

# Stacked kinship CNN vs. GBLUP for genomic predictions of additive and complex continuous phenotypes

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**Supplementary Figure S1:** plot of the first two principal components (PC1, PC2) from the principal component analysis (PCA) of the 26,503 SNP genotypes from 1,033 Holstein-Friesian cows used in the study. Between brackets, the percentage of the variability explained by the two components.

