



Figure S1. Accuracy with GBS data in the expanding prediction set and SNP array data (solid lines) or GBS data (dashed lines) in training. Training on SNP array data involved 1,000 individuals, while training on GBS data involved the same number of individuals and genome-wide sequence read depth as in the prediction set. Different marker densities are shown in top-left – a) 3K, top-right – b) 10K, bottom-left – c) 60K, and bottom-right – d) 300K.