Interpretation of the marker test results.

Table 3 in the document presenting results from the analysis of MVPs gives the key statistical parameters required to make best use of MVPs as predictors of phenotypic differences between animals of the same breed managed alike and also for the best use of MVPs in the calculations of estimated breeding values. These parameters are for each analysed dataset:

- Phenotypic Variance for the trait σ^2_P
- Variance of the MVP
- Heritability of the analysed trait h^2
- Genetic correlation between MVP and the trait r_g
- % genetic variance explained by the MVP r^2_g
- Regression coefficient of phenotype on MVP

The phenotypic variance and the heritability in all datasets show that considerable phenotypic differences between the animals existed and that some component of the phenotypic differences between animals has a genetic base, i.e. is heritable. As the individual datasets are quite small the standard errors for heritabilities are quite large.

Predicting expected Phenotypic Differences from MVPs:

Table 2 shows the maximum and minimum MVP observed in the four different datasets available at this time. It is expected that we observe similar extreme differences in other populations of similar breed type. Our results indicate that only a fraction of the differences in MVP between any two animals will be observed as differences in the phenotypic performance of animals managed alike and under a production system similar to the one in CRC1. The regression coefficient b (last column in table 3) provides these values for each trait. Given the rather small size of our calibration datasets it might be best to average some of those values until more accurate coefficients can be calculated.

An example: MSA marble score.

MVP difference between extreme animals within CRC1 purebred animals is 1.40, and the average regression coefficient is 0.195. We therefore predict a 0.27 MSA marble score difference of these two extreme animals. Using the standard deviation of the MVP (σ_P = 0.18) one can expect that the best half of a mob of cattle selected on the basis of MVP would differ from the worst half by 0.29 in MVP and consequently by 0.06 of a marble score once their carcasses get assessed after about 100 days in the feedlot.

Estimation of Breeding Values:

For the estimation of breeding values the genetic correlation r_g between MVP and trait for which we want to estimate the breeding value is the important statistical coefficient. In BREEDPLAN estimated genetic correlations between different traits is commonly used and MVPs can be thought of as another trait with a heritability very close to 1.0 and a correlation with other traits of r_g. While we have reported only the

genetic correlation with the target trait we expect that some MVP are also correlated to other traits.

The genetic correlation is also the expected accuracy of the EBV as reported by BREEDPLAN (called reliability by Pfizer) from using only the MVP for an animal. It should be noted that MVPs on relatives will not increase the accuracy. As with the regression coefficient it may be necessary to average the correlation across similar datasets until more data become available.

An example: Tenderness

The second and fourth datasets are Indicus cattle, the genetic correlations estimated for MVP Tenderness and Shear force are 0.28 and 0.55 to give an weighted average 0.37. So an EBV based only on GeneSTAR MVP has an accuracy of 0.37. It is not practical to select animals based on their own tenderness because they have to be slaughtered first, but if we could select animals on their own tenderness, the accuracy would be 0.55 equal the square root of the heritability (0.30).

One point to note is that the phenotypes of relatives can contribute to an animals EBV and increase the accuracy even if the animal's phenotype has been recorded.

These are the first results presented from an independent analysis of commercially available Marker Breeding Values, in this case Pfizer Genetics GeneSTAR MVPs. The data is clearly limited and we have insufficient animals tested to provide breed specific information. However the Beef CRC with support of the MLA is cooperating with Pfizer Genetics and other companies to add more independent test results to allow the Australian beef cattle producers to better judge the value of this new technology.