

CORRECTION

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Correction: Expanding the application of haplotype-based genomic predictions to the wild: a case of antibody response against *Teladorsagia circumcincta* in Soay sheep

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Following publication of the original article it was reported that there was an error in Fig. 4 and in the ‘Future studies’ subsection.

In Fig. 4 the legend title was ‘SH’ and has been corrected to ‘Analysis’. The correct Fig. 4 is provided in this Correction.

In the ‘Future studies’ subsection the following sentence had the word ‘references’ in place of missing references: “Furthermore, several other methods can be used for fitting haplotypes in GP analyses (references), and future studies could compare alternative methods.”

The correct sentence including the missing references is: “Furthermore, several other methods can be used for fitting haplotypes in GP analyses [25, 26, 47], and future studies could compare alternative methods.”

The original article has been updated.

The online version of the original article can be found at <https://doi.org/10.1186/s12864-023-09407-0>.

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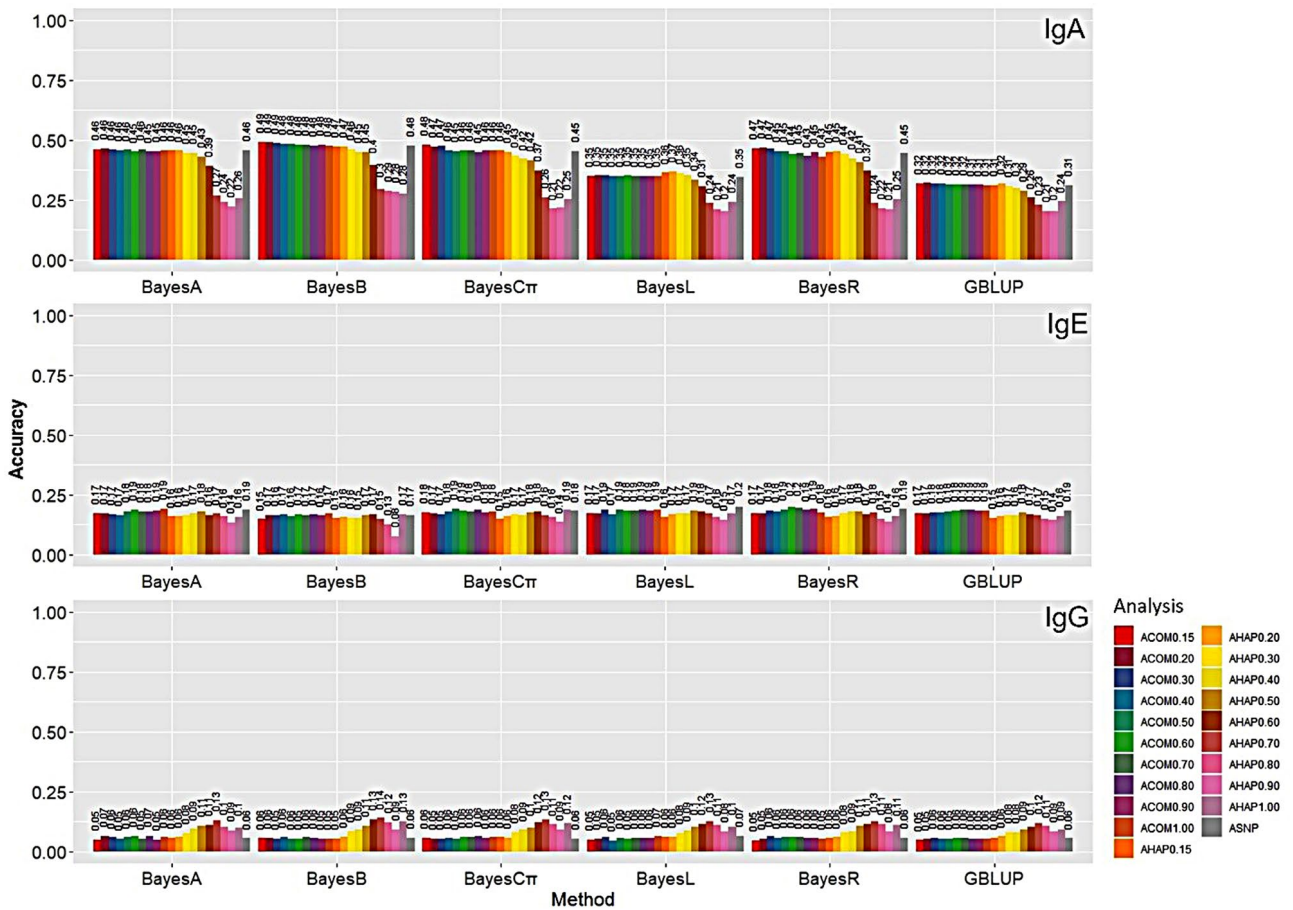


Fig. 4 The estimates of genomic prediction accuracy of IgA, IgE, and IgG applying different methods and analyses. The genomic prediction accuracy was measured by the correlation between adjusted phenotypes (y_c) and GEBV for the validation subset. Methods under evaluation were GBLUP, BayesA, BayesB, BayesCrr, BayesLasso, and BayesR based on different analyses, including ASNP, ACOM0.15, ACOM0.20, ACOM0.30, ACOM0.40, ACOM0.50, ACOM0.60, ACOM0.70, ACOM0.80, ACOM0.90, ACOM1.00, AHAPO.15, AHAPO.20, AHAPO.30, AHAPO.40, AHAPO.50, AHAPO.60, AHAPO.70, AHAPO.80, AHAPO.90, and AHAPO.100. Definitions of the analyses are given in Tables 3 and 4

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