

## **Construction of Genetic Linkage Map and QTL Mapping for Fiber Quality in Upland Cotton**

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A comprehensive genetic linkage map was constructed using 270  $F_{2:7}$  recombinant inbred lines from a cross between two upland cotton cultivars Yumian 1 and T586. The linkage map comprised of 604 loci and 57 linkage groups ordered into 25 chromosomes, spanning 3106.9 cM, and approximately accounting for the 69.87% of the whole cotton genome with an average genetic distance of 5.15 cM between two markers. Based on interval mapping, 29 QTLs affecting fiber quality were identified, including 5 QTLs for fiber length, 7 QTLs for fiber uniformity, 10 QTLs for fiber strength, 2 QTLs for fiber elongation, and 5 QTLs for fiber fineness. Seventeen QTLs were mapped on A sub-genome chromosomes, and 12 on D sub-genome.