

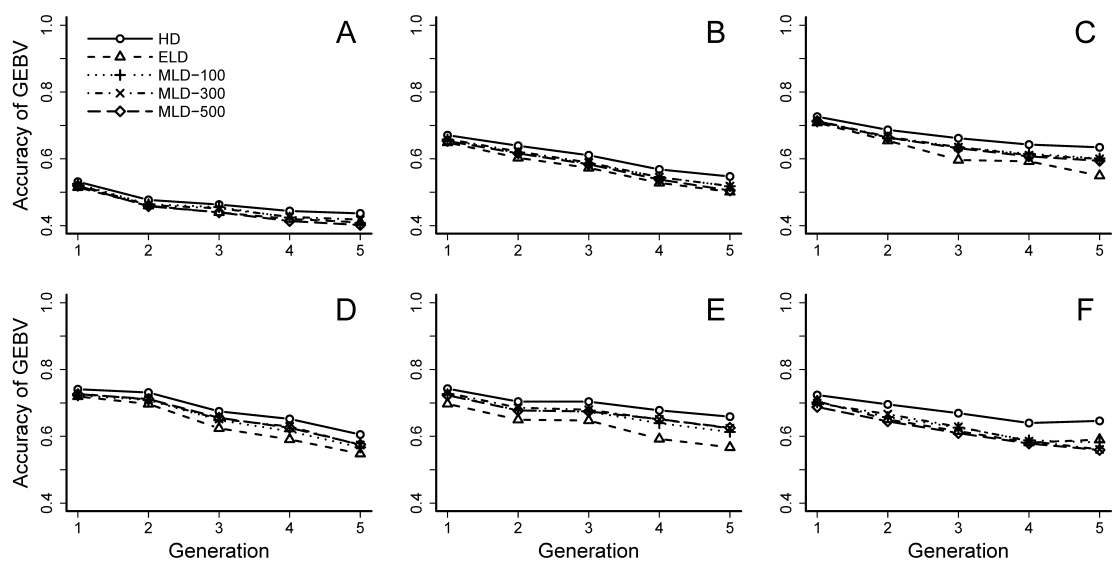
## **Accuracy of genomic prediction using mixed low-density marker panels**

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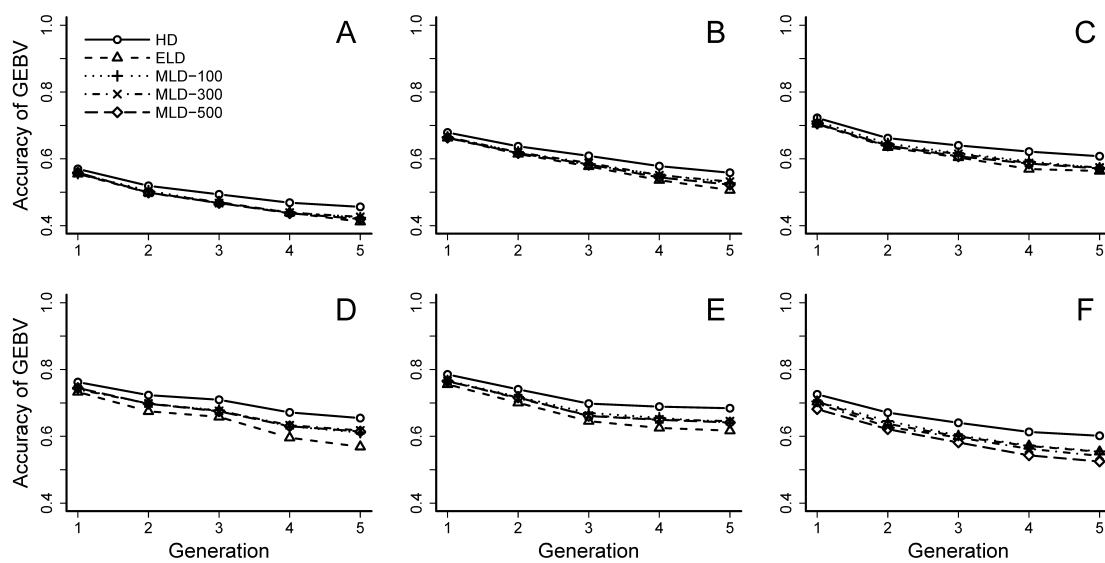
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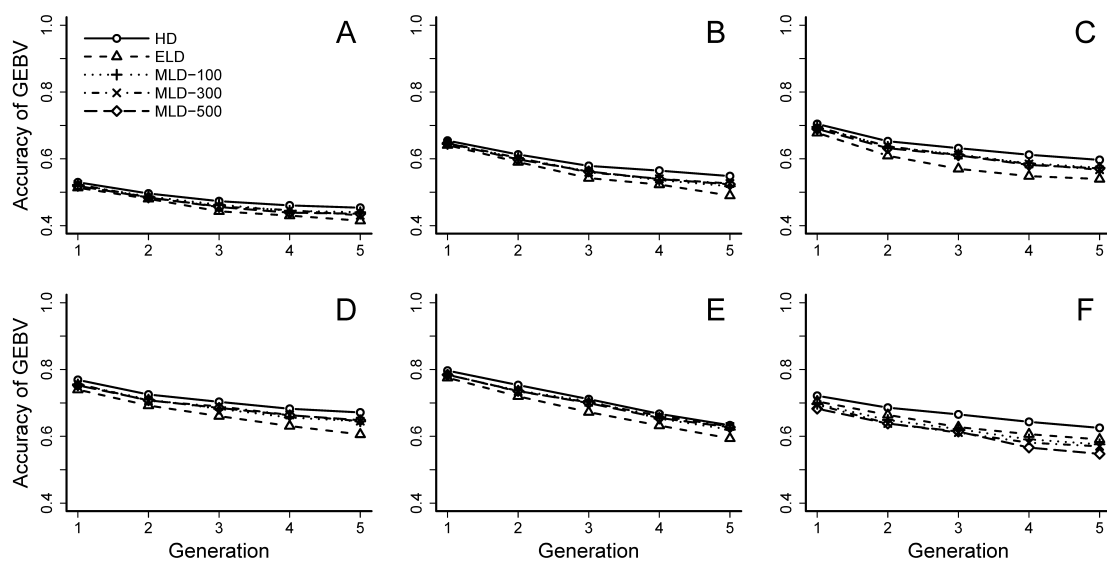
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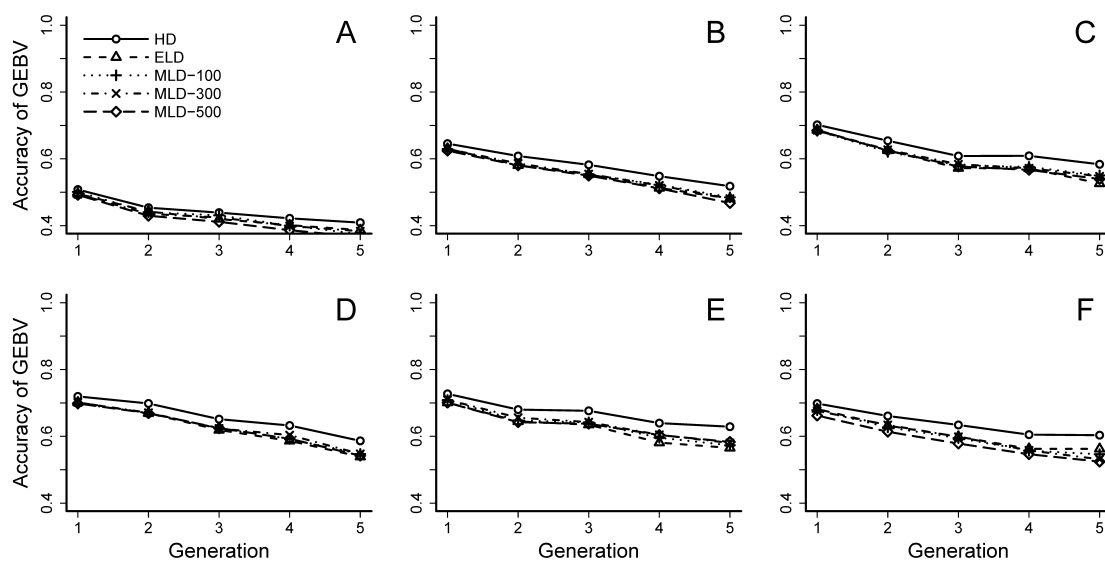
**Figure S1.** Accuracy of genomic estimated breeding value (GEBV) using BayesB for different type of chip with 500 quantitative trait loci (QTL) (Trait T1-T6 for A, B, C, E, and F, respectively). MLD-100, MLD-300, MLD-500 mean mixed low-density (MLD) panel (containing 1000 single-nucleotide polymorphisms (SNP) ) with 100, 300, 500 effective SNP, respectively. Evenly spaced low-density panel (ELD). High-density SNP panels (HD).



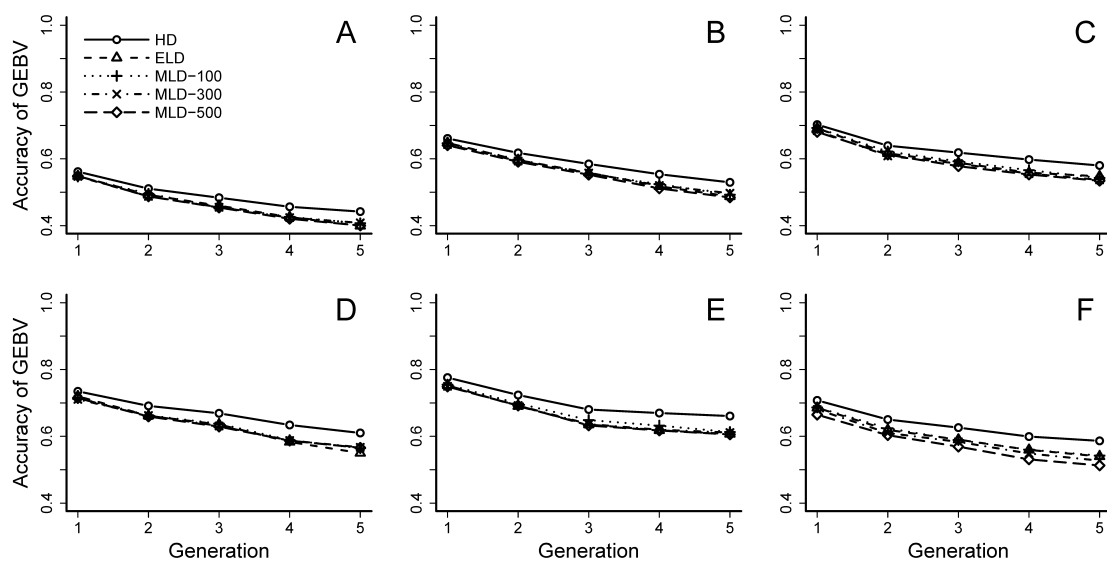
**Figure S2.** Accuracy of genomic estimated breeding value (GEBV) using BayesB for different type of chip with 1000 quantitative trait loci (QTL) (Trait T1-T6 for A, B, C, E, and F, respectively). MLD-100, MLD-300, MLD-500 mean mixed low-density (MLD) panel (containing 1000 single-nucleotide polymorphisms (SNP) ) with 100, 300, 500 effective SNP, respectively. Evenly spaced low-density panel (ELD). High-density SNP panels (HD).



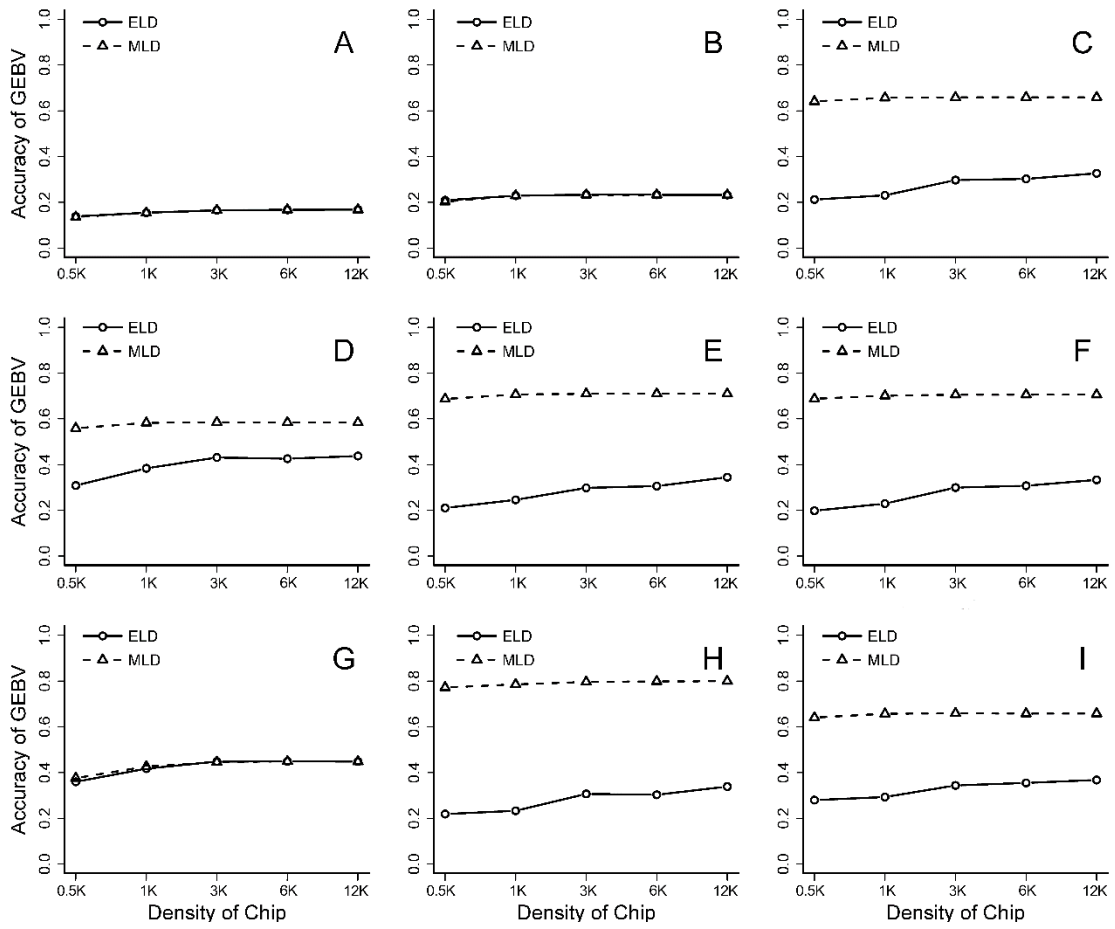
**Figure S3.** Accuracy of genomic estimated breeding value (GEBV) using GBLUP for different type of chip with 100 quantitative trait loci (QTL) (Trait T1-T6 for A, B, C, E, and F, respectively). MLD-100, MLD-300, MLD-500 mean mixed low-density (MLD) panel (containing 1000 single-nucleotide polymorphisms (SNP) ) with 100, 300, 500 effective SNP, respectively. Evenly spaced low-density panel (ELD). High-density SNP panels (HD).



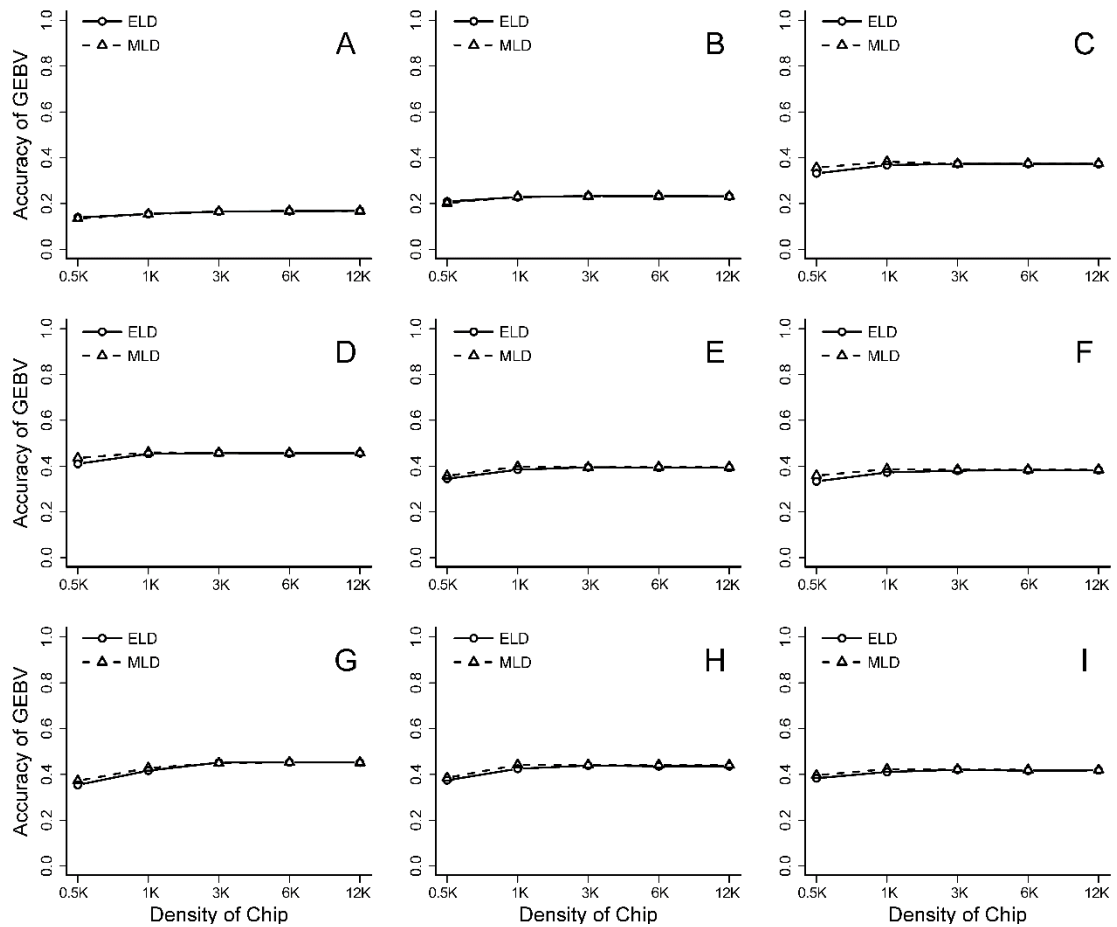
**Figure S4.** Accuracy of genomic estimated breeding value (GEBV) using GBLUP for different type of chip with 500 quantitative trait loci (QTL) (Trait T1-T6 for A, B, C, E, and F, respectively). MLD-100, MLD-300, MLD-500 mean mixed low-density (MLD) panel (containing 1000 single-nucleotide polymorphisms (SNP) ) with 100, 300, 500 effective SNP, respectively. Evenly spaced low-density panel (ELD). High-density SNP panels (HD).



**Figure S5.** Accuracy of genomic estimated breeding value (GEBV) using GBLUP for different type of chip with 1000 quantitative trait loci (QTL) (Trait T1-T6 for A, B, C, E, and F, respectively). MLD-100, MLD-300, MLD-500 mean mixed low-density (MLD) panel (containing 1000 single-nucleotide polymorphisms (SNP) ) with 100, 300, 500 effective SNP, respectively. Evenly spaced low-density panel (ELD). High-density SNP panels (HD).



**Figure S6.** Accuracy of genomic estimated breeding value (GEBV) for growth and meat quality trait using BayesB for pH of leg muscle (LMpH), pH of breast muscle (BMpH), dressed weight (DW), breast muscle weight (BMW), leg muscle weight (LMW), wing weight (WW), abdominal fat pad weight (AFW), feet weight (FW), heart, liver, gizzard, and glandular stomach weights (HLGGW) (scenarios A, B, C, D, E, F, G, H and I). Mixed low-density panel (MLD). Evenly spaced low-density panel (ELD).



**Figure S7.** Accuracy of genomic estimated breeding value (GEBV) for growth and meat quality trait using GBLUP for pH of leg muscle (LMpH), pH of breast muscle (BMpH), dressed weight (DW), breast muscle weight (BMW), leg muscle weight (LMW), wing weight (WW), abdominal fat pad weight (AFW), feet weight (FW), heart, liver, gizzard, and glandular stomach weights (HLGGW) (scenarios A, B, C, D, E, F, G, H and I). Mixed low-density panel (MLD). Evenly spaced low-density panel (ELD).