

Supplemental Figure 3. Goodness of fit for pairwise genetic relatedness against pedigrees, before and after correcting for marker redundancy. Observed genomic relationship matrix for Dataset One (A) and Dataset Two (B) plotted against coancestry calculated from extended pedigrees in NumericwareN. The line of best fit for Dataset One (m = 0.19, b = 0.53, $r^2 = 0.13$) and Dataset Two (m = 0.07, b = 0.82, $r^2 = 0.20$) are given in orange. Outlier genotype pairs have the ID and breeding group number in call-outs.