

**Table S1 Traits statics during the seedling stage of RIL, together with their parents and natural population.**

Trait	Parents		Recombinant Inbred Lines				Natural Population					
	9311	PA64s	Minimum	Maximum	Mean	Skewness	Kurtosis	Minimum	Maximum	Mean	Skewness	Kurtosis
CSL	16.10	13.75	8.10	18.00	14.09	0.19	0.33	8.40	28.90	16.37	0.42	-0.17
CFW	0.63	0.43	0.29	0.75	0.45	1.03	1.95	0.05	0.17	0.09	0.90	1.50
CDW	0.12	0.08	0.07	0.13	0.09	0.80	0.69	0.01	0.04	0.02	0.74	0.78
SL	11.25	9.35	7.30	15.90	10.54	0.54	0.78	7.80	27.90	13.90	1.03	2.26
FW	0.53	0.37	0.28	0.68	0.42	0.89	1.16	0.05	0.14	0.08	0.83	1.82
DW	0.11	0.08	0.06	0.13	0.09	0.56	0.48	0.01	0.04	0.02	1.36	4.78
SR	0.78	0.88	0.41	1.00	0.91	-1.95	5.06	0.18	1.00	0.92	-2.69	7.76

CSL, CFW, CDW indicate shoot length, fresh weight, and dry weight of the seedlings in control groups. SL, FW, DW indicate shoot length, fresh weight, and dry weight of the seedling in treat groups. SR indicates survival rate.

**Table S2 Candidate QTLs identified by GWAS.**

Traits	Linkage-QTL	Chromosome	LeadSNP	P-value
CDW	<i>qCDW_ind1</i>	1	15695725	6.66E-07
	<i>qCDW_ind5</i>	5	6378944	2.30E-07
CFW	<i>qCFW_ind6</i>	6	4678729	3.65E-07
	<i>qCFW_ind9</i>	9	20789266	2.14E-07
	<i>qCFW_ind10</i>	10	2803244	8.33E-10
	<i>qCFW_ind11</i>	11	6077844	3.83E-07
CSL	<i>qCSL_ind2</i>	2	18612268	2.11E-06
	<i>qCSL_ind5-1</i>	5	403333	1.21E-06
	<i>qCSL_ind5-2</i>	5	2578370	6.01E-07
	<i>qCSL_ind10</i>	10	400257	2.50E-07
DW	<i>qDW_ind1</i>	1	30643464	1.02E-07
	<i>qDW_ind2-1</i>	2	7355144	9.42E-07
	<i>qDW_ind2-2</i>	2	24214962	3.96E-08
	<i>qDW_ind4-1</i>	4	9055746	9.39E-07
	<i>qDW_ind4-2</i>	4	21035439	4.65E-07
	<i>qDW_ind5-1</i>	5	11499534	1.48E-07
	<i>qDW_ind5-2</i>	5	13221663	9.11E-08
	<i>qDW_ind5-3</i>	5	24370635	2.48E-07
	<i>qDW_ind7</i>	7	17922137	1.68E-08
	<i>qDW_ind8</i>	8	3190430	5.58E-08
	<i>qDW_ind9</i>	9	96431	6.19E-07
	<i>qDW_ind10</i>	10	475876	3.00E-08
	FW	<i>qFW_ind1-1</i>	1	16851744
<i>qFW_ind1-2</i>		1	24043619	6.51E-07
<i>qFW_ind2-1</i>		2	942193	3.57E-07
<i>qFW_ind2-2</i>		2	7740802	1.50E-08
<i>qFW_ind5-1</i>		5	4809270	7.41E-07
<i>qFW_ind6-1</i>		6	5692071	2.79E-07
<i>qFW_ind6-2</i>		6	24763407	6.04E-07
<i>qFW_ind8-1</i>		8	3190537	4.57E-08
<i>qFW_ind10-1</i>		10	2628436	2.12E-07
SL	<i>qSL-ind1</i>	1	33159557	4.72E-07
	<i>qSL-ind7</i>	7	11408739	6.30E-07
	<i>qSL-ind8-1</i>	8	17106337	4.82E-08
	<i>qSL-ind8-2</i>	8	25945911	8.80E-07
	<i>qSL-ind10</i>	10	503514	1.93E-07
	<i>qSL-ind11-1</i>	11	7271380	5.25E-08
	<i>qSL-ind11-2</i>	11	23654774	8.13E-07
SR	<i>qSL-ind12</i>	12	13518162	3.11E-07
	<i>qSR_ind1-1</i>	1	4578608	3.38E-08

Traits	Linkage-QTL	Chromosome	LeadSNP	P-value
SR	<i>qSR_ind1-2</i>	1	10087572	4.32E-08
	<i>qSR_ind1-3</i>	1	11948923	1.07E-07
	<i>qSR_ind1-4</i>	1	13042387	8.68E-08
	<i>qSR_ind1-5</i>	1	13624893	1.63E-07
	<i>qSR_ind1-6</i>	1	16073967	1.09E-07
	<i>qSR_ind1-7</i>	1	33427195	4.08E-08
	<i>qSR_ind1-8</i>	1	42815810	1.87E-07
	<i>qSR_ind2-1</i>	2	6483259	3.98E-08
	<i>qSR_ind2-2</i>	2	17903021	7.25E-07
	<i>qSR_ind2-3</i>	2	24662672	1.32E-08
	<i>qSR_ind3-1</i>	3	300929	7.32E-08
	<i>qSR_ind3-2</i>	3	3521746	4.58E-07
	<i>qSR_ind3-3</i>	3	4746385	1.79E-07
	<i>qSR_ind3-4</i>	3	13376526	1.84E-09
	<i>qSR_ind3-5</i>	3	14164909	7.67E-08
	<i>qSR_ind3-6</i>	3	21467558	1.85E-07
	<i>qSR_ind3-7</i>	3	23196721	3.64E-07
	<i>qSR_ind3-8</i>	3	30362842	1.43E-07
	<i>qSR_ind3-9</i>	3	33481705	9.35E-08
	<i>qSR_ind4-1</i>	4	732698	1.85E-07
	<i>qSR_ind4-2</i>	4	1396038	1.74E-07
	<i>qSR_ind4-3</i>	4	4422893	1.68E-07
	<i>qSR_ind4-4</i>	4	4666903	2.16E-08
	<i>qSR_ind4-5</i>	4	7134602	7.62E-08
	<i>qSR_ind4-6</i>	4	11833339	6.22E-08
	<i>qSR_ind4-7</i>	4	12634503	6.85E-08
	<i>qSR_ind4-8</i>	4	16315342	8.00E-09
	<i>qSR_ind4-9</i>	4	18765786	1.67E-08
	<i>qSR_ind4-10</i>	4	21029822	5.33E-07
	<i>qSR_ind4-11</i>	4	23343879	1.33E-07
	<i>qSR_ind4-12</i>	4	28705929	5.40E-08
	<i>qSR_ind5-1</i>	5	5121670	6.19E-07
	<i>qSR_ind5-2</i>	5	8961002	1.00E-07
	<i>qSR_ind5-3</i>	5	9275531	1.60E-07
	<i>qSR_ind5-4</i>	5	9952329	9.85E-09
	<i>qSR_ind5-5</i>	5	10209130	2.24E-07
	<i>qSR_ind5-6</i>	5	11913110	2.42E-07
	<i>qSR_ind5-7</i>	5	12494751	6.47E-07
	<i>qSR_ind5-8</i>	5	13131662	4.25E-08
	<i>qSR_ind5-9</i>	5	15936997	2.25E-08
<i>qSR_ind5-10</i>	5	19749618	2.32E-07	

Traits	Linkage-QTL	Chromosome	LeadSNP	P-value
SR	<i>qSR_ind5-11</i>	5	22802644	9.50E-08
	<i>qSR_ind6-1</i>	6	2468598	3.12E-08
	<i>qSR_ind6-2</i>	6	14109103	1.34E-10
	<i>qSR_ind6-3</i>	6	16845854	5.38E-08
	<i>qSR_ind6-4</i>	6	17469133	2.59E-08
	<i>qSR_ind6-5</i>	6	18513585	1.66E-09
	<i>qSR_ind7-1</i>	7	3660372	1.95E-07
	<i>qSR_ind7-2</i>	7	14451289	5.75E-08
	<i>qSR_ind7-3</i>	7	17387084	7.11E-10
	<i>qSR_ind7-4</i>	7	18007927	1.97E-07
	<i>qSR_ind8-1</i>	8	2397636	2.27E-08
	<i>qSR_ind8-2</i>	8	3071479	8.71E-08
	<i>qSR_ind8-3</i>	8	4063203	4.25E-07
	<i>qSR_ind8-4</i>	8	4259130	2.31E-08
	<i>qSR_ind8-5</i>	8	9473199	1.02E-08
	<i>qSR_ind8-6</i>	8	16039302	7.84E-07
	<i>qSR_ind8-7</i>	8	16678638	3.13E-07
	<i>qSR_ind8-8</i>	8	22515168	3.15E-08
	<i>qSR_ind9-1</i>	9	1746880	6.04E-08
	<i>qSR_ind9-2</i>	9	15261914	2.36E-07
	<i>qSR_ind9-3</i>	9	21645459	4.88E-07
	<i>qSR_ind9-4</i>	9	22745472	1.79E-09
	<i>qSR_ind10-1</i>	10	3989989	4.80E-07
	<i>qSR_ind10-2</i>	10	6939742	4.86E-08
	<i>qSR_ind10-3</i>	10	7875075	4.23E-08
	<i>qSR_ind11-1</i>	11	936305	1.17E-07
	<i>qSR_ind11-2</i>	11	11009454	6.90E-08
	<i>qSR_ind11-3</i>	11	18865118	2.21E-07
	<i>qSR_ind11-4</i>	11	21818005	4.53E-07
	<i>qSR_ind12-1</i>	12	119359	5.87E-08
	<i>qSR_ind12-2</i>	12	565346	8.69E-08
	<i>qSR_ind12-3</i>	12	7817107	6.47E-10
	<i>qSR_ind12-4</i>	12	11011200	3.89E-07
	<i>qSR_ind12-5</i>	12	11629746	2.04E-07
	<i>qSR_ind12-6</i>	12	16671789	1.69E-07
<i>qSR_ind12-7</i>	12	26525394	4.45E-10	

CSL, CFW, CDW indicate shoot length, fresh weight, and dry weight of the seedlings in control groups. SL, FW, DW indicate shoot length, fresh weight, and dry weight of the seedling in treat groups. SR indicates survival rate.

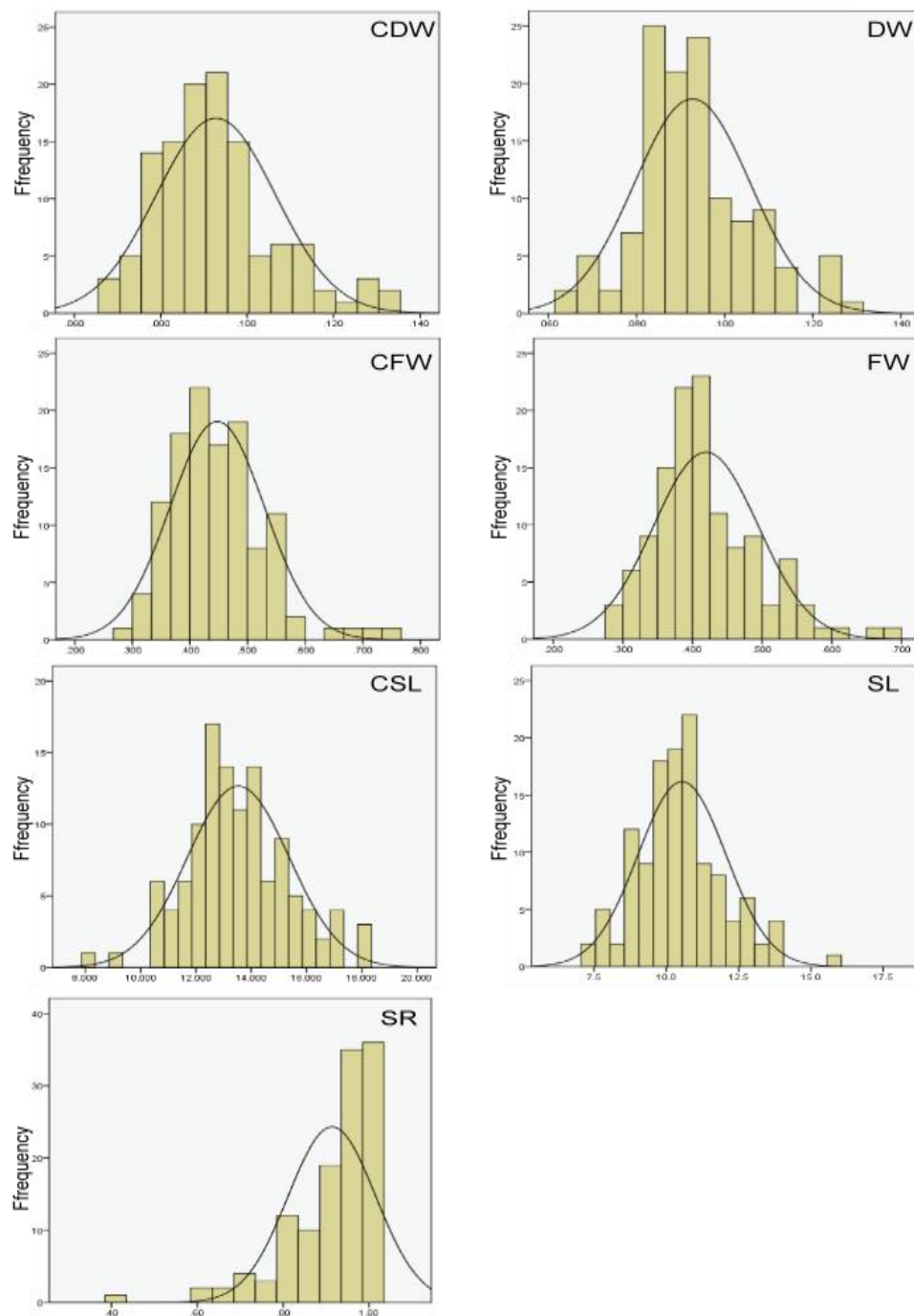
**Table S3 Annotation information of candidate genes identified in GWAS and linkage analysis.**

Chromosome	Candidate Gene	Start	End	Comment Information
6	<i>LOC_Os06g10770</i>	5621926	5625701	peptidase putative expressed
6	<i>LOC_Os06g10780</i>	5629416	5631997	AP2 domain containing protein expressed
6	<i>LOC_Os06g10790</i>	5633354	5635721	lectin-like receptor kinase putative expressed
6	<i>LOC_Os06g10800</i>	5636936	5637931	zinc finger family protein putative expressed
6	<i>LOC_Os06g10810</i>	5638272	5641660	phosphate carrier protein mitochondrial precursor putative expressed
6	<i>LOC_Os06g10820</i>	5642245	5642880	helix-loop-helix DNA-binding domain containing protein expressed
6	<i>LOC_Os06g10830</i>	5648264	5650906	retrotransposon protein putative unclassified expressed
6	<i>LOC_Os06g10840</i>	5653538	5653942	expressed protein
6	<i>LOC_Os06g10850</i>	5657850	5661265	lipase putative expressed
6	<i>LOC_Os06g10860</i>	5663968	5665309	glucosyltransferase putative expressed
6	<i>LOC_Os06g10870</i>	5665965	5667013	retrotransposon protein putative unclassified expressed
6	<i>LOC_Os06g10880</i>	5677080	5682126	bZIP transcription factor putative expressed
6	<i>LOC_Os06g10890</i>	5688535	5690095	sterol carrier protein-2 putative expressed
7	<i>LOC_Os07g30280</i>	17902640	17904772	csAtPR5 putative expressed
7	<i>LOC_Os07g30300</i>	17907341	17912298	small G protein family protein putative expressed
7	<i>LOC_Os07g30310</i>	17914477	17924844	retrotransposon protein putative Ty3-gypsy subclass expressed
7	<i>LOC_Os07g30320</i>	17934883	17940840	retrotransposon protein putative Ty3-gypsy subclass expressed
7	<i>LOC_Os07g30330</i>	17945639	17947265	cytokinin-O-glucosyltransferase 2 putative expressed
7	<i>LOC_Os07g30340</i>	17956245	17956571	retrotransposon protein putative unclassified

**Table S4 KEGG pathway analysis of DEGs**

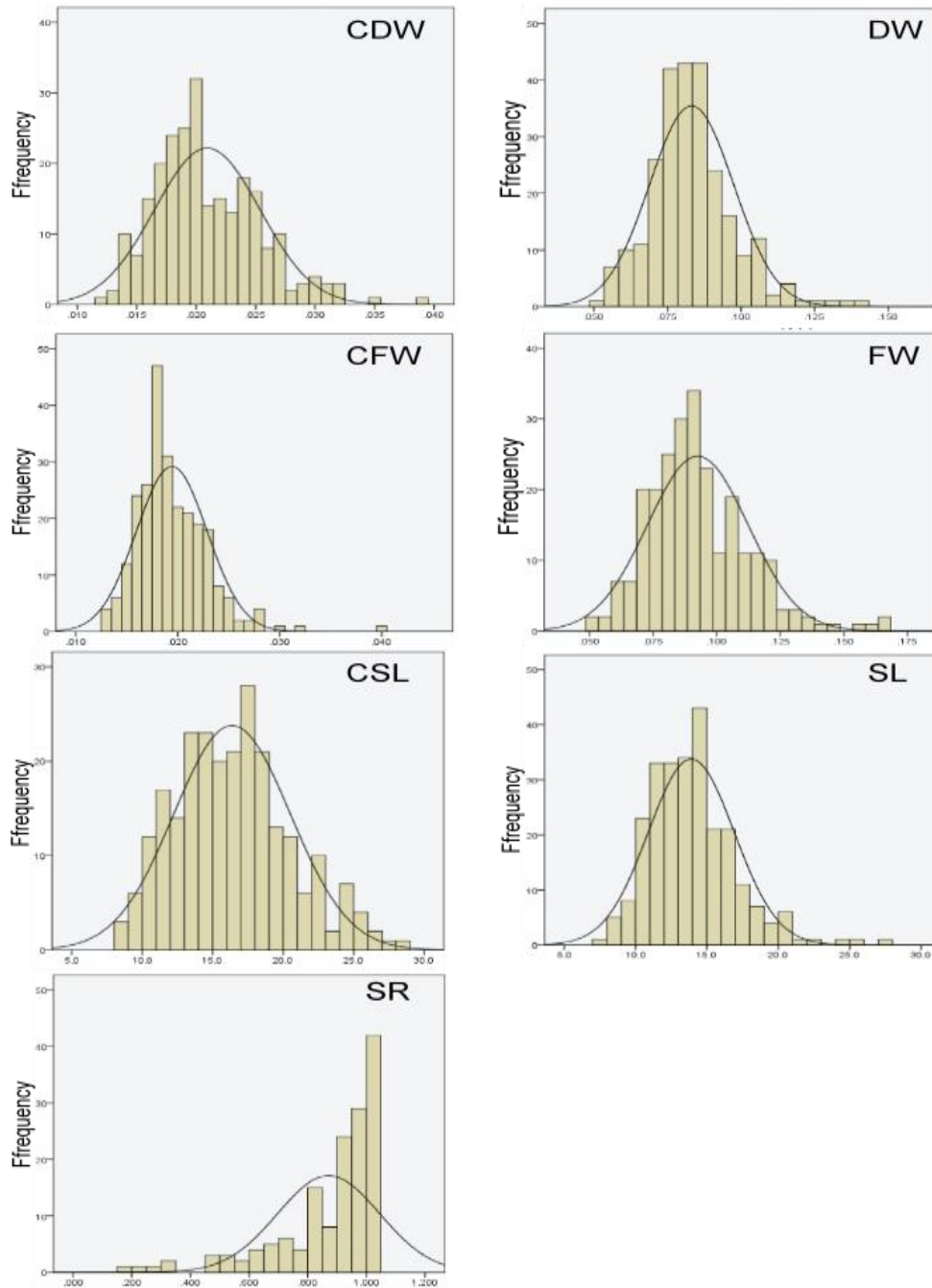
#Term	Database	ID	Input number	Background number	P-Value	Corrected P-Value
Metabolic pathways	KEGG PATHWAY	osa01100	112	2290	1.41E-10	3.04E-08
Pyruvate metabolism	KEGG PATHWAY	osa00620	14	86	2.10E-07	9.68E-06
Starch and sucrose metabolism	KEGG PATHWAY	osa00500	18	161	6.78E-07	2.91E-05
Biosynthesis of unsaturated fatty acids	KEGG PATHWAY	osa01040	7	28	2.22E-05	0.000484901
Carbon metabolism	KEGG PATHWAY	osa01200	20	271	5.34E-05	0.000908139
Fatty acid metabolism	KEGG PATHWAY	osa01212	10	75	5.36E-05	0.000908139
Biosynthesis of secondary metabolites	KEGG PATHWAY	osa01110	54	1177	5.78E-05	0.000908455
Carbon fixation in photosynthetic organisms	KEGG PATHWAY	osa00710	10	77	6.55E-05	0.000917033
Phenylpropanoid biosynthesis	KEGG PATHWAY	osa00940	17	233	0.000214794	0.001948271
Plant hormone signal transduction	KEGG PATHWAY	osa04075	17	240	0.0002968	0.002654711
Cysteine and methionine metabolism	KEGG PATHWAY	osa00270	11	119	0.000450026	0.003602569
Amino sugar and nucleotide sugar metabolism	KEGG PATHWAY	osa00520	13	161	0.000476415	0.003602569
Limonene and pinene degradation	KEGG PATHWAY	osa00903	3	8	0.002232842	0.011454978
MAPK signaling pathway - plant	KEGG PATHWAY	osa04016	11	151	0.002699569	0.013582207
Huntington disease	PANTHER	P00029	5	36	0.003483573	0.01739086
Valine, leucine and isoleucine degradation	KEGG PATHWAY	osa00280	5	45	0.008192552	0.037685741
Glycine, serine and threonine metabolism	KEGG PATHWAY	osa00260	6	68	0.010704714	0.048208643

**Fig. S1 Normal distribution maps of biomass traits and survival rate in the RIL in control and treatment groups.**



CSL, CFW, CDW indicate shoot length, fresh weight, and dry weight of the seedlings in control groups. SL, FW, DW indicate shoot length, fresh weight, and dry weight of the seedling in treat groups. SR indicates survival rate.

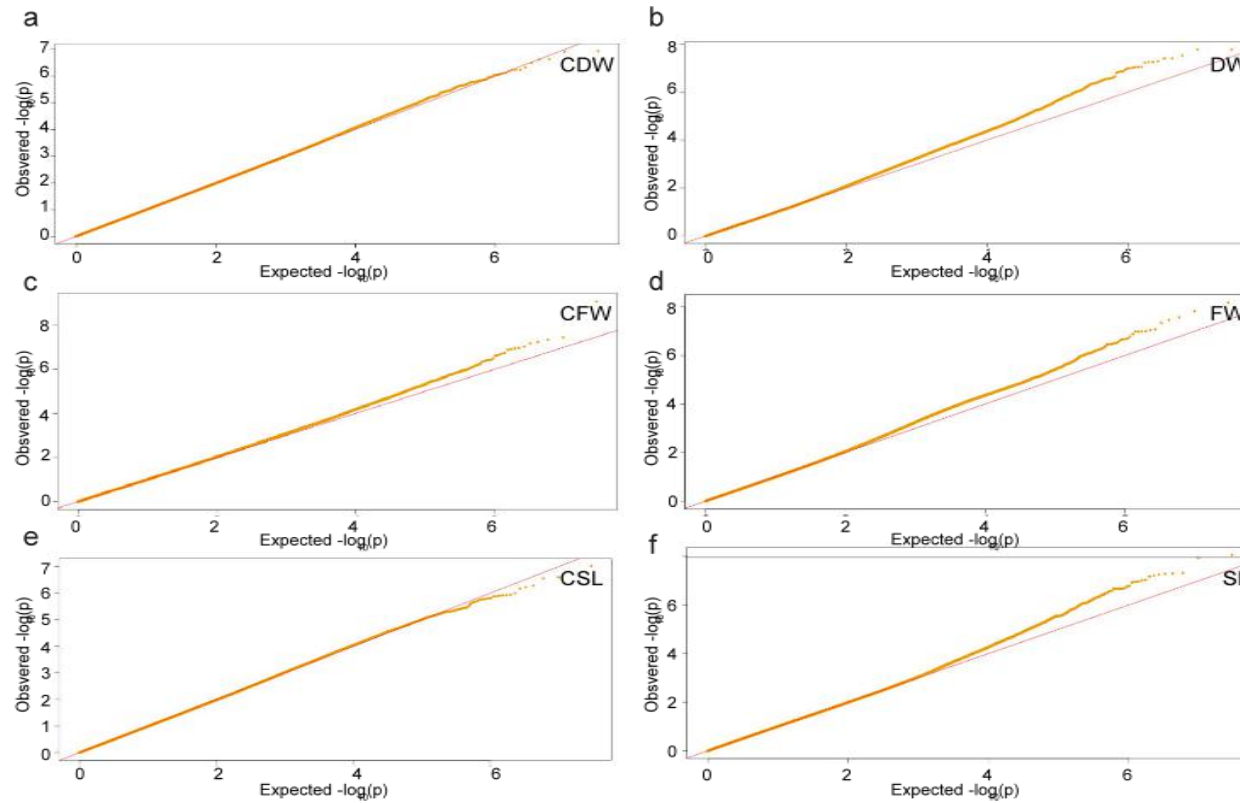
**Fig. S2 Normal distribution maps of biomass traits and survival rate in the natural population in control and treatment groups.**



CSL, CFW, CDW indicate shoot length, fresh weight, and dry weight of the seedlings in control groups. SL, FW, DW indicate shoot length, fresh weight, and dry weight of the seedling in treat groups. SR indicates survival rate.



**Fig. S3 QQplots for Genome-wide association analysis in the treatment and control groups of the natural population.**



CSL, CFW, CDW indicate shoot length, fresh weight, and dry weight of the seedlings in control groups. SL, FW, DW indicate shoot length, fresh weight, and dry weight of the seedling in treat groups. SR indicates survival rate.