

Supplementary Figures

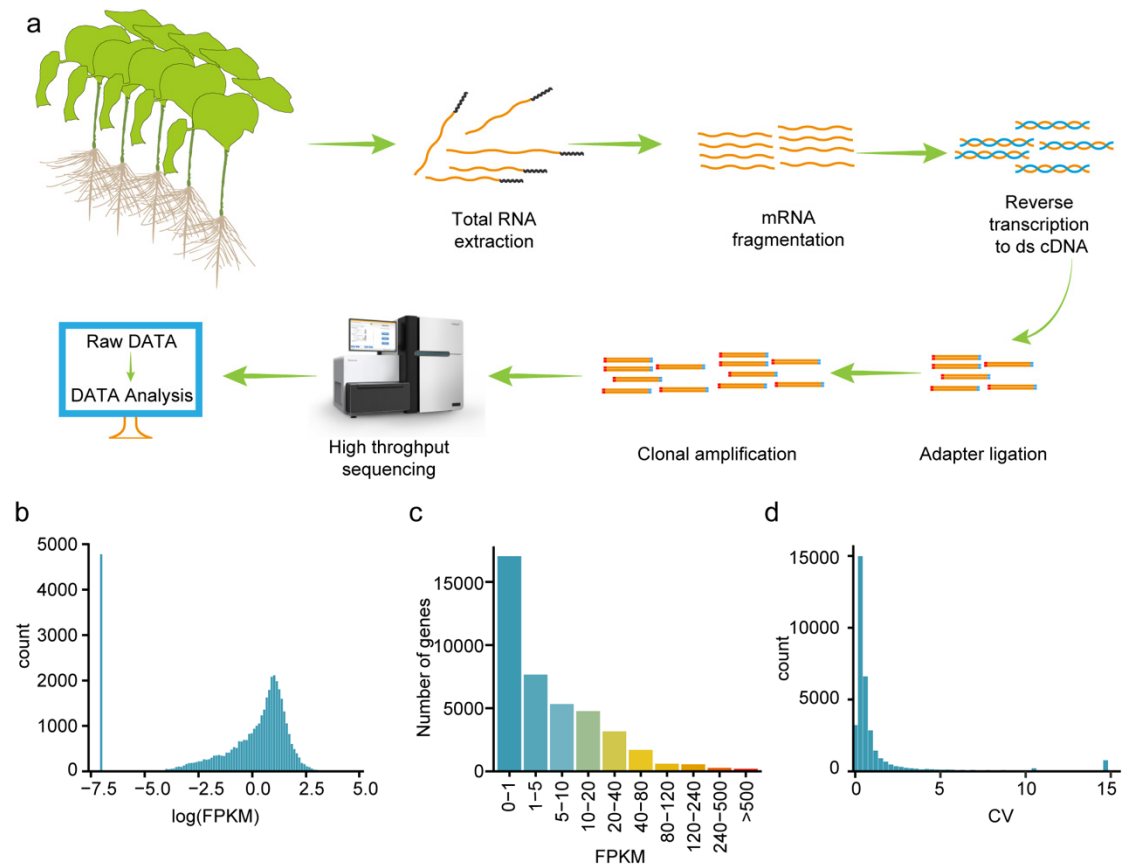


Figure S1. Overall statistics of RNA-Seq. (a) Analysis process for RNA-Seq (b) The histogram of $\log_{10}$ (FPKM). (c) FPKM statistic of genes. (d) The histogram of coefficient of variation (CV) for FPKM.

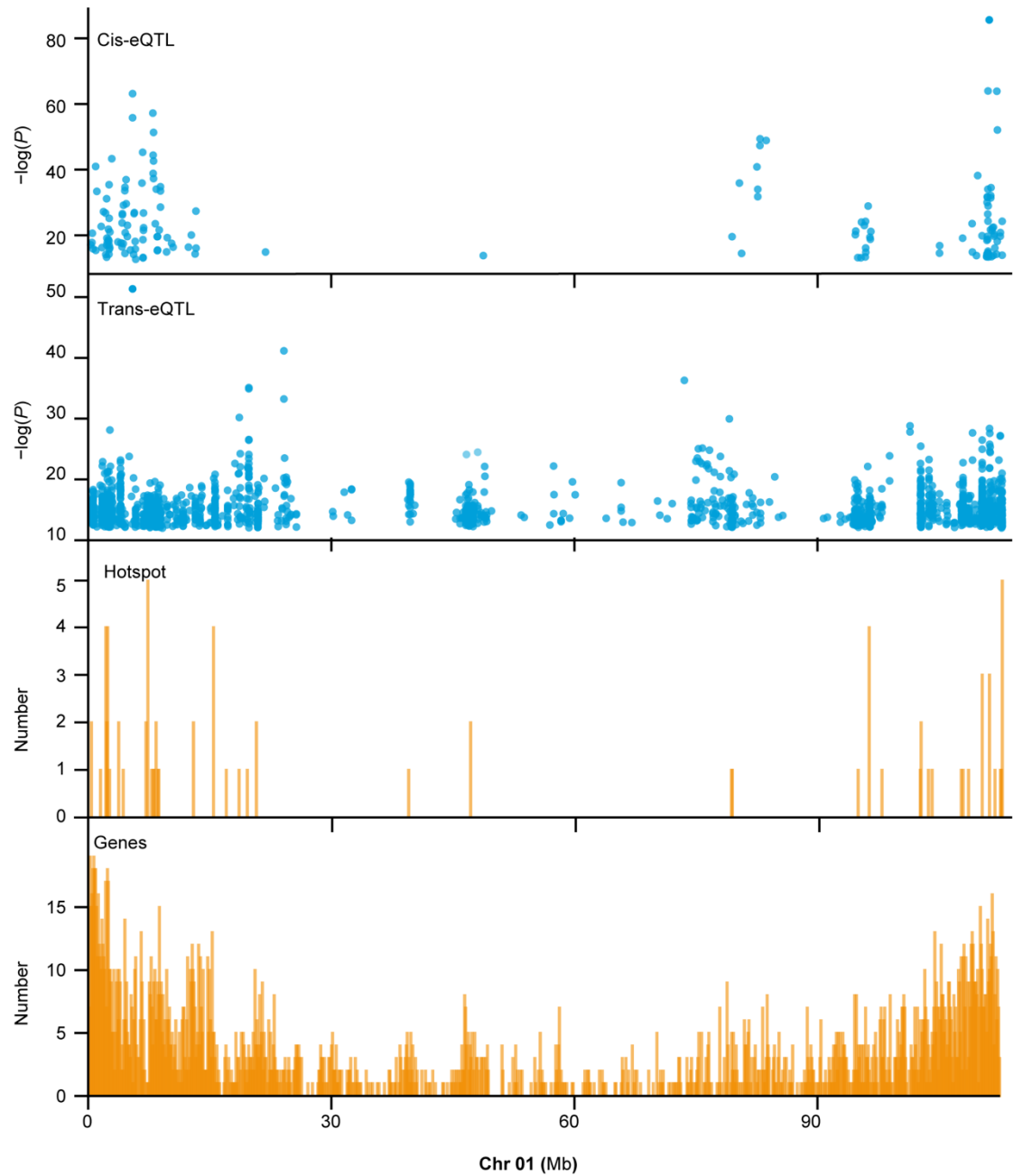


Figure S2. Integration of eQTLs and hotspots for chromosome 01. (a) Cis-eQTL (p -value $< 1e-5$) association plot. (b) Trans-eQTL (p -value $< 1e-5$) association plot. (c) Histogram of hotspots . (d) Density of gene in a 1 Mb window.

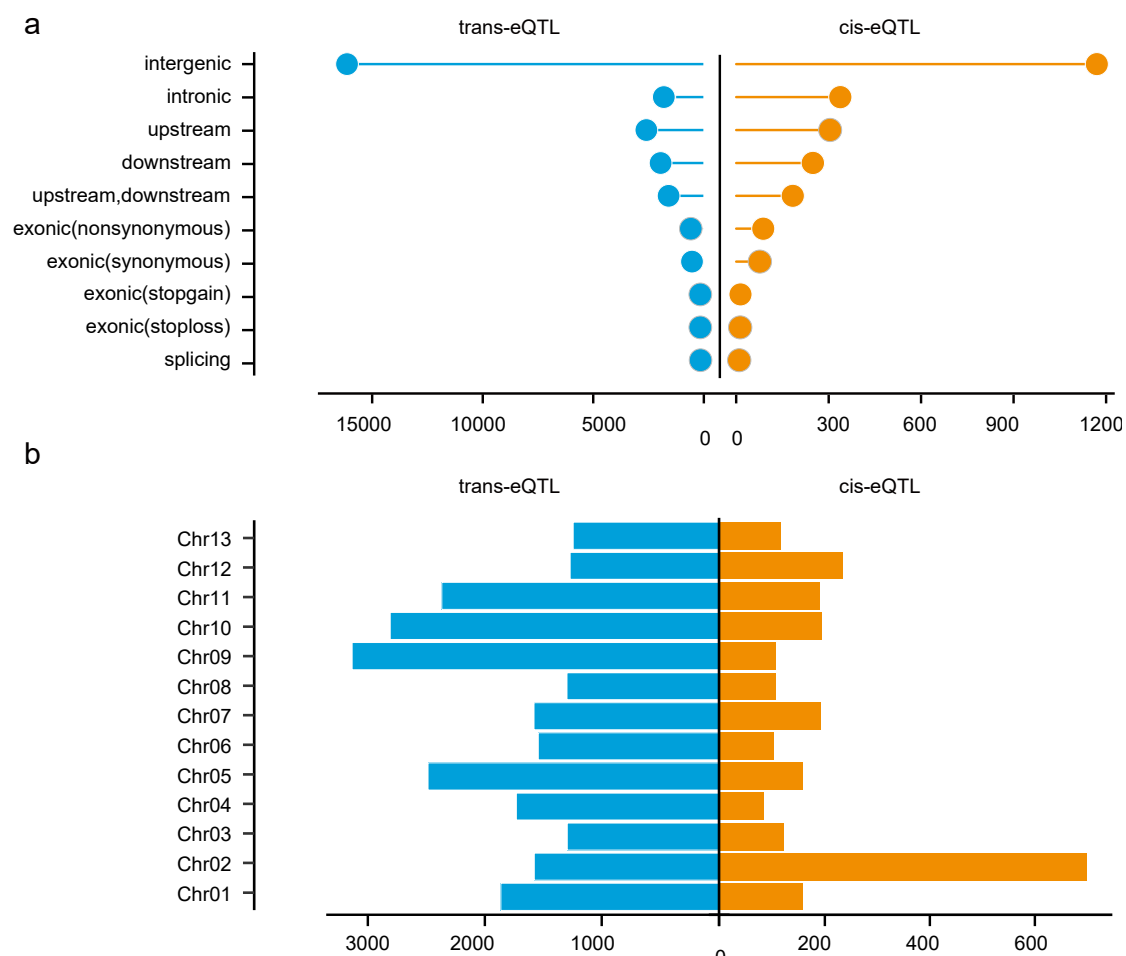


Figure S3. Number of cis-eQTLs and trans-eQTLs in different functional categories. (a) Number of cis-eQTLs and trans-eQTLs across functional categories. (b) Number of cis-eQTLs and trans-eQTLs in each chromosome.

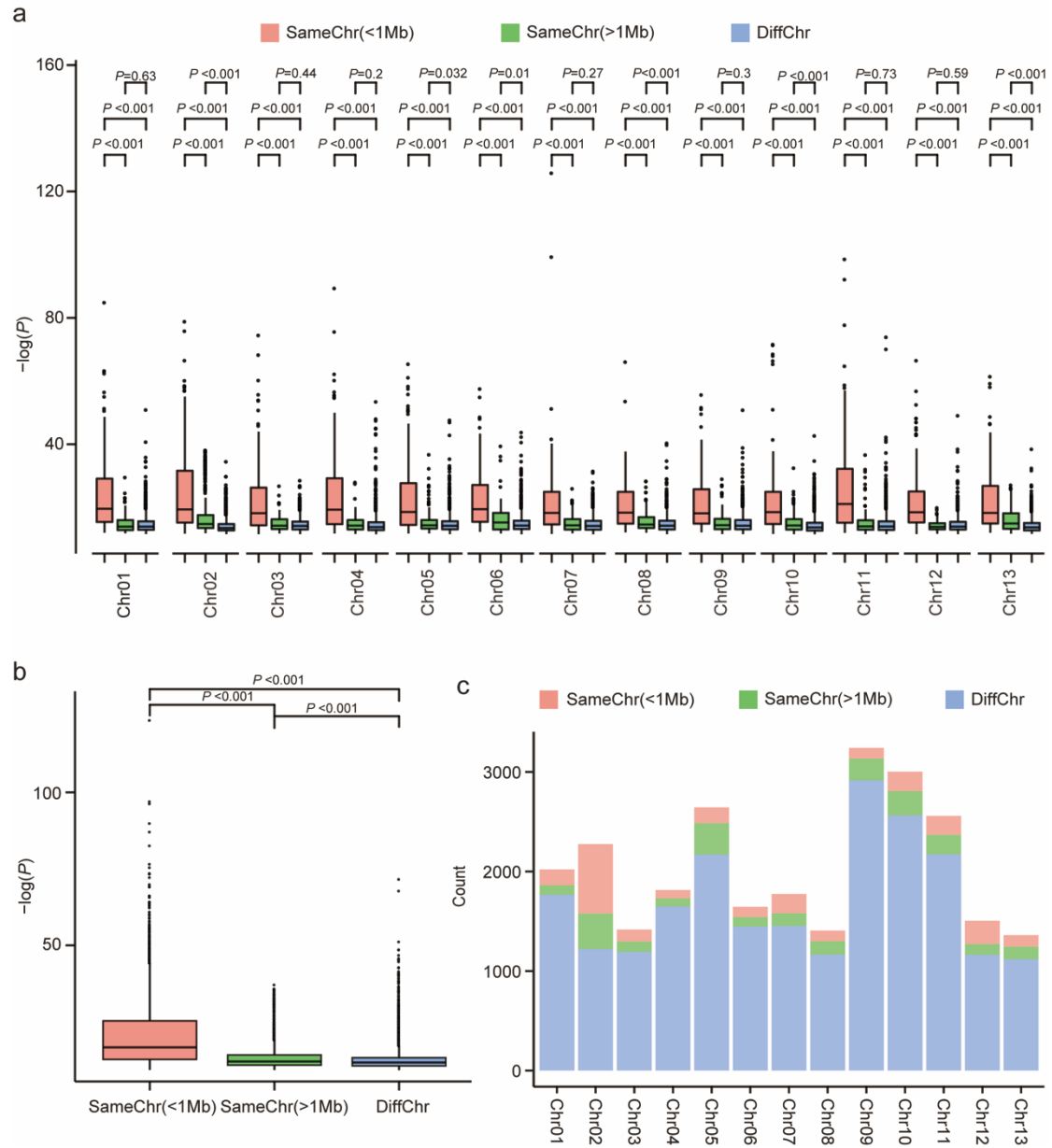


Figure S4. The variation in p -value for the distance between eQTL and eGene. (a) The comparison of significance (p -values) between intra-chromosomal eQTLs (SameChr) and inter-chromosomal eQTLs (DiffChr) for each chromosome. The intra-chromosomal eQTLs were divided into those with a distance of more than 1 Mb (SameChr (>1Mb)) and less than 1 Mb (SameChr (<1Mb)). (b) The comparison of significance (p -values) between SameChr (<1Mb), SameChr (>1Mb) and DiffChr. (c) The number of SameChr (<1Mb), SameChr (>1Mb) and DiffChr for each chromosome.

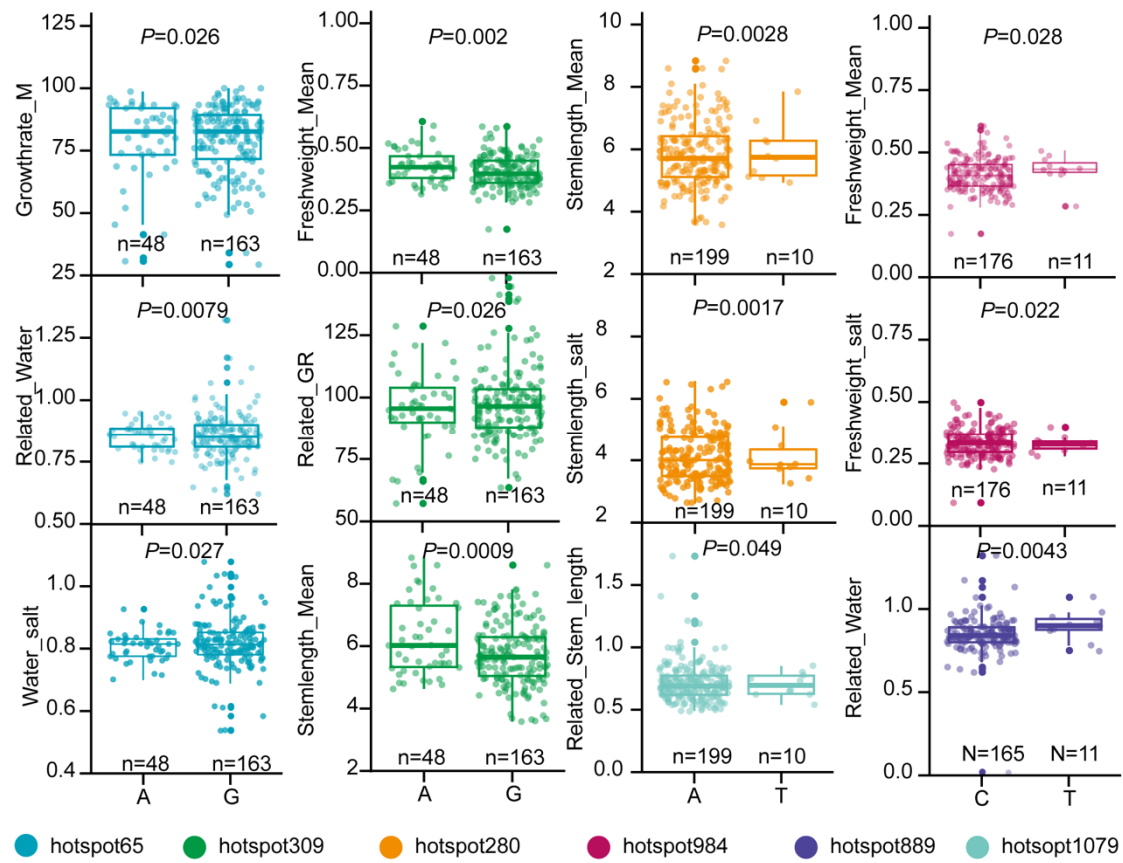


Figure S5. The significant divergence of the traits between different alleles of the lead SNP for 6 of the top 10 hotspots.

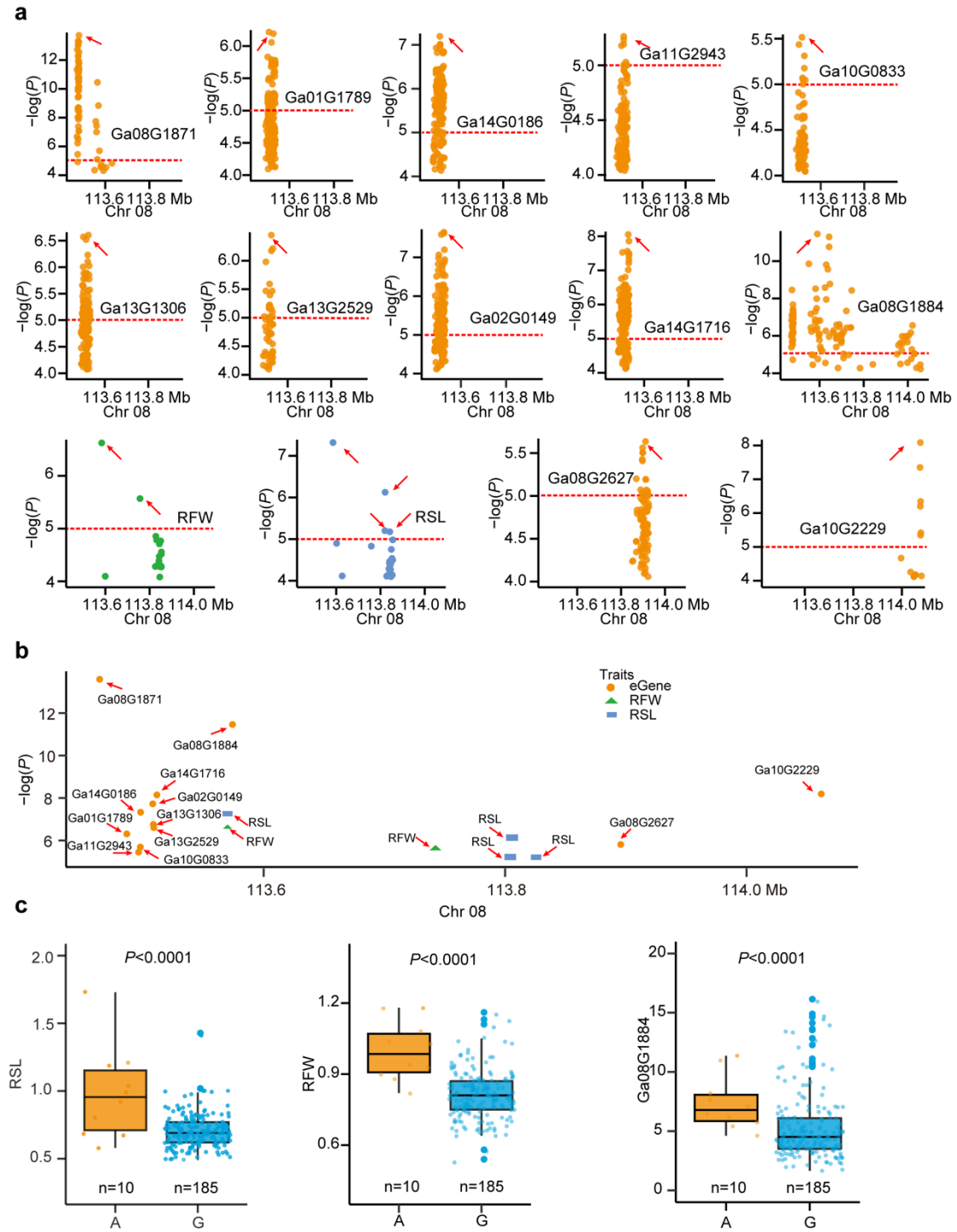


Figure S6. Integration of QTL and eQTL on Chr08:113453649-114064078. (a) Manhattan plot of GWAS and eQTL signal on Chr08:113453649-114064078. (b) Manhattan plot of QTL and eQTL signal on Chr08:113453649-114064078. (c) The divergence of traits and expression of *Ga08G1884* between different alleles of the lead SNP.

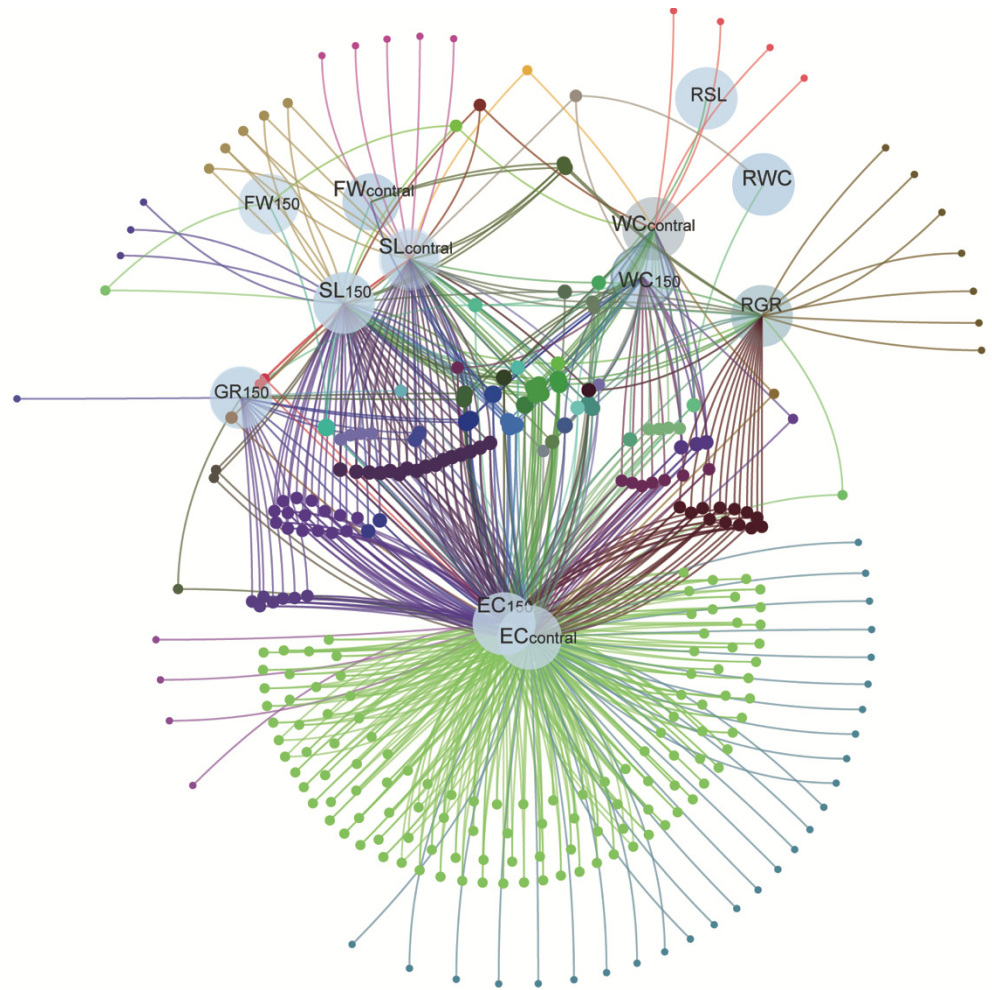


Figure S7. The network of traits and hotspot 309-related genes. The colorful points were hotspot 309-related genes. Grey points represented traits. Lines represent a significant correlation between the points.

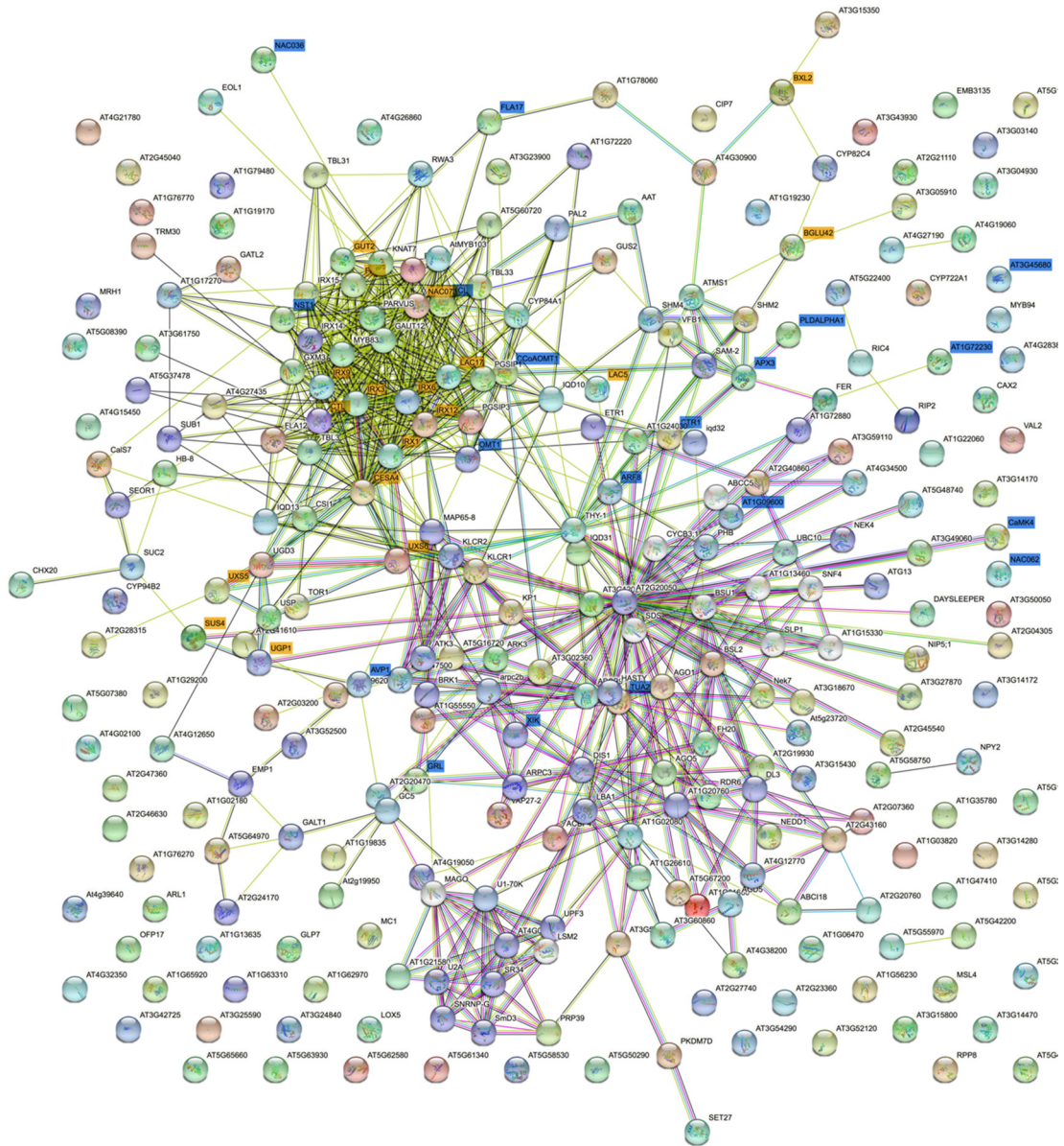


Figure S8. The network of *Arabidopsis thaliana* homologous genes for eGene of hotspot 309 by STRIGN. The genes highlighted in orange were homologous genes of cotton related with salt stress cotton. The genes highlighted in blue were homologous genes of cotton related with cell wall bio-synthesis.

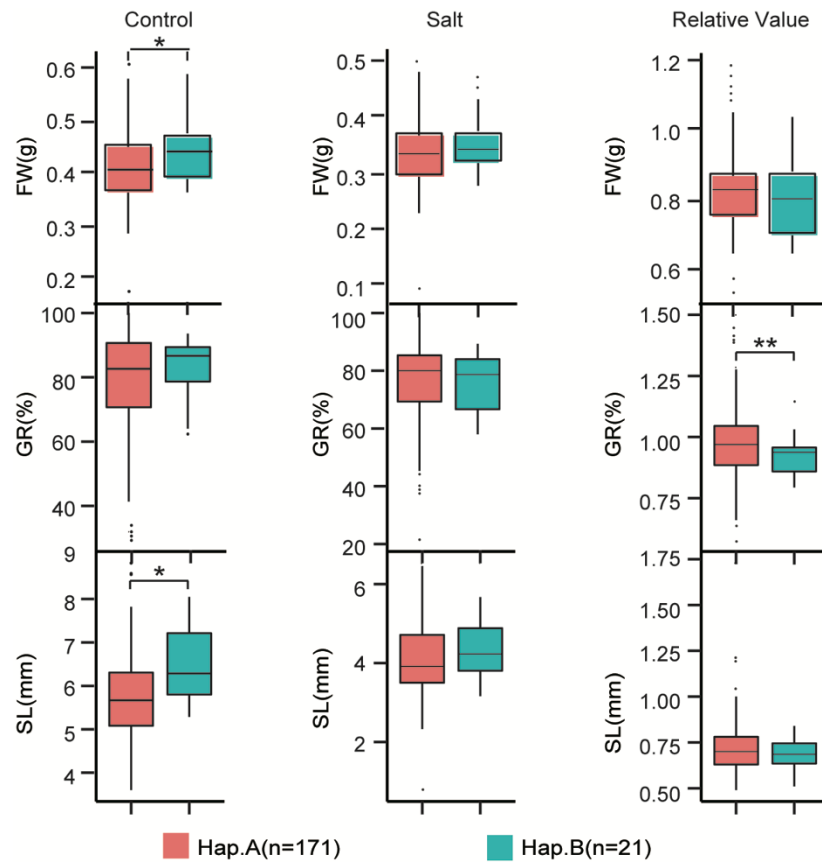


Figure S9. The traits of GRcontrol and GR150 was no different between Hap. B and Hap. A.

Supplementary Tables

Table S1. Summary of RNA-Seq data in this study.

sample	reads number	mapping
GA0001	36816366	91.05%
GA0002	27624118	92.08%
GA0003	29161426	93.93%
GA0005	30597874	94.77%
GA0006	34770050	95.19%
GA0007	29383329	94.86%
GA0008	27985385	95.25%
GA0009	37809408	92.93%
GA0010	28749746	95.07%
GA0011	29352912	93.55%
GA0012	28582015	92.07%
GA0013	27530729	94.90%
GA0014	27211068	94.38%
GA0015	28673820	93.98%
GA0016	28012329	95.22%
GA0017	29642195	94.86%
GA0018	29371273	94.37%
GA0019	30426101	95.39%
GA0020	27302226	95.41%
GA0021	27143086	94.42%
GA0022	27442714	94.39%
GA0023	27979518	92.62%
GA0096	34998821	93.55%
GA0097	37627028	90.70%
GA0098	37633402	89.98%
GA0099	38487522	89.47%
GA0100	30729013	91.00%

GA0101	34703953	92.78%
GA0102	46015829	91.71%
GA0103	40047870	89.96%
GA0104	37047935	91.47%
GA0105	35231664	93.29%
GA0004	28110114	94.98%
GA0106	30940677	86.38%
GA0107	31837256	91.51%
GA0108	36707699	93.59%
GA0109	38002298	86.80%
GA0110	38098934	90.72%
GA0111	33691433	93.35%
GA0112	34862843	89.70%
GA0113	43259652	92.89%
GA0114	27569607	91.82%
GA0115	34947880	90.83%
GA0034	31362573	92.90%
GA0035	27978457	91.76%
GA0036	30324468	88.74%
GA0037	37026651	89.50%
GA0038	36707176	92.70%
GA0039	38244394	92.81%
GA0040	35855882	92.45%
GA0041	35642258	93.14%
GA0042	39751303	92.50%
GA0043	33589579	91.34%
GA0044	38710386	91.15%
GA0045	38056237	92.07%
GA0046	41714369	92.94%
GA0047	40854869	91.74%
GA0048	39893060	91.17%
GA0049	37710093	93.30%
GA0050	36907744	93.18%
GA0051	37635799	87.46%
GA0052	37345663	92.02%
GA0053	39325994	90.27%
GA0054	46201167	92.57%
GA0055	40075382	92.94%
GA0056	36907071	90.86%
GA0057	40925028	92.84%
GA0058	39719355	90.85%
GA0059	38112405	91.48%
GA0060	45385423	86.15%
GA0062	28502411	92.38%
GA0063	29538315	91.61%
GA0064	28116188	86.81%
GA0065	28708380	92.57%
GA0066	29939398	92.63%
GA0068	27883053	93.54%
GA0069	33254965	93.69%
GA0070	28449405	91.68%
GA0071	33031684	85.49%
GA0072	32443356	86.92%
GA0073	34511186	93.78%
GA0074	35953815	89.94%
GA0075	38427361	91.52%
GA0076	39241487	91.40%
GA0077	40169741	91.15%
GA0078	39564872	89.66%
GA0079	40530657	89.87%
GA0080	35888447	87.15%
GA0081	32856829	88.11%

GA0082	35709213	88.77%
GA0083	33972715	89.99%
GA0084	36107206	89.53%
GA0085	33727984	90.87%
GA0086	32782221	89.18%
GA0087	31842695	87.26%
GA0088	32804267	86.70%
GA0089	37232428	91.22%
GA0090	35365881	93.35%
GA0091	35673949	92.58%
GA0093	32222235	91.73%
GA0094	36483851	87.11%
GA0095	32306255	93.23%
GA0116	34363921	85.82%
GA0117	34314547	93.93%
GA0118	26921467	92.13%
GA0119	28945523	86.08%
GA0120	32103578	86.22%
GA0121	40609699	92.74%
GA0122	34177991	93.34%
GA0123	31966417	89.65%
GA0124	32373243	93.84%
GA0125	27660321	91.44%
GA0126	30995817	91.45%
GA0127	38680605	89.21%
GA0128	30180943	92.12%
GA0129	28971001	88.36%
GA0130	36669541	92.57%
GA0131	34188453	88.03%
GA0132	28584780	92.61%
GA0133	27712691	88.75%
GA0134	36058275	93.17%
GA0135	30205236	92.83%
GA0136	33453647	91.71%
GA0137	35085736	91.68%
GA0138	27462946	86.11%
GA0139	31644257	92.40%
GA0140	35834877	93.09%
GA0141	31601199	92.72%
GA0142	33395176	86.51%
GA0143	33562054	89.50%
GA0144	34090980	87.26%
GA0145	34475799	87.90%
GA0146	38980372	93.88%
GA0147	34690064	91.80%
GA0148	34412396	91.07%
GA0149	31617212	92.34%
GA0150	33200184	86.64%
GA0151	33464967	89.17%
GA0152	34716070	92.69%
GA0153	36980106	91.48%
GA0154	29950302	90.76%
GA0155	30146170	91.84%
GA0156	43815201	91.81%
GA0157	35657387	93.30%
GA0158	36979166	89.88%
GA0159	37081754	89.85%
GA0160	35203085	89.99%
GA0161	34982943	91.45%
GA0162	35098388	86.35%
GA0163	33154216	87.21%
GA0164	37720850	92.42%

GA0165	33656097	93.03%
GA0166	43234366	93.54%
GA0167	35445130	91.38%
GA0168	34896901	92.18%
GA0169	31701837	86.63%
GA0170	35454473	92.46%
GA0171	36548774	90.90%
GA0172	35964221	86.78%
GA0173	32958405	91.28%
GA0174	36093498	93.77%
GA0175	32346400	94.13%
GA0177	34080403	94.59%
GA0178	37477894	93.75%
GA0179	38979785	92.62%
GA0180	39782899	90.93%
GA0181	36243827	94.46%
GA0182	34728905	92.49%
GA0183	33852190	93.86%
GA0184	32243716	93.86%
GA0185	40508985	93.43%
GA0187	43693474	93.04%
GA0188	33900121	93.48%
GA0189	37520624	93.38%
GA0190	37187243	92.99%
GA0191	40769105	93.64%
GA0192	37226612	93.83%
GA0193	39538512	94.41%
GA0194	38599061	94.24%
GA0195	38277866	94.05%
GA0206	38692208	93.48%
GA0207	36030138	93.14%
GA0208	42088024	89.98%
GA0209	28206635	94.24%
GA0210	33423557	93.59%
GA0211	39317230	94.12%
GA0213	36937665	93.56%
GA0214	40253351	93.77%
GA0215	35022673	93.80%
GA0061	31599756	94.35%
GA0092	31698387	93.62%
GA0176	35695185	93.64%
GA0186	40509184	93.41%
GA0024	32975556	93.13%
GA0025	31019076	92.08%
GA0026	32219035	92.79%
GA0027	34323257	90.71%
GA0028	26788020	92.66%
GA0029	29025456	87.48%
GA0030	32184692	92.12%
GA0031	32047039	90.81%
GA0032	27844483	92.20%
GA0033	29550015	91.60%
GA0196	38004168	92.63%
GA0197	35150437	93.08%
GA0198	39082544	93.84%
GA0199	33778640	92.99%
GA0200	32984044	93.85%
GA0201	34147075	94.65%
GA0202	33467173	94.20%
GA0203	34964569	93.22%
GA0204	35217953	93.86%
GA0205	42775437	92.80%

Table S2. Gene expression statistics.

FPKM	Number of genes	Percentage
0-1	16935	41.35%
1-5	7609	18.58%
5-10	5293	12.92%
10-20	4738	11.57%
20-40	3135	7.65%
40-80	1678	4.10%
80-120	581	1.42%
120-240	543	1.33%
240-500	262	0.64%
>500	186	0.45%

Table S3. Statistics of significant SNP associated with treatments.

Control treatment		Salt treatment		Relative treatment	
Treatment	Number	Treatment	Number	Treatment	number
GR _{control}	12	GR ₁₅₀	4	RGR	0
FW _{control}	22	FW ₁₅₀	989	RFW	20
SL _{control}	39	SL ₁₅₀	57	RSL	40
WC _{control}	634	WC ₁₅₀	387	RWC	25
EC _{control}	1874	EC ₁₅₀	49	REC	8

Table S4. QTL(Chr08:113453649-114064078)-related gene expression and traits.

QTL Type	Traits	CHR	Site	Pvalue	Type	GeneID	Annotation	reference
	Ga01G1789	Chr08	113484533	7.24E-07	Trans-eQTLs		Disease resistance-responsive family protein [Theobroma cacao]	Faisal et.al 2020
	Ga02G0149	Chr08	113506218	2.84E-08	Trans-eQTLs		Pyridine nucleotide-disulfide oxidoreductase domain-containing 2 [Gossypium arboreum]	
	Ga04G1991	Chr08	113483025	1.91E-06	Trans-eQTLs		Glycerol-3-phosphate dehydrogenase [NAD(P)+] [Gossypium arboreum]	Katarzyna et.al 2012
	Ga08G1871	Chr08	113462536	3.57E-14	Cis-eQTLs		Nitrate transporter 1.5 -like protein [Gossypium arboreum]	Hong et.al 2017
eQT L	Ga08G1873	Chr08	113484348	1.26E-06	Cis-eQTLs		Phosphoribosyltransferase family protein [Theobroma cacao]	
	Ga08G1884	Chr08	113571400	5.70E-12	Cis-eQTLs		Actin-regulating kinase PRK1 [Gossypium arboreum]	Yong-hua et.al 2018
	Ga08G2627	Chr08	113892910	2.57E-06	Trans-eQTLs		Leucoanthocyanidin dioxygenase, putative [Theobroma cacao]	Ilya et.al 2006; Muhammad et.al 2020
	Ga10G0833	Chr08	113495059	3.37E-06	Trans-eQTLs		Asparticase nepenthesin-1 [Gossypium arboreum]	Behnaz et.al 2013; Anna et.al 2015
	Ga10G2229	Chr08	114059004	1.07E-08	Trans-eQTLs		2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [Gossypium arboreum]	Ming et.al 2015

Ga11G29	Chr0	1134	5.91E	Trans-	Transcription factor PIF3 -like protein	Trijatmiko et.al 2004; Barah et.al 2013
43	8	9361	-06e	QTLs	[Gossypium arboreum]	
Ga13G13	Chr0	1135	2.93E	Trans-	hypothetical protein F383_37108	Xiao et.al 2013
06	8	0581	-07e	QTLs	[Gossypium arboreum]	
Ga13G19	Chr0	1134	1.34E	Trans-	Arginine/serine-rich 45	Albaqami et.al 2019
20	8	8042	-06e	QTLs	[Theobroma cacao]	
Ga13G19	Chr0	1134	2.71E	Trans-	Cytochrome P450 71D10, putative	Kim et.al 2019
49	8	9799	-06e	QTLs	[Theobroma cacao]	
Ga13G25	Chr0	1135	4.15E	Trans-	hypothetical protein F383_01057	[Gossypium arbo- reum]
29	8	0622	-07e	QTLs		
Ga14G01	Chr0	1134	7.84E	Trans-	hypothetical protein F383_14723	[Gossypium arbo- reum]
86	8	9529	-08e	QTLs		
Ga14G17	Chr0	1135	1.15E	Trans-	hypothetical protein F383_08088	[Gossypium arbo- reum]
16	8	0951	-08e	QTLs		
Re- lated_Ste m_length	Chr0	1135	5.98E	-08		
Re- lated_Ste m_length	Chr0	1138	7.77E	-06		
Re- lated_Ste m_length	Chr0	1138	9.34E	-07		
Re- lated_Ste m_length	Chr0	1138	8.30E	-06		

Table S5. Correlation between the traits of the QTL (Chr08:113453649-114064078).

Traits 1	Traits 2	Correlation(Pearson)	Pvalue
Ga02G0149	Ga01G1789	0.24258691	0.00035274
Ga13G1306	Ga01G1789	0.17722032	0.00954827
Ga13G1920	Ga01G1789	0.43395495	3.42E-11
Ga13G1949	Ga01G1789	0.3989369	1.53E-09
Ga13G2529	Ga01G1789	0.40774376	6.14E-10
Ga14G0186	Ga01G1789	0.53342923	4.63E-17
Ga14G1716	Ga01G1789	0.29911842	8.92E-06
Ga08G1873	Ga02G0149	0.16903908	0.01349884
Ga10G2229	Ga02G0149	0.31985959	1.87E-06
Ga13G1306	Ga02G0149	0.27070606	6.27E-05
Ga13G1920	Ga02G0149	0.31200262	3.43E-06
Ga13G2529	Ga02G0149	0.21775474	0.00138487
Ga14G0186	Ga02G0149	0.34217145	3.06E-07
Ga08G2627	Ga04G1991	-0.152191	0.02634836
Ga11G2943	Ga04G1991	0.40119076	1.22E-09
Ga13G1306	Ga04G1991	0.36606202	3.73E-08
Ga13G1920	Ga04G1991	0.39055504	3.58E-09
Ga13G1949	Ga04G1991	0.37626841	1.44E-08
Ga13G2529	Ga04G1991	0.29688009	1.05E-05
Ga14G0186	Ga04G1991	0.36163173	5.58E-08
Ga14G1716	Ga04G1991	0.25623831	0.00015621
Ga08G1873	Ga08G1871	0.19143813	0.00505539
Ga10G2229	Ga08G1871	0.30389987	6.29E-06
Ga13G1306	Ga08G1871	0.23552156	0.0005283

Ga13G1920	Ga08G1871	0.22466948	0.00096011
Ga14G0186	Ga08G1871	0.18254584	0.0075632
Ga13G1920	Ga08G1873	0.15979455	0.01962636
Ga13G1949	Ga08G1873	0.16728075	0.01451481
Ga13G2529	Ga08G1873	0.32345433	1.41E-06
Ga14G1716	Ga08G1873	0.27835607	3.78E-05
Ga10G2229	Ga08G1884	0.13501228	0.0490837
Ga13G1306	Ga08G1884	0.40098941	1.24E-09
Ga13G1920	Ga08G1884	0.38894145	4.20E-09
Ga13G1949	Ga08G1884	0.37794282	1.23E-08
Ga13G2529	Ga08G1884	0.33931789	3.89E-07
Ga14G1716	Ga08G1884	0.35477938	1.03E-07
Ga10G2229	Ga08G2627	-0.1356092	0.04808173
Ga10G2229	Ga10G0833	0.13635845	0.04684829
Ga13G1306	Ga10G0833	0.49994094	7.19E-15
Ga13G1920	Ga10G0833	0.7108621	4.33E-34
Ga13G1949	Ga10G0833	0.51827425	4.87E-16
Ga13G2529	Ga10G0833	0.50752419	2.41E-15
Ga14G0186	Ga10G0833	0.60652279	8.67E-23
Ga14G1716	Ga10G0833	0.45280973	3.65E-12
Ga13G1920	Ga10G2229	0.18620436	0.00642141
Ga14G0186	Ga10G2229	0.20749966	0.00233661
Ga13G1306	Ga11G2943	0.44305894	1.18E-11
Ga13G1949	Ga11G2943	0.56970834	1.00E-19
Ga13G2529	Ga11G2943	0.28323386	2.72E-05
Ga14G0186	Ga11G2943	0.2746939	4.83E-05
Ga14G1716	Ga11G2943	0.34817399	1.83E-07
Ga13G1949	Ga13G1306	0.32805238	9.79E-07
Ga13G2529	Ga13G1306	0.27822601	3.82E-05
Ga14G0186	Ga13G1306	0.35556018	9.61E-08
Ga14G1716	Ga13G1306	0.34884097	1.73E-07
Ga11G2943	Ga13G1920	0.32119804	1.69E-06
Ga13G1949	Ga13G1920	0.4130495	3.49E-10
Ga13G2529	Ga13G1920	0.41860018	1.91E-10
Ga14G0186	Ga13G1920	0.6091201	5.09E-23
Ga14G1716	Ga13G1920	0.29198557	1.48E-05
Ga13G2529	Ga13G1949	0.58596373	4.97E-21
Ga14G0186	Ga13G1949	0.4512425	4.42E-12
Ga14G1716	Ga13G1949	0.40957557	5.06E-10
Related_FreshW	Ga13G1949	-0.1534525	0.0261719
Ga14G0186	Ga13G2529	0.51102794	1.44E-15
Ga14G1716	Ga13G2529	0.45822352	1.87E-12
Ga14G1716	Ga14G0186	0.34294214	2.87E-07
Related_FreshW	Related Stem length	0.70119252	2.16E-32

Table S6. Gene ontology (GO) enrichment of hotspot 309.

Annot Term	Anno- tated	Signif- icant	p-valuePadj	GeneID
GO:00 plant-type secondary 09834 cell wall biogenesis	8	5	8.40E-09 2.18E-09	Ga03G2054,Ga07G2381,Ga11G230738,Ga11G3582,Ga13G2817
GO:00 translational initiation 06413	16	3	0.0007 0.0093 157 040744	Ga09G1034,Ga09G1869,Ga12G00
GO:00 cellular protein modifi- 06464 cation process	7	2	0.0026 0.0227 3061 986	Ga12G0229,Ga13G2148
GO:00 phenylpropanoid meta- 09698 bolic process	1	1	0.0115 0.0594 626 5243	Ga10G2561
GO:00 cellular response to iron 10106 ion starvation	1	1	0.0115 0.0594 626 5243	Ga08G1251

GO:0032259	methylation	28	2	0.0406 8614	0.0661 1498	Ga08G1237,Ga12G0336
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Table S7. KEGG enrichment analysis of hotspots309.

AnnotTerm	Anno- tated	Sig- nifi- cant	p- value	Padj	GeneID
ko04144 Endocytosis	215	7	0.000 370293726	0.011 3726	Ga03G0161,Ga04G0145,Ga07G0340,Ga08G0374,Ga10G1624,Ga10G3060,Ga13G1791
ko00940 Phenylpropanoid biosynthesis	232	7	0.000 5855193726	0.011 3726	Ga04G0313,Ga08G1237,Ga10G0561,Ga10G2561,Ga11G0347,Ga12G0336,Ga11G2107
ko00460 Cyanoamino acid metabolism	65	4	0.000 724959372614G1502	0.011 3726	Ga10G1527,Ga11G0347,Ga11G3514,Ga14G1502
ko00670 One carbon pool by folate	31	3	0.000 9483893726	0.011 3726	Ga03G2541,Ga10G1527,Ga14G1502
ko00520 Amino sugar and nucleotide sugar metabolism	189	6	0.001 147819372612G1218,Ga12G2624,Ga13G1828	0.011 3726	Ga01G0796,Ga02G0822,Ga08G0443,Ga12G1218,Ga12G2624,Ga13G1828
ko00500 Starch and sucrose metabolism	316	7	0.003 48672	0.030 2182	Ga01G0796,Ga05G0384,Ga06G0858,Ga08G0443,Ga11G0347,Ga12G1218,Ga13G1828
ko00053 Ascorbate and aldarate metabolism	70	3	0.009 7171118426	0.072 18426	Ga02G0079,Ga02G0822,Ga12G1218
ko00360 Phenylalanine metabolism	153	4	0.015 653527479111G1604	0.101 11G1604	Ga04G0313,Ga10G0561,Ga10G2561,Ga11G1604
ko00480 Glutathione metabolism	121	3	0.040 8794919259	0.236 19259	Ga02G0079,Ga08G0610,Ga11G3514

Table S8. KEGG ontology (KO) enrichment analysis of hotspot309.

An- not	Term	An- no- tated	Sig- nifi- cant	p- value	Padj	GeneID
K10999	K10999 cellulose synthase A [EC:2.4.1.12] (A)	18	5	3.40E-07	2.69E-05	Ga05G0095,Ga07G0463,Ga07G052381,Ga08G0544,Ga10G2710
K11593	K11593 eukaryotic translation initiation factor 2C (A)	15	4	6.62E-06	0.000 26163	Ga09G1032,Ga09G1034,Ga09G1869,Ga12G0044
K10406	K10406 kinesin family member C2/C3 (A)	21	4	2.79E-05	0.000 73485	Ga01G1003,Ga07G1406,Ga08G1402,Ga11G0822
K08857	K08857 NIMA (never in mitosis gene a)-related kinase [EC:2.7.11.1] (A)	12	3	0.000 12942	0.002 47674	Ga02G1456,Ga08G0755,Ga09G1422
K15285	K15285 solute carrier family 35, member E3 (A)	13	3	0.000 16719	0.002 47674	Ga01G2415,Ga05G1100,Ga08G2334
K02184	K02184 formin 2 (A)	3	2	0.000 21946	0.002 47674	Ga11G3744,Ga12G1033
K16547	K16547 protein NEDD1 (A)	3	2	0.000 21946	0.002 47674	Ga10G0239,Ga10G0241
K17086	K17086 transmembrane 9 superfamily member 2/4 (A)	18	3	0.000 46227	0.004 56492234	Ga05G0576,Ga05G0636,Ga14G56492234

K124 71	K12471 epsin (A)	5	2	0.000 0.006 7233 349	Ga03G0161,Ga10G1624
K116 99	K11699 RNA-dependent RNA polymerase [EC:2.7.7.48] (A)	6	2	0.001 0.008 0788 5228	Ga05G0583,Ga07G0092
K184 42	K18442 brefeldin A-inhibited guanine nucleotide-exchange protein (A)	8	2	0.001 0.014 9912 3008	Ga04G0145,Ga08G0374
K006 95	K00695 sucrose synthase [EC:2.4.1.13] (A)	10	2	0.003 0.020 1643 8321	Ga05G0384,Ga06G0858
K057 50	K05750 NCK-associated pro- tein 1 (A)	1	1	0.008 0.042 6153 7284	Ga14G2625
K079 99	K07999 matrix metalloprotein- ase-20 (enamelysin) [EC:3.4.24.-] (A)	1	1	0.008 0.042 6153 7284	Ga11G3250
K110 93	K11093 U1 small nuclear ribo- nucleoprotein 70kDa (A)	1	1	0.008 0.042 6153 7284	Ga10G2030
K006 00	K00600 glycine hydroxyme- thyltransferase [EC:2.1.2.1] (A)	17	2	0.009 0.042 1947 7284	Ga10G1527,Ga14G1502
K110 00	K11000 callose synthase [EC:2.4.1.-] (A)	17	2	0.009 0.042 1947 7284	Ga04G1728,Ga14G1699
K094 22	K09422 myb proto-oncogene protein, plant (A)	216	6	0.010 0.047 9283 9631	Ga01G2601,Ga08G1352,Ga11G 12G0584,Ga12G1064,G 2a13G2645
K130 66	K13066 caffeic acid 3-O-me- thyltransferase [EC:2.1.1.68] (A)	24	2	0.017 0.048 9437 8812	Ga08G1237,Ga12G0336
K136 48	K13648 alpha-1,4-galac- turonosyltransferase [EC:2.4.1.43] (A)	25	2	0.019 0.051 3956 0752	Ga01G0796,Ga13G1828
K093 38	K09338 homeobox-leucine zip- per protein (A)	68	3	0.020 0.053 8069 0241	Ga05G1392,Ga07G0275,Ga10G 73057

Table S9. Cell wall biosynthesis-related genes and salt stress response of hotspot309.

GeneID	Type	Gene Name	nr annotation	Model name	Short description
Ga05G1026	cellwall	UXS6	UDP-glucuronic acid decarboxylase 1 [Gossypium arbo- reum]	AT2G28760. 3	UDP-XYL synthase 6
Ga01G2357	cellwall	UXS5	UDP-glucuronic acid decarboxylase 1 [Gossypium arbo- reum]	AT3G46440. 2	UDP-XYL synthase 5
Ga08G0443	cellwall	UGPA	UTP--glucose-1- phosphate uri- dyltransferase [Gossypium arbo- reum]	AT3G03250. 1	UDP-GLUCOSE PY- ROPHOSPHORY- LASE 1
Ga05G0384	cellwall	SS	sucrose synthase 3 [Gossypium arbo- reum]	AT3G43190. 1	sucrose synthase 4
Ga05G0369	cellwall	Polygalac- turonase	putative polygalac- turonase [Gossypium arboreum]	AT1G19170. 1	Pectin lyase-like super- family protein

Ga06G0835cellwall	Polygalacturonase	putative polygalacturonase [Gossypium arboreum]	AT3G42950.1	Pectin lyase-like superfamily protein
Ga06G1973cellwall	LAC5	Laccase 12 [Theobroma cacao]	AT2G40370.1	laccase 5
Ga11G0039cellwall	LAC4	Laccase-17-like protein [Gossypium arboreum]	AT5G60020.1	laccase 17
Ga10G0166cellwall	LAC22	Laccase-22 [Gossypium arboreum]	AT2G38080.1	Laccase/Diphenol oxidase family protein
Ga09G1756cellwall	LAC17	Laccase 17 [Theobroma cacao]	AT5G60020.1	laccase 17
Ga11G0041cellwall	LAC17	Laccase 17 isoform 1 [Theobroma cacao]	AT5G60020.1	laccase 17
Ga09G1729cellwall	IRX9	putative beta-1,4-xylotransferase IRX9-like protein [Gossypium arboreum]	AT2G37090.1	Nucleotide-diphosphosugar transferases superfamily protein
Ga13G2817cellwall	IRX7	putative glucuronoxylan glucuronosyltransferase IRX7-like protein [Gossypium arboreum]	AT2G28110.1	Exostosin family protein
Ga01G2197cellwall	IRX12	Laccase/Diphenol oxidase family protein [Theobroma cacao]	AT2G38080.1	Laccase/Diphenol oxidase family protein
Ga04G0648cellwall	IRX12	Laccase-4-like protein [Gossypium arboreum]	AT2G38080.1	Laccase/Diphenol oxidase family protein
Ga11G0024cellwall	IRX12	Laccase/Diphenol oxidase family protein isoform 1 [Theobroma cacao]	AT2G38080.1	Laccase/Diphenol oxidase family protein
Ga03G2054cellwall	IRX10	putative beta-1,4-xylotransferase IRX10-like protein [Gossypium arboreum]	AT1G27440.1	Exostosin family protein
Ga09G0843cellwall	CTL2	chitinase-like protein [Gossypium hirsutum]	AT3G16920.1	chitinase-like protein 2
Ga10G1044cellwall	CTL2	Chitinase-like protein 2 [Gossypium arboreum]	AT3G16920.1	chitinase-like protein 2
Ga01G1918cellwall	COBL4	COBRA-like protein 4 [Gossypium arboreum]	AT5G15630.1	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family
Ga08G0607cellwall	COBL4	COBRA-like protein 4 [Gossypium arboreum]	AT5G15630.1	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family
Ga11G2338cellwall	COBL4	COBRA-like protein 4 [Gossypium arboreum]	AT5G15630.1	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family
Ga10G2710cellwall	CESA8	cellulose synthase A1 [Gossypium barbadense]	AT4G18780.1	cellulose synthase family protein

Ga05G0095cellwall	CESA7	CESA8 [Gossypium hirsutum]	AT5G17420.1	Cellulose synthase family protein
Ga07G0463cellwall	CESA7	Cellulose synthase A catalytic subunit 7 [UDP-forming] -like protein [Gossypium arboreum]	AT5G17420.1	Cellulose synthase family protein
Ga07G2381cellwall	CESA4	Cellulose synthase A catalytic subunit 4 [UDP-forming] -like protein [Gossypium arboreum]	AT5G44030.1	cellulose synthase A4
Ga08G0544cellwall	CESA4	Cellulose synthase A catalytic subunit 3 [UDP-forming] -like protein [Gossypium arboreum]	AT5G44030.1	cellulose synthase A4
Ga07G1428cellwall	BXL2	putative beta-D-xylosidase 2 -like protein [Gossypium arboreum]	AT1G02640.1	beta-xylosidase 2
Ga11G0347cellwall	BGLU42	Beta-glucosidase, putative [Theobroma cacao]	AT5G36890.2	beta glucosidase 42
Ga05G2284salt	TUA	alpha-tubulin [Gossypium hirsutum]	AT1G50010.1	tubulin alpha-2 chain
Ga01G1596salt	Protein kinase	hypothetical protein F383_22386 [Gossypium arboreum]	AT1G09600.1	Protein kinase superfamily protein
Ga07G0340salt	PLD1	Phospholipase D alpha 1 [Theobroma cacao]	AT3G15730.1	phospholipase D alpha 1
Ga08G0131salt	NPF2.3	Major facilitator superfamily protein, putative [Theobroma cacao]	AT3G45680.1	Major facilitator superfamily protein
Ga11G2976salt	NAC096	NAC domain-containing 4 -like protein [Gossypium arboreum]	AT2G17040.1	NAC domain containing protein 36
Ga11G2975salt	NAC062	NAC domain-containing 4 -like protein [Gossypium arboreum]	AT3G49530.1	NAC domain containing protein 62
Ga01G1785salt	NAC043	NAC domain-containing protein [Gossypium hirsutum]	AT2G46770.1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
Ga10G0673salt	FLA17	fasciclin-like arabinogalactan protein 15 [Gossypium hirsutum]	AT5G06390.1	FASCICLIN-like arabinogalactan protein 17 precursor
Ga09G1563salt	CTR1	Serine/threonine-protein kinase CTR1 [Gossypium arboreum]	AT5G03730.2	Protein kinase superfamily protein
Ga11G3008salt	CRK3	CDPK-related protein kinase [Gossypium arboreum]	AT2G46700.1	CDPK-related kinase 3
Ga08G1237salt	COMT	Caffeic acid 3-O-methyltransferase	AT5G54160.1	O-methyltransferase 1

Ga12G0336salt	COMT	[Gossypium arbo- reum] Caffeic acid 3-O-me- thyltransferase [Gossypium arbo- reum]	AT5G54160.1	O-methyltransferase 1
Ga02G0079salt	APX3	Ascorbate peroxi- dase isoform 1 [The- obroma cacao]	AT4G35000.1	ascorbate peroxidase 3
Ga10G2561salt	4CL1	4-coumarate--CoA ligase 1 [Gossypium arbo-reum]	AT1G51680.1	4-coumarate:CoA ligase 1

Table S10. KEGG Fst and DEG statistics.

type	Contras- tive study	carbon metabo- lism	genetic processing	lipid me- tabolism	protein processing	regulation	Secondary metabo- lism	other
DE	SC_YER	0	1	5	3	2	0	0
DE	SC_YZR	1	1	9	4	0	3	2
DE	YER_YZ R	0	0	0	2	0	5	2
Fst	SC_YER	2	0	0	1	2	3	1
Fst	SC_YZR	0	0	2	3	0	3	1
Fst	YER_YZ R	0	1	2	0	0	5	0

Table S11. Statistics of duplicated gene pairs of different types.

Type	Ka/Ks>1	Ka/Ks1<1	Mean of Ka/Ks
DSD	0.03530107	0.96469893	0.4212519
PD	0.05089059	0.94910942	0.5359288
TD	0.04673457	0.95326543	0.4907648
TRD	0.01506616	0.98493384	0.3238082
WGD	0.00103665	0.99896335	0.2195169

Table S12. Primers used in this study.

Primer name	Sequence	Purpose
pLL00R-proGa01G0472-HindIII-F	ACGGCCAGTGCCAAGCTTGCAG-GAAATGAAAAGGGGAA	For LUC activity assay
pLL00R-proGa01G0472-SalI-R	GGATCCTCTAGAGTCGACCGACATTGAC-CATCATATCG	For LUC activity assay