

Figure S1. The frequency distribution of all traits for 146 rapeseed accessions. The x-axis indicates the ranges of phenotypic data for each trait; the y-axis indicates the number of individuals. SL, silique length; SMI, siliques on main inflorescence; SS, seeds per silique; TSW, thousand seeds weight; SYP, seed yield per plant; DWP, dry weight per plant; GV, germination vigor; GR, germination rate; RSDI, relative salt damage index.

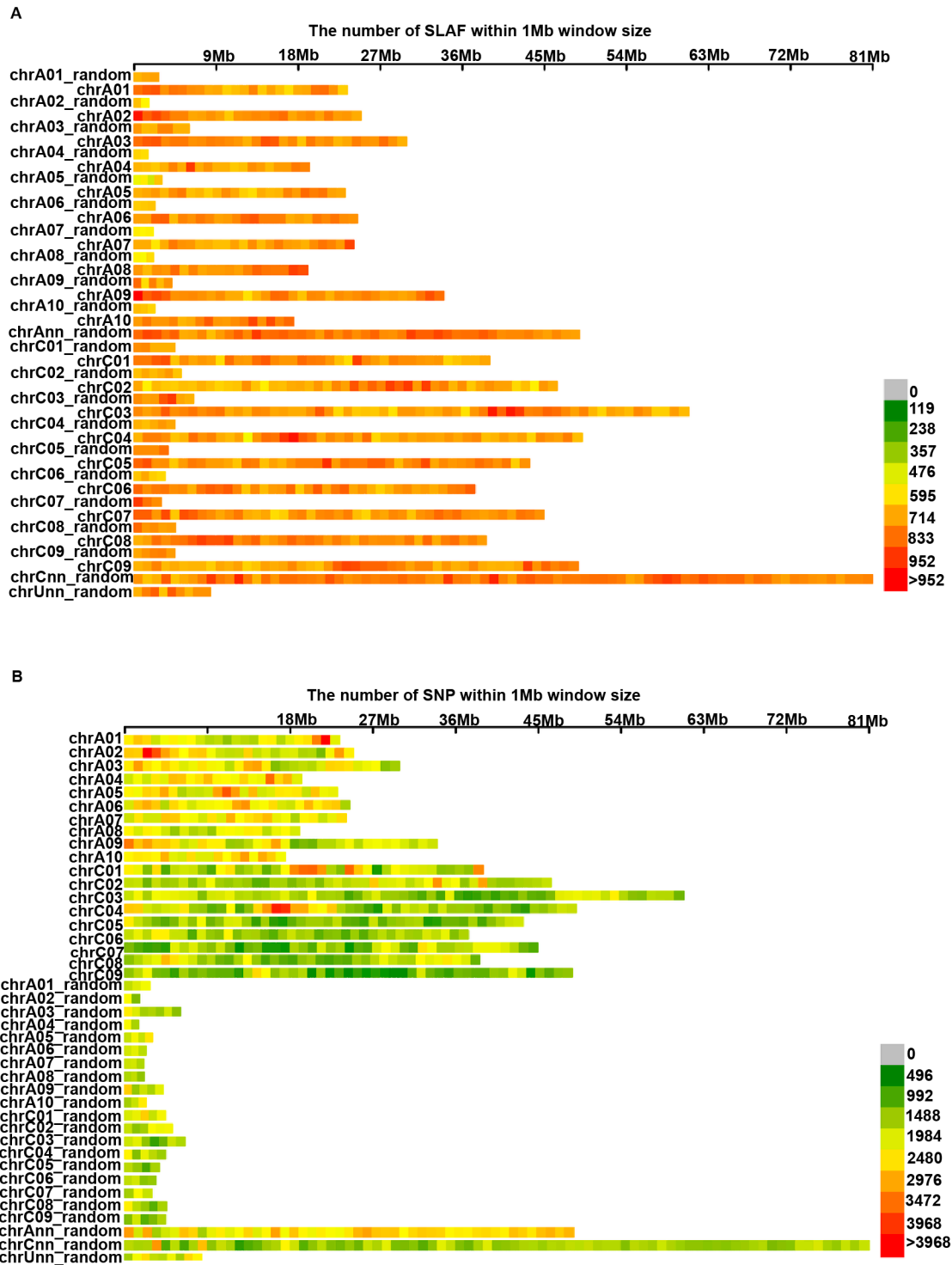
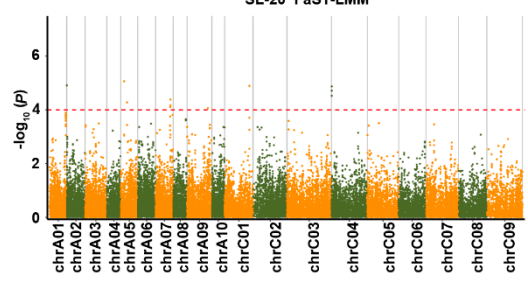
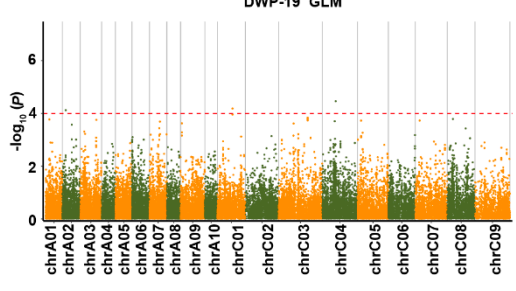
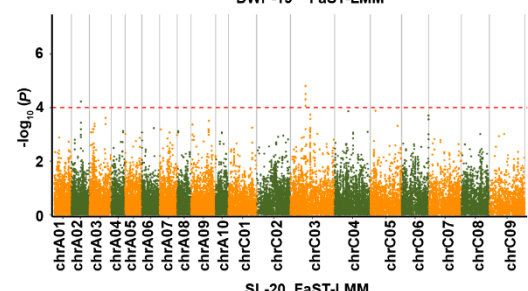
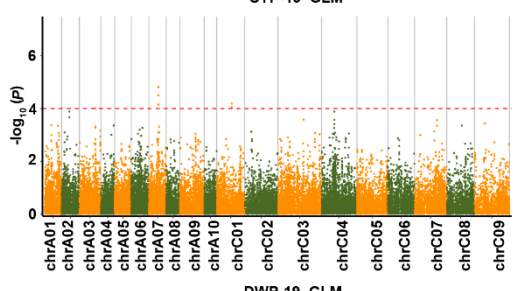
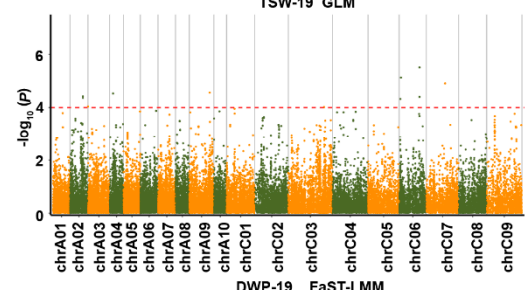
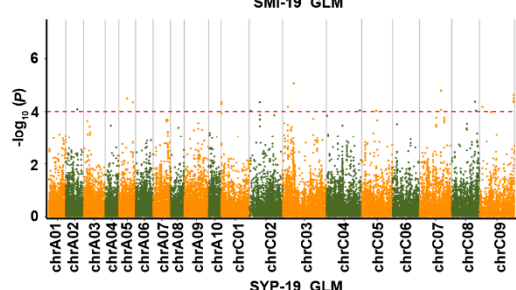
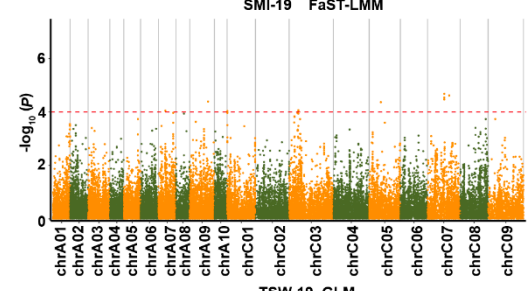
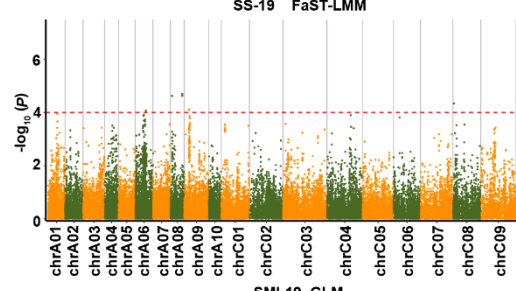
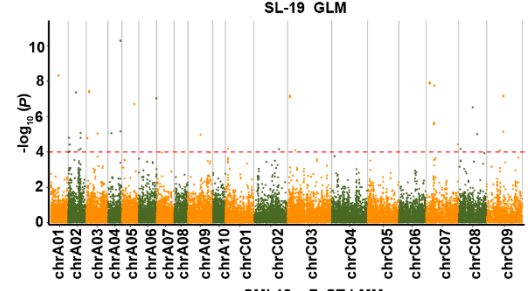
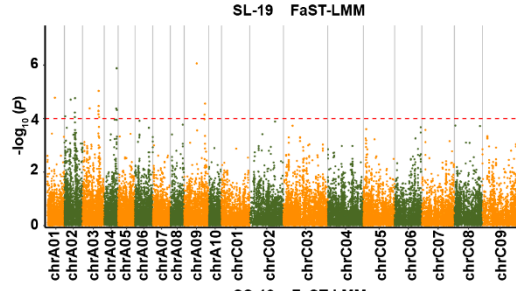


Figure S2. Distribution of the specific-locus amplified fragment (A) and SNPs (B) on the 19 rapeseed chromosomes. Each row represents one chromosome and the colors indicate the number of SLAF tags or SNPs within a Mb window.



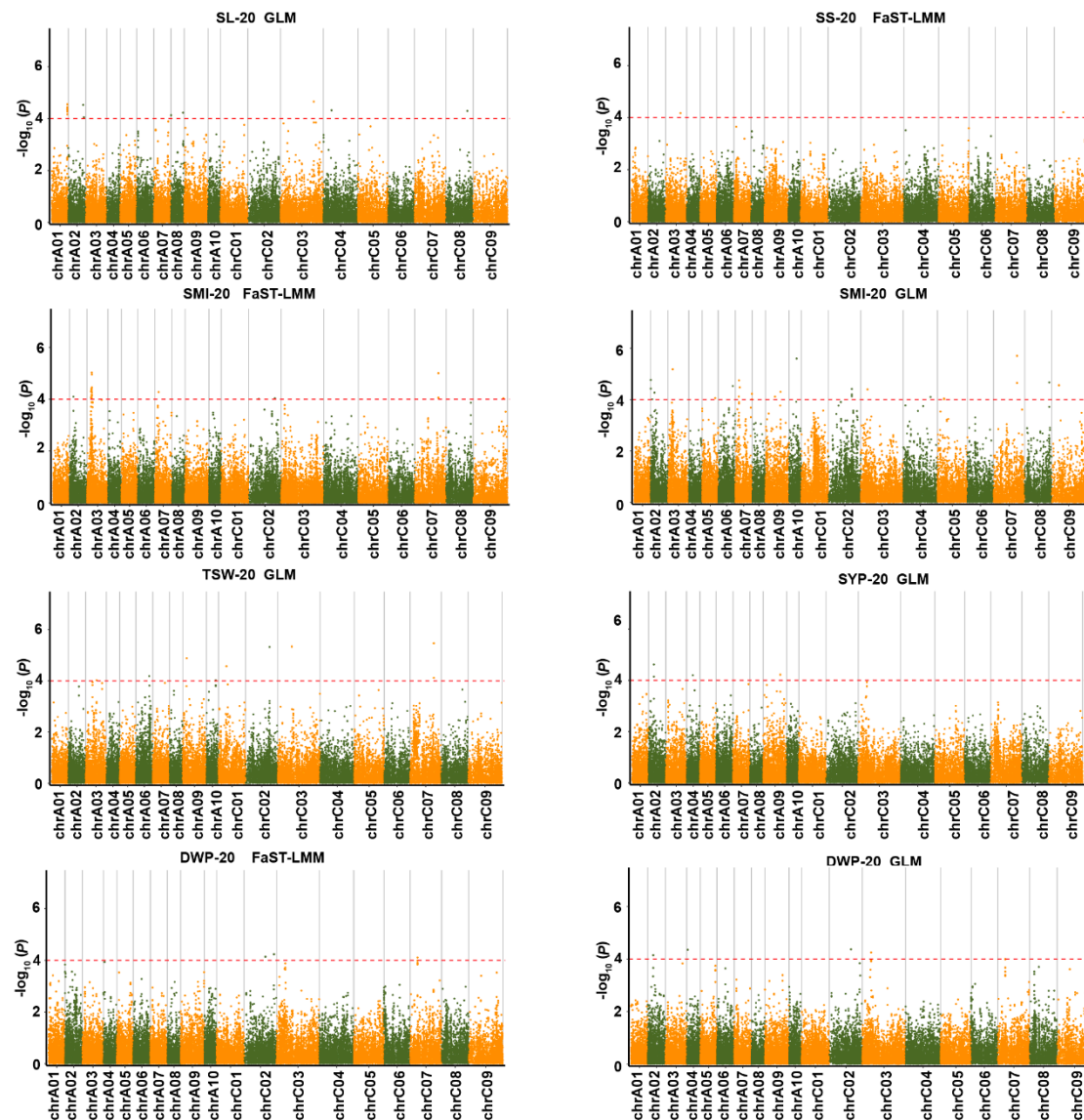


Figure S3. Manhattan plots from association analysis of six yield-related traits using the optimal statistical models in two year (2019, 2020). The X-axis indicates the nineteen chromosomes and the Y-axis represents $-\log_{10}(P)$ values of the SNP marker. The red dashed line represents the significant threshold ($P < 0.0001$). GLM, general linear model; FaST-LMM, factored spectrally transformed linear mixed model. SL, silique length; SMI, siliques on main inflorescence; SS, seeds per silique; TSW, thousand seeds weight; SYP, seed yield per plant; DWP, dry weight per plant.