Figure S1 – Population clusters in Ames-H, inferred by *k*-means clustering (*k* = 4). Hybrids are differentiated by tester (B47 or PHZ51) and represented on principal component (PC) 1 and PC 2 or 3. Validation sets in Ames-H were obtained by partition into 10 sets within each population cluster and tester group. Points outlined in black correspond to one of the 10 validation sets in Ames-H, and exemplify the preserved structure by population cluster and tester within each validation set. Principal components and proportions of genomic variance explained were computed based on WGS SNPs in the Goodman association panel.