

Figure S1. Quantile–quantile (QQ) plots from GWAS for leaf types for each year. The blue line represents the expected distribution of p -values, and the red dotted line indicates a reference or threshold. The observed p -values are shown as blue dots.

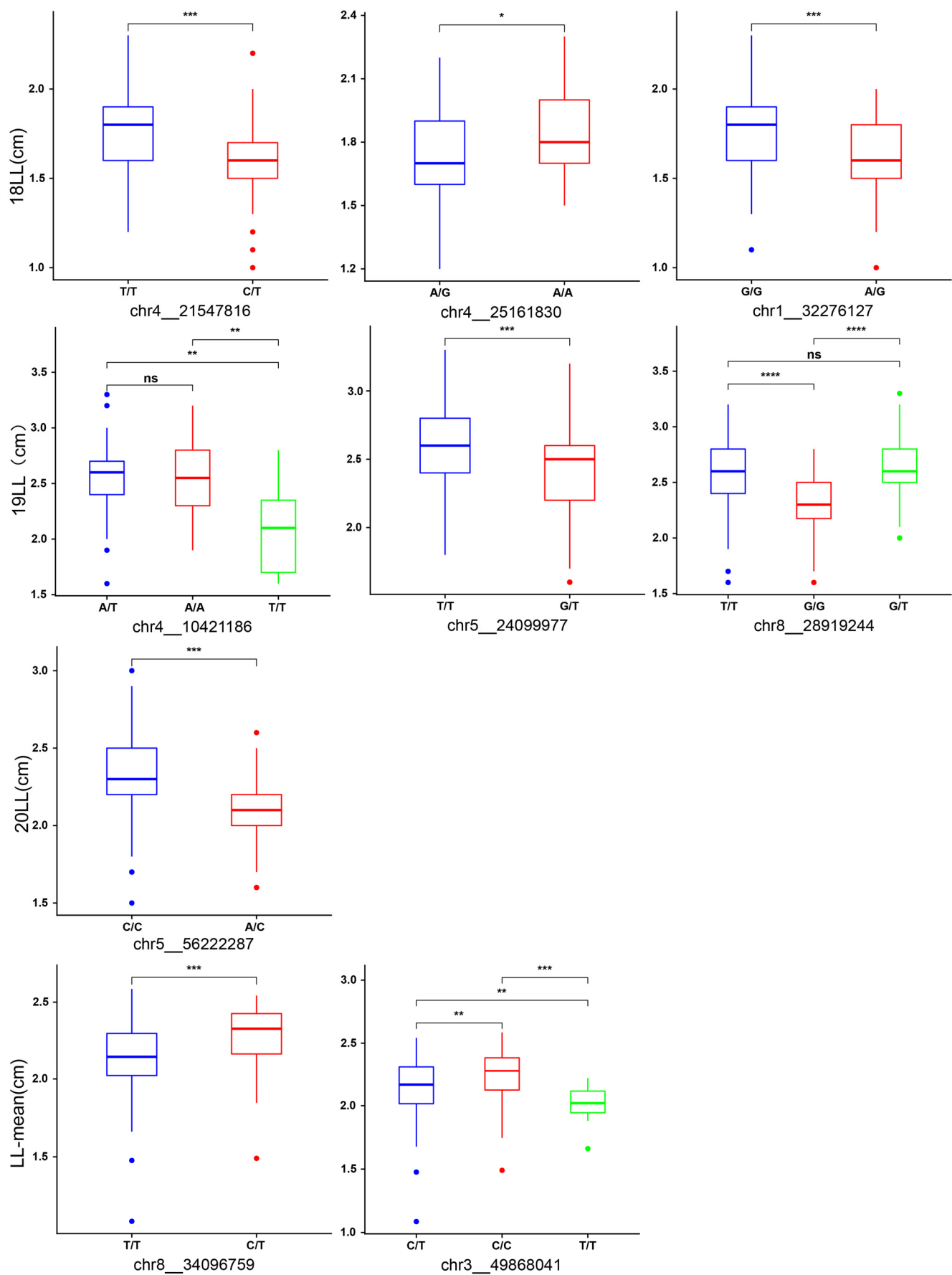


Figure S3. Haplotype analysis of SNP related to leaf length (LL).

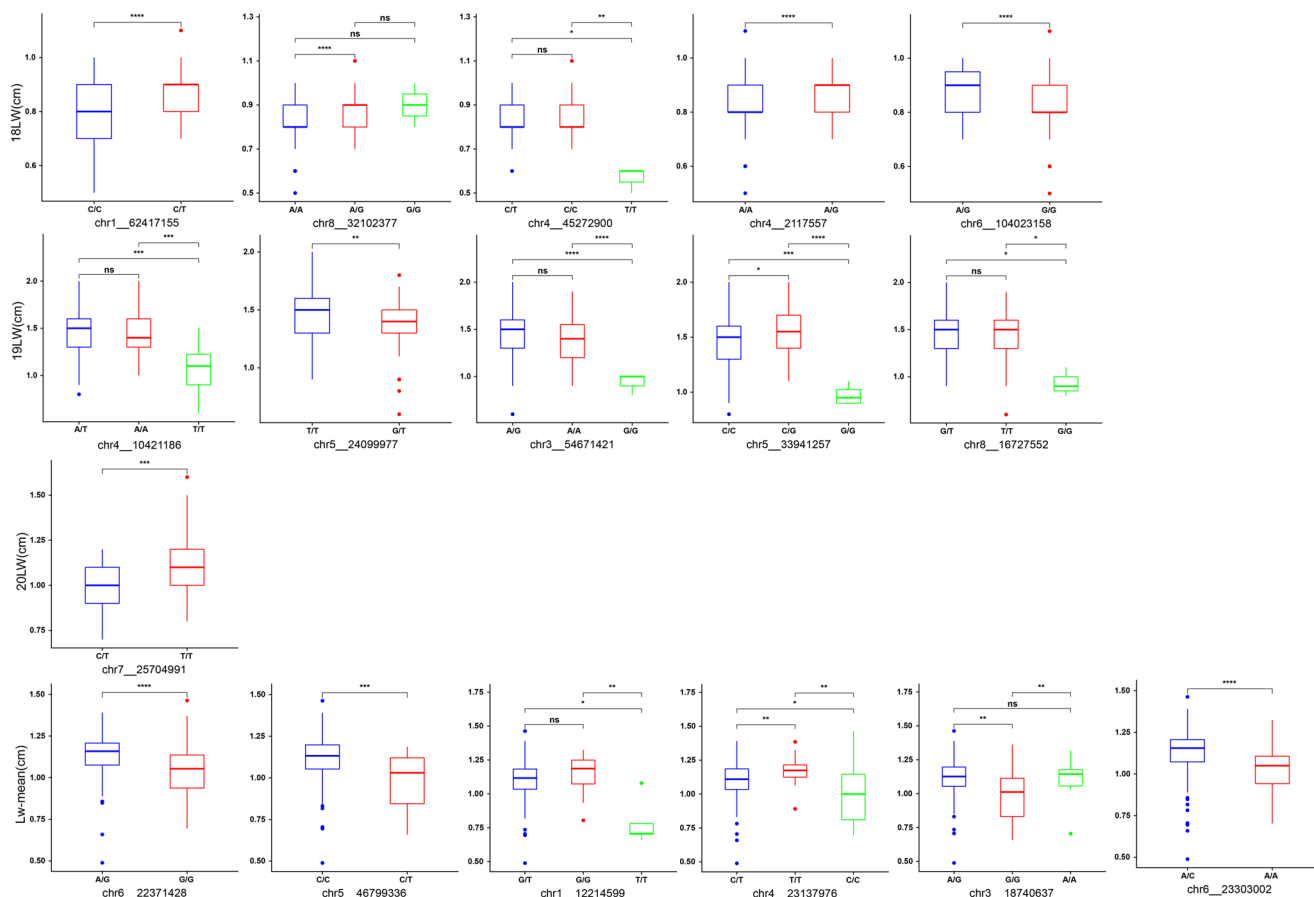


Figure S4. Haplotype analysis of SNP related to leaf width (LW).

Table S1. Details of the 13 Chinese cultivars.

Taxa	Accession	Name	Improvement of Breeding status	Region
B10	CF032020	Zhongmu No.1	Cultivar	China
B140	CF002722	Xinmu	Cultivar	China
B141	CF020901	Gannong No.3	Cultivar	China
B145	CF000715	Gongnong No.1	Cultivar	China
B148	CF020976	Guyuan	Cultivar	China
B152	CF030056	Xinjiangdaye	Cultivar	China
B159	PI502646	Gongnong	Cultivar	China
B160	PI499544	D2675	Cultivar	China
B161	PI502647	Humeng	Cultivar	China
B172	PI491400	Wuming	Cultivar	China
B173	PI491401	Wulumuqi	Cultivar	China
B9	PI430638	Yuhisian	Cultivar	China
B93	PI430636	Tingsi	Cultivar	China

Table S2. Candidate gene prediction and functional annotation.

Trait	Marker	Gene Model	Chromosome	Position			BLAST-P		
				Start-Pos	End-Pos	Strand	Annotation	E-Value	%ID
18LL	chr4__21547816	Msa0540020	4	21527816	21567816	-	TATA-binding protein-associated factor BTAF1 isoform X1	0	95.68%
	chr4__25161830	Msa0541350	4	25141830	25181830	+	CAX-interacting protein 4	4.00×10^{-78}	89.15%
	chr1__32276127	Msa0018930	1	32256127	32296127	+	transmembrane protein, putative	3.00×10^{-25}	49.38%
18LW	chr1__62417155	Msa0034420	1	62397155	62437155	+	putative E3 ubiquitin-protein ligase RF4 isoform X2	0	97.17%
		Msa0034430	1	62397155	62437155	+	endonuclease/exonuclease/phosphatase family protein	0	95.44%
		Msa0034440	1	62397155	62437155	-	putative histone acetyltransferase	4.00×10^{-76}	78.53%
	chr8__32102377	Msa1189740	8	32082377	32122377	-	GDSL esterase/lipase At5g22810	3.00×10^{-87}	70.44%
	chr4__45272900	Msa0549940	4	45252900	45292900	-	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic	0	95.99%
		Msa0549950	4	45252900	45292900	+	organ-specific protein P4	3.00×10^{-57}	92.71%
		Msa0549960	4	45252900	45292900	-	BURP domain protein USPL1	0	96.01%
19LL	chr4__10421186	Msa0534800	4	10401186	10441186	+	protein FAR1-RELATED SEQUENCE 5-like	0	86.65%
		Msa0534810	4	10401186	10441186	+	Ulp1 protease family, carboxy-terminal domain protein	0	80.25%
	chr8__28919244	Msa1188590	8	28899244	28939244	+	CTP synthase	0	96.52%
		Msa1188600	8	28899244	28939244	-	zinc finger CCCH domain-containing protein 37	0	97.48%
	chr4__10421186	Msa0534800	4	10401186	10441186	+	protein FAR1-RELATED SEQUENCE 5-like	0	86.65%
19LW		Msa0534810	4	10401186	10441186	+	Ulp1 protease family, carboxy-terminal domain protein	0	80.25%
	chr3__54671421	Msa0362890	3	54651421	54691421	-	E3 ubiquitin-protein ligase KEG	0	96.87%
	chr8__16727552	Msa1181920	8	16707552	16747552	-	probable polygalacturonase At3g15720	6.00×10^{-156}	69.19%
		Msa1181930	8	16707552	16747552	-	Ulp1 protease family, carboxy-terminal domain protein	5.00×10^{-121}	50.12%
		Msa1181970	8	16707552	16747552	-	polygalacturonase	0	77.12%
20LL	chr5__56222287	Msa0738440	5	56202287	56242287	+	26S proteasome non-ATPase regulatory subunit 7 homolog A	0	95.09%
		Msa0738450	5	56202287	56242287	+	probable LRR receptor-like serine/threonine-protein kinase At3g47570	0	77.90%
		Msa0738480	5	56202287	56242287	+	probable LRR receptor-like serine/threonine-protein kinase At3g47570	0	87.06%
LL-mean	chr8__34096759	Msa1190810	8	34076759	34116759	+	ribonuclease 3-like protein 2	0	92.69%
		Msa1190820	8	34076759	34116759	-	metallothionein-like protein type 3	1.00×10^{-36}	100%
	chr3__49868041	Msa0360500	3	49848041	49888041	-	DEAD-box ATP-dependent RNA helicase 38	0	71.73%
		Msa0360510	3	49848041	49888041	-	acetyltransferase (GNAT) domain protein	4.00×10^{-147}	67.85%
LW-mean	chr6__22371428	Msa0879720	6	22351428	22391428	+	F-box/FBD/LRR-repeat protein At4g26340	2.00×10^{-163}	65.74%
	chr5__46799336	Msa0733480	5	46779336	46819336	-	probable ribonuclease P/MRP protein subunit POP5	1.00×10^{-109}	100%

	Msa0733510	5	46779336	46819336	+	sm-like protein LSM3A	4.00×10^{-62}	100%
chr1__12214599	Msa0008500	1	12194599	12234599	-	hydroquinone glucosyltransferase	1.00×10^{-67}	86.05%
	Msa0008520	1	12194599	12234599	+	protein ATAF2 isoform X1	0	95.58%
