Figure S3. Prediction accuracies of GBLUP, EGBLUP, LEGBLUP, and HGBLUP using simulated data for a trait with the following features, $h^2 = 0.5$, $\sigma_a^2/\sigma_{aa}^2 = 3:1$. (a). Scenario 1: only additive effects were simulated; (b) Scenario 2: additive and global epistatic effects were simulated; (c) Scenario 3: additive and digenic local epistatic effects were simulated, effects were assumed to be independent; (d) Scenario 4: additive, digenic and higher-order local epistatic effects were simulated, effects were assumed to be independent; (e) Scenario 5: additive and digenic local epistatic effects were simulated, effects were assumed to be correlated; (f) Scenario 6: additive, digenic and higher-order local epistatic effects were simulated, effects were assumed to be correlated; GBLUP: genome-wide best linear unbiased prediction; EGBLUP: extended genome-wide best linear unbiased prediction; LEGBLUP: locally extended genome-wide best linear unbiased prediction; HGBLUP: haplotype-based genome-wide best linear unbiased prediction. Standard errors of the estimated prediction accuracies are indicated by whiskers. The LEGBLUP and HGBLUP models were implemented with different window length (i.e. number of SNPs), varying from 2 to 5.