Evaluation of the 2b-RAD method for genomic selection in scallop breeding

Jinzhuang Dou, Xue Li, Qiang Fu, Wenqian Jiao, Yangping Li, Tianqi Li, Yangfan Wang, Xiaoli Hu, Shi Wang[*]*, & Zhenmin Bao*[*]

Supplementary Figures

Figure S1. Principal component analysis (a) and genetic kinships (b) of the simulated 20 full-sib families using the markers derived from the low-density panel (2,364). The numbers in brackets refer to the proportion of variance explained.

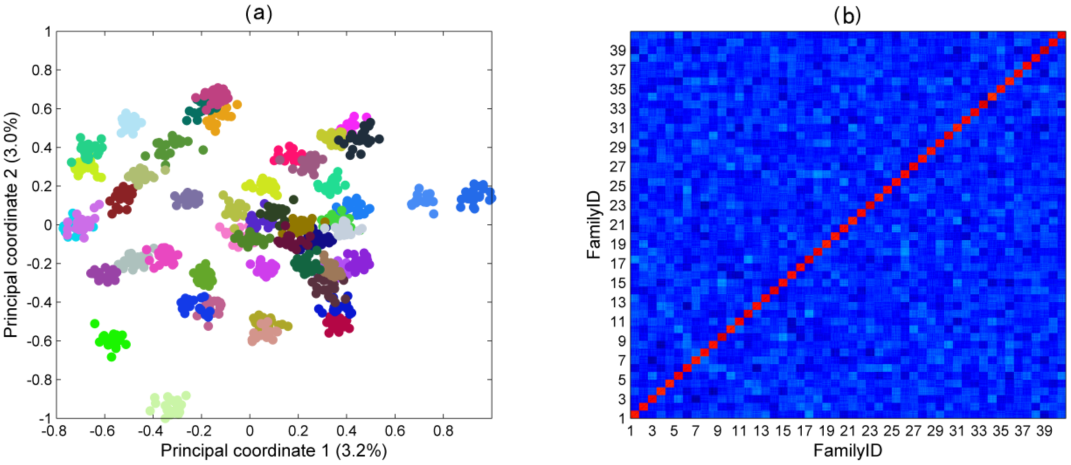

Figure S2. Accuracy of GEBVs estimated from a family-based dataset considering the dominant effects (Simulation 3). The vertical bar indicates the prediction accuracy under each scenario. The x-axis indicates the proportion of explained variation of additive effects, whereas the y-axis indicates the proportion of explained variation of dominant effects.