

File S1: Special case of synthetics with $N_p = 2$.

Synthetics with $N_p = 2$ and $N_R = 1$ represent a special case, because in scenario *Re-LD_A-Ped*, $r_{g,\hat{g}}$ could not be calculated as all *TS* and *RSC* individuals are full-sibs and, therefore, all predicted breeding values are identical. For $N_R \geq 2$, variation in pedigree relationships between the *TS* and the *RSC* emerges, resulting in $r_{g,\hat{g}} \geq 0.2$ (Figure 6). Surprisingly, $r_{g,\hat{g}}$ in scenario *Re-LD_A-SNP* was largely unaffected by recombination, most likely because the newly generated variation in pedigree relationships was small compared with the variation in Mendelian sampling already present for $N_R = 1$. The much smaller standard deviation of pedigree relationships than genomic relationships between the *TS* and *RSC* shown in Figures S4C and S4D supports this explanation.