

SUPPORTING INFORMATION

**Shoupu He^{1,2,†}, Gaofei Sun^{1,3,†}, Longyu Huang^{2,†}, Daigang Yang², Panhong Dai², Dayun Zhou²,
Yuzhen Wu², Xiongfeng Ma², Xiongming Du^{1,2}, Shoujun Wei^{2,*}, Jun Peng^{2,*}, Meng Kuang^{1,2,*}**

**¹Research Base, Anyang Institute of Technology, State Key Laboratory of Cotton Biology,
Anyang, China**

²Institute of Cotton Research of the Chinese Academy of Agricultural Sciences, Anyang, China

**³Department of Computer Science and Information Engineering/Data Mining Institute,
Anyang Institute of Technology, Anyang, China**

Genomic divergence in cotton germplasm related to maturity and heterosis

SUPPLEMENTARY FIGURES

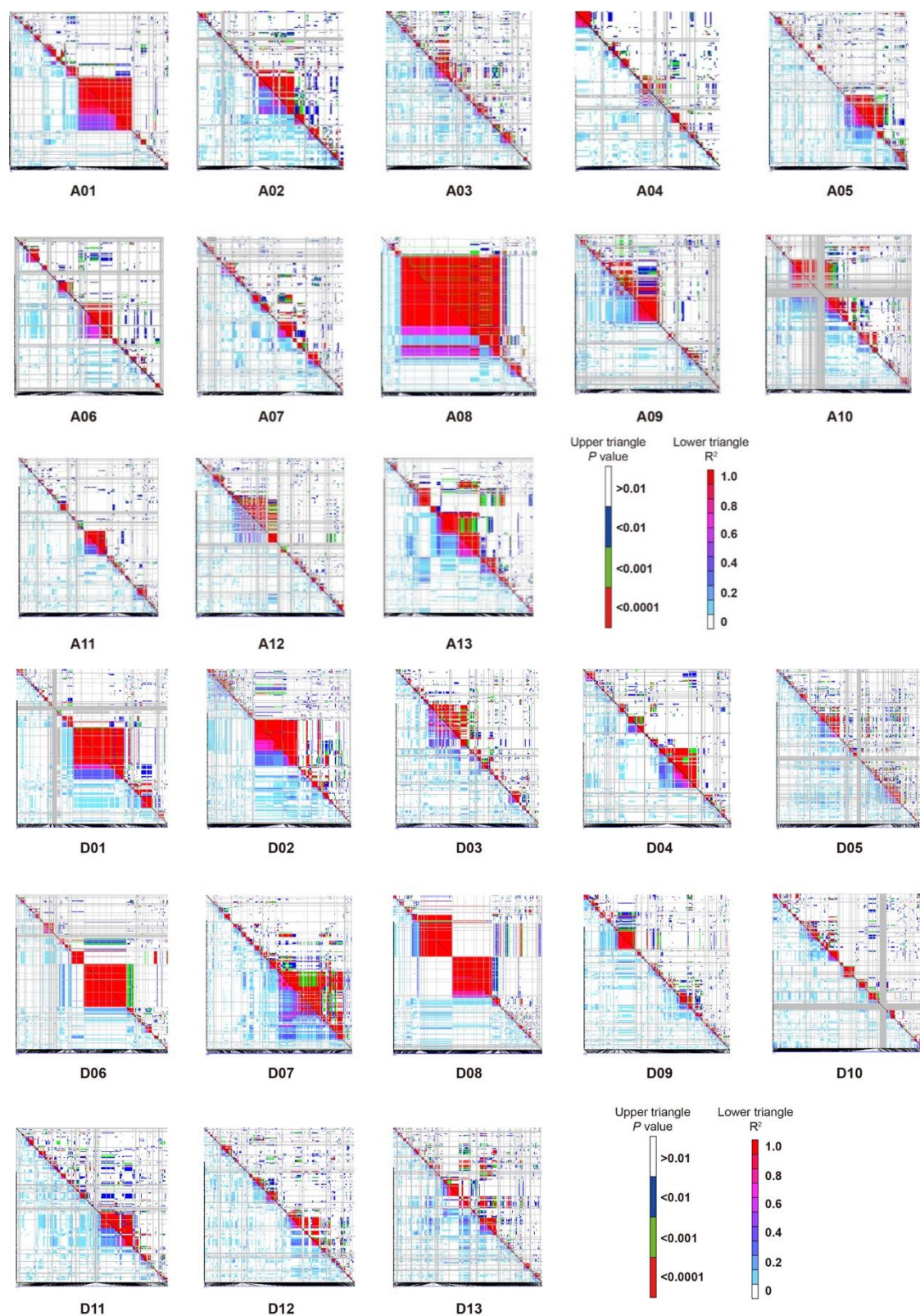


Figure S1. The whole-genome linkage disequilibrium (LD) map of upland cotton based on all the inbred *G. hirsutum* lines and 10,552 single-locus SNP markers.

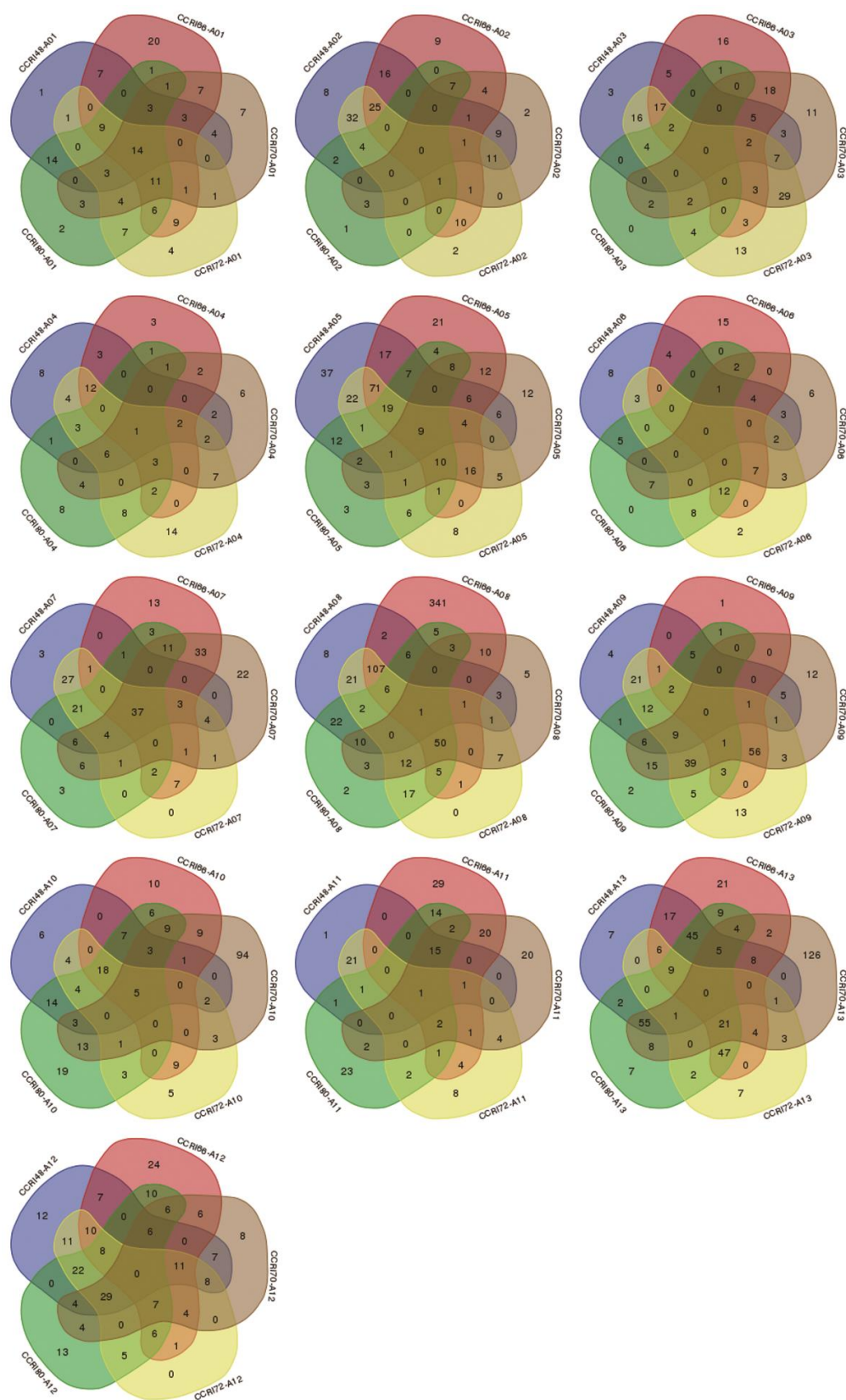


Figure S2. Venn diagrams of all shared and unique theoretical heterozygous loci among the five hybrids represented in the At subgenome.

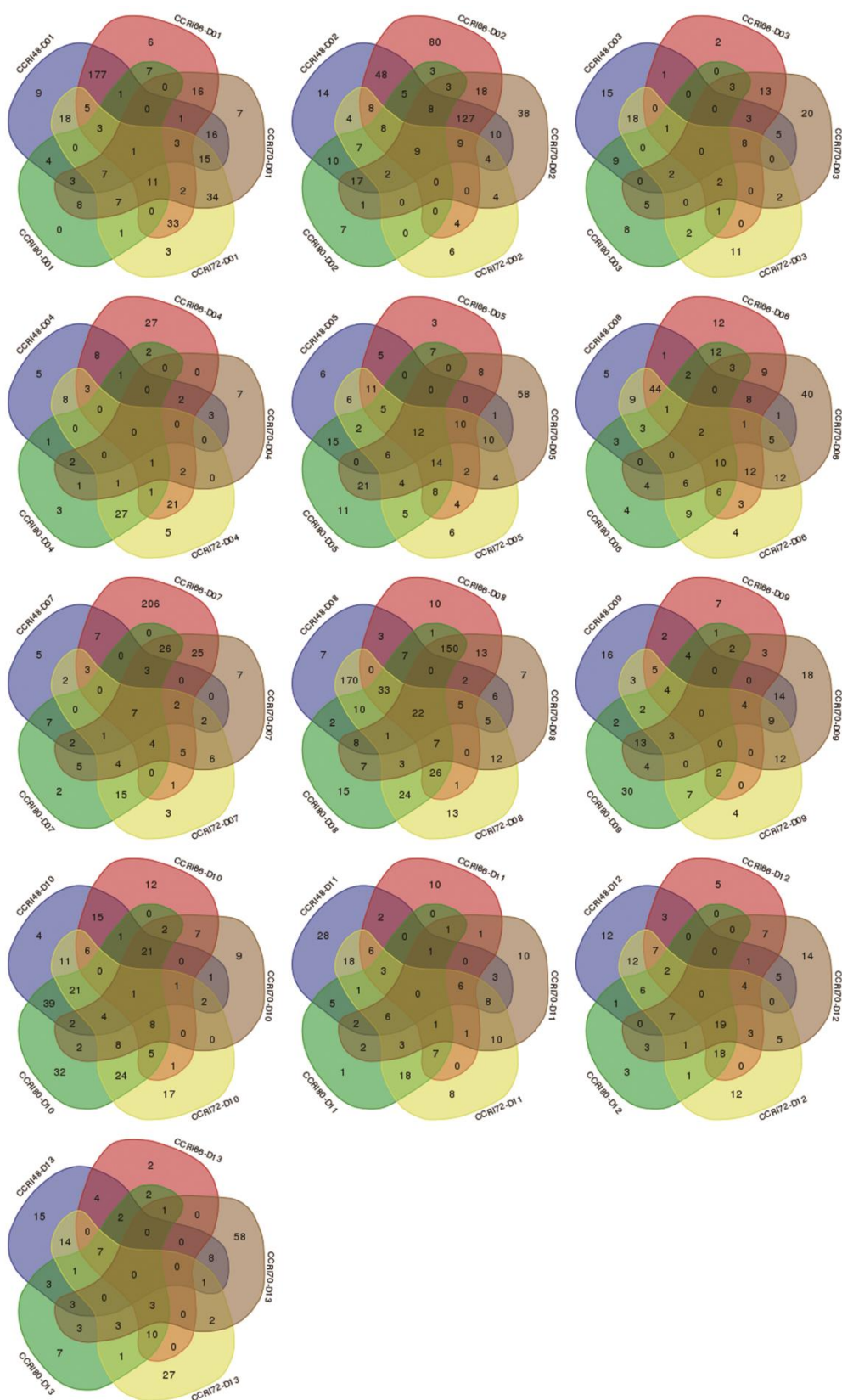


Figure S3. Venn diagrams of all shared and unique theoretical heterozygous loci among the five hybrids represented in the Dt subgenome.

SUPPLEMENTARY TABLES

Table S1-S6 were available online as separated excel files.