	-0,000325	0,000271	-0,000459	0,001211	0,000618
ARS-BFGL-NGS-3964	0,001211	-0,001234	-0,000003	0,000018	0,000298	0,000246	-0,000004	0,000046
ARS-BFGL-NGS-98203	-0,000687	-0,000129	0,000681	0,000397	-0,000430	-0,000478	0,000805	-0,000895
ARS-BFGL-BAC-31722	0,000726	-0,000388	0,000301	-0,000238	-0,000037	0,000184	-0,000150	-0,000120
ARS-BFGL-BAC-6557	0,000406	-0,000140	-0,000363	-0,000298	-0,000030	-0,000448	0,000369	0,000348
ARS-BFGL-BAC-14857	-0,000796	0,000017	-0,000007	0,000063	0,000179	0,000379	0,000630	0,000109
Hapmap53766-ss46526150	-0,000797	-0,000387	-0,000219	0,000206	0,000264	-0,000127	0,000048	0,001226
ARS-BFGL-NGS-115971	-0,000251	-0,000173	0,000880	-0,000356	0,000236	0,000066	-0,000810	0,000766
ARS-BFGL-NGS-62826	0,000132	-0,000710	0,000265	0,000433	-0,000280	-0,000613	0,000139	0,000257

**25K SNP Makers AND 23 Different Breeds' Keys**

# Results - Breed Keys



BREED	BMA	BON	BOR	CHL	DRB	HFD	JER	NGI	TUL
BMA	0.99	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BMA	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BON	0.01	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BON	0.01	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BOR	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00
BOR	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00
CHL	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00
CHL	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00
DRB	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00
DRB	0.00	0.00	0.00	0.00	0.99	0.00	0.00	0.00	0.00
HFD	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00
HFD	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00
JSE	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00
JSE	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00
NGI	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00
NGI	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00
TUL	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.01
TUL	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	1.00

# Results - Breed Keys

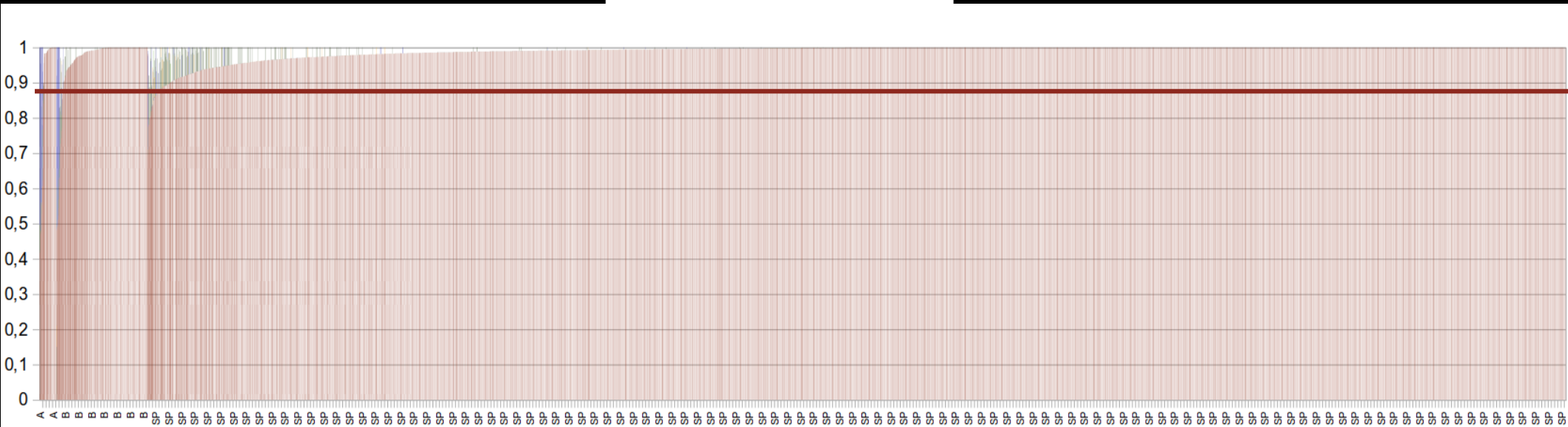


ID	BON	BMA	DRB	CHL	NGI	BOR	JER
CHL M BL 140056	6,0%	0,0%	6,5%	<b>98,7%</b>	7,6%	0,0%	0,0%
JER DQHV0830	0,0%	0,0%	0,0%	0,0%	0,0%	0,0%	<b>99,7%</b>
BON F WJK 030494	<b>99,5%</b>	0,0%	0,0%	0,0%	0,0%	0,0%	0,0%
DRB M BV 020370	6,0%	0,0%	<b>97,7%</b>	0,0%	0,0%	0,0%	0,0%
NGI F SHL 020083	0,0%	0,0%	0,0%	0,0%	<b>98,5%</b>	0,0%	0,0%



## 9 208 – Genotypes of Breed A

$7 / 8 = 0.87\%$



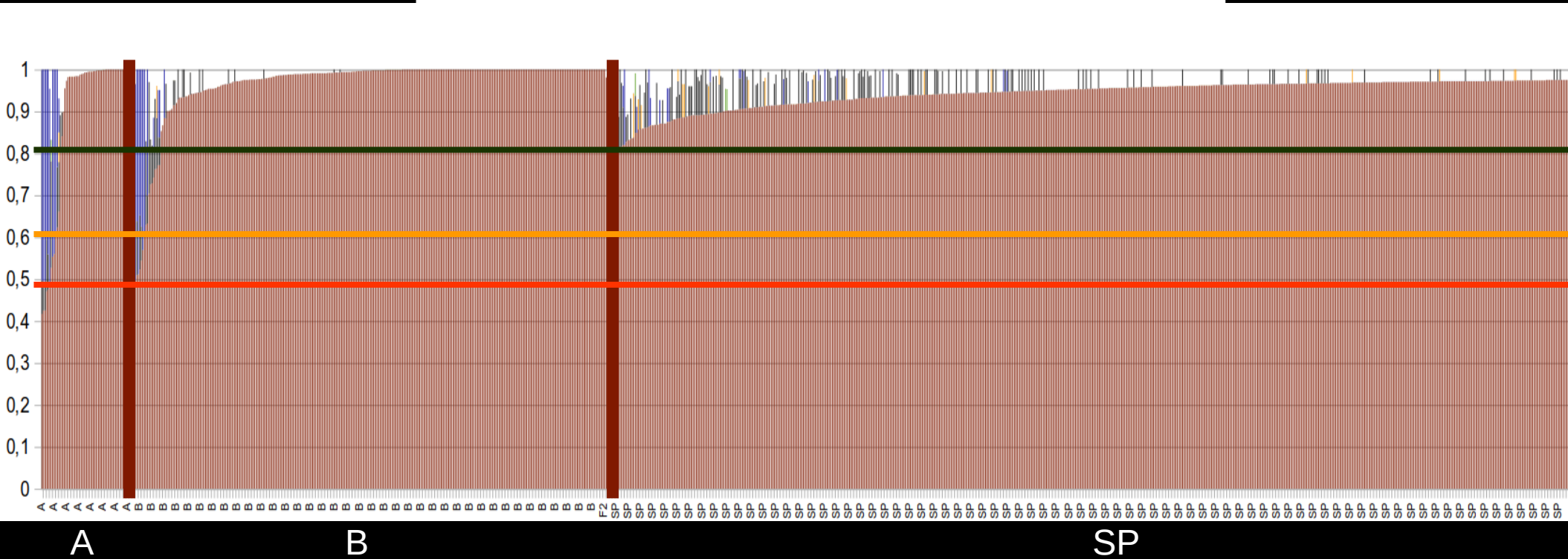
A

B

SP

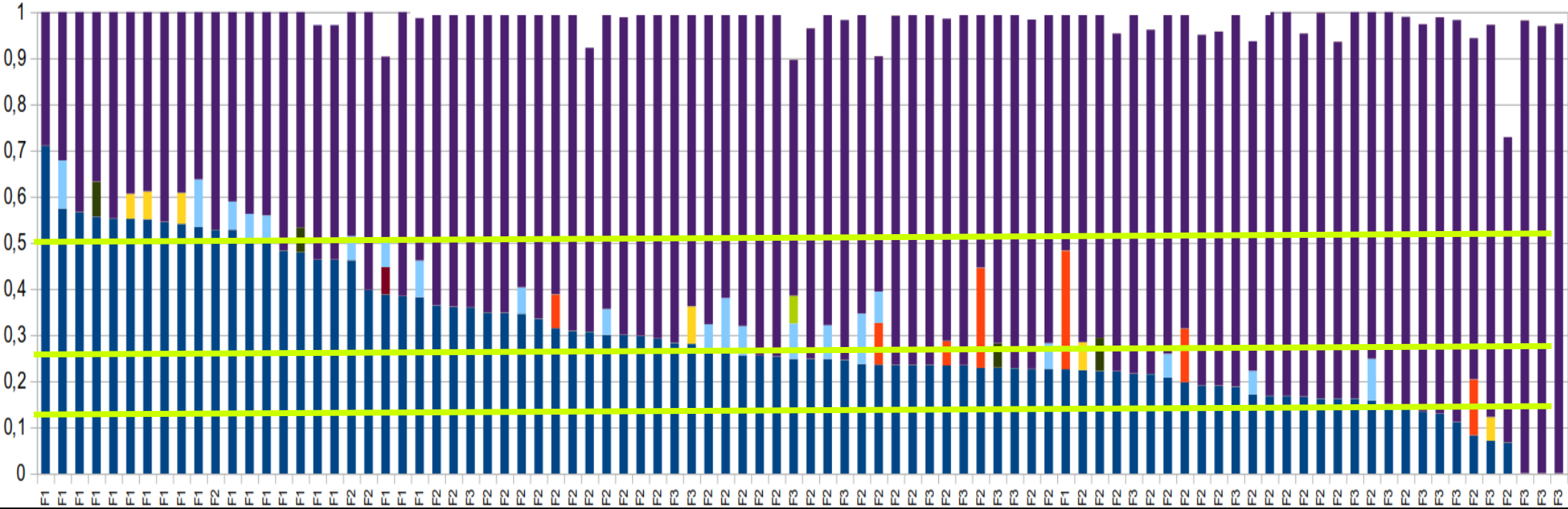


## Selected – Breed A Genotypes





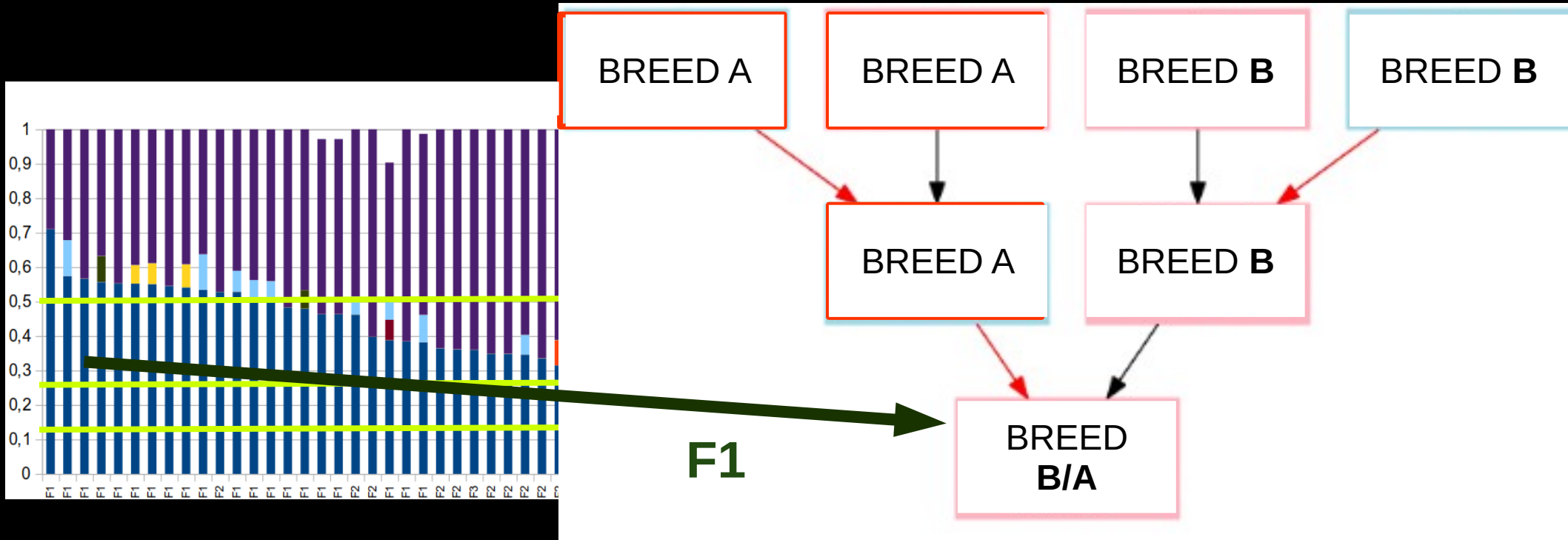
## Breed A Introduced into Breed B



# Results - Breed Keys



[SABeefBulls.com](http://SABeefBulls.com)



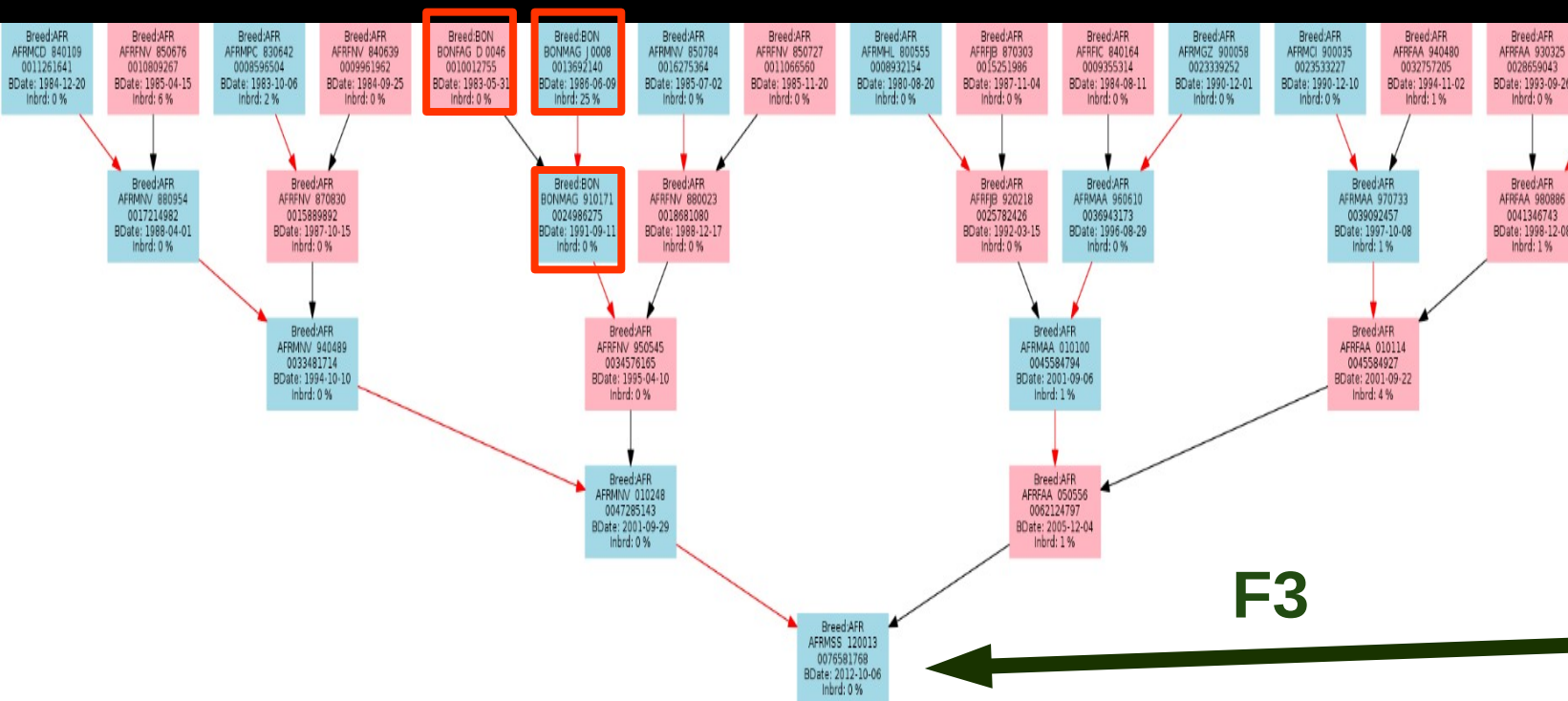




# Results - Breed Keys



## SABeeFBulls.com



F3

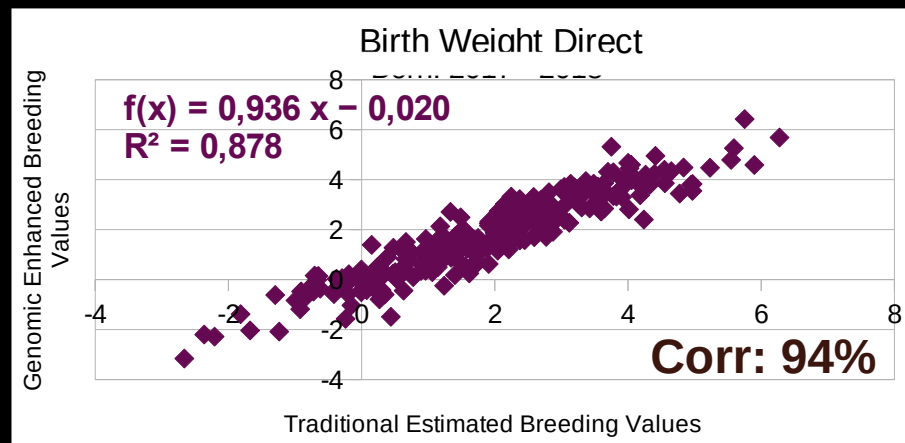
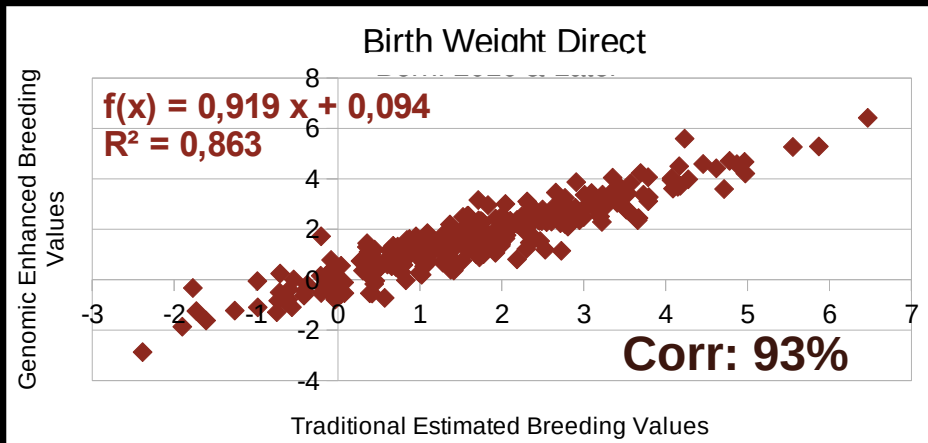
LOGIX-Profit through genetics



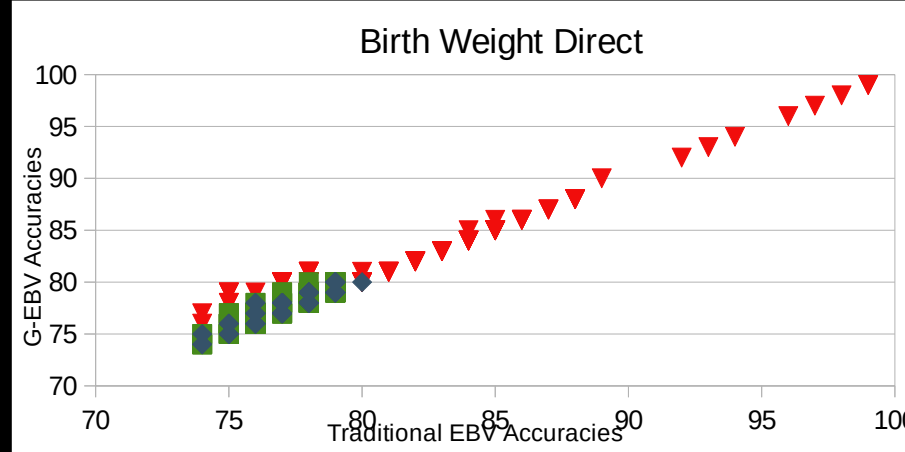
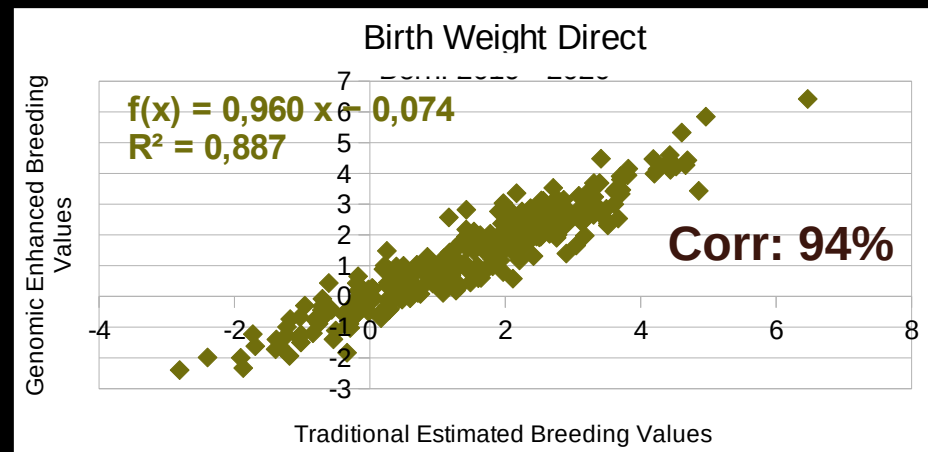
# Discussion

- Between 2% and 8% pedigree errors discovered and corrected where an alternative parent could be identified
- Where parentage could not be corrected: H-matrix used to correct for the error in the A-matrix
- Correcting incorrect parentages is critical for reliable Breeding Value predictions
- Addressing one of the main reasons why Breeding Values might be unstable over time
- Even if this is the only advantage that this technology offers, it outweighs genotyping cost by ensuring more accurate and reliable predictions for selection and genetic progress

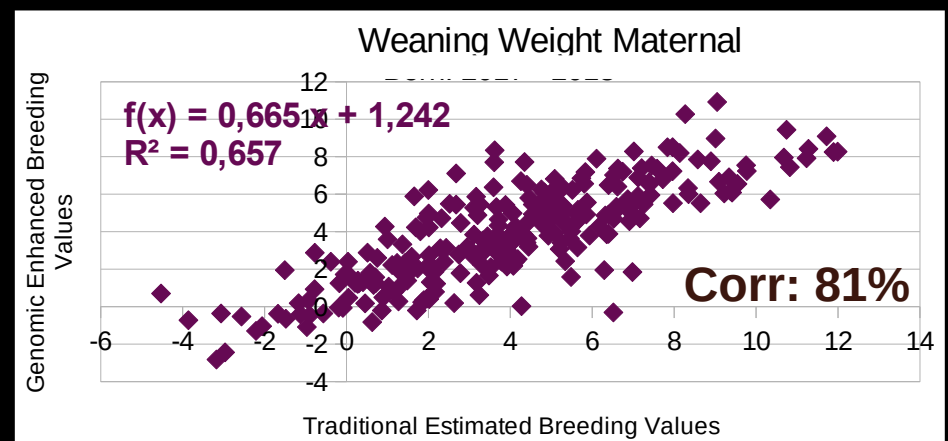
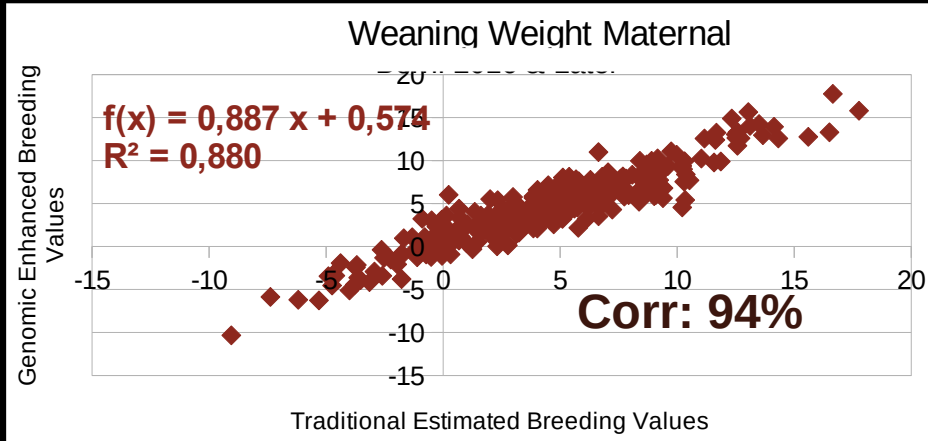
# Results - High Heritable & Sufficient Data



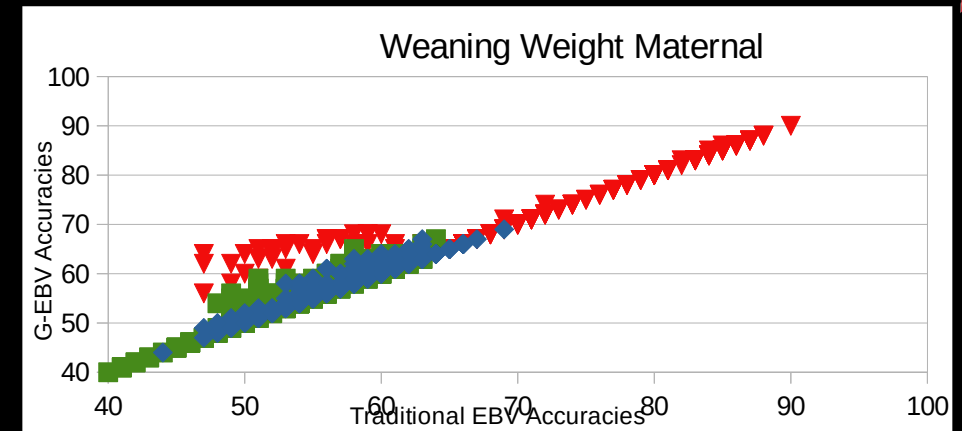
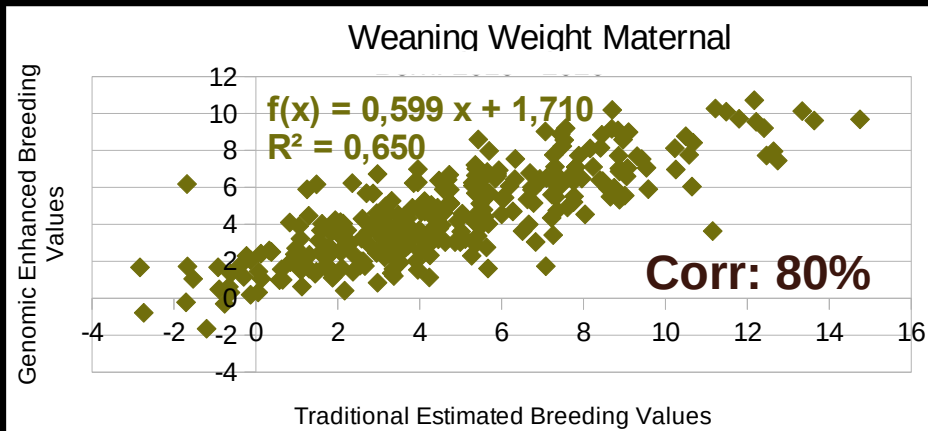
$h^2 = 0.31$



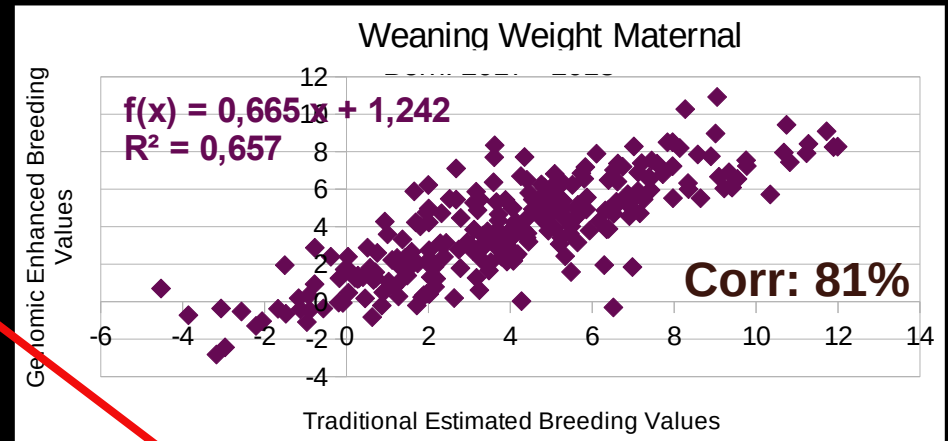
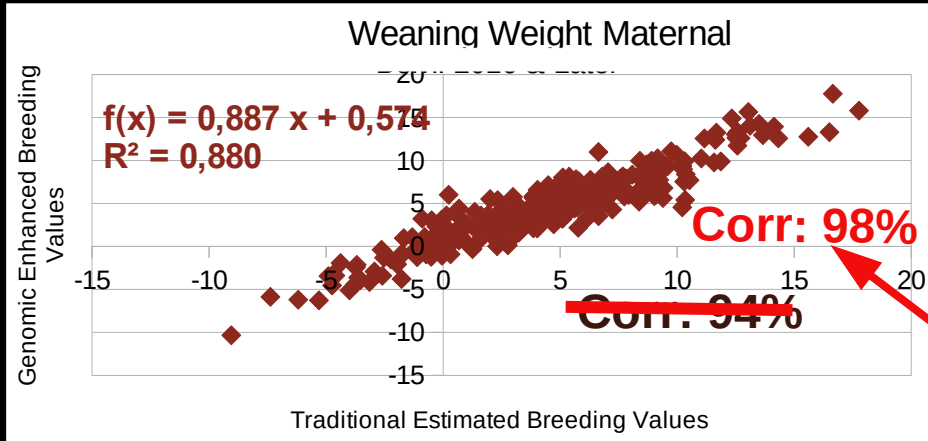
# Results – Maternal Traits



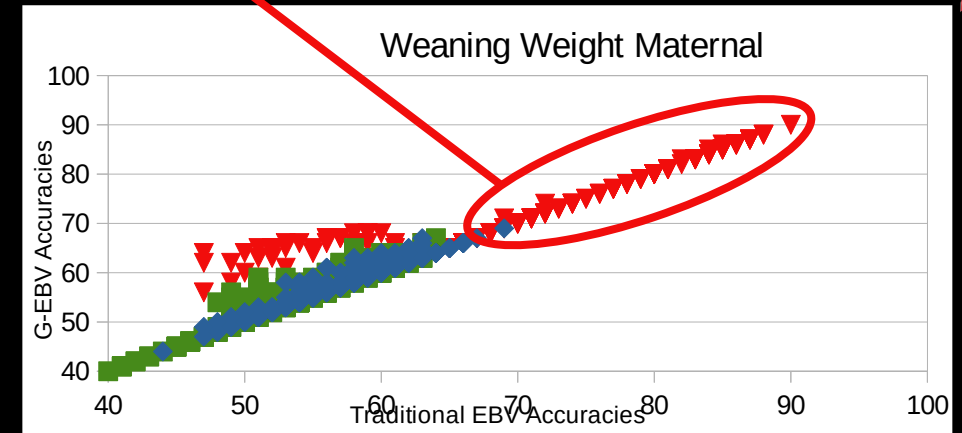
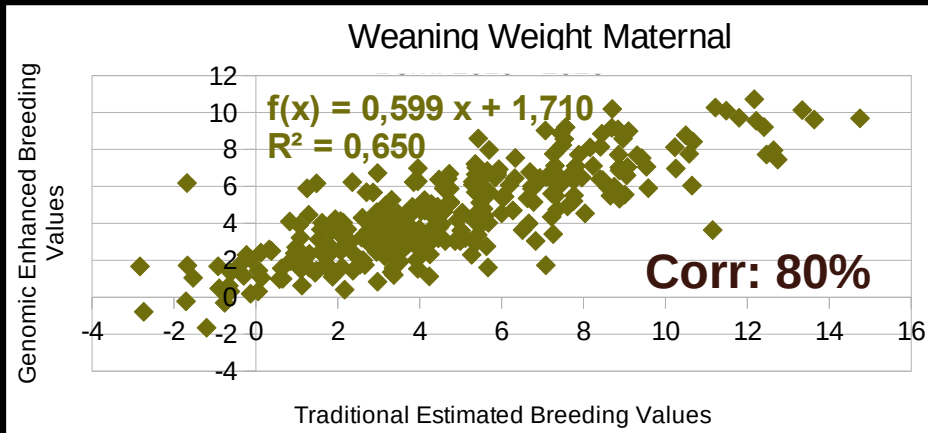
$h^2 = 0.15$



# Results – Maternal Traits

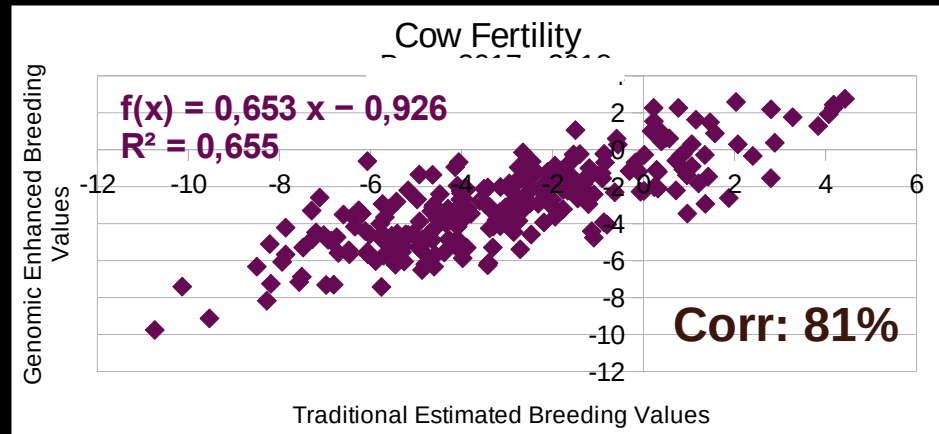
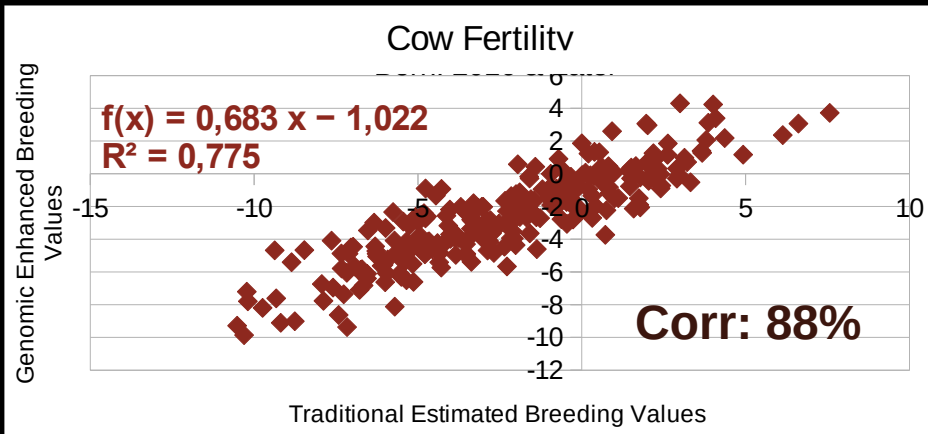


$h^2 = 0.15$

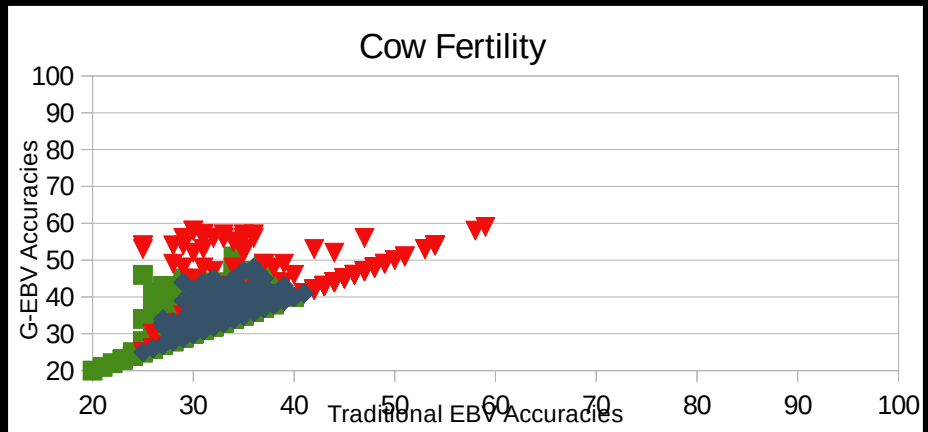
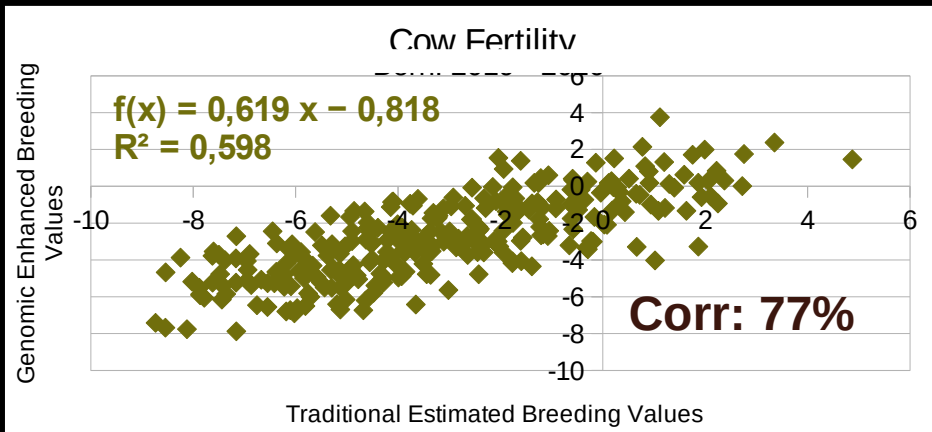


# Results – Lower Heritable Traits

LOGIX-Profitt through genetics

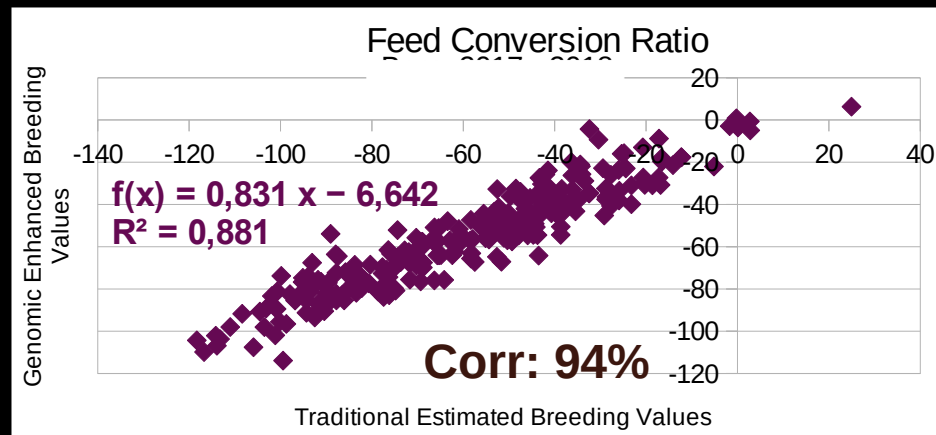
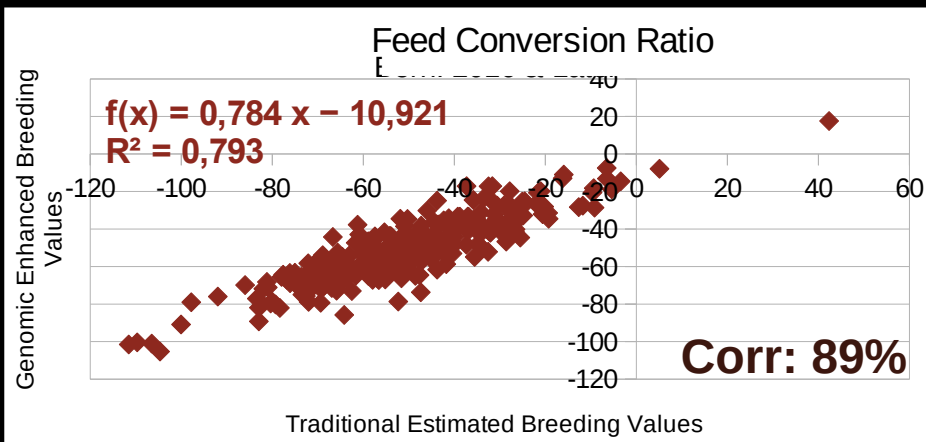


$h^2 = 0.10$

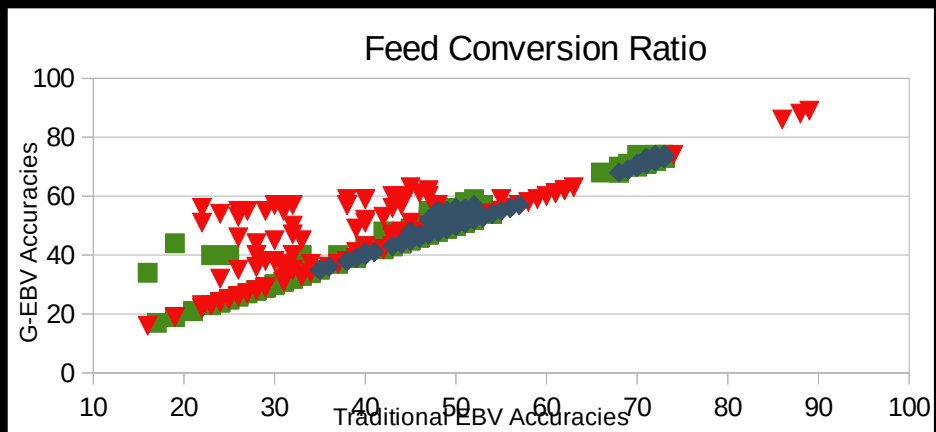
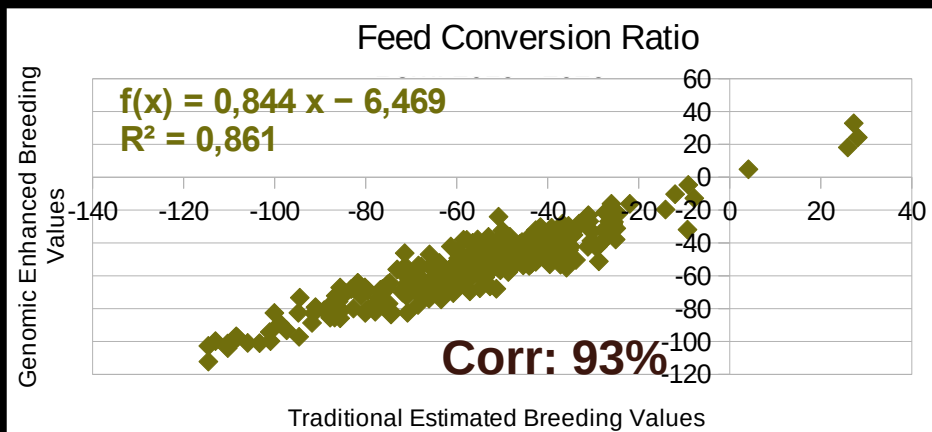


LOGIX

# Results – New, Difficult & Expensive Traits



$h^2 = 0.31$





# Conclusions & Prospects

- Big likelihood for 2<sup>nd</sup> round BGP – all Stud Book recorded beef breeds moving over to SS-BLUP
- Slow uptake in dairy also due to false marketing (AI and Pharmaceutical companies)
- Relative expensive genomic tests (€40.28 vs €18.00) is challenging
- Need for more focus on single (or limited) gene markers services (eg. Scrapie resistance, Dermatosparaxis)
- Realisation of need to change over to genomic information
  - Accurate & stable genetic merit predictions
    - Sex limited, maternal, limited recording
  - Parentage verification & exploration
  - Fast tracking upgrading
  - Deleterious & advantageous mutations



# LOGIX

## Thank You

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Profit through genetics