SA STAMBOEK
STUD BOOK

RE-RANKING OF IMPORTED ANGUS SIRES FOLLOWING INTEGRATION OF FOREIGN GENOTYPES INTO A NATIONAL GENOMIC EVALUATION

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ANGUS

INTRODUCTION

- The Angus Cattle Breeders Society of South Africa was formed in 1917
  - Complete pedigree contains 280 194 animals

- Number of imported sires has rapidly increased in the last 15 years:
  - 2 847 imported sires from 18 countries
  - 1 710 sires from the USA & 627 from Canada
  - 192 from Zimbabwe & 177 from Namibia

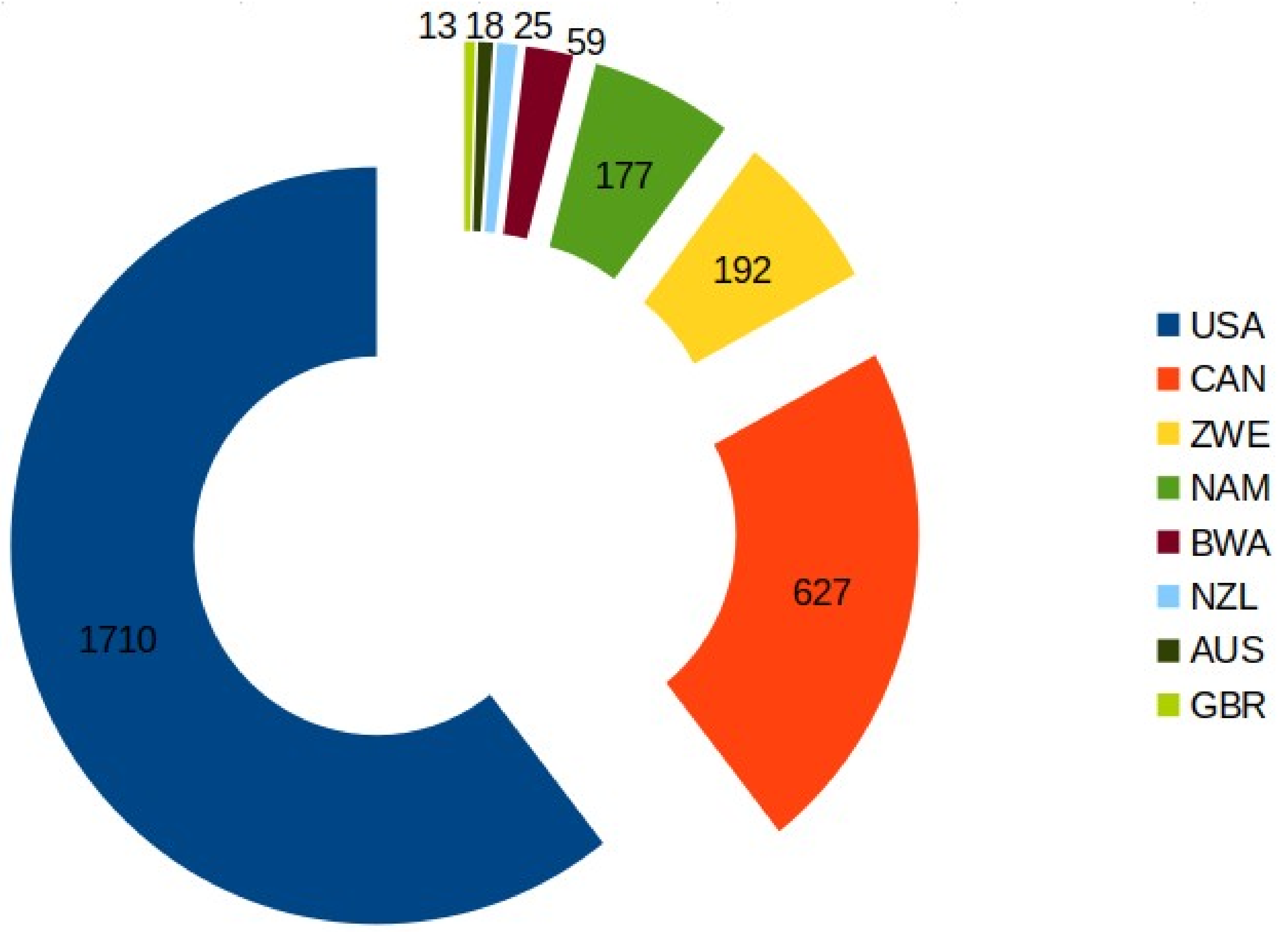


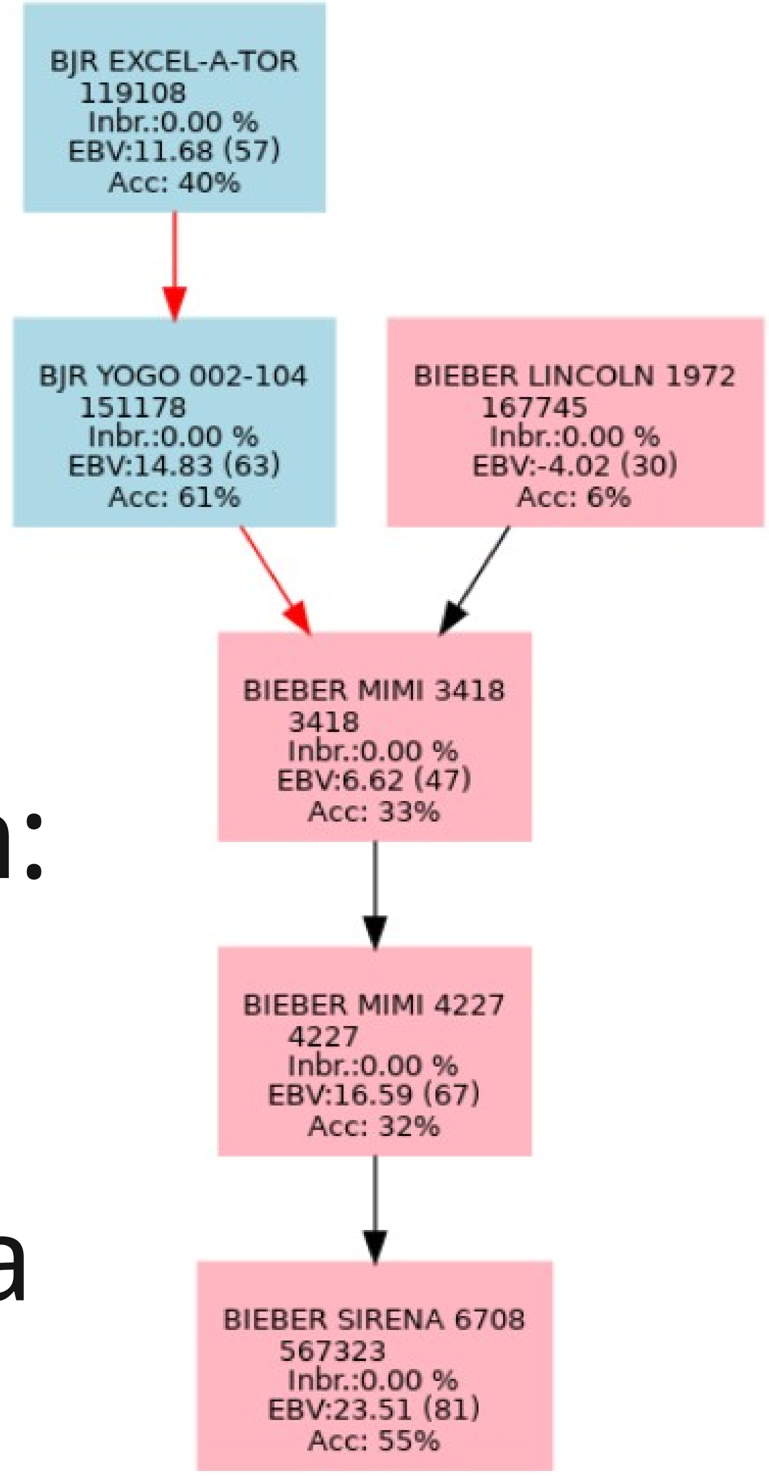
Figure 1: Top 8 Countries of imported Angus sires

INTRODUCTION

- Limitations of Imported Angus bulls within the South African national genetic evaluation:

- Limited pedigree depth
- Limited progeny records & performance data under local conditions (Škorput *et al*.,2025)

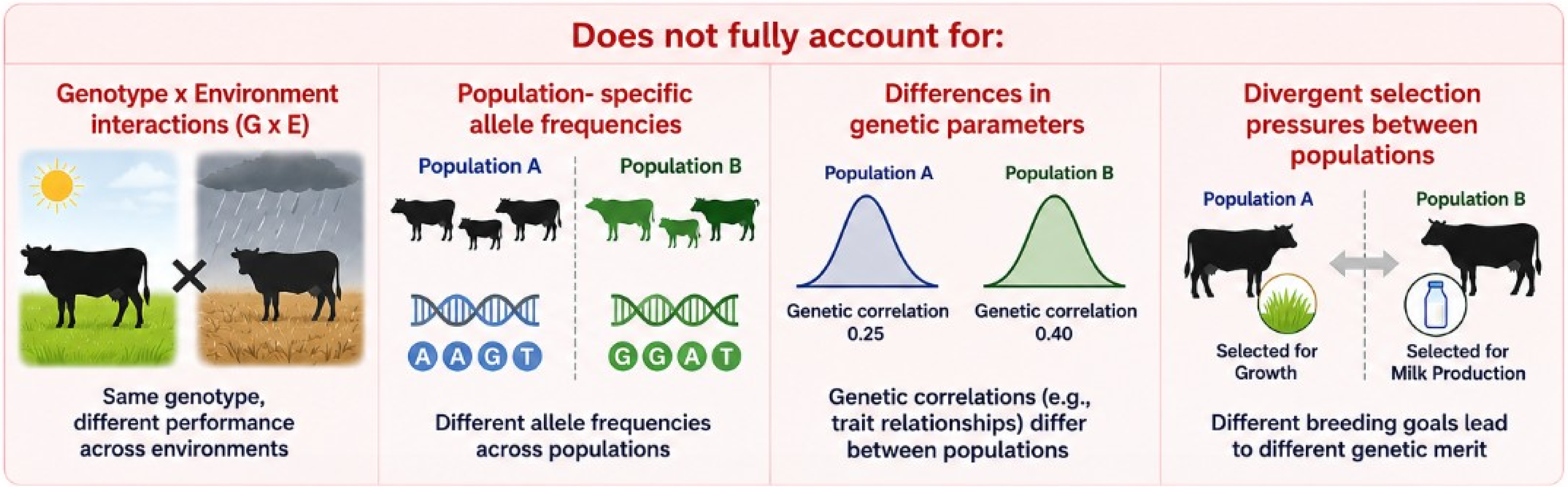
- Angus Society of South Africa have implemented a single-step genomic evaluation since March 2026, allowing for the inclusion of imported bulls genotypes



Problem Statement

- Historically, country-of-origin percentiles were blended into the local evaluation until sufficient local progeny records were available

- avoids initial underestimation of Pedigree-based Breeding Values (EBVs)



Does not fully account for:

Genotype x Environment interactions (G x E)

Same genotype, different performance across environments

Population- specific allele frequencies

Different allele frequencies across populations

Differences in genetic parameters

Genetic correlations (e.g., trait relationships) differ between populations

Divergent selection pressures between populations

Different breeding goals lead to different genetic merit

Aim & Objective

Aim: To determine whether the integration of genomic data influences the ranking of imported sires within the national genomic evaluation

Objective: Compare EBVs and sire rankings obtained from multi-trait pedigree-based EBVs to those derived from the Multi-trait Single-Step Genomic BLUP (MT ssGBLUP) evaluation

Traits evaluated:

- Birth Weight Direct (BWD), Weaning Weight Direct (WWD) and Weaning Weight Maternal (WWM)

Materials

- 194 imported Angus sires with genotypes
  - Provided pedigree information
  - Available progeny records
  - Genotypes generated via semen companies (2022)

- Evaluated within the entire population:
  - 280 194 animals in the pedigree
  - 20 852 registered active animals (6 244 males & 14 609 females)

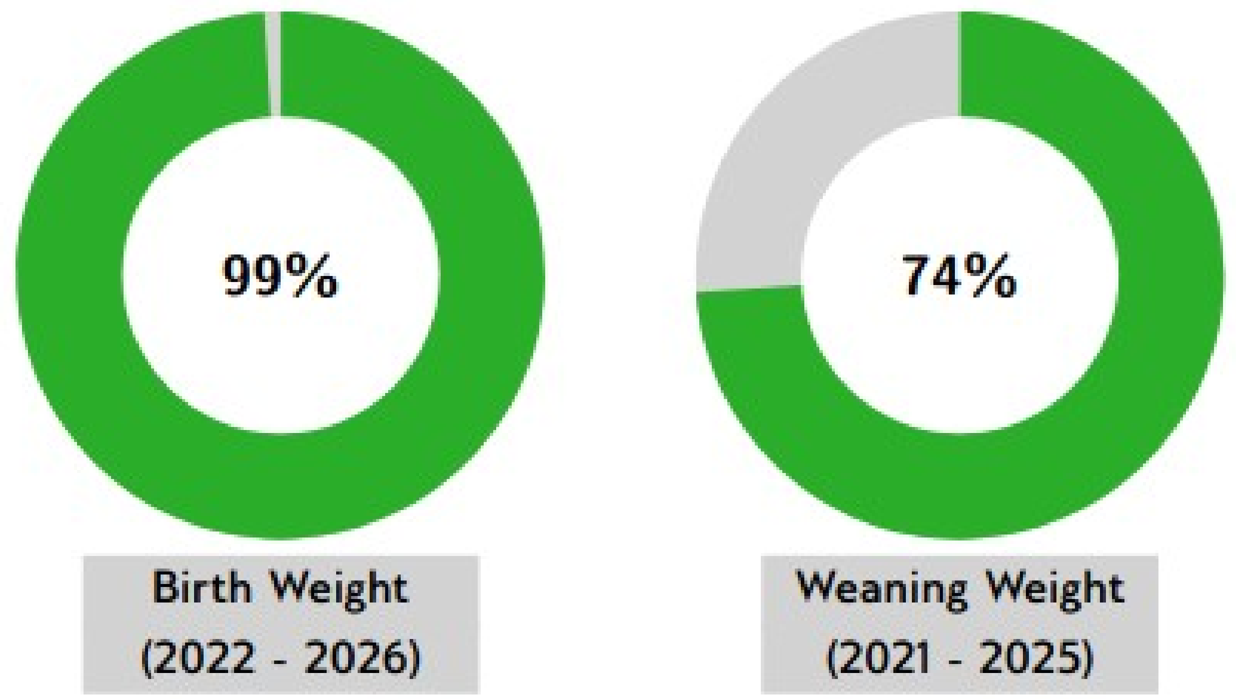
Trait	Number of animal measured	Number of males measured	Number of females measured
Birth weight	139 173	55 892	83 281
Weaning weight	106 220	41 690	64 530

- Total genotyped population of 1 427 animals (63% Male & 37% Female)

Materials: Model

$$y_{ijklmnop} = \mu + cg_i + sex_j + age_k + parity_l + age\_of\_dam_m + Pe_n + mat_o + animal_p + e_{ijklmnop}$$

y = birth or weaning weights of animal p
μ = mean weight
cg_i = contemporary group I (herd x year x season x treatment group x birth status) of animal p
sex_j = sex j of animal p
age_k = age k of animal p
$parity_l$ = parity status (1 or >1) l of dam of animal p
$age\_of\_dam_m$ = linear and quadratic regressions on age of the dam of animal p
PE_n = random permanent environmental effect n associated with the dam of animal p
mat_o = random maternal additive genetic effect of dam o of animal p
$animal_p$ = random direct additive genetic effect of animal p
$e_{ijklmnop}$ = random residual effect



Methods

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} + A_{22}^{-1} \end{bmatrix}$$

- Breeding values
  - Estimated using MiX99 (Lidauer *et al*., 2016)
  - MT PBLUP versus MT ssGLUP with inclusion of H^{-1} matrix

- Genotyped population
  - Quality control & imputation to density of 51k autosomal SNPs (Fimpute v3; Sargolazei, 2014)
  - Using the PVR1 method (VanRaden, 2008) alongside a weighting factor of 0.1 the Genomic Relationship Matrix (GRM) was constructed using the HGInv program (Strandén, 2014) and blended with the pedigree-based relationship matrix (A_{22}) using RelaX2 to produce the G^{-1} matrix, which was provided to Mix99 for internal H^{-1} construction in ssGBLUP

Results: EBVs vs GEBVs

Pearson Correlations between PBLUP & ssGBLUP for the 194 imported Angus Sires

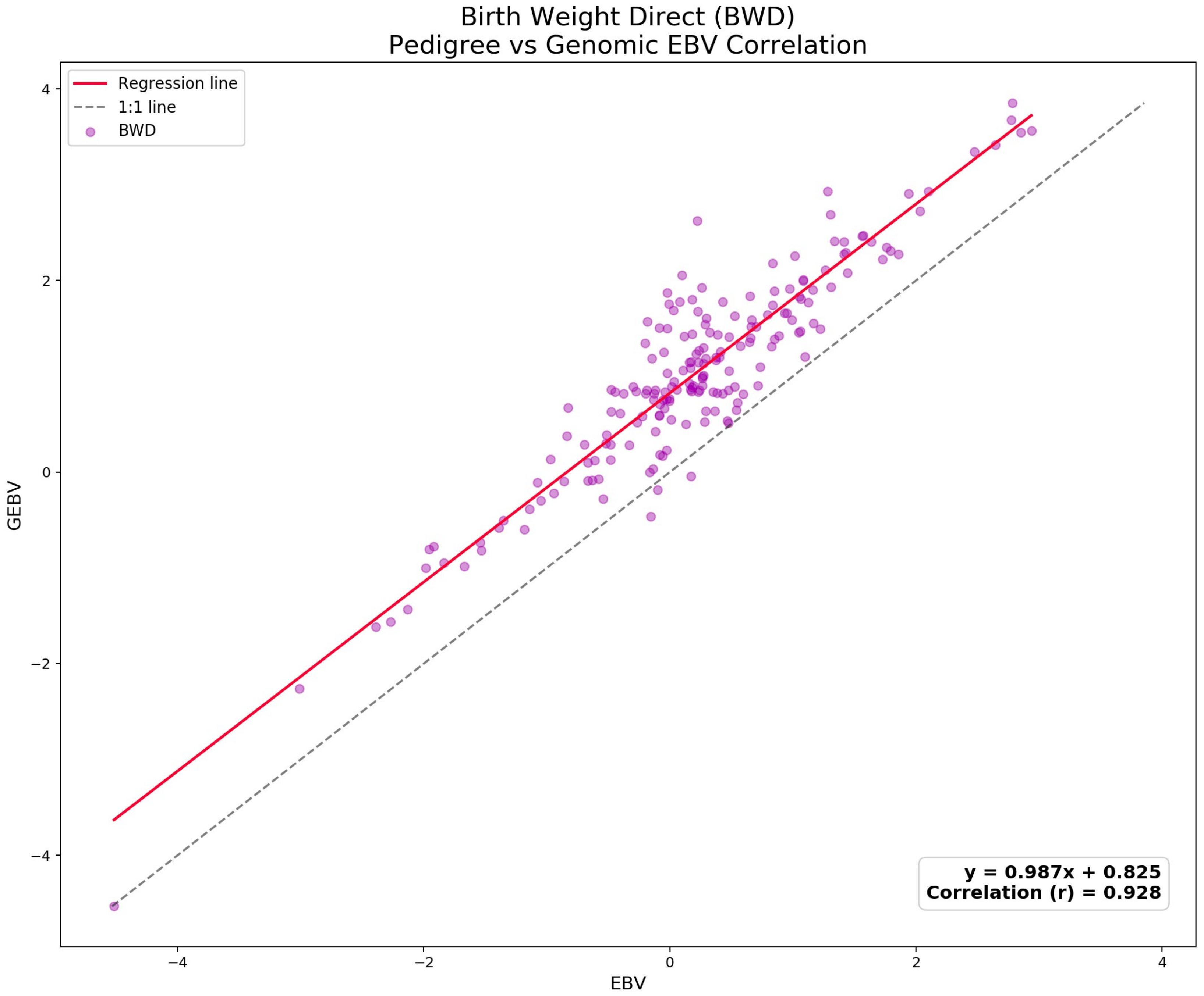


Figure 1: Birth Weight Direct (r = 0.9)

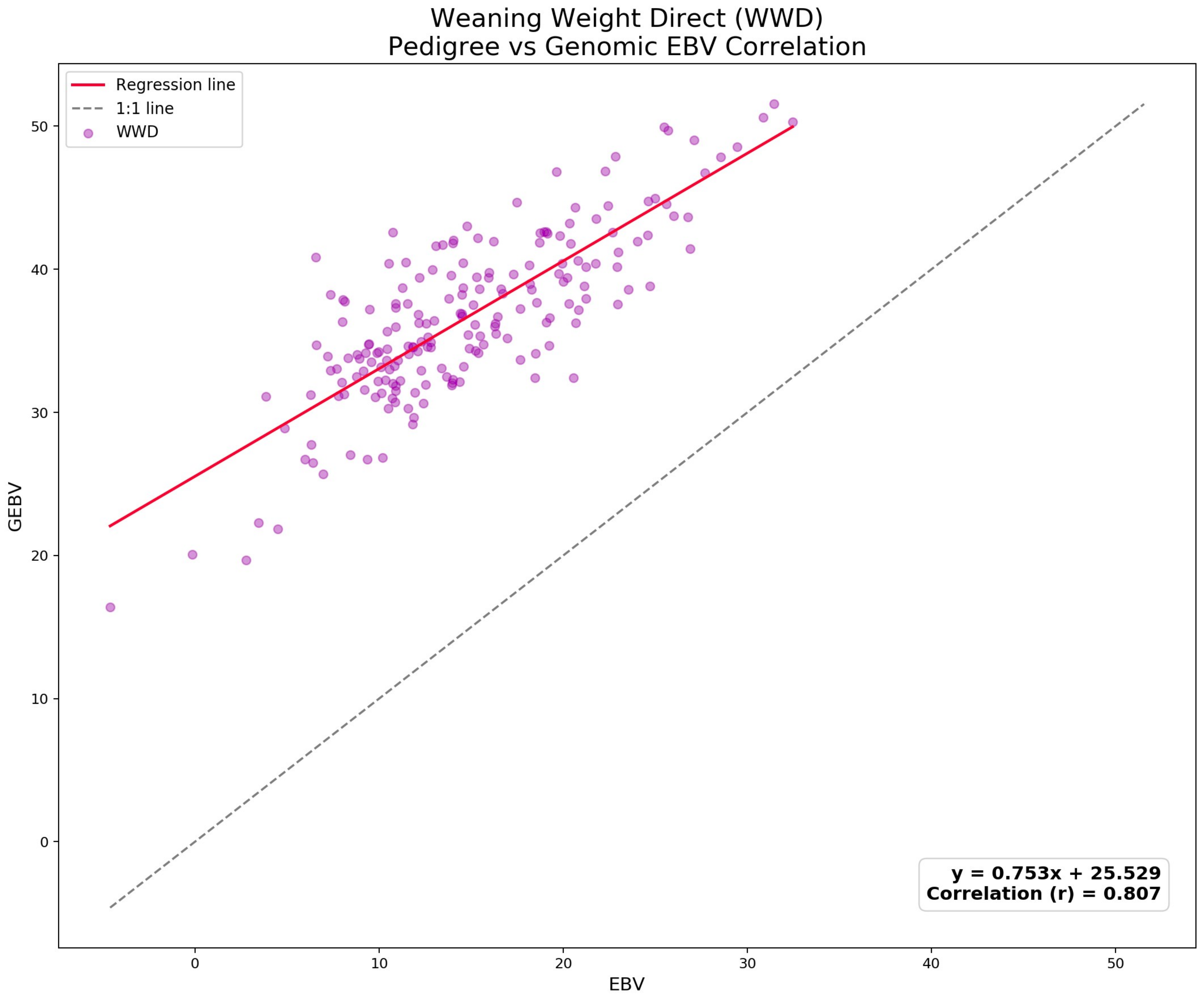


Figure 2: Weaning Weight Direct (r = 0.8)

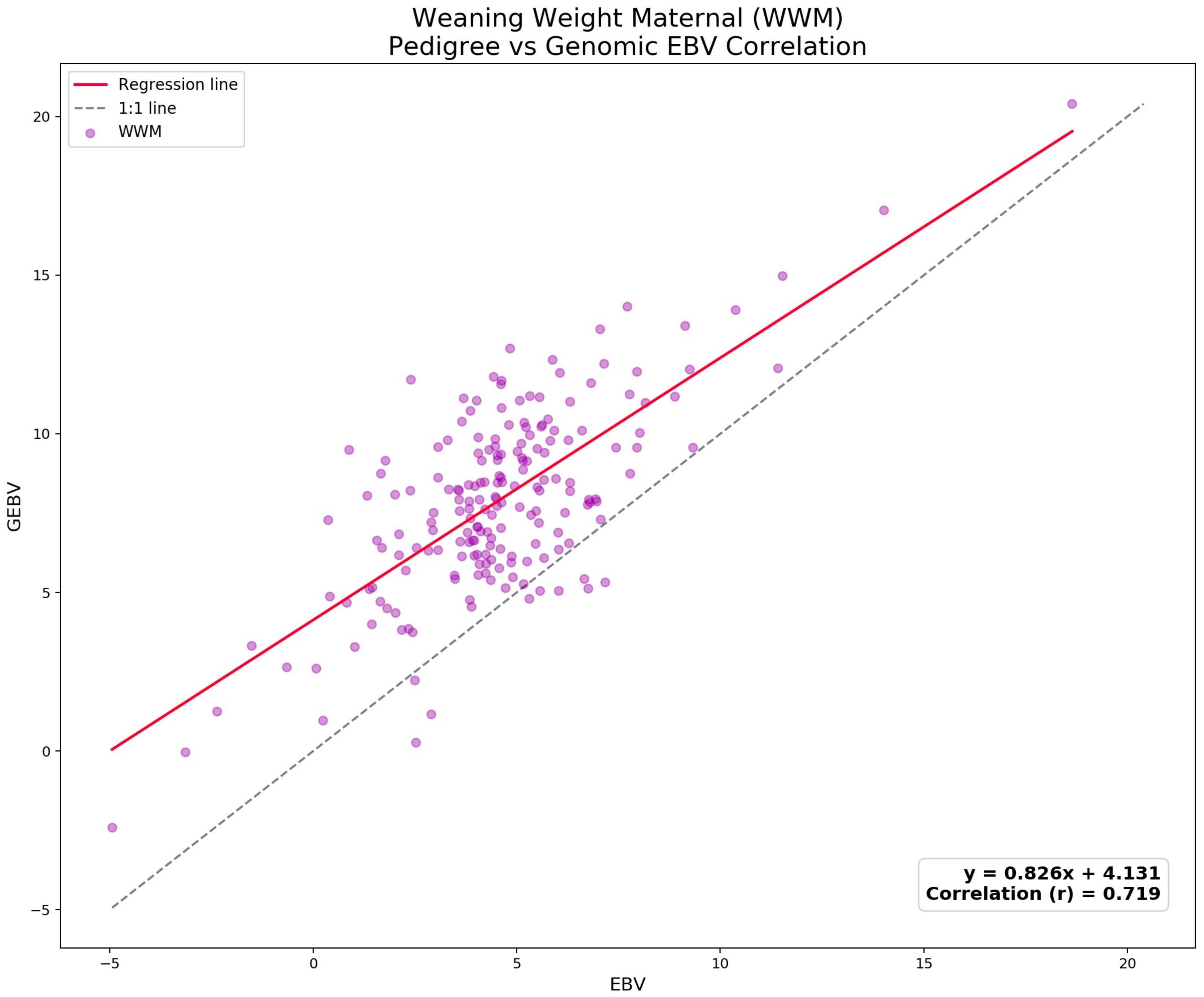
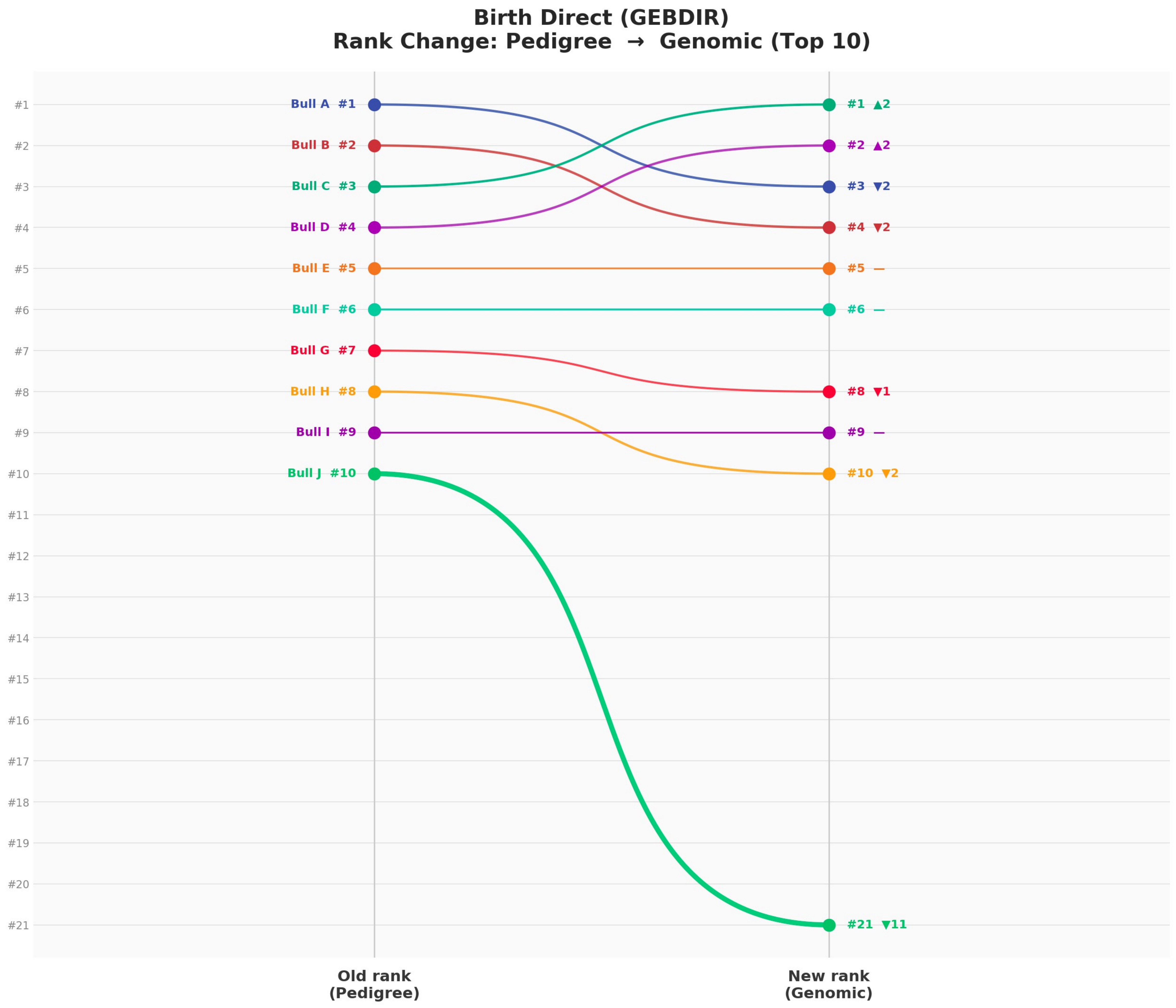


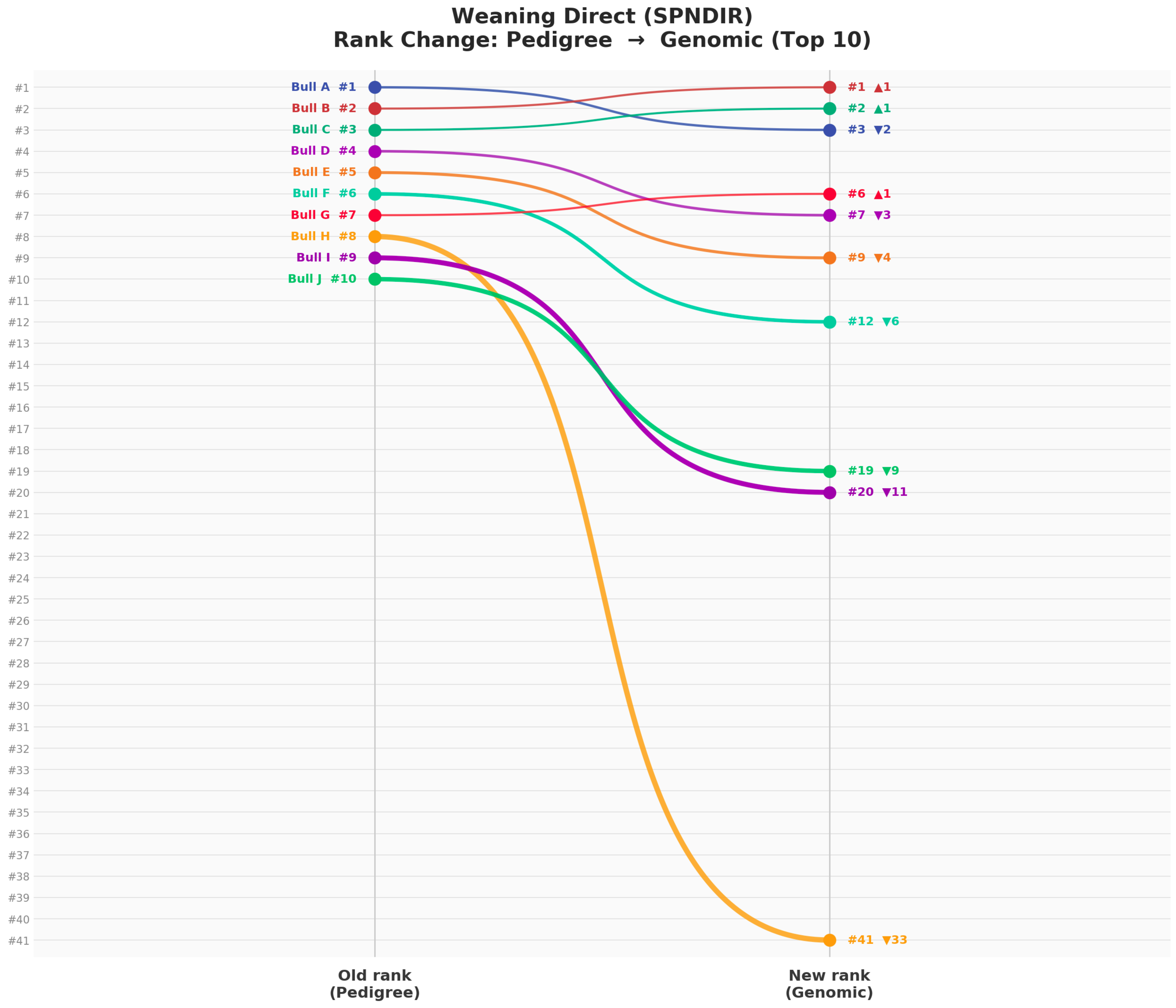
Figure 3: Weaning Weight Maternal (r = 0.7)

Results: BWD & WWD

Ranking change of the imported Angus bulls between evaluations (Top 10 ranked on PBLUP)



Birth Direct (GEBDIR)
Rank Change: Pedigree → Genomic (Top 10)



Weaning Direct (SPNDIR)
Rank Change: Pedigree → Genomic (Top 10)

Results: WWM

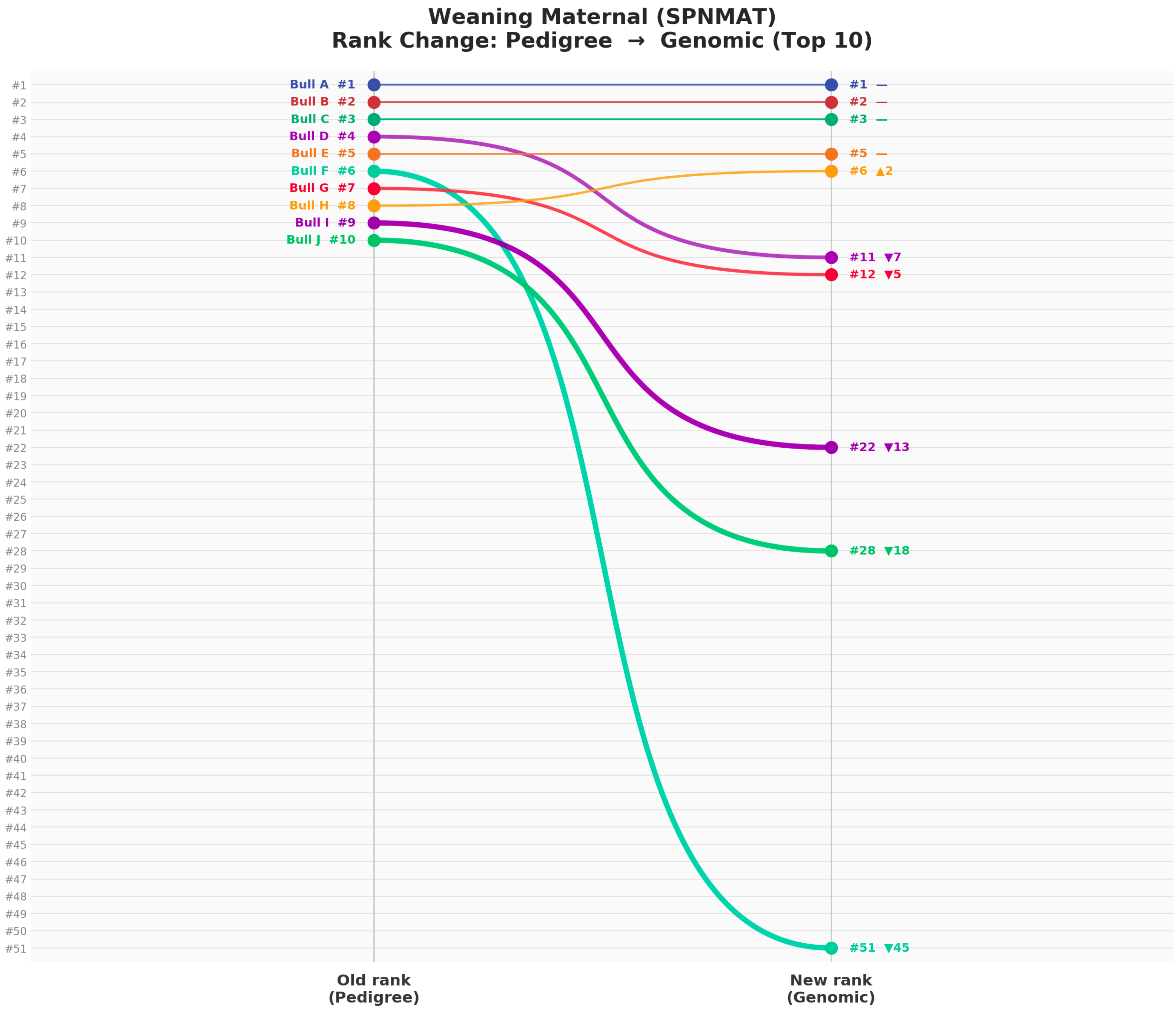


Table: Average change in rank according to the number of progeny

Progeny group	Number in group	Average rank movement
0 progeny	67	35.7 positions
1 - 5	32	32.8 positions
6 - 20	44	29.8 positions
21 -50	28	22.2 positions
51+	22	19.5 positions

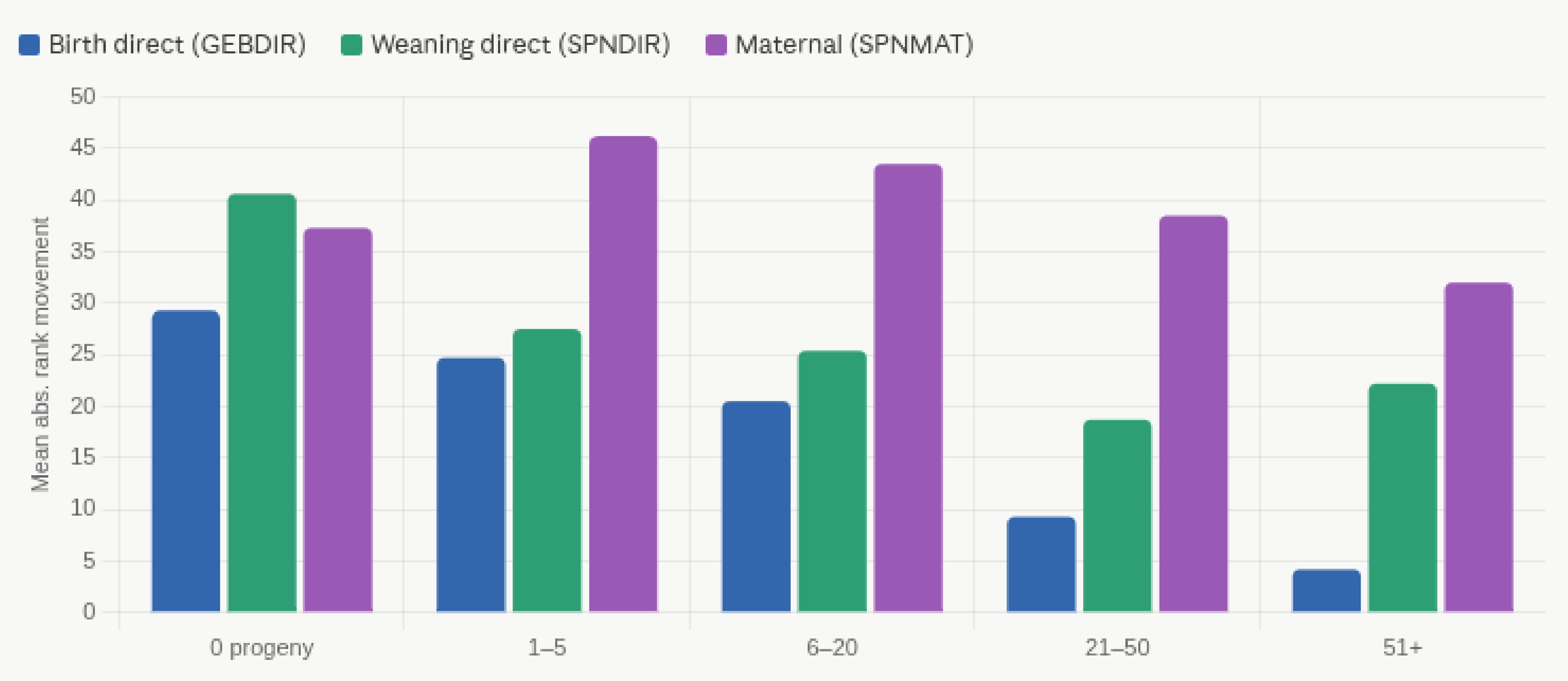


Figure: Average change in ranking for each trait in each progeny group

Discussion

- **EBV values universally increased**
  - The mean EBV difference revealed a consistent upward shift across all three traits (BWD +0.82, WWD +21.87, WWM +3.34) upon the integration of genomic information.
  - Genomic reference population captures realized genetic relationships that were unaccounted for in the pedigree BLUP run

- **Rank changes and effect of progeny records**
  - Animals with no progeny showed the largest average rank movement (35.7 positions), nearly double that of animals with 51+ progeny (19.5 positions)
  - Consistent with published observations of ssGBLUP where genomic information improves the prediction of genetic merit for young, unmeasured or unproven animals
  - Majority of the largest rank movers had two or fewer progeny

Adekale, D., Liu, Z., Evans, R., Pabiou, T., Reents, R., Segelke, D. & Tetens, J. 2025. The impact of deregressed foreign breeding values on national beef cattle single-step genomic evaluation. Genetics Selection Evolution, 57:37. https://doi.org/10.1186/s12711-025-00982-2
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Discussion

- **Maternal trait**
  - WWM showed consistently large rank movements across all progeny record groups (lowest h^2 of three traits analysed)
  - Suggests that increase in direct progeny records does not stabilize maternal EBVs the way it does for direct growth traits
  - A bull can have many progeny but still lack the specific daughter performance data needed to anchor his maternal EBV
  - Effect compounded by limited pedigree depth for imported bulls
  - Due to only 37% of the genomic reference population being females this may cause the large rank movement seen within the maternal trait

- **Movement within the entire Angus bull population evaluated**
  - BWD: barely shifted as a whole group
  - WWD: Imported bulls moved from the bottom half into the upper half, 159 of the 194 improved
  - WWM: Group moved closer to the population median, 140 out of 194 improved

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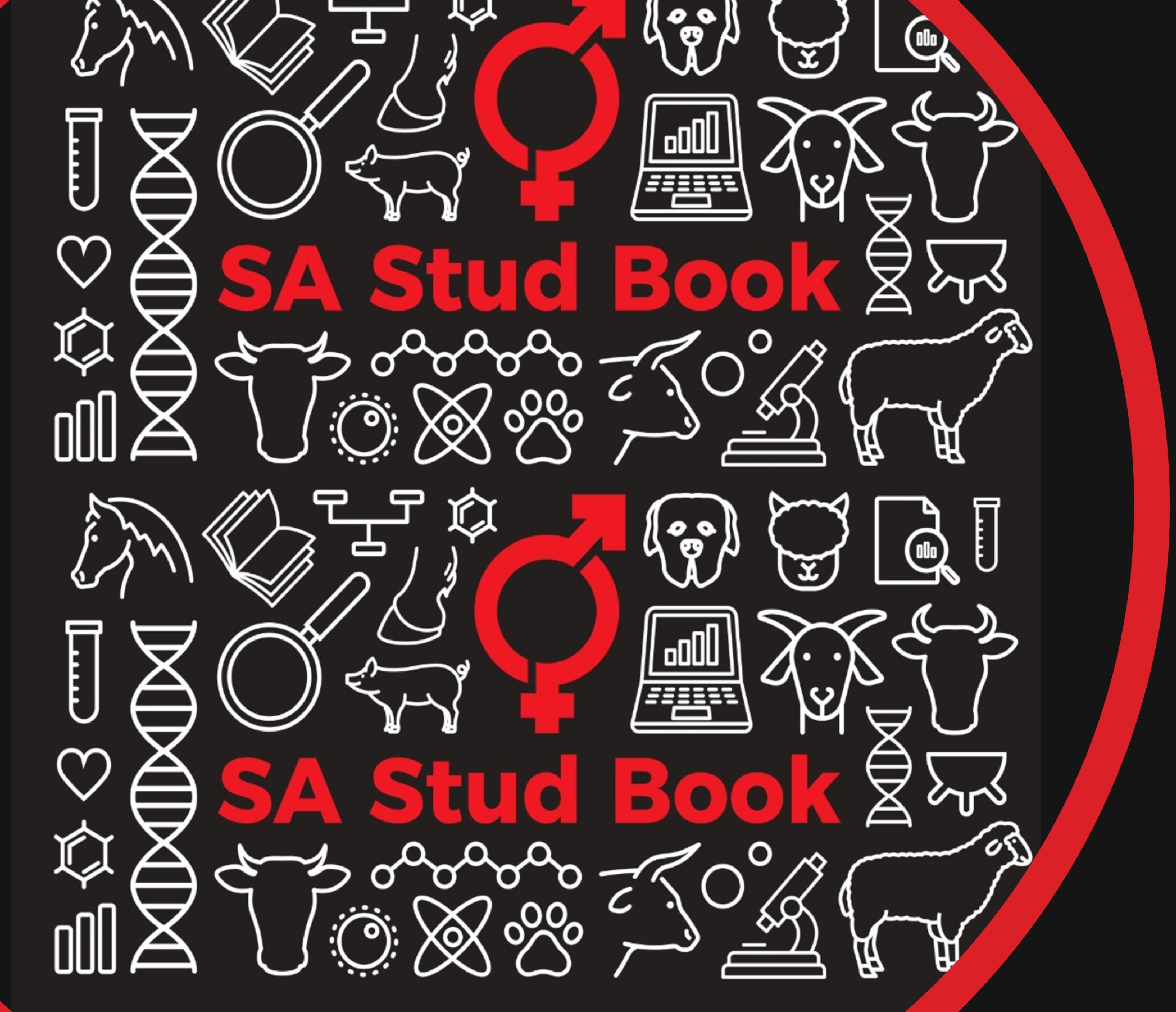
CONCLUSIONS

- The inclusion of genomic information via ssGBLUP resulted in a systemic upward shift in EBVs across all three traits, reflecting the capture of realised genetic relationships that pedigree-based BLUP alone was unable to account for
- Genomic information had the greatest impact on animals with limited pedigree depth and less progeny records
- Maternal EBVs proved uniquely resistant to stabilisation by progeny count, reflecting the biological requirement for locally-recorded daughter performance data, and highlighting the need for continued development of the maternal genomic reference population
- Resulted in an overall improvement of these bulls ranks within the entire male Angus population in South Africa
- Recommendation: Encourage breeders to test more cows (matriarch cows) who are representative of the population and who have measured calves



Thank you!

Grazie!

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