Supplementary Table 11 Significant GWAS signals for fiber quality-related traits.

Trait	Chromos-ome	Position	Major allele	Minor allele	Minor allele freq.	*P* value	QTL hotspots
Fiber length	A01	43,738,677	A*	G	0.06	1.2×10^{-7}	FQ2; Said *et al.*, 2015[13]
	A06	75,968,621	G*	A	0.19	2.2×10^{-8}	
	A06	91,942,101	C	A*	0.16	3.1×10^{-7}	Liu *et al.*, 2016[14]
	D07	50,345,184	C	T*	0.14	1.9×10^{-7}	
Fiber uniformity	D09	9,787,159	G*	A	0.06	1.0×10^{-7}	
Micronaire value	D03	6,838,694	T	C*	0.13	3.7×10^{-7}	FQ8; Said *et al.*, 2015[13]
	D10	7,022,160	C	T*	0.46	1.8×10^{-7}	
	D10	23,063,270	T	C*	0.06	3.5×10^{-7}	
Fiber elongation rate	A07	54,633,604	A	T*	0.46	4.1×10^{-7}	
	D04	47,796,313	G	A*	0.46	4.8×10^{-8}	
Fiber strength	A12	6,593,191	G*	A	0.48	2.0×10^{-8}	
Short fiber rate	A01	9,043,901	G*	A	0.07	2.8×10^{-7}	
	A03	22,313,040	A*	G	0.18	3.3×10^{-8}	
	A05	23,119,434	G*	A	0.11	6.3×10^{-8}	
	A06	29,442,697	C*	A	0.08	1.8×10^{-7}	
	A11	27,027,214	A*	C	0.07	$1.0 \times 1^{0-7}$	
	A12	3,999,622	T	C*	0.37	1.1×10^{-7}	
	D08	19,049,523	T	G*	0.33	3.1×10^{-9}	
	D11	63,562,989	T*	G	0.12	2.3×10^{-8}	

*favorable SNP alleles.

Supplementary Table 12 Expression and annotation of candidate genes identified by GWAS (included as a separate excel file).

Supplementary Table 13 Summary of homoeologous gene pairs with selection signals in at least one subgenome (included as a separate excel file).