

# BULL DISCOVERY

## Powered by genomics

Genomics has a wide and varied range of uses within modern Angus breeding programs, from confirming important parentage details or genetic condition status through to improving confidence when making breeding decisions.



Utilising the varied applications of genomics to better identify elite sires within their herd is just one-way breeders can benefit from the technology.

The following case study examines the use of genomic testing in the herd of a current Angus Australia member.

### When Genomic Testing

Genomics enables a more informed selection decision to be made, through higher accuracy EBVs. This decision can be made earlier in an animal's life and can be hugely valuable when making breeding and purchasing decisions.

Genomic testing when incorporated into a breeding value will cause;

- No change in the average breeding value for a group of animals.
- An increase in the spread of breeding values between animals in the group, driven by movement in individual EBVs and re-ranking within the group.
- The accuracy of the breeding values to increase, with a greater increase in accuracy for hard to measure compared to easy to record traits.

Genomics does this by better describing the relationship between the tested animal and the reference population. As relationships can be developed between not only pedigree relations but also animals that share genes in common.

## Examining the Bulls

The following case study examines the identification of an elite herd sire from a group of 138 bulls and the impact genomics has on their selection. The bulls represent a range of different genetics, including local and international sires.

The use of genomic testing confirmed important parentage information ensuring that all data used in the bulls' EBV calculation, as part of this analysis, is coming from an accurate pedigree.

## Average Breeding Value

When genomic information is included into the calculation of the breeding values, we see very little or no change in the average breeding value of the 138 bulls (Table 1). When examining those breeding values which recorded a slight positive or negative movement it is important to context the movement in relation to the magnitude of the breeding value. For instance, +3 kg in 111 kg, as seen in 600 day weight represents a less than 2.5% movement.

Table 1 - Average change in the bulls breeding values with the incorporation of genomic information

	BWT (kg)	200 (kg)	400 (kg)	600 (kg)	MCW (kg)	SS (cm)	CWT (kg)	EMA (cm <sup>2</sup> )	RIB (mm)	P8 (mm)	RBY (%)	IMF (%)
No Genomics	+3.9	+48	+85	+111	+86	+1.7	+62	+5.8	-0.1	-0.4	+0.4	+2.1
Genomics Included	+4.1	+49	+87	+114	+88	+1.6	+64	+5.8	-0.1	-0.4	+0.4	+2.1
BV Difference	+0.2	+1	+2	+3	+2	-0.1	+2	0	0	0	0	0

Table 2 - Breeding value spread for the bulls with and without the incorporation of genomic information

No Genomics												
EBV	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
Min.	+0.3	+34	+64	+79	+47	-1.2	+37	+2.8	-2.8	-4.4	-1.4	+1.0
Avg.	+3.9	+48	+85	+111	+86	+1.7	+62	+5.8	-0.1	-0.4	+0.4	+2.1
Max.	+9.1	+64	+113	+148	+151	+3.8	+87	+10	+4.3	+5.1	+3	+3.4
Genomics Included												
EBV	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
Min.	-1.5	+32	+54	+69	+16	-1.5	+29	0	-3.5	-5.3	-2.5	+0.2
Avg.	+4.1	+49	+87	+114	+88	+1.6	+64	+5.8	-0.1	-0.4	+0.4	+2.1
Max.	+10.3	+73	+127	+168	+170	+5	+96	+12.3	+5.3	+6.1	+3.9	+4.4

## Individual Movement and Ranking

The re-ranking of individuals significantly affected the bulls with the highest EBVs for each trait. Bulls shown in red fell outside the highest 15 for the trait with the inclusion of genomics. Bulls in yellow were previously in the highest 15, but changed position, while the bulls in green moved into the highest 15 with the inclusion of genomics (Table 3).

## Breeding Value Spread

The spread of breeding values for the group, has increased significantly with the inclusion of genomic information (Table 2). The increase in spread has come about from the individual movement in breeding values, which has resulted in the re-ranking of bulls within the group.

This occurs because with genomics we have better understanding of the genes the animal inherited and how they perform. This greater understanding allows the breeding value calculation to not only develop pedigree links but also links with animals that share genes in common.

This increase in breeding value spread is a valuable feature of genomic testing, because not only does it enable breeders to examine better described traits but enables separation of animals, which previously may have had very similar breeding values.

Importantly the change in ranking doesn't mean an individual's breeding value moved. For example, the bull M223 was the highest EBV bull for 200 day weight without genomics. Despite the inclusion of genomics resulting in no change to his breeding value, his ranking moved to 6th with genomics included (Table 3). This was the result of the movement of the other bulls.

On average, the inclusion of genomics caused 5 new bulls to enter the highest 15 for each of the examined traits. Of the highest 15, on average 1 bull remained in the same ranking position across the examined traits.

The correlation between the EBVs for each trait with and without genomic information (Table 4), supports what was observed in the re-ranking of the 15 highest EBV bulls, highlighting that a large amount of re-ranking was observed in breeding values with the inclusion of genomics.

If we look at the re-ranking of the bulls as a group we see further evidence to support this. The heat map

demonstrates the movement of bulls as a group with the inclusion of genomics for the breeding values, which are used to calculate the Angus Breeding Index (ABI). The ABI captures the bulls movement across a range of traits (Figure 1).

The heat map shows that of the 13 bulls originally in the highest 10 percent of the group (total of the far-right column), 8 remained in the highest 10 percent with the inclusion of genomics. 3 bulls dropped to be ranked in the highest 20 percent of the group, while 2 bulls dropped to be ranked in the highest 30 percent (see far-right column).

Table 3 – Ranking top 15 bulls for each trait, with and without the inclusion of genomic information (Red=dropped outside top 15 with genomic inclusion, Yellow= changed rank order but remained in the top 15, Green=moved into the top 15 with genomic inclusion)

No Genomics												
Rank	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBV	IMF
1	M63	M223	M149	M81	M81	M174	M81	M149	M42	M249	M300	M197
2	M289	M198	M223	M223	M287	M307	M177	M242	M8	M53	M131	M167
3	M8	M81	M198	M333	M250	M109	M149	M153	M29	M238	M271	M188
4	M212	M225	M225	M198	M46	M263	M103	M131	M308	M307	M214	M90
5	M20	M148	M148	M149	M333	M298	M225	M177	M249	M42	M202	M289
6	M162	M149	M118	M225	M223	M65	M148	M163	M65	M38	M133	M82
7	M165	M102	M81	M245	M225	M223	M248	M214	M20	M308	M149	M225
8	M53	M118	M248	M46	M198	M321	M83	M111	M176	M120	M89	M102
9	M169	M186	M237	M148	M186	M315	M46	M202	M45	M29	M328	M80
10	M89	M237	M102	M83	M83	M142	M237	M300	M145	M20	M242	M117
11	M140	M248	M186	M287	M156	M328	M8	M38	M23	M145	M156	M140
12	M141	M240	M103	M102	M323	M275	M223	M248	M307	M118	M275	M240
13	M14	M257	M240	M257	M220	M333	M165	M99	M53	M117	M248	M63
14	M155	M197	M257	M156	M6	M57	M257	M81	M120	M315	M64	M198
15	M179	M188	M290	M118	M256	M259	M98	M148	M54	M198	M174	M223
Genomics Included												
RANK	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBV	IMF
1	M63	M225	M148	M245	M287	M307	M81	M300	M65	M249	M300	M104
2	M8	M81	M225	M81	M245	M54	M103	M214	M29	M145	M64	M167
3	M329	M102	M245	M225	M250	M275	M83	M242	M35	M315	M214	M197
4	M289	M240	M102	M46	M81	M65	M149	M274	M308	M307	M280	M188
5	M89	M245	M81	M287	M46	M177	M225	M153	M8	M29	M242	M90
6	M212	M223	M103	M333	M83	M315	M148	M111	M42	M212	M237	M53
7	M179	M103	M248	M83	M333	M333	M177	M156	M120	M53	M275	M82
8	M155	M148	M46	M156	M156	M32	M46	M163	M249	M123	M99	M117
9	M14	M198	M118	M148	M234	M194	M245	M64	M145	M308	M131	M236
10	M106	M149	M223	M102	M6	M321	M156	M21	M53	M8	M89	M156
11	M321	M248	M149	M38	M220	M142	M248	M148	M176	M38	M285	M323
12	M141	M333	M240	M103	M80	M109	M86	M202	M45	M238	M217	M80
13	M169	M83	M198	M6	M280	M263	M287	M99	M162	M65	M274	M125
14	M99	M287	M83	M223	M320	M298	M21	M42	M179	M162	M170	M243
15	M311	M118	M142	M149	M186	M89	M142	M321	M63	M179	M272	M35

Table 4 – Correlation between bulls breeding value with and without genomics

	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
Correlation	0.85	0.85	0.84	0.88	0.87	0.87	0.86	0.71	0.84	0.85	0.79	0.78

		Bull Percentile (No Genomics)									
		91-100	81-90	71-80	61-70	51-60	41-50	31-40	21-30	11-20	1-10
Bull Percentile (Genomics)	1-10	0	0	0	0	0	0	1	0	2	8
	11-20	0	0	0	0	0	1	1	4	7	3
	21-30	0	0	1	2	0	1	0	7	0	2
	31-40	0	2	0	2	0	4	3	2	2	0
	41-50	0	1	1	2	4	1	0	0	0	0
	51-60	0	2	2	3	3	4	3	2	0	0
	61-70	0	1	3	4	0	1	1	0	0	0
	71-80	2	1	2	2	1	5	1	1	0	0
	81-90	3	5	3	2	2	1	0	0	1	0
	91-100	8	2	3	0	0	0	0	0	0	0

Figure 1 - Percentile band movement of bulls for ABI with the incorporation of genomic information

## Breeding value accuracy

The final area to examine is the change in the accuracy of EBVs. The accuracy for all EBVs increased, with an average increase of between 6% to 12%, depending on the trait. A greater increase in accuracy was observed in the hard to measure traits (CWT, IMF, etc.) compared to the traits that are more routinely recorded (BWT, 400, etc.) (Table 5).

The improvement in accuracy allows greater confidence when making breeding and purchasing decisions.

Table 5 - Average EBV accuracy change in the bulls breeding values with the incorporation of genomic information

	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
No Genomics Accuracy	64%	60%	60%	62%	58%	55%	52%	50%	52%	52%	48%	47%
Genomics Included Accuracy	71%	69%	67%	69%	64%	64%	60%	58%	62%	59%	54%	57%
Accuracy Difference	+7%	+9%	+7%	+7%	+6%	+9%	+12%	+8%	+10%	+7%	+6%	+10%



## What genomics has delivered to bull selection

The genomic testing of the bulls has enabled a better understanding and ability to identify the top performing animals through an increase in the spread and accuracy of breeding values within the group.

Based on the highest 15 bulls across the examined traits, a third of the bulls identified were not present in the list prior to genomic testing (Table 3).

These bulls may not have been considered as potential sire options because of their rank within the group, if genomic testing was not performed, and therefore the breeding program could not benefit for their genetic contribution.

By implementing genomic testing, these bulls were identified and the breeder had the opportunity to select them for use within the breeding program, highlighting that genomics enables a more informed decision to be made earlier in an animal's life.

Genomic testing the bulls also has a number of additional benefits to those bulls which were not selected for use within the breeding program. Genomics added value to them as sale bulls through confirmation of pedigree, improved reliability of genetic condition status, and improved breeding value accuracy.

### For more information contact Angus Australia:

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## Take Home Messages

Genomics increases the accuracy and spread of breeding values

Average breeding value doesn't change for the tested group

Genomics enables a more informed selection decision to be made earlier in an animals life



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