



Supplementary Figure S1. Distribution of SNPs in 1Mb bin along the chromosomes. The SNP identified between CDC Stanley and CDC Landmark with WGS were genotyped in 48 DH lines which were skim-sequenced at **a)** mean raw sample coverage of 0.88x, and down sampling from the original sequence data to simulate low coverage samples as **b)** 0.1x, **c)** 0.05x and **d)** 0.01x