

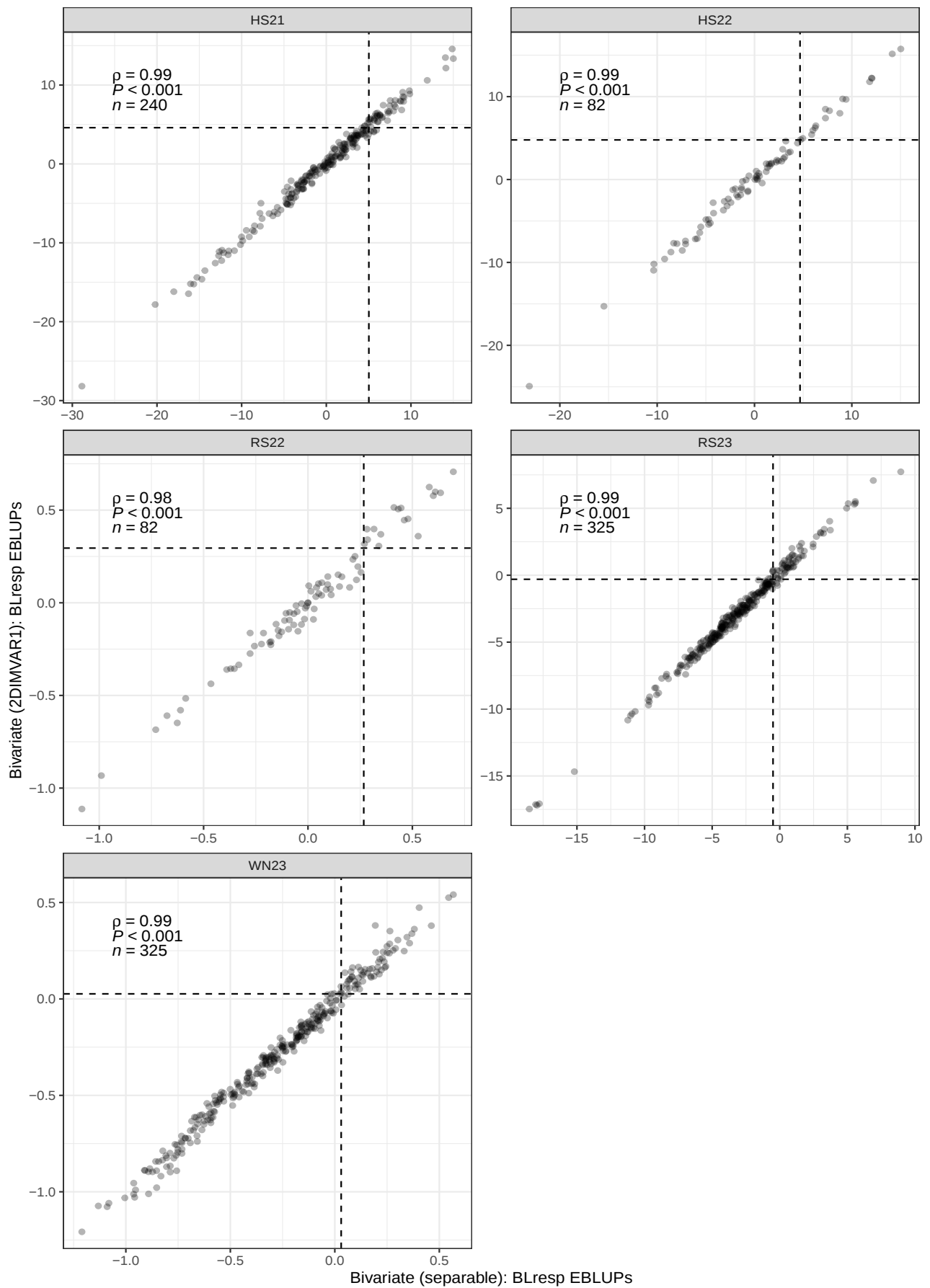


Fig.S2. The EBLUPs of BLresp derived from bivariate genomic model with flexible 2DIMVAR1 residual structure against the historic three-way separable structure. Here, only datasets that showed significant improvement in 2DIMVAR1 model (see Table 4) were included. The cut-off for top 20% of genotypes was indicated with vertical dotted lines for separable and horizontal dotted lines for 2DIMVAR1. ρ represents the Spearman's rank correlation coefficient between the two sets of EBLUPs while n represents the number of genotypes in each dataset. Note: the non-additive EBLUPs were used for datasets HS21, HS22 and RS22 (additive not significant), while additive EBLUPs were used for remaining datasets.