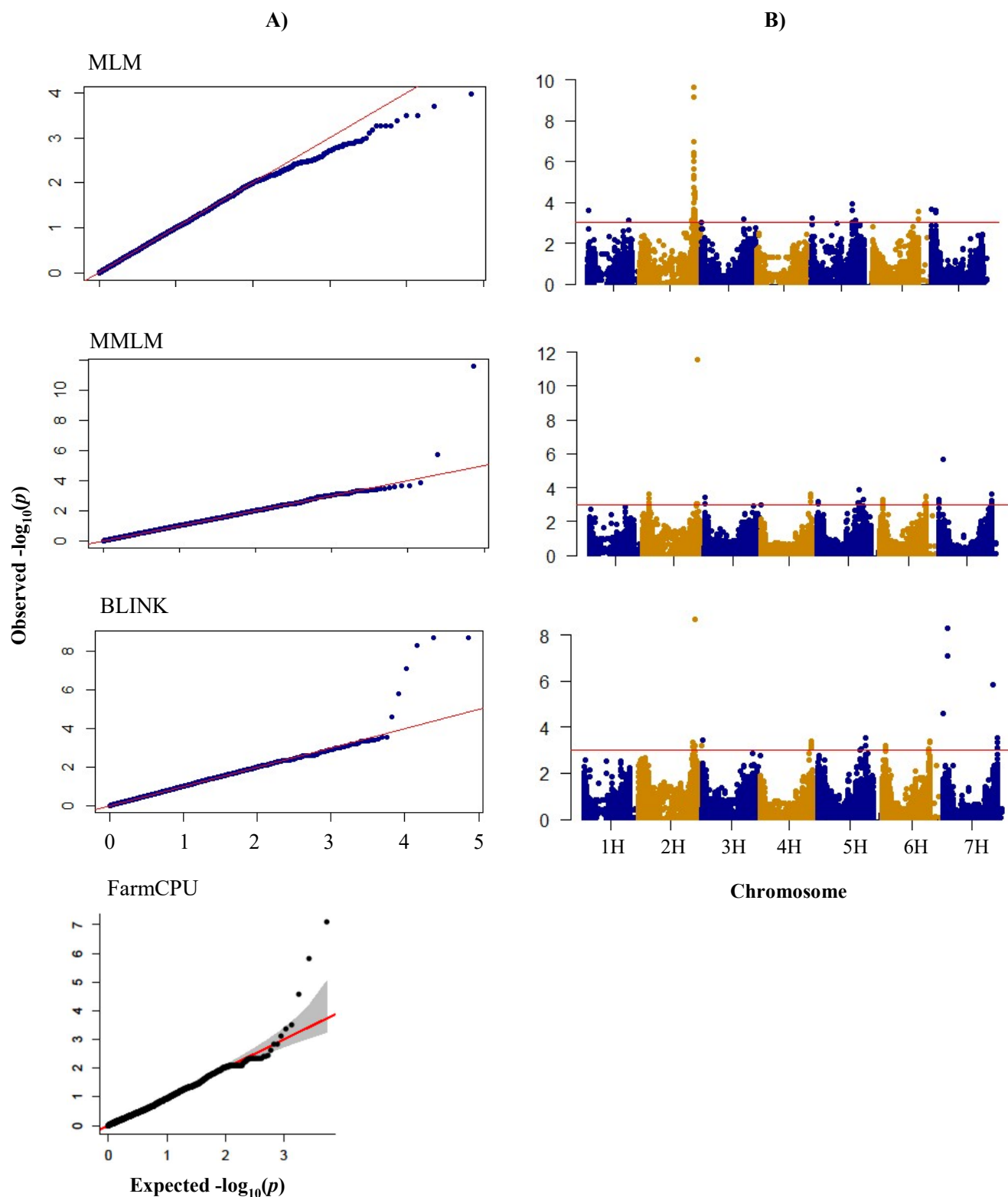
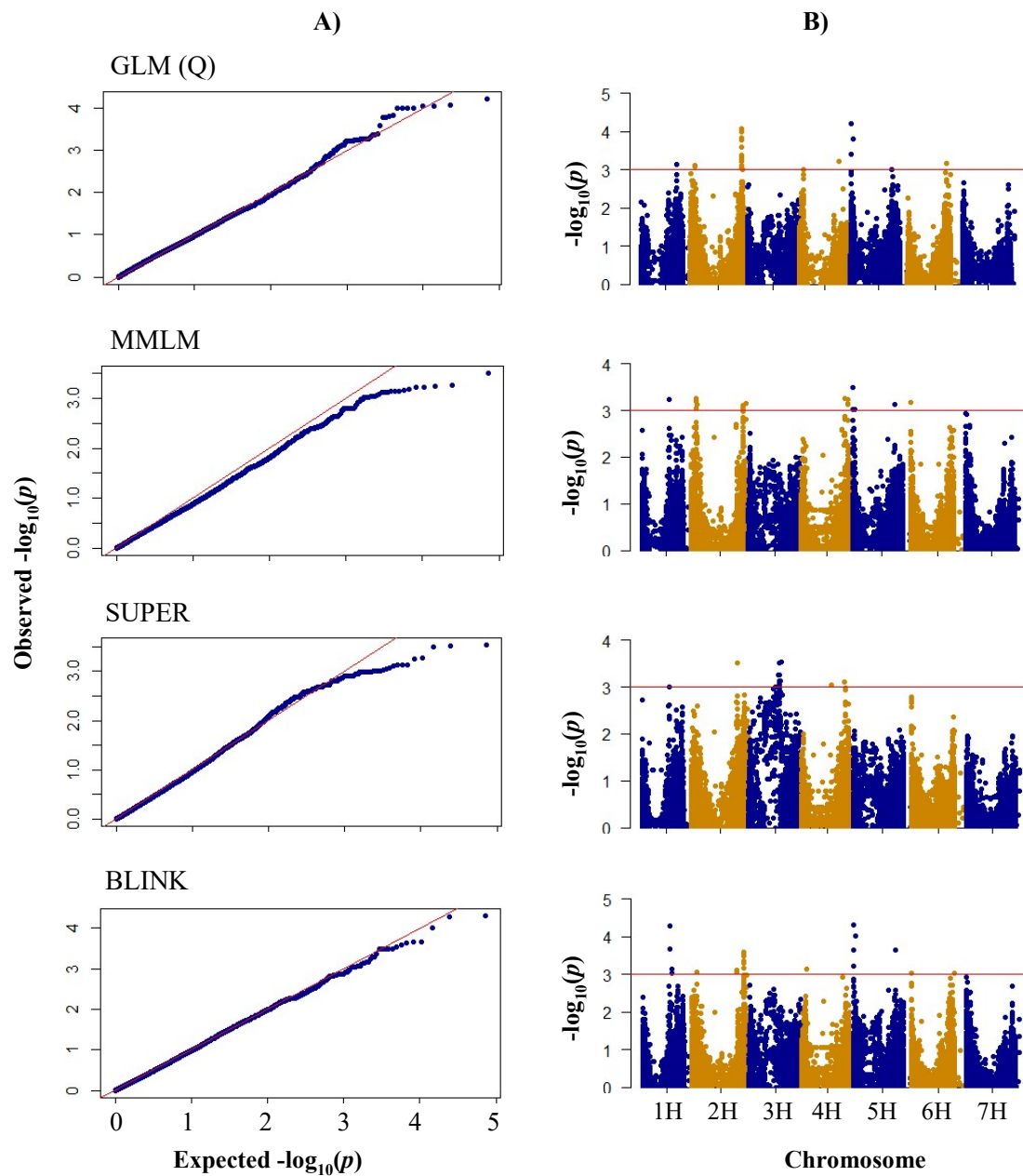


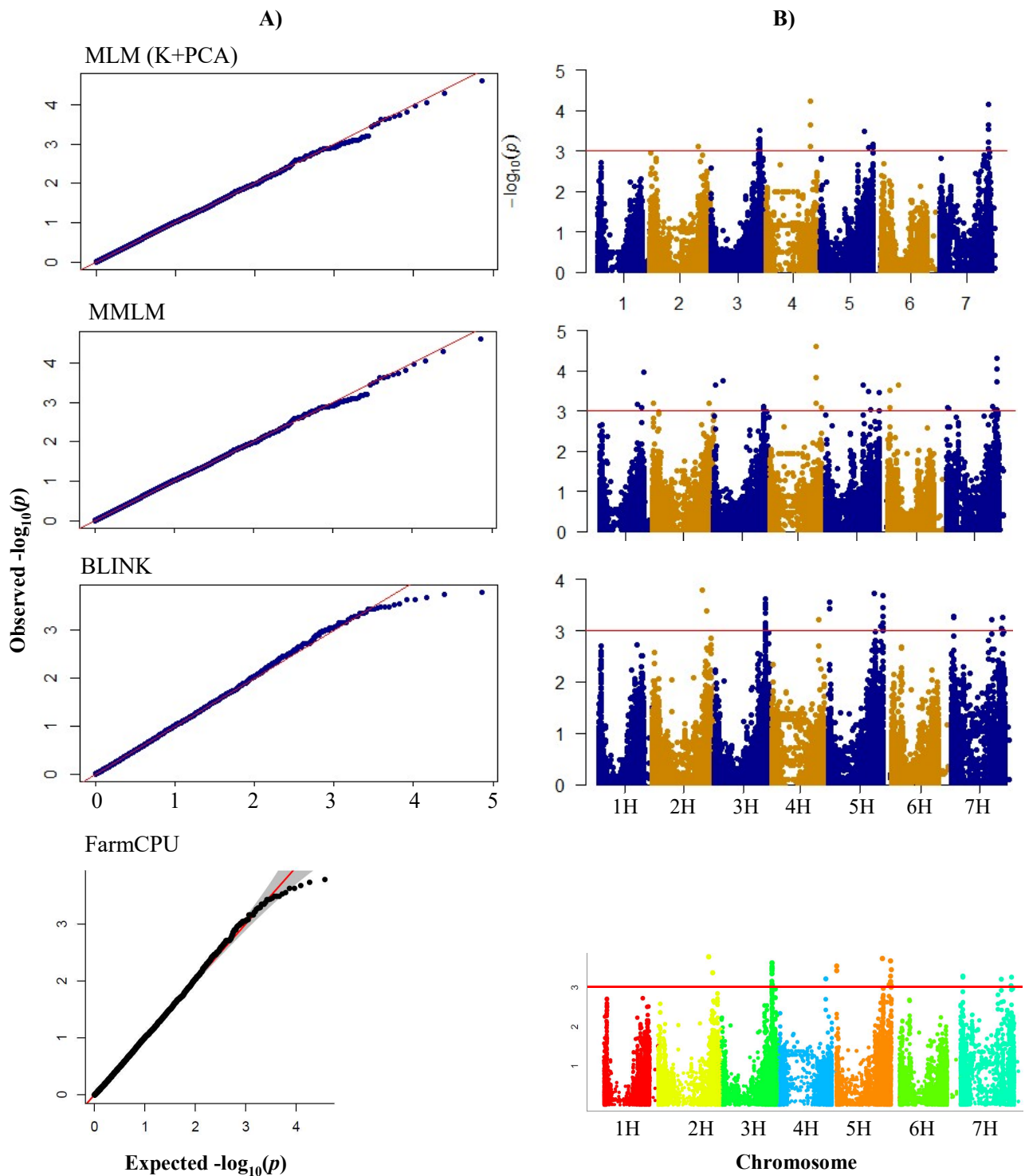
**Figure S1.** Genome-wide association mapping of barley leaf rust resistance at the seedling stage for *P. hordei* isolate SRT-MRC. a) Quantile-Quantile (Q-Q) plots of marker-trait association using MMLM, BLINK, SUPER, and FarmCPU models in GAPIT3. (b) The Manhattan plots shows  $-\log_{10}$  of  $p$ -values from genome-wide association mapping against the positions of SNPs on all chromosomes of barley using MMLM, BLINK, SUPER, and FarmCPU models in GAPIT3. The red horizontal line indicates significance threshold)  $p < 0.001$  [ $-\log_{10}(p)=3$ ]).



**Figure S2.** Genome-wide association mapping of barley leaf rust resistance at the seedling stage for *P. hordei* isolate SRT-SAT. a) Quantile-Quantile (Q-Q) plots of marker-trait association using MLM (K+PCA) in Tassel, and MMLM, BLINK, and FarmCPU models in GAPIT3. (b) The Manhattan plots shows  $-\log_{10}$  of  $p$ -values from genome-wide association mapping against the positions of SNPs on all chromosomes of barley using using MLM (K+PCA) in Tassel, and MMLM, BLINK, and FarmCPU models in GAPIT3. The red horizontal line indicates significance threshold)  $p < 0.001$  [ $-\log_{10}(p) = 3$ ].



**Figure S3.** Genome-wide association mapping of barley leaf rust resistance at the adult plant stage at Sidi Allal Tazi station in 2017 (APR-SAT17). a) Quantile-Quantile (Q-Q) plots of marker-trait association using GLM (Q) in Tassel, and MMLM, SUPER, and BLINK models in GAPIT3. (b) The Manhattan plots shows  $-\log_{10}$  of  $p$ -values from genome-wide association mapping against the positions of SNPs on all chromosomes of barley using GLM (Q) in Tassel, and MMLM, SUPER, and BLINK models in GAPIT3.. The red horizontal line indicates significance threshold)  $p < 0.001$  [ $-\log_{10}(p)=3$ ]).



**Figure S4.** Genome-wide association mapping of barley leaf rust resistance at the adult plant stage at Sidi Allal Tazi station in 2019 (APR-SAT19). a) Quantile-Quantile (Q-Q) plots of marker-trait association using MLM (K +PCA) in Tassel, and MMLM, BLINK, and FarmCPU models in GAPIT3. (b) The Manhattan plots shows  $-\log_{10}$  of  $p$ -values from genome-wide association mapping against the positions of SNPs on all chromosomes of barley MLM (K+PCA) in Tassel, and MMLM, BLINK, and FarmCPU models in GAPIT3. The red horizontal line indicates significance threshold  $p < 0.001$  [ $-\log_{10}(p) = 3$ ].