

Supplementary Figures

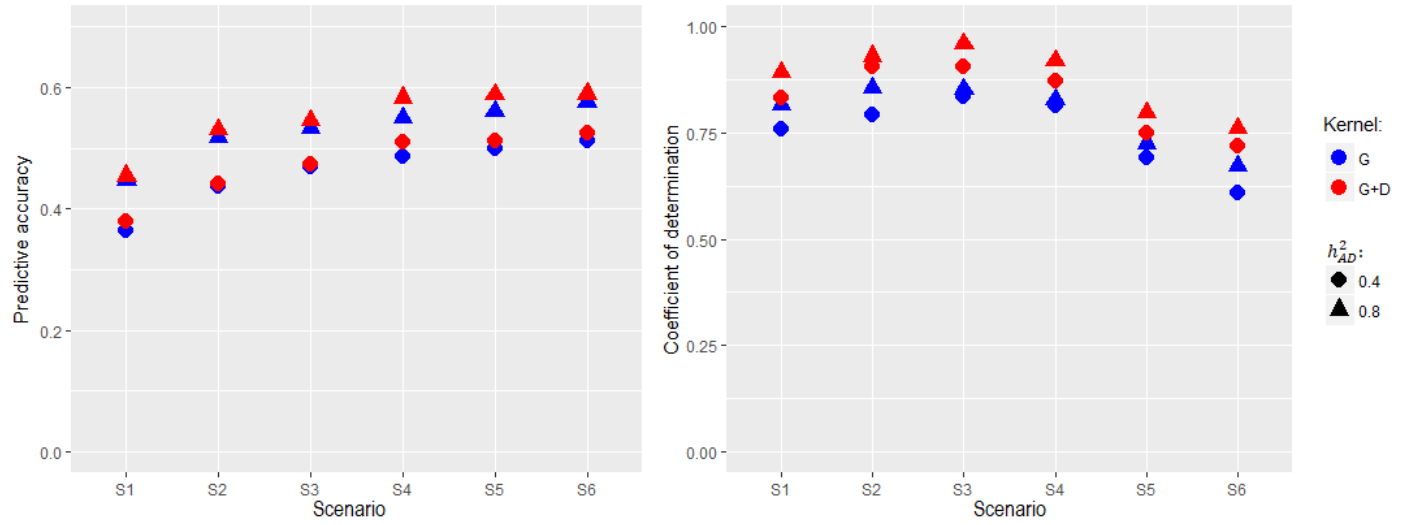


Figure S1: Relationship between prediction accuracies (left panel) and connectedness measures (right panel) under an additive and dominance scenario based on the K -means clustering using the genomic relationship matrix. The magnitude of the relationship level was steadily increased from scenario 1 (S1) to scenario 6 (S6). **G**: additive genomic kernel relationship matrix. **D**: dominance genomic kernel relationship matrix. h^2_{AD} : broad sense heritability including additive and dominance variation.

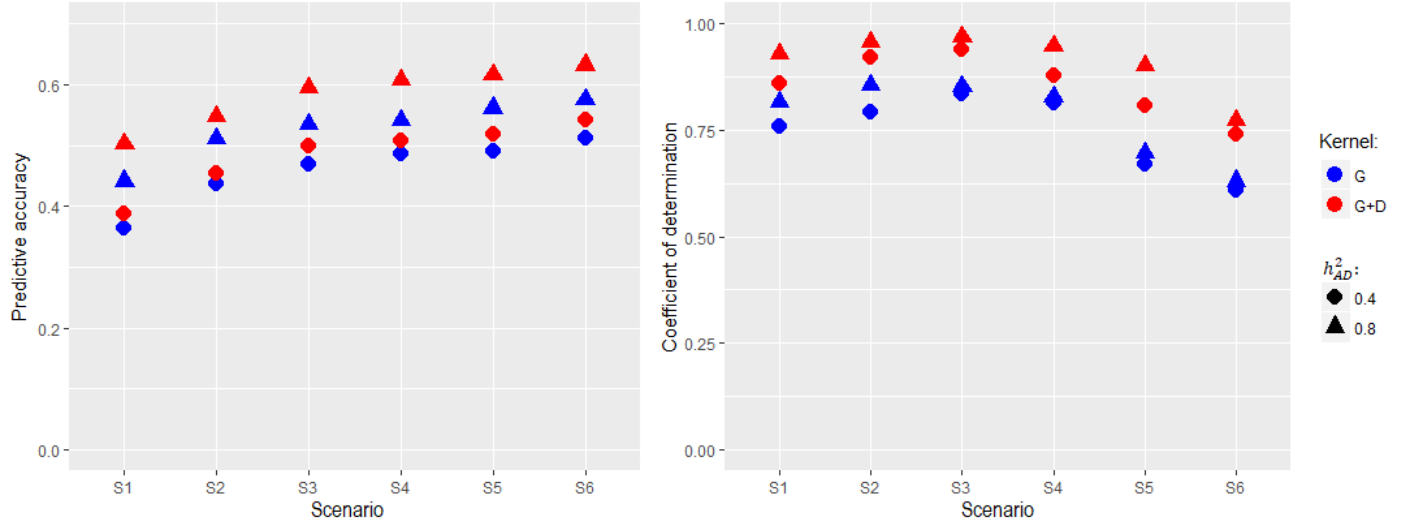


Figure S2: Relationship between prediction accuracies (left panel) and connectedness measures (right panel) under an additive and dominance scenario based on the K -means clustering using the multi-kernel genomic and dominance relationship matrix. The magnitude of the relationship level was steadily increased from scenario 1 (S1) to scenario 6 (S6). **G**: additive genomic kernel relationship matrix. **D**: dominance genomic kernel relationship matrix. h^2_{AD} : broad sense heritability including additive and dominance variation.

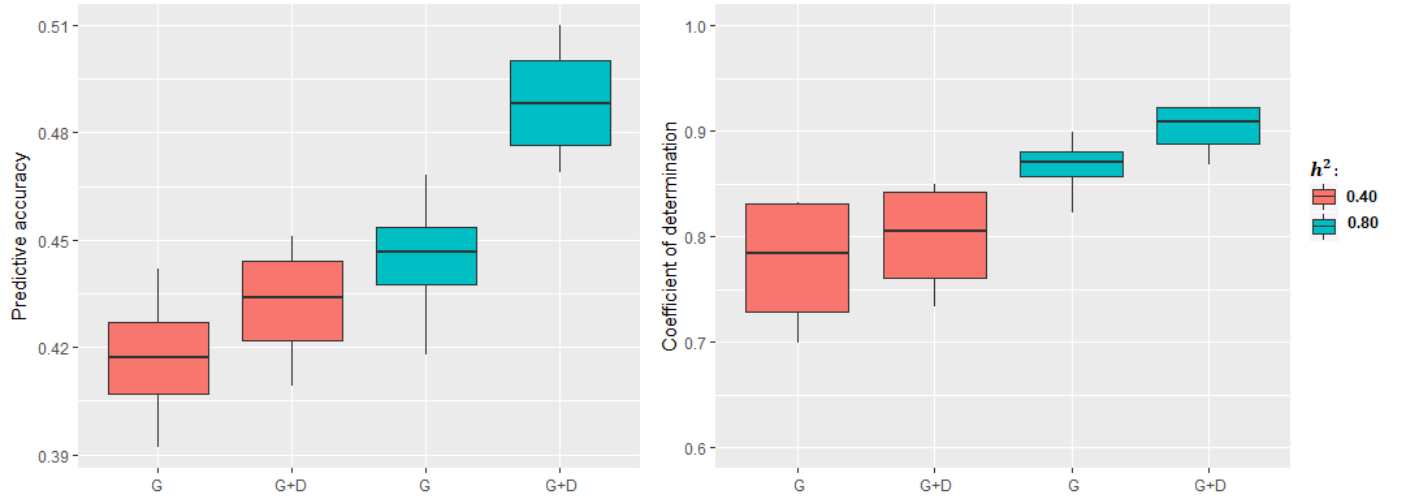


Figure S3: Relationship between prediction accuracies (left panel) and connectedness measures (right panel) under an additive and dominance scenario based on forward validation. **G**: additive genomic kernel relationship matrix. **D**: dominance genomic kernel relationship matrix. h^2 : heritability.