**Impact of including growth, carcass and feed efficiency traits in the breeding goal for combined milk and beef production systems**

P. Hietala and J. Juga

**Supplementary Material S3**

*Calculation of accuracies of genomic breeding values for residual feed intake indicator traits*

The accuracies of DGVs ($r\_{gg}$) for RFI\_T and RFI\_I were calculated using a formula described by Daetwyler *et al*. (2008 and 2010):

$$r\_{gg}=w\sqrt{\frac{Nr^{2}}{Nr^{2}+M\_{e}}}$$

where $N$ is the number of animals in the reference population, $r^{2}$ is the reliability of EBV of the trait in the reference population and $w$ denotes the square root of the proportion of the total genetic variance explained by markers. For $w$ the value of 0.9 was used, which is empirically determined for different traits in dairy cattle using a 50k SNP chip (Erbe *et al*., 2013). $M\_{e}$is the effective number of independent segregating chromosome segments defined as described by Goddard (2009):

$$M\_{e}=\frac{2N\_{e}L}{log⁡(4N\_{e}L)}$$

where $N\_{e}$ is the effective population size and $L$ is the average length of a chromosome in Morgans. The used values for $N\_{e}$and $L$were 176 and 30, respectively (M. Koivula, Natural Resources Institute Finland, Jokioinen, Finland, personal communication). When defining the accuracy of DGVs the size of the reference populations were assumed to be 2 000 bulls with own records for RFI\_T and 2 000 proven bulls with EBVs based on 50 daughter records for RFI\_I.

*Additional references*

Erbe M, Gredler B, Seefried FR, Bapst B and Simianer H 2013. A function accounting for training set size and marker density to model the average accuracy of genomic prediction. PLoS ONE 8, e81046.

Goddard M 2009. Genomic selection: Prediction of accuracy and maximisation of long term response. Genetica 136, 245–257.