Figure S4 Linear canonical analyses determining the relationships between kinship levels based on SNP allele matches and genomic relationship scores. The SNP50 BeadChip data of 789 sires was used to calculate the genome-wide identity-by-state and the genomic relationship (GR) coefficients of each possible pair of individuals. Pairs were grouped according to their level of kinship and canonical scores were calculated using the discriminant analysis module of the JMPIN software. The modified output of this software analysis is given as described in the legend for Fig. 1, including the pair counts and the values of group means, which are specified in tables. Dot colors indicate the familial relation and kinship level according to the key on the right. **A.** Discriminant analysis using the genomic relationship coefficients as a single covariant. **B.** Discriminant analysis using three covariants (X', Y' and GR).