

Table S1 Reported genes related with PH in maize

Gene name	Gene number V4	Chr	V4-start	V4-end
CNR13	Zm00001d027722	1	12170863	12175121
RPH1	Zm00001d028073	1	21990180	22006881
PHYB1	Zm00001d028905	1	50443216	50455013
BR2	Zm00001d031871	1	204748411	204755635
AN1	Zm00001d032961	1	244858795	244867417
BRD1	Zm00001d033180	1	253162491	253166753
GRAS8	Zm00001d033680	1	270918085	270919977
PHYC1	Zm00001d034038	1	281978994	281984348
AMP1	Zm00001d034383	1	291472441	291480873
Zfl2	Zm00001d002449	2	12914091	12917068
PRR95	Zm00001d006212	2	201957643	201963953
KOB1	Zm00001d039284	3	1009359	1014295
VATE	Zm00001d039331	3	2013965	2017590
D1	Zm00001d039453	3	4745784	4752166
GA3ox2	Zm00001d039634	3	9745817	9747450
MADS69	Zm00001d042315	3	160591489	160591701
TE1	Zm00001d042445	3	167821561	167825000
GA20ox3	Zm00001d042611	3	173559174	173562022
ELF3.1	Zm00001d044232	3	222542813	222548835
PHYC2	Zm00001d013262	5	7372367	7382139
D9	Zm00001d013465	5	12228329	12230206
NA2	Zm00001d014887	5	67026171	67030023
SPL12	Zm00001d015410	5	89049594	89053097
BV1	Zm00001d016487	5	164505621	164508106
COL3	Zm00001d017176	5	188033144	188034257
TOC1b	Zm00001d017241	5	190060998	190063941
MADS3	Zm00001d018667	7	2191954	2203098
NF-YC	Zm00001d020874	7	135216263	135216865
zmm28	Zm00001d022088	7	169844061	169849722
GlGZ1a	Zm00001d008826	8	21787238	21795721
EMF1L1	Zm00001d010894	8	132435792	132443091
Rap2.7	Zm00001d010988	8	136011962	136013101
GA20ox5	Zm00001d012212	8	170115789	170118570
GAD5	Zm00001d045563	9	26822040	26825680
PHYB2	Zm00001d047632	9	137491058	137497818
PRR7	Zm00001d047761	9	141194049	141202987
MADS1	Zm00001d048474	9	156960598	156980213
D53	Zm00001d023208	10	130112	134842
CCT10	Zm00001d024909	10	94430850	94433404
ACS7	Zm00001d026060	10	137296427	137304511

Table S2 The distribution of markers on the linkage map of the IMF₂ population

Chr.	Number of markers	Physical distance (Mb)	Genetic distance (cM)	Average distance (cM)	<5 cM Gap
1	649	306.04	363.61	0.56	646
2	576	244.07	278.50	0.48	575
3	449	231.84	202.35	0.45	446
4	177	241.96	153.83	0.87	173
5	68	223.53	128.80	1.89	62
6	354	173.17	179.60	0.51	352
7	208	181.01	151.26	0.73	201
8	342	180.80	188.29	0.55	338
9	63	155.18	113.51	1.80	57
10	183	149.04	133.10	0.73	180
Total	3069	2086.65	1892.83	0.86	3030

Table S3 Variance components and proportion of the phenotypic variance contributed by each variance component in the hybrid population

Traits	δ^2_a	δ^2_d	δ^2_{aa}	δ^2_{ad}	δ^2_{dd}	δ^2_ε	h^2_a	h^2_d	h^2_{aa}	h^2_{ad}	h^2_{dd}	h^2
PH	230.98	25.89	29.41	21.23	19.51	35.95	0.636	0.071	0.081	0.058	0.054	0.900
EH	76.12	5.61	6.55	5.93	4.73	10.94	0.693	0.051	0.060	0.054	0.043	0.901
PHAE	121.61	13.36	18.68	11.68	11.35	21.37	0.614	0.067	0.094	0.059	0.057	0.891
TL	7.87	1.08	1.07	0.91	0.84	1.83	0.579	0.079	0.079	0.067	0.062	0.866
AENN	0.14	0.01	0.02	0.02	0.01	0.03	0.612	0.065	0.085	0.068	0.056	0.886
AILAE	1.14	0.19	0.27	0.16	0.15	0.29	0.521	0.085	0.123	0.072	0.067	0.868

Notes: All genetic variance σ^2 is calculated by $\sigma^2 = \sigma_a^2 + \sigma_d^2 + \sigma_{aa}^2 + \sigma_{ad}^2 + \sigma_{dd}^2 + \sigma_\varepsilon^2$;

h_a^2 , the genetic proportion of additive effect, calculated by $h_a^2 = \sigma_a^2/\sigma^2$;

h_d^2 , the genetic proportion of dominance effect, calculated by $h_d^2 = \sigma_d^2/\sigma^2$;

h_{aa}^2 , the genetic proportion of additive-by-additive effect, calculated by $h_{aa}^2 = \sigma_{aa}^2/\sigma^2$;

h_{ad}^2 , the genetic proportion of additive-by-dominance effect, calculated by $h_{ad}^2 = \sigma_{ad}^2/\sigma^2$;

h_{dd}^2 , the genetic proportion of dominance-by-dominance effect, calculated by $h_{dd}^2 = \sigma_{dd}^2/\sigma^2$.

PH, plant height; EH, ear height; PHAE, plant height above-ear; TL, tassel length;

AENN, above-ear node number; AILAE, average internode length above-ear.

Table S4 QTL mapping results of the six traits in the IMF₂ population

Env.	Trait	Chr.	Pos.	Left Marker	Right Marker	LOD	PVE(%)	Add.	Dom.	Left CI	Right CI
BLUE	PH	1	47	S1_11671250	S1_12716397	8.4	2.6	-4.71	0.34	45.5	47.5
BLUE	PH	1	141	S1_110002889	S1_143444026	7.9	2.4	-4.04	0.84	140.5	141.5
BLUE	PH	1	289	S1_269329879	S1_270329585	26.2	9.3	-8.23	0.91	288.5	289.5
BLUE	PH	2	83	S2_39095425	S2_39116916	5.7	1.7	-3.73	-0.14	82.5	84.5
BLUE	PH	2	162	S2_177887793	S2_178768823	18.6	6.0	6.60	0.44	161.5	162.5
BLUE	PH	2	170	S2_184489684	S2_184507538	18.2	5.9	-6.47	1.48	168.5	170.5
BLUE	PH	2	191	S2_194953435	S2_195895088	11.2	3.4	-4.89	2.16	188.5	192.5
BLUE	PH	3	142	S3_202756748	S3_204515987	38.7	15.3	10.70	1.13	141.5	142.5
BLUE	PH	3	144	S3_204886397	S3_205197635	16.7	5.5	-6.40	1.23	143.5	144.5
BLUE	PH	4	49	S4_24524787	S4_25776067	10.1	3.1	-5.02	-0.17	47.5	49.5
BLUE	PH	5	0	S5_191242515	S5_189324793	12.7	3.9	-5.59	1.20	0	0.5
BLUE	PH	6	72	S6_98444313	S6_100494561	15.5	4.9	-6.31	0.73	71.5	73.5
BLUE	PH	7	57	S7_35657556	S7_103970149	5.5	1.7	-3.85	0.41	55.5	57.5
BLUE	PH	7	148	S7_179889058	S7_179890872	6.0	1.8	-3.75	0.42	147.5	149.5
BLUE	PH	8	124	S8_136858916	S8_155239245	7.1	2.0	-1.78	5.62	122.5	124.5
BLUE	PH	8	188	S8_179303074	S8_181044202	6.3	1.9	1.05	5.43	186.5	188
BLUE	EH	2	53	S2_14173718	S2_15005821	6.3	5.0	2.47	1.43	51.5	54.5
BLUE	EH	2	189	S2_194070269	S2_194953435	9.5	7.3	-2.94	1.29	188.5	191.5
BLUE	EH	2	277	S2_242359991	S2_243177289	11.2	8.9	3.24	1.31	275.5	278
BLUE	EH	3	46	S3_16736078	S3_16972714	5.0	3.8	-2.10	1.50	42.5	48.5
BLUE	EH	3	78	S3_129403674	S3_130034086	14.0	11.7	3.81	0.85	77.5	78.5
BLUE	EH	4	22	S4_7358055	S4_7659118	4.5	3.4	2.19	-0.52	21.5	23.5
BLUE	EH	4	58	S4_32408665	S4_36804605	8.7	6.7	-2.80	1.04	56.5	59.5
BLUE	EH	5	3	S5_179758728	S5_170980192	5.9	4.4	-2.40	0.57	0	7.5
BLUE	EH	6	68	S6_96214388	S6_99027644	4.9	4.1	-2.33	0.82	65.5	69.5
BLUE	EH	7	4	S7_730311	S7_1414806	5.3	4.1	1.93	-1.32	0	4.5
BLUE	PHAE	1	141	S1_110002889	S1_143444026	9.9	6.4	-4.15	0.48	140.5	141.5
BLUE	PHAE	1	289	S1_269329879	S1_270329585	20.2	13.7	-6.08	1.53	288.5	289.5
BLUE	PHAE	2	12	S2_2805295	S2_3408488	8.3	5.1	-4.22	-0.13	11.5	12.5
BLUE	PHAE	2	169	S2_183498880	S2_184489684	8.9	5.6	-3.85	1.14	168.5	170.5
BLUE	PHAE	2	273	S2_241126960	S2_241790578	10.3	6.8	-4.45	-0.45	270.5	274.5
BLUE	PHAE	4	47	S4_22850445	S4_24524787	5.6	3.5	-3.27	0.13	44.5	49.5
BLUE	PHAE	6	73	S6_98444313	S6_100494561	6.2	3.9	-3.21	1.83	71.5	74.5
BLUE	PHAE	6	114	S6_151999143	S6_152608758	12.7	8.4	5.14	1.08	112.5	115.5
BLUE	PHAE	7	140	S7_177749949	S7_178153031	5.7	3.4	-2.96	-1.95	139.5	140.5
BLUE	PHAE	8	123	S8_136858916	S8_155239245	4.3	2.8	0.30	4.06	121.5	124.5
BLUE	PHAE	8	188	S8_179303074	S8_181044202	4.5	2.7	2.75	1.93	186.5	188
BLUE	TL	1	41	S1_10852905	S1_11128611	5.2	2.7	-0.80	0.41	38.5	42.5
BLUE	TL	1	199	S1_192436850	S1_192760939	5.9	2.9	-0.89	0.21	197.5	199.5
BLUE	TL	1	283	S1_266537872	S1_267030175	7.7	3.9	0.98	0.01	282.5	283.5
BLUE	TL	1	290	S1_273002635	S1_273836450	26.5	15.8	-1.99	0.28	289.5	291.5
BLUE	TL	2	0	S2_41033	S2_1083914	6.9	3.4	-0.96	0.49	0	1.5

BLUE	TL	2	250	S2_235056628	S2_235788869	8.7	4.5	-1.07	-0.19	249.5	250.5
BLUE	TL	2	272	S2_241126960	S2_241790578	7.5	4.0	-0.97	-0.37	269.5	274.5
BLUE	TL	3	175	S3_224216705	S3_225346839	4.4	2.2	0.76	0.04	174.5	175.5
BLUE	TL	4	0	S4_3571676	S4_4611545	5.5	2.7	0.87	0.25	0	4.5
BLUE	TL	6	99	S6_138542031	S6_139900816	11.1	5.8	1.24	-0.56	98.5	99.5
BLUE	TL	7	47	S7_13644694	S7_15921898	17.5	9.9	-1.63	-0.42	45.5	47.5
BLUE	TL	7	140	S7_177749949	S7_178153031	9.8	5.0	-1.16	0.30	139.5	140.5
BLUE	AENN	1	28	S1_7345988	S1_8152527	4.1	0.6	-0.09	-0.03	27.5	29.5
BLUE	AENN	1	360	S1_304587897	S1_304932473	7.0	1.1	-0.12	0.01	358.5	360.5
BLUE	AENN	2	278	S2_243537180	S2_244109746	12.6	2.0	-0.17	-0.03	277.5	278
BLUE	AENN	3	150	S3_207962098	S3_208325684	13.2	2.0	0.17	0.03	149.5	151.5
BLUE	AENN	4	57	S4_32408665	S4_36804605	10.3	1.6	-0.15	0.01	56.5	59.5
BLUE	AENN	4	141	S4_242286166	S4_242888414	4.9	0.7	0.10	0.00	139.5	141.5
BLUE	AENN	5	0	S5_191242515	S5_189324793	8.0	1.2	-0.13	-0.03	0	0.5
BLUE	AENN	6	35	S6_76077187	S6_83127386	59.1	14.5	-0.44	0.00	34.5	35.5
BLUE	AENN	6	46	S6_73928215	S6_82194026	74.4	20.9	0.55	-0.01	45.5	46.5
BLUE	AENN	8	54	S8_17292863	S8_18462606	56.1	12.8	0.42	-0.05	52.5	54.5
BLUE	AENN	8	56	S8_18951887	S8_20499409	27.6	4.9	-0.26	-0.04	55.5	56.5
BLUE	AENN	9	87	S9_153044666	S9_154838789	10.8	1.7	-0.15	0.02	86.5	88.5
BLUE	AILAE	1	89	S1_42291652	S1_43645958	4.8	2.0	-0.29	0.07	88.5	89.5
BLUE	AILAE	1	141	S1_110002889	S1_143444026	14.5	6.6	-0.50	0.13	140.5	141.5
BLUE	AILAE	1	219	S1_210138844	S1_211116324	14.2	6.4	-0.50	0.09	218.5	220.5
BLUE	AILAE	1	292	S1_273608504	S1_275164590	10.9	4.7	-0.43	0.11	291.5	292.5
BLUE	AILAE	2	17	S2_4668065	S2_4864056	5.1	2.1	-0.29	-0.13	15.5	17.5
BLUE	AILAE	2	54	S2_14173718	S2_15005821	10.4	4.6	0.45	0.07	52.5	54.5
BLUE	AILAE	2	87	S2_41241033	S2_41648818	30.6	15.8	-0.87	0.07	86.5	88.5
BLUE	AILAE	2	185	S2_190810969	S2_191462633	8.5	3.7	-0.41	-0.03	183.5	185.5
BLUE	AILAE	4	78	S4_135623178	S4_135622314	7.0	2.9	-0.35	0.09	77.5	78.5
BLUE	AILAE	6	1	S6_479526	S6_2409227	5.0	2.1	-0.06	-0.42	0	3.5
BLUE	AILAE	6	61	S6_94245221	S6_95056892	17.5	8.3	-0.60	0.18	59.5	62.5
BLUE	AILAE	6	123	S6_156584507	S6_157124016	5.4	2.3	0.31	0.01	121.5	124.5
BLUE	AILAE	7	105	S7_167277540	S7_170257603	7.3	3.1	0.38	-0.09	104.5	107.5
BLUE	AILAE	10	27	S10_4281712	S10_4476300	10.6	4.7	-0.46	-0.15	24.5	27.5
BLUE	AILAE	10	97	S10_140119850	S10_140696756	9.5	4.1	0.43	0.01	95.5	98.5
2ILY	PH	1	105	S1_62856959	S1_64040706	10.0	8.9	-7.33	-0.99	102.5	107.5
2ILY	PH	1	292	S1_273608504	S1_275164590	9.7	8.4	-6.71	2.30	291.5	292.5
2ILY	PH	2	184	S2_190810969	S2_191462633	9.0	7.9	-6.68	2.63	182.5	185.5
2ILY	PH	3	138	S3_198495467	S3_199019661	8.5	7.2	6.42	0.89	136.5	138.5
2ILY	PH	4	58	S4_32408665	S4_36804605	9.6	8.1	-6.60	2.93	56.5	58.5
2ILY	PH	5	0	S5_191242515	S5_189324793	4.3	3.5	-4.41	2.49	0	0.5
2ILY	PH	6	60	S6_93872487	S6_94245221	4.2	3.5	-4.72	-1.12	59.5	62.5
2ILY	EH	2	233	S2_223195826	S2_223464405	10.3	7.8	-4.24	1.15	232.5	234.5
2ILY	EH	2	269	S2_239761722	S2_241119338	12.0	9.2	4.47	1.17	267.5	269.5
2ILY	EH	3	47	S3_16736078	S3_16972714	5.8	4.4	-3.19	1.49	45.5	48.5

21LY	EH	3	78	S3_129403674	S3_130034086	10.1	7.9	4.29	0.45	77.5	78.5
21LY	EH	10	2	S10_1296064	S10_1562457	5.3	3.8	2.95	-0.35	0	3.5
21LY	PHAE	1	105	S1_62856959	S1_64040706	11.6	12.6	-6.15	1.05	102.5	107.5
21LY	PHAE	1	134	S1_93741990	S1_101472296	4.6	4.5	-0.36	5.69	133.5	135.5
21LY	PHAE	1	292	S1_273608504	S1_275164590	5.4	5.3	-4.04	0.75	291.5	292.5
21LY	PHAE	2	12	S2_2805295	S2_3408488	4.3	4.2	-3.85	-1.22	10.5	12.5
21LY	PHAE	2	184	S2_190810969	S2_191462633	6.1	6.3	-4.46	1.26	182.5	185.5
21LY	PHAE	4	76	S4_110627655	S4_133437637	5.9	5.9	-4.35	1.07	74.5	77.5
21LY	TL	1	139	S1_98961699	S1_105867233	4.6	2.3	-1.12	-0.10	137.5	139.5
21LY	TL	1	295	S1_279919454	S1_279982555	6.0	3.0	-1.24	0.50	294.5	295.5
21LY	TL	4	0	S4_3571676	S4_4611545	4.8	2.4	1.22	0.38	0	4.5
21LY	TL	7	141	S7_178253113	S7_178653254	30.8	19.4	-3.55	0.12	140.5	141.5
21LY	TL	10	34	S10_5605708	S10_7375307	6.6	3.4	-1.48	-0.03	33.5	35.5
21LY	AENN	2	16	S2_4668065	S2_4864056	8.7	1.8	-0.18	-0.02	15.5	16.5
21LY	AENN	2	278	S2_243537180	S2_244109746	5.6	1.2	-0.14	-0.01	277.5	278
21LY	AENN	3	138	S3_198495467	S3_199019661	12.0	2.5	0.20	0.02	137.5	138.5
21LY	AENN	4	76	S4_110627655	S4_133437637	70.3	25.6	-0.68	-0.03	75.5	76.5
21LY	AENN	6	26	S6_28516337	S6_30754790	8.7	1.8	0.17	0.00	25.5	26.5
21LY	AILAE	1	113	S1_73973616	S1_74159005	10.1	10.7	-0.59	0.23	112.5	113.5
21LY	AILAE	1	272	S1_257870704	S1_257980045	14.1	15.5	-0.81	0.12	271.5	273.5
21LY	AILAE	2	13	S2_3876621	S2_4277587	4.4	4.3	-0.39	-0.23	12.5	13.5
21LY	AILAE	2	86	S2_40420633	S2_40560337	6.9	7.2	-0.56	0.05	84.5	86.5
21LY	AILAE	6	72	S6_98444313	S6_100494561	7.2	7.4	-0.56	-0.01	71.5	73.5
21XT	PH	1	47	S1_11671250	S1_12716397	4.7	0.8	-4.34	1.05	45.5	47.5
21XT	PH	1	141	S1_110002889	S1_143444026	72.4	24.3	-21.76	0.65	140.5	141.5
21XT	PH	1	164	S1_118075679	S1_115182187	55.8	15.4	17.10	0.26	163.5	164.5
21XT	PH	1	289	S1_269329879	S1_270329585	16.9	3.3	-8.20	1.13	288.5	289.5
21XT	PH	2	190	S2_194070269	S2_194953435	20.9	4.2	-9.24	3.24	188.5	191.5
21XT	PH	3	142	S3_202756748	S3_204515987	13.5	2.7	7.37	1.73	141.5	142.5
21XT	PH	4	14	S4_5651041	S4_6039804	4.1	0.7	4.02	0.55	11.5	17.5
21XT	PH	4	49	S4_24524787	S4_25776067	5.8	1.0	-4.81	-0.62	47.5	50.5
21XT	PH	5	0	S5_191242515	S5_189324793	12.3	2.2	-6.86	2.49	0	0.5
21XT	PH	6	69	S6_96214388	S6_99027644	14.3	2.8	-8.08	1.01	68.5	69.5
21XT	PH	7	53	S7_67238775	S7_53422226	13.3	2.6	7.61	0.54	52.5	53.5
21XT	PH	7	57	S7_35657556	S7_103970149	32.2	7.2	-13.47	1.82	56.5	57.5
21XT	PH	8	6	S8_2200273	S8_2437582	6.3	1.1	4.66	2.31	5.5	6.5
21XT	PH	8	124	S8_136858916	S8_155239245	10.5	1.9	-1.89	9.31	123.5	124.5
21XT	PH	8	188	S8_179303074	S8_181044202	5.6	1.0	1.05	6.79	186.5	188
21XT	EH	1	157	S1_112127208	S1_113123793	18.0	8.6	5.38	0.59	156.5	157.5
21XT	EH	1	167	S1_156170224	S1_156411308	26.5	13.2	-6.95	-0.48	166.5	167.5
21XT	EH	2	233	S2_223195826	S2_223464405	12.6	5.5	-4.40	1.81	232.5	234.5
21XT	EH	2	277	S2_242359991	S2_243177289	7.8	3.4	3.42	1.42	275.5	278
21XT	EH	3	47	S3_16736078	S3_16972714	7.5	3.3	-3.52	1.09	45.5	48.5
21XT	EH	3	84	S3_145600894	S3_139135638	18.6	8.8	5.79	-0.47	83.5	84.5

21XT	EH	5	3	S5_179758728	S5_170980192	13.5	6.0	-4.87	0.44	1.5	4.5
21XT	EH	8	75	S8_56604393	S8_52875891	10.8	4.7	-4.35	-0.29	74.5	76.5
21XT	EH	9	30	S9_12500206	S9_12698428	6.6	2.8	3.32	-0.70	29.5	31.5
21XT	PHAE	1	141	S1_110002889	S1_143444026	13.2	6.7	-6.69	0.53	140.5	141.5
21XT	PHAE	1	286	S1_268575537	S1_268584138	14.4	7.2	7.07	2.41	285.5	286.5
21XT	PHAE	1	289	S1_269329879	S1_270329585	38.5	23.8	-12.84	1.78	288.5	289.5
21XT	PHAE	2	180	S2_188907014	S2_190762998	13.3	6.6	-6.97	1.43	179.5	180.5
21XT	PHAE	7	105	S7_167277540	S7_170257603	6.5	3.1	4.90	-0.82	104.5	106.5
21XT	PHAE	8	122	S8_136858916	S8_155239245	4.6	2.2	1.07	5.34	120.5	123.5
21XT	PHAE	10	26	S10_4281712	S10_4476300	4.2	2.1	-4.06	-0.66	23.5	27.5
21XT	TL	1	207	S1_197842519	S1_198043688	5.6	3.3	-1.01	-0.23	205.5	207.5
21XT	TL	1	269	S1_257231788	S1_257870704	8.0	5.1	1.34	-0.11	267.5	270.5
21XT	TL	1	290	S1_273002635	S1_273836450	12.5	8.0	-1.55	0.21	289.5	291.5
21XT	TL	2	248	S2_233403203	S2_233476723	8.7	5.4	-1.29	-0.05	246.5	248.5
21XT	TL	2	274	S2_241126960	S2_241790578	8.9	5.5	-1.31	-0.32	271.5	274.5
21XT	TL	3	96	S3_157561325	S3_158611286	4.5	2.7	-0.12	1.34	95.5	96.5
21XT	TL	3	119	S3_181430700	S3_183054245	8.6	5.5	1.37	0.23	118.5	120.5
21XT	TL	6	115	S6_151999143	S6_152608758	8.2	5.3	1.35	0.19	112.5	115.5
21XT	TL	7	47	S7_13644694	S7_15921898	16.9	11.7	-2.00	-0.23	46.5	47.5
21XT	TL	8	128	S8_157390197	S8_162606948	8.2	5.1	1.29	0.09	126.5	128.5
21XT	AENN	1	227	S1_215648855	S1_216312177	24.6	5.7	0.24	-0.03	226.5	227.5
21XT	AENN	1	231	S1_219091374	S1_219345086	16.5	3.7	-0.20	0.01	230.5	231.5
21XT	AENN	1	362	S1_304940162	S1_305107918	4.5	0.9	-0.10	-0.02	360.5	363
21XT	AENN	2	156	S2_173967687	S2_174134822	5.3	1.1	-0.11	0.00	154.5	156.5
21XT	AENN	2	278	S2_243537180	S2_244109746	13.9	3.0	-0.18	-0.04	277.5	278
21XT	AENN	3	48	S3_16736078	S3_16972714	15.5	3.3	-0.19	-0.02	46.5	48.5
21XT	AENN	3	98	S3_158989326	S3_160473752	15.2	3.4	0.19	0.04	97.5	98.5
21XT	AENN	3	150	S3_207962098	S3_208325684	11.2	2.3	0.16	0.03	149.5	151.5
21XT	AENN	6	35	S6_76077187	S6_83127386	47.8	13.9	-0.40	0.02	34.5	35.5
21XT	AENN	6	46	S6_73928215	S6_82194026	67.0	23.9	0.54	0.01	45.5	46.5
21XT	AENN	8	54	S8_17292863	S8_18462606	6.9	1.4	0.12	-0.06	51.5	55.5
21XT	AENN	9	79	S9_145088102	S9_151217105	9.3	1.9	-0.15	-0.04	77.5	79.5
21XT	AENN	10	100	S10_140832404	S10_143210614	6.6	1.3	-0.12	0.04	99.5	102.5
21XT	AILAE	1	141	S1_110002889	S1_143444026	4.2	3.2	-0.35	0.12	140.5	141.5
21XT	AILAE	1	207	S1_197842519	S1_198043688	6.3	4.8	-0.46	-0.02	205.5	207.5
21XT	AILAE	1	273	S1_257980045	S1_258441675	8.9	7.0	-0.56	0.17	272.5	274.5
21XT	AILAE	2	147	S2_157225575	S2_157225727	5.0	3.8	-0.40	0.15	146.5	149.5
21XT	AILAE	2	188	S2_193721872	S2_193814824	6.6	5.0	-0.46	0.19	185.5	188.5
21XT	AILAE	3	108	S3_171642559	S3_171710537	7.6	6.0	-0.47	0.22	106.5	109.5
21XT	AILAE	6	60	S6_93872487	S6_94245221	17.6	15.2	-0.85	0.08	59.5	61.5
21XT	AILAE	6	114	S6_151999143	S6_152608758	9.4	7.5	0.59	0.13	112.5	115.5
21XT	AILAE	9	13	S9_6587462	S9_9205824	9.3	7.8	-0.56	0.09	11.5	14.5
21XX	PH	1	129	S1_88452861	S1_89644712	7.2	3.6	4.48	1.33	128.5	129.5
21XX	PH	1	179	S1_174128698	S1_180370264	22.0	12.1	-8.63	2.39	178.5	179.5

21XX	PH	1	318	S1_292331671	S1_292615519	11.5	5.9	-6.23	-0.18	316.5	319.5
21XX	PH	2	180	S2_188907014	S2_190762998	8.8	4.4	-5.33	0.48	179.5	181.5
21XX	PH	3	78	S3_129403674	S3_130034086	6.7	3.4	4.54	0.10	77.5	78.5
21XX	PH	3	155	S3_212187491	S3_213465208	6.3	3.1	4.32	0.71	154.5	157.5
21XX	PH	4	57	S4_32408665	S4_36804605	7.9	3.9	-4.76	1.62	56.5	58.5
21XX	PH	6	72	S6_98444313	S6_100494561	16.0	8.4	-7.41	0.49	71.5	73.5
21XX	PH	6	94	S6_133193926	S6_134042655	14.4	7.7	7.08	-0.47	93.5	94.5
21XX	PH	6	133	S6_158799634	S6_159593586	4.5	2.3	3.69	0.24	130.5	135.5
21XX	PH	8	0	S8_245739	S8_625088	4.2	2.0	3.61	1.19	0	0.5
21XX	PH	9	49	S9_68994370	S9_91946183	6.0	3.0	-4.38	-0.55	48.5	49.5
21XX	EH	1	47	S1_11671250	S1_12716397	5.2	3.9	-2.11	0.32	44.5	47.5
21XX	EH	1	179	S1_174128698	S1_180370264	7.2	5.4	-2.34	0.91	178.5	181.5
21XX	EH	2	190	S2_194070269	S2_194953435	6.5	4.9	-2.25	0.63	188.5	191.5
21XX	EH	2	277	S2_242359991	S2_243177289	16.3	12.9	3.48	1.52	276.5	278
21XX	EH	3	78	S3_129403674	S3_130034086	8.3	6.4	2.57	-0.46	77.5	78.5
21XX	EH	5	0	S5_191242515	S5_189324793	5.9	4.3	-2.07	0.88	0	0.5
21XX	EH	5	70	S5_1397619	S5_120544	6.1	4.6	-2.31	0.10	68.5	70.5
21XX	EH	6	52	S6_88267885	S6_89083642	7.4	5.4	-2.43	0.39	51.5	52.5
21XX	EH	6	99	S6_138542031	S6_139900816	4.2	3.1	1.85	-0.07	98.5	99.5
21XX	EH	8	102	S8_109465772	S8_110495388	4.3	3.2	-1.75	-0.53	101.5	102.5
21XX	EH	10	6	S10_1562457	S10_2048136	5.1	4.0	2.03	-0.29	3.5	7.5
21XX	PHAE	1	110	S1_71985240	S1_72906175	4.9	3.6	-0.17	4.99	108.5	111.5
21XX	PHAE	1	317	S1_291664004	S1_292331671	10.4	8.3	-5.39	-0.61	315.5	318.5
21XX	PHAE	2	274	S2_241126960	S2_241790578	8.4	6.5	-4.53	1.31	272.5	274.5
21XX	PHAE	3	74	S3_127113244	S3_128626658	4.1	3.1	3.06	1.04	73.5	75.5
21XX	PHAE	3	193	S3_230739332	S3_231276686	5.1	4.2	1.06	5.01	191.5	193.5
21XX	PHAE	4	76	S4_110627655	S4_133437637	7.8	6.0	-4.47	0.15	74.5	77.5
21XX	PHAE	6	72	S6_98444313	S6_100494561	5.3	4.0	-3.70	0.32	71.5	74.5
21XX	PHAE	6	114	S6_151999143	S6_152608758	11.8	9.6	5.73	1.36	112.5	115.5
21XX	TL	1	41	S1_10852905	S1_11128611	5.7	4.7	-1.24	0.56	38.5	42.5
21XX	TL	1	318	S1_292331671	S1_292615519	4.7	3.7	-1.16	0.27	316.5	320.5
21XX	TL	2	108	S2_57300855	S2_57733024	5.0	3.9	1.12	0.43	107.5	109.5
21XX	TL	2	271	S2_241126960	S2_241790578	4.7	3.8	-1.14	-0.12	269.5	274.5
21XX	TL	3	121	S3_183054245	S3_184601636	6.4	5.2	1.38	0.02	119.5	122.5
21XX	TL	4	77	S4_133437637	S4_133642844	6.5	5.1	-1.39	-0.17	74.5	77.5
21XX	TL	6	95	S6_134042655	S6_136571957	11.4	9.3	1.85	0.00	93.5	96.5
21XX	TL	7	47	S7_13644694	S7_15921898	13.4	11.7	-2.10	-0.19	46.5	47.5
21XX	TL	8	173	S8_176950316	S8_177160597	6.3	5.3	1.45	0.33	169.5	175.5

Notes: PH, plant height; EH, ear height; PHAE, plant height above-ear; TL, tassel length; AENN, above-ear node number; AILAE, average internode length above-ear. Env., environment; Chr. chromosome; Pos., position; PVE, phenotypic variance explained the QTL; Add, additive effect; Dom, dominance effect; Add., additive effect; Dom. dominance effect; CI., confidence interval; Negative and positive values in add. and dom. indicates the effects are from the parent Zheng58 and PH6WC, respectively.

Table S5 Epistatic QTL identified for the traits of BLUE values in the IMF₂ population

Trait	Chr. i	Pos. i	Marker interval i	Chr. j	Pos. j	Marker interval j	LOD	PVE(%)	Add i	Add j	Dom i	Dom j	Add by Add	Add by Dom	Dom by Add	Dom by Dom	Major effect
PH	1	45	S1_11671250 - S1_12716397	9	20	S9_9724404 - S9_10722507	6.2	9.3	-4.33	2.23	1.09	0.50	-5.94	0.89	-1.69	-0.59	aa
PH	1	190	S1_184630453 - S1_185850186	7	130	S7_176443705 - S7_177637932	5.0	5.1	0.65	1.44	6.04	3.97	0.99	-2.38	-0.83	-10.77	dd
PH	1	320	S1_292331671 - S1_292615519	1	360	S1_304587897 - S1_304932473	5.0	4.9	-1.26	-0.95	-2.68	-4.41	-1.29	0.39	1.42	9.75	dd
PH	2	0	S2_41033 - S2_1083914	3	85	S3_145600894 - S3_139135638	5.9	5.0	-4.43	-1.44	2.30	1.37	0.51	5.53	4.43	-2.91	ad
PH	2	50	S2_13574260 - S2_14088283	5	30	S5_13546996 - S5_11683352	6.5	5.7	3.59	-1.18	-2.42	-0.31	-0.62	-6.19	4.24	4.75	ad
PH	2	260	S2_239274384 - S2_239370993	10	105	S10_140832404 - S10_143210614	5.8	5.7	-1.58	0.74	-5.44	-3.83	1.66	3.48	-3.52	8.04	dd
PH	3	5	S3_3982403 - S3_4175085	6	145	S6_162432992 - S6_162563453	5.4	3.7	1.91	4.20	1.30	0.87	-2.56	-2.32	-5.68	-1.59	ad
PH	3	10	S3_4595954 - S3_5495815	9	0	S9_3990742 - S9_4441847	5.3	4.3	-0.47	3.03	3.53	2.95	0.53	1.76	-5.97	-5.16	ad
PH	3	15	S3_5809538 - S3_7393597	5	25	S5_19952245 - S5_13744674	6.1	6.3	1.32	4.37	1.67	1.65	-1.78	-1.66	-7.23	2.10	ad
PH	3	90	S3_150288145 - S3_152243848	7	50	S7_25644859 - S7_27939165	5.3	3.5	1.82	-1.05	-0.79	0.04	-3.72	-3.29	2.33	0.02	aa
EH	1	25	S1_4908782 - S1_6322458	9	10	S9_5071229 - S9_5606263	5.2	7.2	-0.59	2.18	1.74	0.95	-0.98	0.78	-4.61	-1.22	ad
EH	1	45	S1_11671250 - S1_12716397	10	0	S10_1102942 - S10_1238544	5.9	8.8	-2.19	3.26	1.30	0.34	-1.73	2.10	-3.61	-2.52	ad
EH	2	25	S2_6564039 - S2_6868941	8	80	S8_75939202 - S8_77058745	5.4	7.0	0.53	-1.28	0.17	0.89	-3.08	-0.79	-0.04	-0.74	aa
EH	6	10	S6_3646695 - S6_3830350	10	105	S10_140832404 - S10_143210614	5.0	6.7	0.43	1.28	-1.61	-0.63	2.70	-0.20	-2.76	1.29	ad
EH	6	25	S6_28516337 - S6_30754790	8	85	S8_89837142 - S8_89844495	5.8	6.9	0.77	-1.97	-0.43	-0.41	-1.33	-2.82	2.59	1.05	ad
PHAE	1	0	S1_132093 - S1_2109865	10	80	S10_133899128 - S10_134615174	5.4	3.5	1.59	-1.65	0.89	0.47	0.99	-3.69	4.93	0.36	ad
PHAE	1	5	S1_2897280 - S1_3036249	1	345	S1_300788992 - S1_301043158	5.4	4.0	-0.18	1.04	0.36	0.68	3.27	-1.38	-3.97	-0.10	ad
PHAE	1	65	S1_21287388 - S1_21980824	8	145	S8_171482717 - S8_171837631	5.7	3.8	-0.71	1.62	0.04	-0.98	3.61	2.09	-2.71	1.31	aa
PHAE	1	80	S1_30087860 - S1_30541220	3	105	S3_169453685 - S3_170032493	5.8	3.8	-2.42	1.27	1.83	3.97	2.08	5.36	-2.84	-3.87	ad
PHAE	1	165	S1_113772604 - S1_152424407	5	40	S5_10258023 - S5_8850189	5.6	3.5	-0.70	-2.10	1.83	2.37	0.72	2.15	4.54	-4.81	dd
PHAE	1	205	S1_197314960 - S1_197499396	2	200	S2_200783940 - S2_201609947	5.2	3.6	-1.12	-0.91	2.83	3.29	2.46	-0.05	2.82	-5.37	dd
PHAE	1	245	S1_230038981 - S1_230531645	6	20	S6_9902679 - S6_16653812	5.8	3.8	0.75	0.74	1.18	0.04	4.52	-0.60	-0.81	-1.62	aa
PHAE	2	50	S2_13574260 - S2_14088283	5	30	S5_13546996 - S5_11683352	5.1	4.4	1.61	-1.77	-0.46	-1.06	-1.91	-3.87	3.88	3.81	ad
PHAE	2	55	S2_15450819 - S2_15740493	7	0	S7_730311 - S7_1414806	6.0	4.3	1.45	-1.00	0.68	-0.44	-4.14	-1.32	0.75	2.50	aa
PHAE	2	70	S2_24772111 - S2_24963216	9	30	S9_12500206 - S9_12698428	5.6	3.8	-0.87	-2.26	1.14	-1.05	-2.13	0.74	5.45	0.43	ad
PHAE	2	275	S2_242050148 - S2_242359991	8	25	S8_6154100 - S8_6299217	5.8	3.7	-0.78	1.63	2.35	1.75	-1.99	2.15	-3.69	-5.50	dd
PHAE	3	125	S3_186922295 - S3_187679512	3	150	S3_207962098 - S3_208325684	5.4	3.4	1.48	-0.39	2.12	2.56	-2.47	-1.05	-0.59	-6.56	dd
PHAE	5	70	S5_1397619 - S5_120544	7	130	S7_176443705 - S7_177637932	5.3	3.9	0.87	-1.73	0.12	0.04	4.43	-0.70	3.67	-0.65	aa
PHAE	6	25	S6_28516337 - S6_30754790	6	140	S6_160413362 - S6_161163501	5.2	3.5	-0.47	-0.20	-2.56	-1.02	3.21	1.74	-0.71	4.08	dd

PHAE	6	130	S6_158315087 - S6_158532450	10	15	S10_2372764 - S10_2754874	5.4	3.6	-0.09	-1.61	4.05	1.91	1.88	-0.26	2.70	-6.02	dd
PHAE	7	50	S7_25644859 - S7_27939165	9	100	S9_154838789 - S9_156832816	5.0	3.7	-0.72	-1.88	2.77	3.52	2.79	0.39	4.04	-3.42	ad
PHAE	7	150	S7_180747932 - S7_181089779	10	0	S10_1102942 - S10_1238544	6.8	4.1	0.45	-0.33	-3.32	-1.71	-4.08	-0.60	-1.70	3.98	aa
PHAE	8	120	S8_132313712 - S8_134646229	10	15	S10_2372764 - S10_2754874	6.8	4.3	1.71	-2.90	-0.17	-0.47	2.35	-2.46	4.91	-1.02	ad
PHAE	9	65	S9_114298575 - S9_142292875	10	120	S10_145972304 - S10_147054287	5.6	6.6	-1.56	1.34	4.60	5.53	-1.35	-0.43	-2.18	-10.56	dd
TL	1	35	S1_9997005 - S1_10258020	4	85	S4_149228365 - S4_151063954	5.5	3.6	0.45	-0.74	-0.11	0.27	-0.38	-0.89	1.34	-0.22	ad
TL	1	185	S1_180292075 - S1_181340572	5	40	S5_10258023 - S5_8850189	5.0	4.0	0.37	0.17	1.35	1.23	-0.56	-0.45	-0.06	-2.06	dd
TL	1	250	S1_234268367 - S1_234388480	2	55	S2_15450819 - S2_15740493	5.6	3.9	0.58	-0.92	-0.93	-0.95	-0.53	-0.83	1.32	1.36	dd
TL	1	325	S1_293920109 - S1_294248361	3	110	S3_172731597 - S3_178337993	5.2	4.0	-0.09	0.12	1.10	1.09	-0.82	-0.14	-0.04	-1.72	dd
TL	1	345	S1_300788992 - S1_301043158	9	30	S9_12500206 - S9_12698428	5.0	3.9	-0.17	-0.12	-0.87	-1.15	-0.05	-0.13	0.83	2.00	dd
TL	2	55	S2_15450819 - S2_15740493	4	30	S4_11652202 - S4_11762566	5.3	4.3	-0.71	-0.75	-0.88	-0.52	1.20	0.58	0.58	0.88	aa
TL	2	65	S2_20704326 - S2_20765552	7	145	S7_178653254 - S7_179354212	6.0	4.5	0.13	0.89	0.11	0.22	0.14	-0.33	-1.79	0.11	ad
TL	3	0	S3_3087150 - S3_3103038	10	100	S10_140832404 - S10_143210614	5.2	4.1	-0.59	-0.74	-0.07	-0.43	0.80	0.08	1.57	0.08	ad
TL	4	30	S4_11652202 - S4_11762566	8	180	S8_177983965 - S8_178359010	9.6	6.8	-0.16	1.31	1.11	0.99	-1.03	0.07	-1.54	-1.71	dd
TL	4	45	S4_22850445 - S4_24524787	10	60	S10_56837781 - S10_58446849	5.1	4.9	-0.41	-0.64	1.05	0.39	0.69	0.56	0.66	-1.62	dd
TL	5	10	S5_170980192 - S5_43800877	8	50	S8_15101811 - S8_17292863	5.5	5.1	-0.61	0.67	-0.94	-0.89	-0.22	1.69	-0.79	1.42	ad
TL	6	130	S6_158315087 - S6_158532450	10	75	S10_127954750 - S10_129535696	5.6	3.7	0.56	-0.50	-0.24	-0.43	-0.26	-1.09	0.83	1.00	ad
TL	7	125	S7_172900931 - S7_176067682	10	105	S10_140832404 - S10_143210614	6.3	5.7	0.94	-0.37	0.21	-0.51	0.12	-1.90	0.98	-0.03	ad
TL	8	10	S8_3069086 - S8_3220600	9	95	S9_154838789 - S9_156832816	6.6	6.3	0.34	1.33	0.48	0.39	-1.51	-0.13	-1.09	0.22	aa
TL	9	5	S9_4441314 - S9_5071229	9	110	S9_157944455 - S9_158039498	5.2	4.8	-0.72	0.28	-0.43	0.26	0.80	1.37	0.59	0.31	ad
TL	10	50	S10_14793404 - S10_15031133	10	90	S10_138350431 - S10_138511994	5.1	3.8	-0.89	0.86	-0.49	0.04	-0.25	0.98	-1.63	0.16	ad
AENN	1	0	S1_132093 - S1_2109865	1	50	S1_13761553 - S1_13908602	5.3	4.1	-0.05	-0.01	0.14	0.11	0.08	0.04	0.07	-0.23	aa
AENN	1	50	S1_13761553 - S1_13908602	3	80	S3_135811818 - S3_135985887	7.2	5.5	0.01	0.00	-0.14	-0.13	0.10	0.01	-0.03	0.26	dd
AENN	1	75	S1_25636570 - S1_26614707	7	130	S7_176443705 - S7_177637932	6.5	6.8	-0.05	-0.12	0.04	0.07	-0.02	0.15	0.19	-0.15	ad
AENN	1	140	S1_109846948 - S1_109867103	8	90	S8_98054940 - S8_101866995	5.7	4.3	-0.10	0.03	0.06	0.04	-0.06	0.18	-0.06	-0.04	ad
AENN	1	270	S1_257231788 - S1_257870704	5	75	S5_1356035 - S5_222474229	5.5	4.3	0.01	0.08	-0.14	-0.12	0.00	0.00	-0.15	0.21	dd
AENN	1	345	S1_300788992 - S1_301043158	9	50	S9_91643493 - S9_95189235	7.2	6.1	-0.05	0.01	-0.12	-0.10	-0.10	0.06	-0.10	0.25	dd
AENN	2	75	S2_29361057 - S2_29829813	10	110	S10_143572593 - S10_143794647	7.4	6.0	-0.09	0.02	0.07	0.13	0.06	0.19	-0.07	-0.15	ad
AENN	2	185	S2_190810969 - S2_191462633	8	85	S8_89837142 - S8_89844495	5.2	3.8	0.04	-0.02	-0.04	-0.06	0.11	-0.08	0.02	0.15	dd
AENN	3	125	S3_186922295 - S3_187679512	9	20	S9_9724404 - S9_10722507	5.4	4.1	0.01	-0.07	0.03	0.05	-0.07	-0.06	0.15	-0.12	ad
AENN	5	30	S5_13546996 - S5_11683352	5	50	S5_6421695 - S5_5978052	6.9	5.2	-0.10	0.10	-0.09	-0.08	-0.22	0.12	-0.15	0.00	aa
AENN	7	5	S7_1414806 - S7_3080163	8	0	S8_245739 - S8_625088	5.7	4.5	0.00	-0.02	0.09	0.05	-0.11	0.02	0.04	-0.11	dd
AENN	8	50	S8_15101811 - S8_17292863	8	55	S8_18462606 - S8_18951887	5.0	14.7	0.18	0.01	0.06	0.08	0.23	-0.23	-0.03	0.03	aa

AILAE	1	125	S1_85173860 - S1_84249804	7	40	S7_9193825 - S7_9619402	5.9	6.4	0.22	0.03	0.11	0.19	-0.13	-0.52	-0.32	-0.03	ad
AILAE	1	215	S1_203118803 - S1_204753671	10	105	S10_140832404 - S10_143210614	5.1	5.0	-0.25	-0.12	-0.17	-0.27	0.44	0.35	0.00	0.34	aa
AILAE	2	15	S2_4480978 - S2_4661172	7	140	S7_177749949 - S7_178153031	5.8	6.0	0.30	0.12	-0.24	-0.27	0.02	-0.52	-0.39	0.16	ad
AILAE	2	25	S2_6564039 - S2_6868941	10	20	S10_3671242 - S10_4264931	5.2	5.4	0.13	-0.18	-0.15	-0.37	0.30	-0.21	0.21	0.50	dd
AILAE	3	35	S3_9812175 - S3_10947297	3	195	S3_232292314 - S3_232638036	5.3	4.7	-0.11	0.24	-0.19	-0.06	-0.16	0.20	-0.42	0.45	dd
AILAE	3	120	S3_181430700 - S3_183054245	7	20	S7_1414806 - S7_3080163	5.1	5.2	-0.13	0.21	0.20	0.13	0.07	0.19	-0.55	-0.08	ad
AILAE	6	10	S6_3646695 - S6_3830350	9	35	S9_15133455 - S9_21566415	6.3	5.7	-0.13	0.03	-0.23	-0.23	0.40	0.06	0.08	0.40	aa
AILAE	7	60	S7_110029797 - S7_119718788	8	175	S8_176950316 - S8_177160597	6.0	7.4	-0.03	0.16	0.47	0.35	-0.32	-0.20	-0.20	-0.63	dd
AILAE	8	15	S8_3988651 - S8_4715013	10	35	S10_5605708 - S10_7375307	5.1	5.5	-0.13	-0.15	-0.45	-0.44	0.18	0.36	0.28	0.79	dd

Notes: PH, plant height; EH, ear height; PHAE, plant height above-ear; TL, tassel length; AENN, above-ear node number; AILAE, average internode length above-ear. Chr. chromosome; Pos., position; PVE, phenotypic variance explained the QTL; Add, additive effect; Dom, dominance effect; Add., additive effect; Dom. dominance effect; aa, additive-by-additive effect; ad, additive-by-dominance effect; dd, dominance-by- dominance effect. Negative and positive values in add. and dom. indicates the effects are from the parent Zheng58 and PH6WC, respectively.