

Fig. 1. Heritability of 33 biomarker genes derived from half-sib genetic variances in 10 sire families, estimated by random genetic effect mixed models in ASReml. Biomarkers with heritabilities > 0.15 (red dashed line) are shown in blue and those < 0.15 are shown in pale blue.

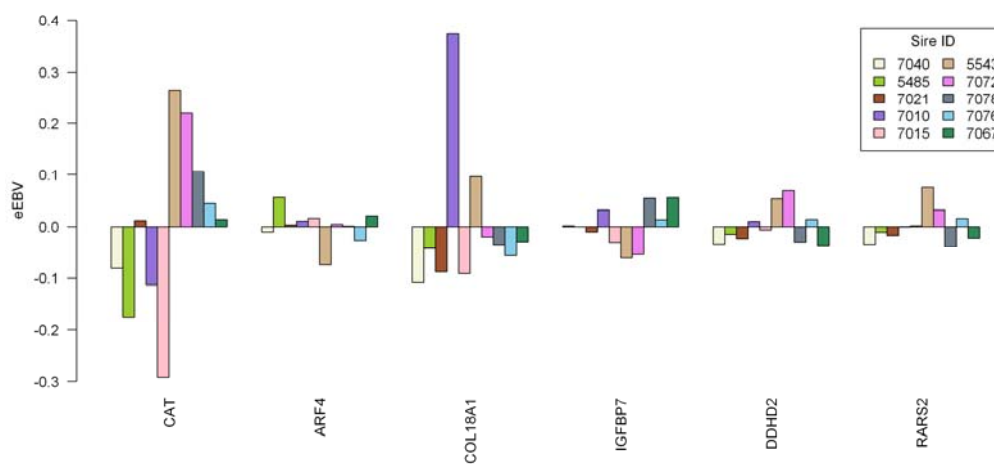


Fig. 2. Expression Estimated breeding values (eEBVs) of sires for the gene expression of 6 biomarkers (heritabilities > 0.15) indicating the transmissible levels of transcript abundance to their progeny.