

Supplementary Material

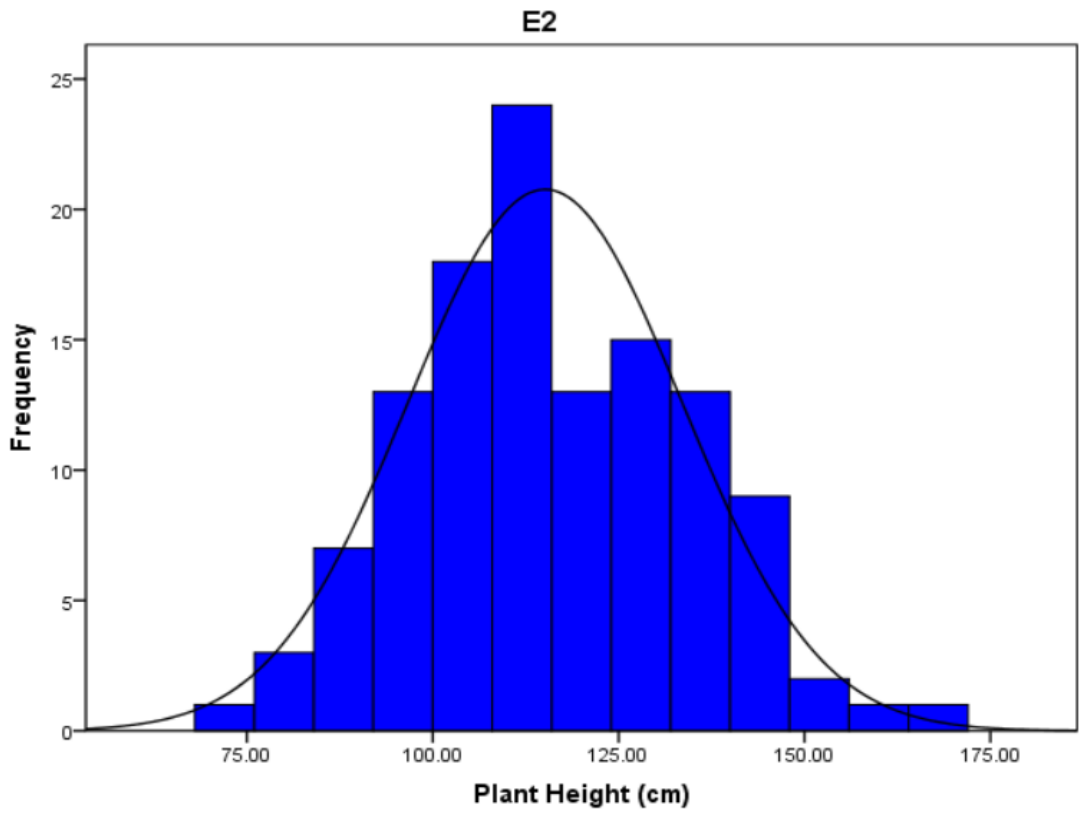
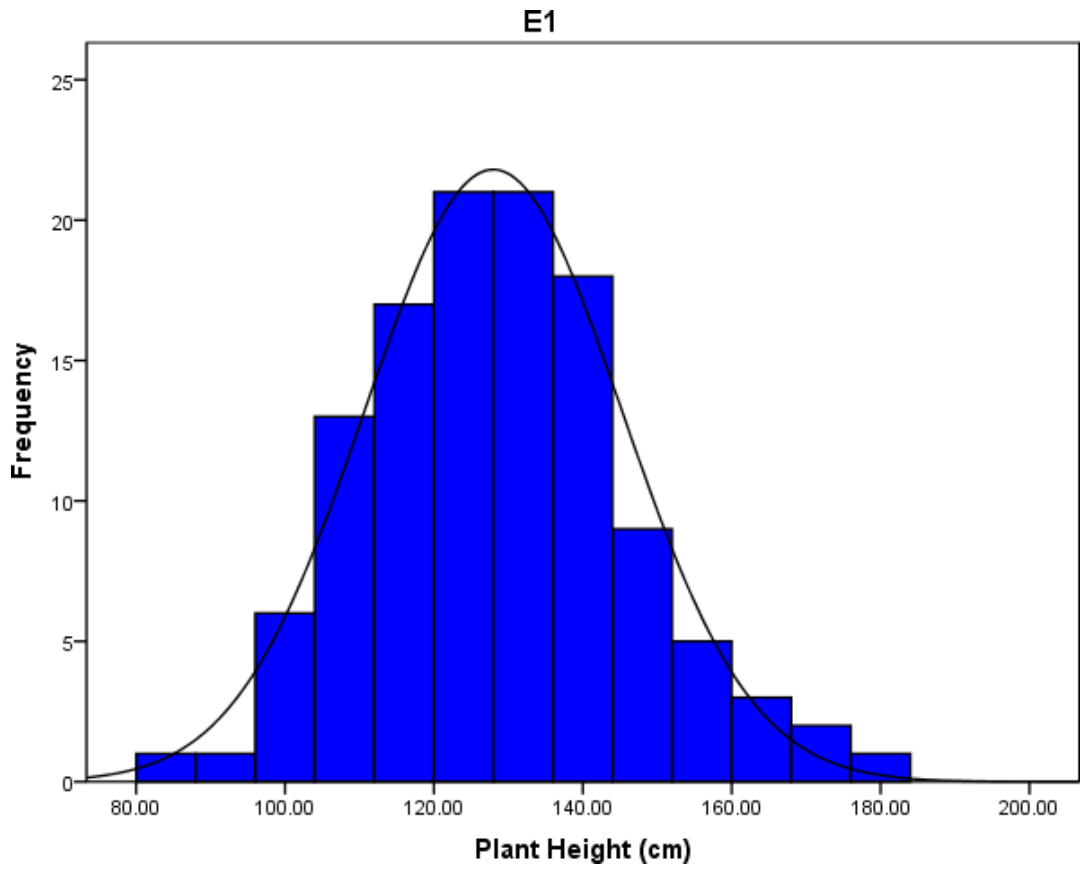
SNP-bin linkage analysis and genome-wide association study of plant height in soybean

Jijiang Wang^A, Bo Hu^A, Shanshan Huang^B, Xiping Hu^B, Mahfishan Siyal^A, Chang Yang^A, Hengxing Zhao^A, Tao Yang^A, Haoran Li^A, Yongqin Hou^A, Cuiqiao Liu^A, Xu Sun^A, Raja Rameez Veesar^A, Wen-Xia Li^{A,}, and Hailong Ning^{A,*}*

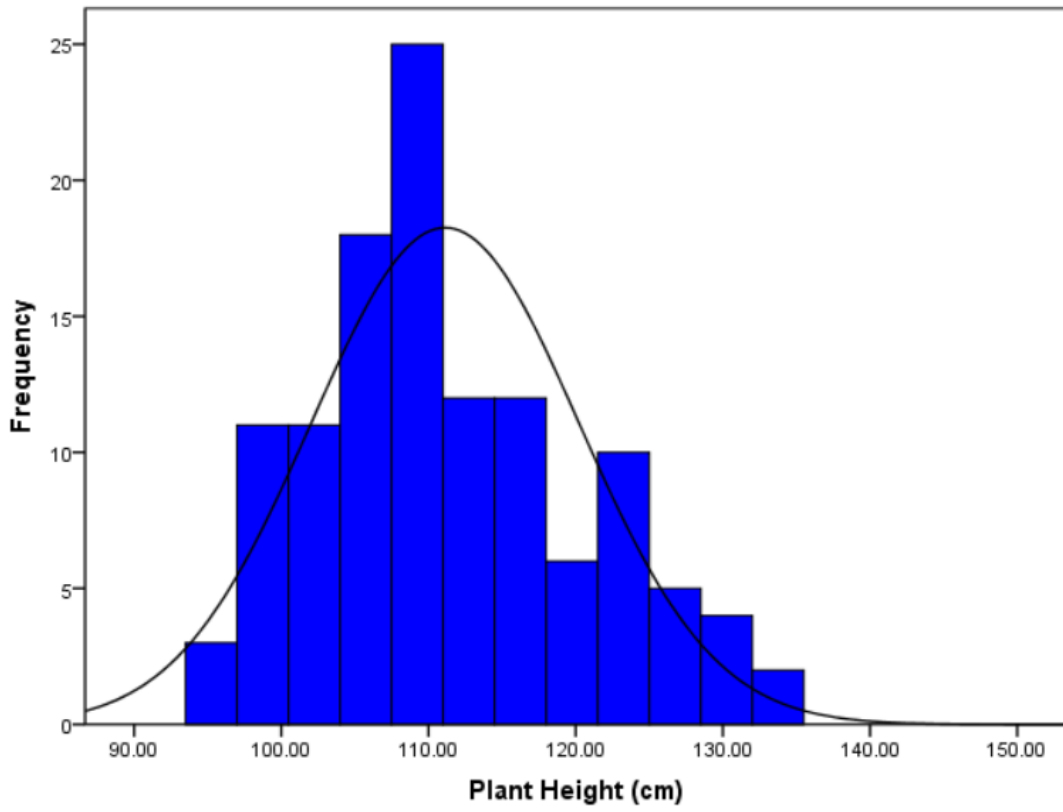
^AKey Laboratory of Soybean Biology, Ministry of Education, Key Laboratory of Soybean Biology and Breeding/Genetics, Ministry of Agriculture, Northeast Agricultural University, Harbin 150030, China.

^BKey Laboratory of Crop Biotechnology Breeding of the Ministry of Agriculture, Beidahuang Kenfeng Seed Co. Ltd, Harbin, China.

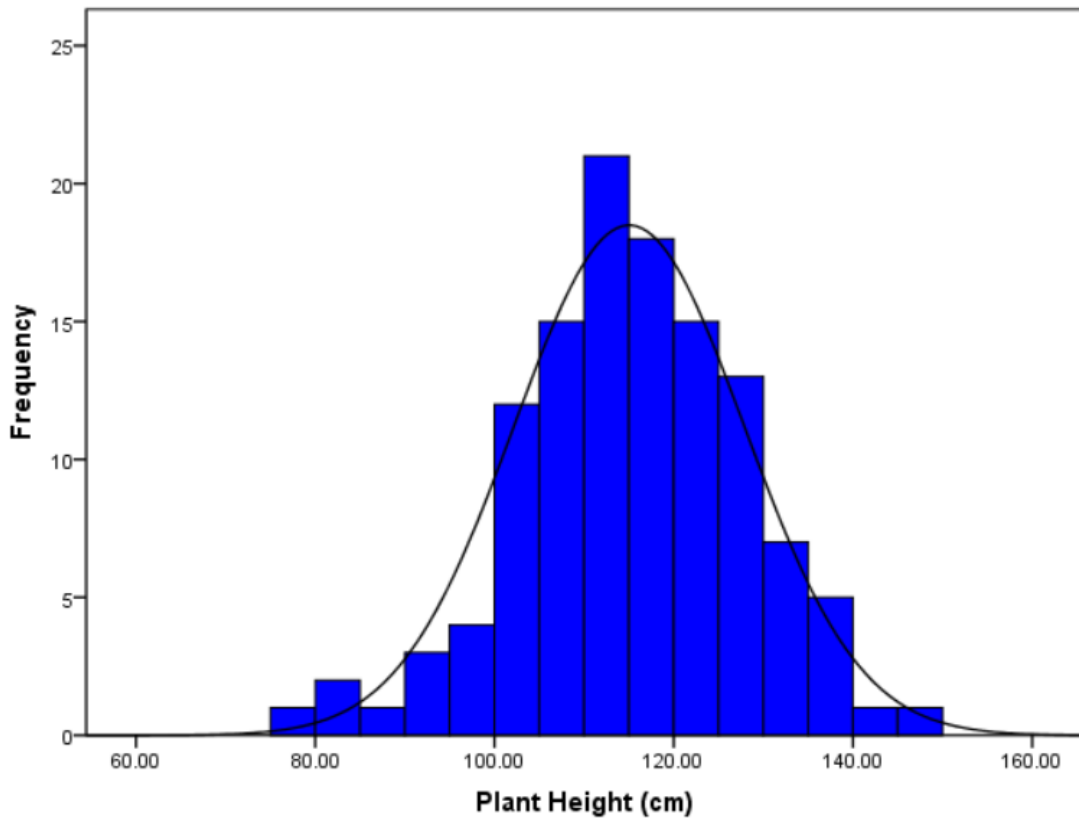
*Correspondence to: Hailong Ning Key Laboratory of Soybean Biology, Ministry of Education, Key Laboratory of Soybean Biology and Breeding/Genetics, Ministry of Agriculture, Northeast Agricultural University, Harbin 150030, China Email: ninghailongneau@126.com and Wen-Xia Li Key Laboratory of Soybean Biology, Ministry of Education, Key Laboratory of Soybean Biology and Breeding/Genetics, Ministry of Agriculture, Northeast Agricultural University, Harbin 150030, China Email: liwenxianeau@126.com

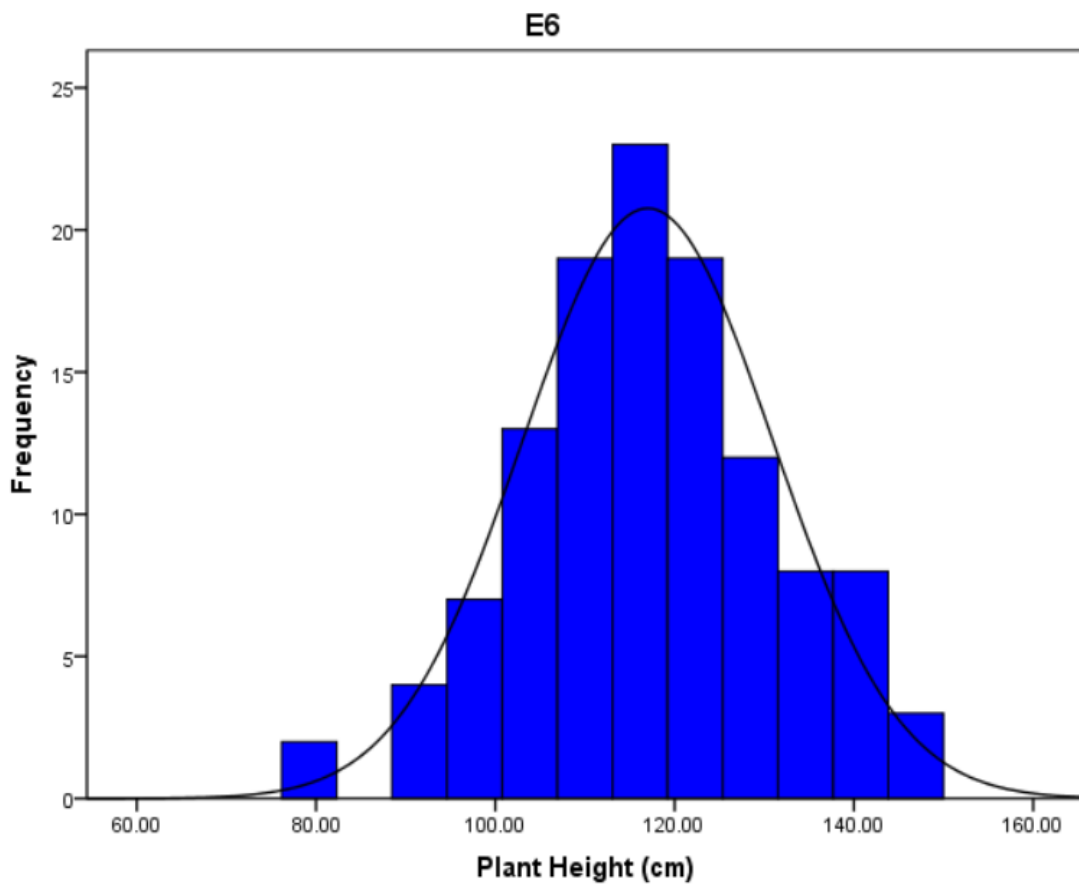
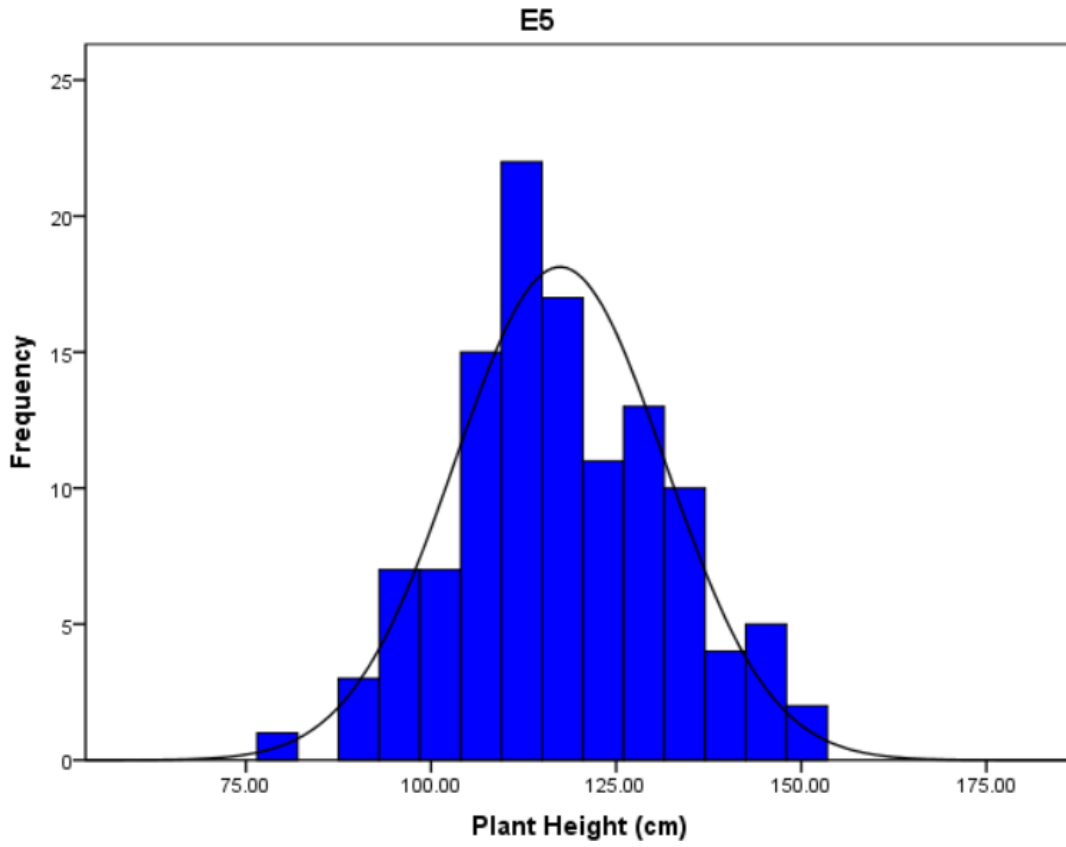


E3

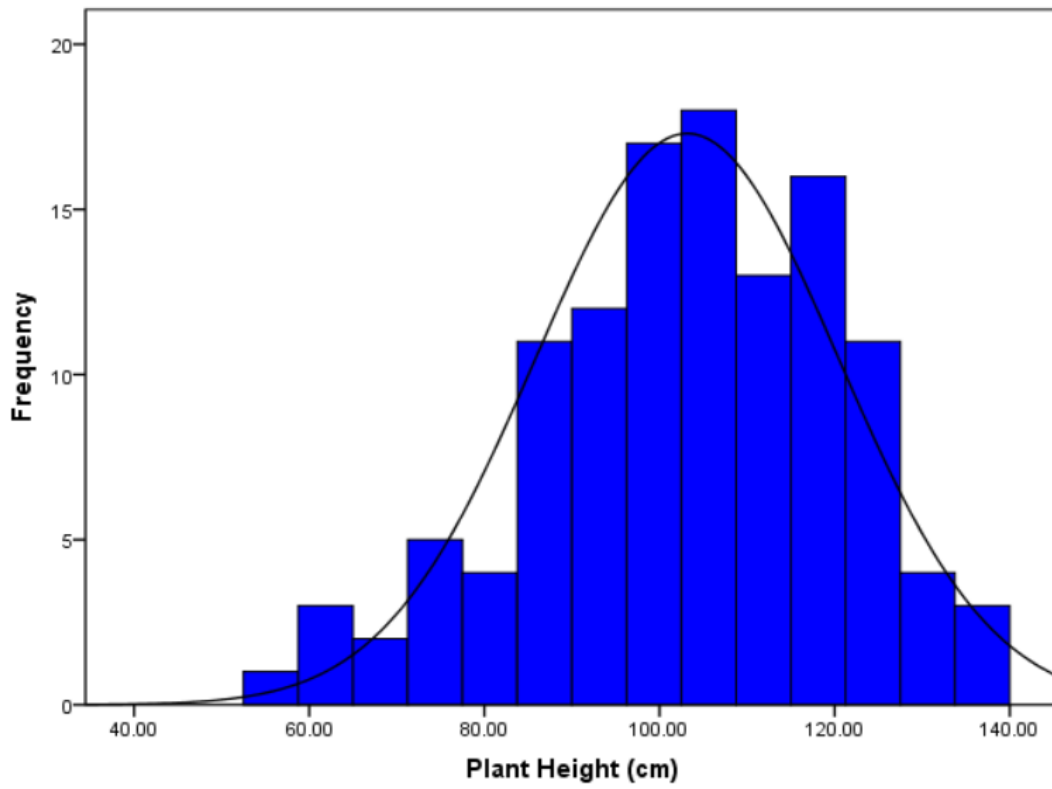


E4

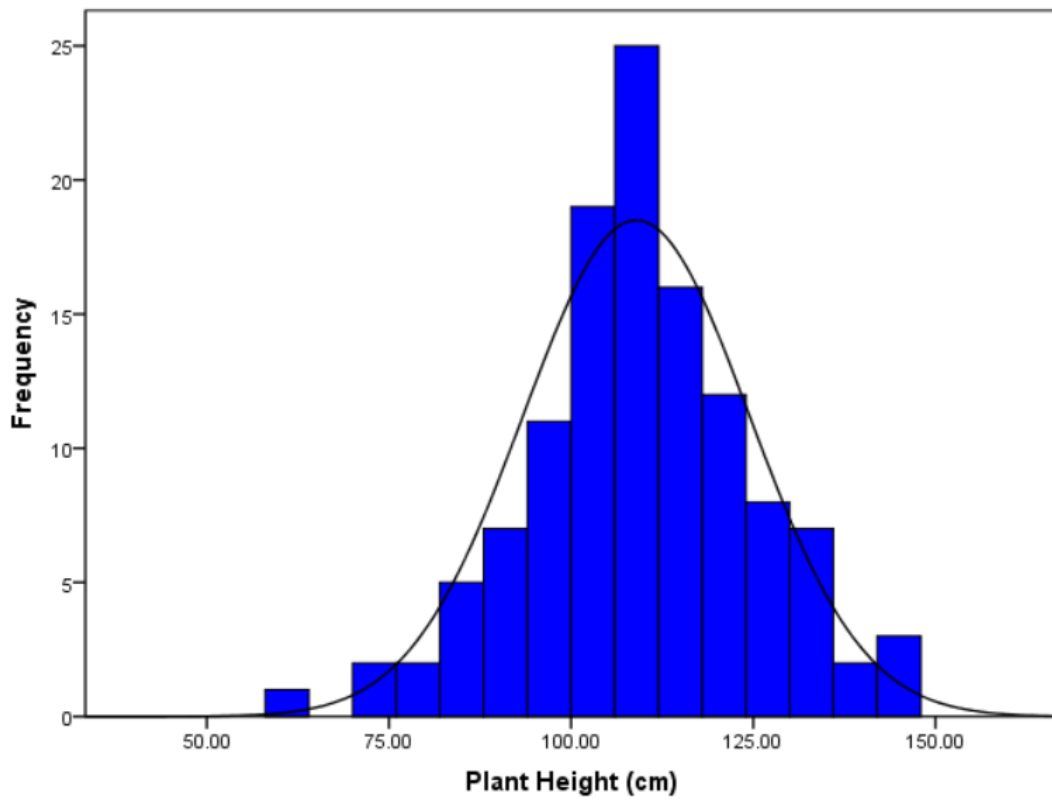


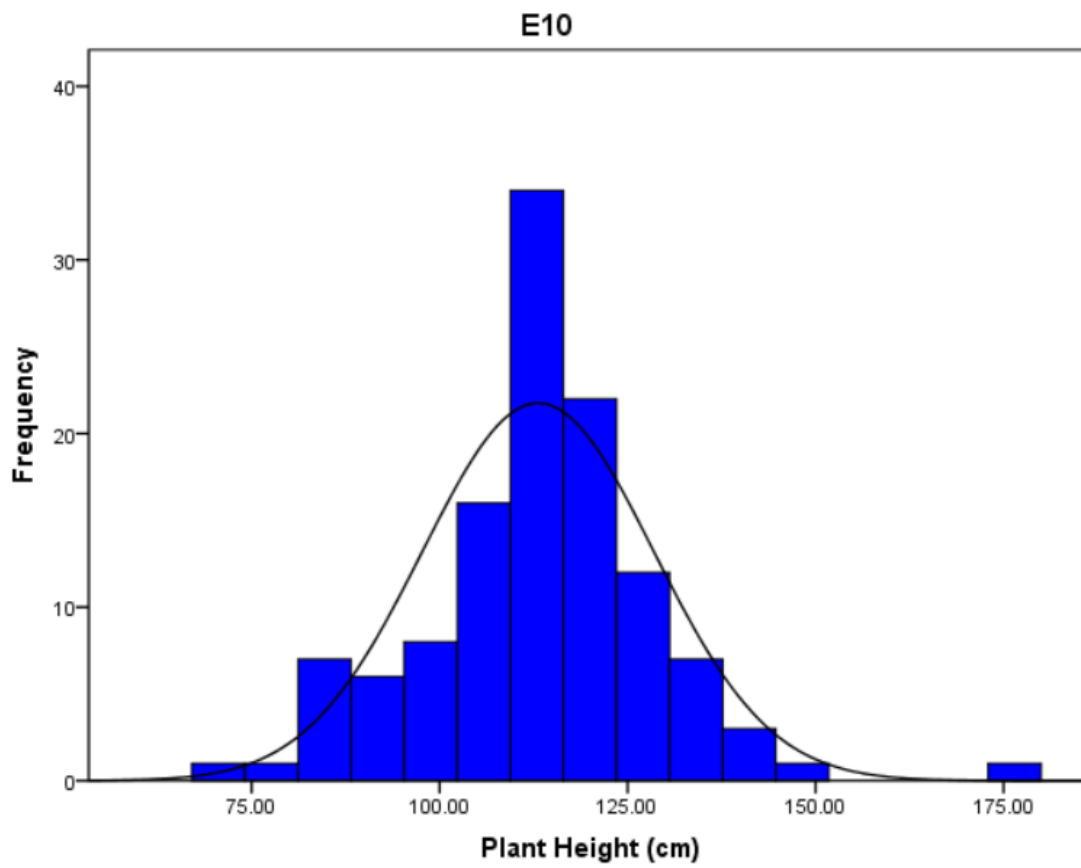
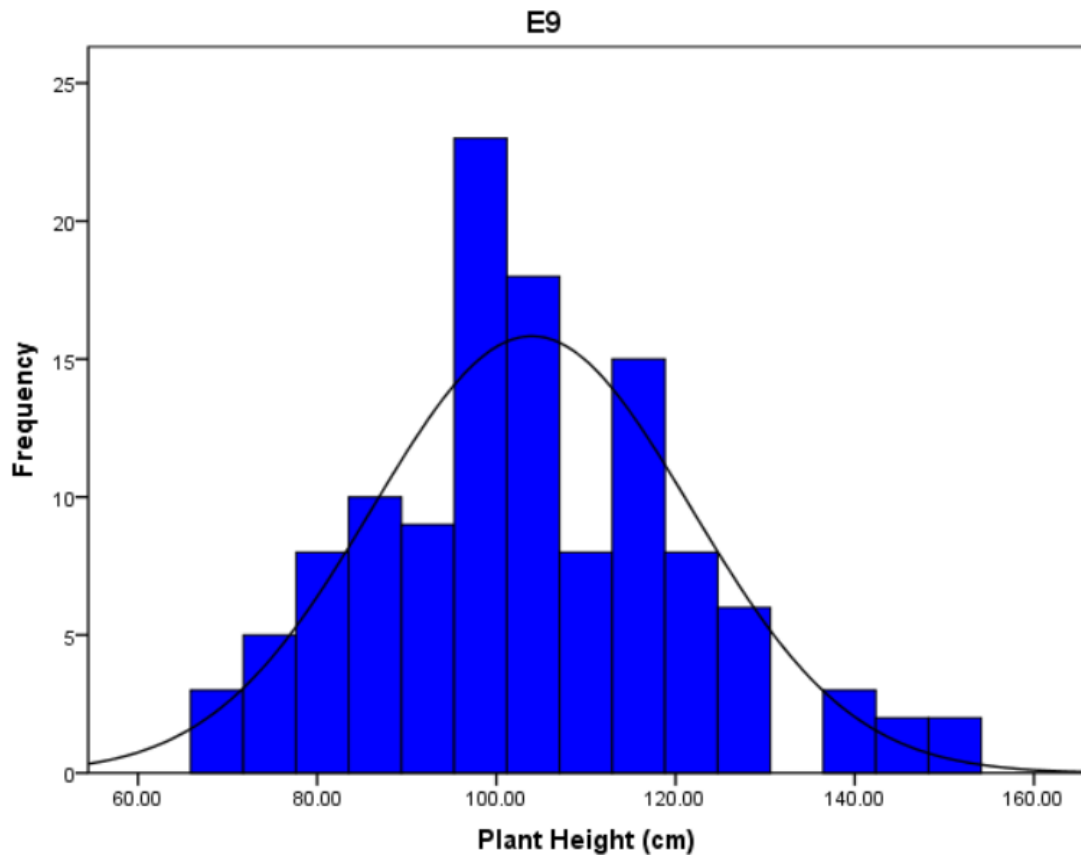


E7

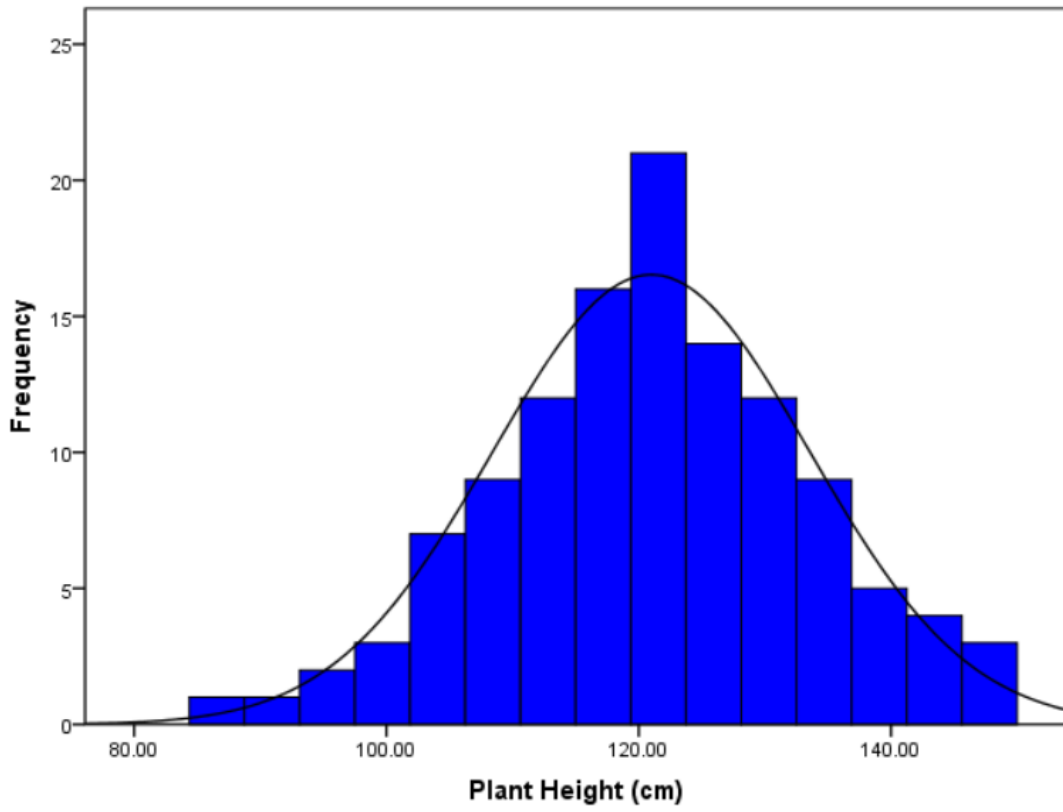


E8

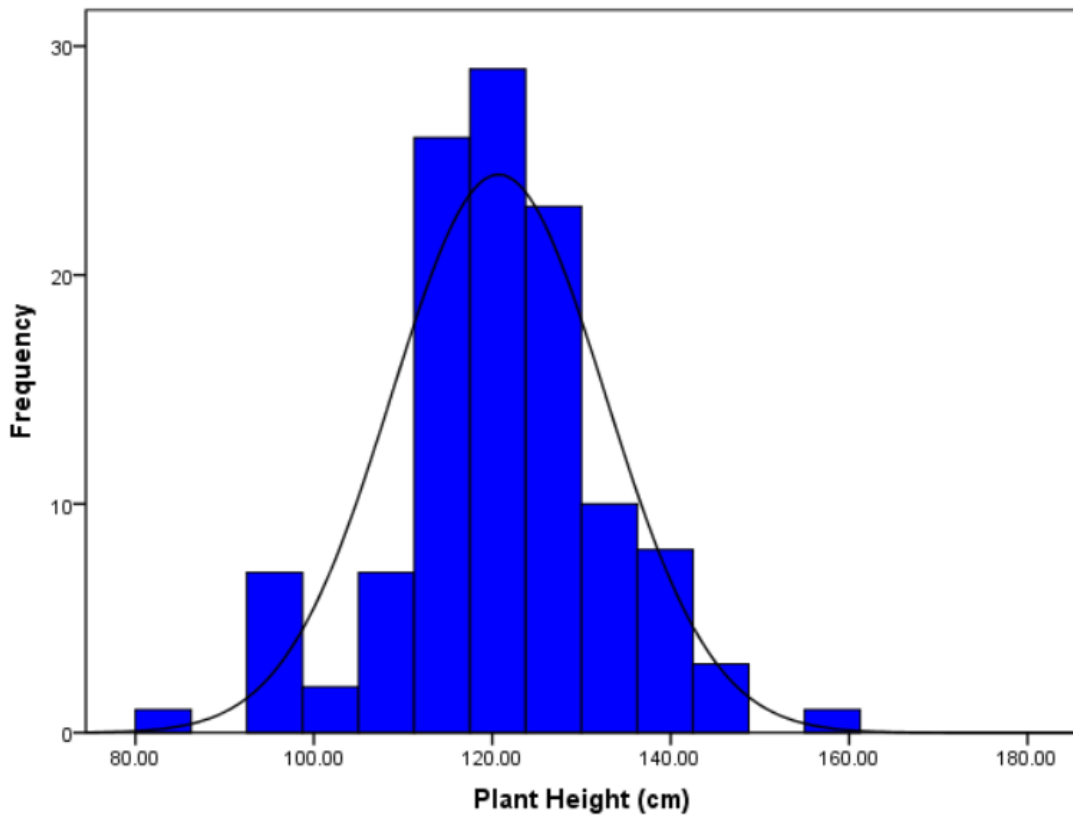




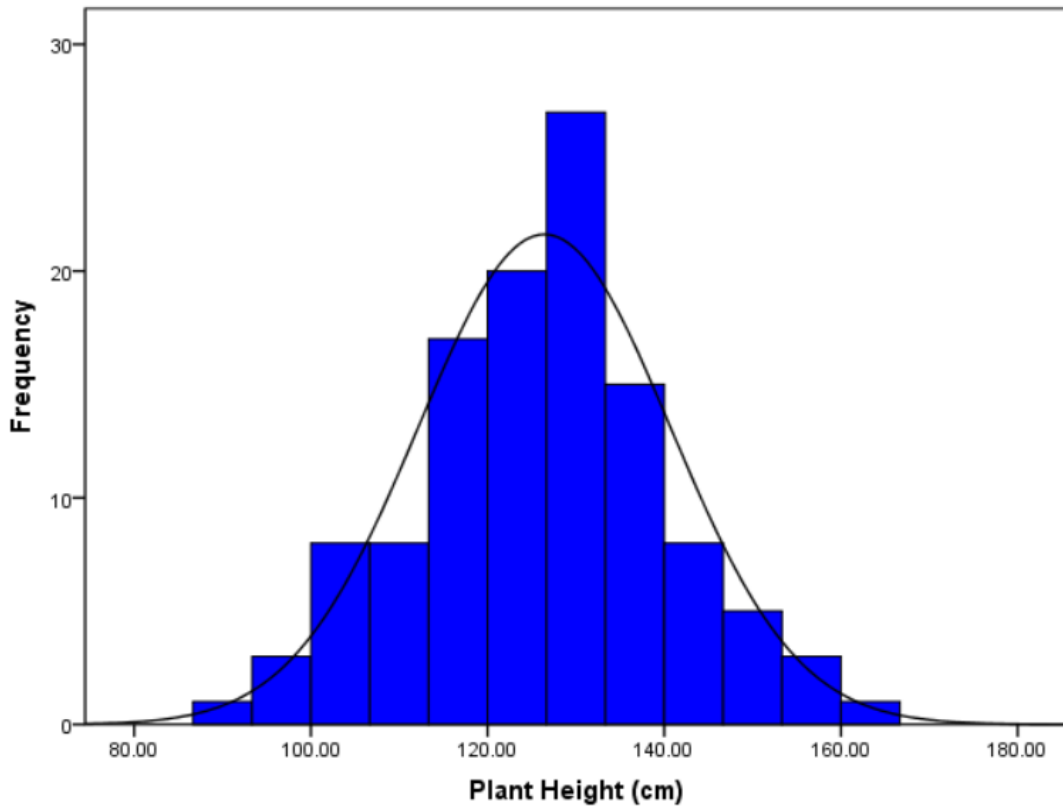
E11



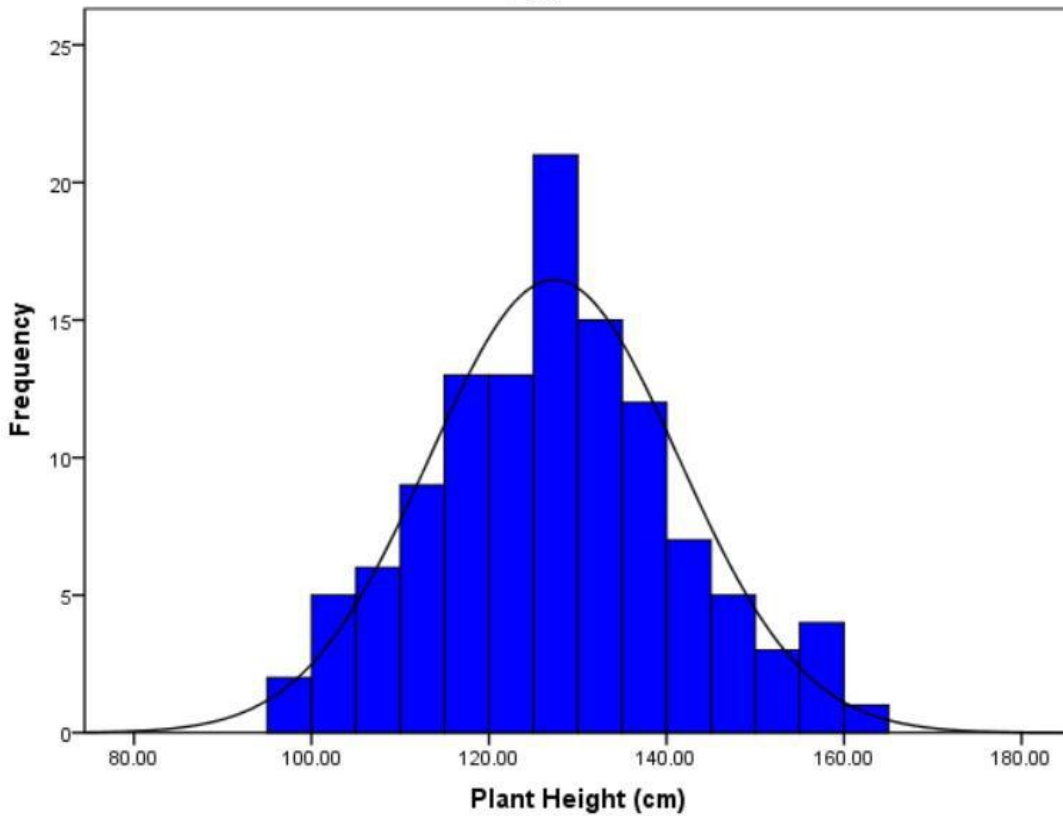
E12



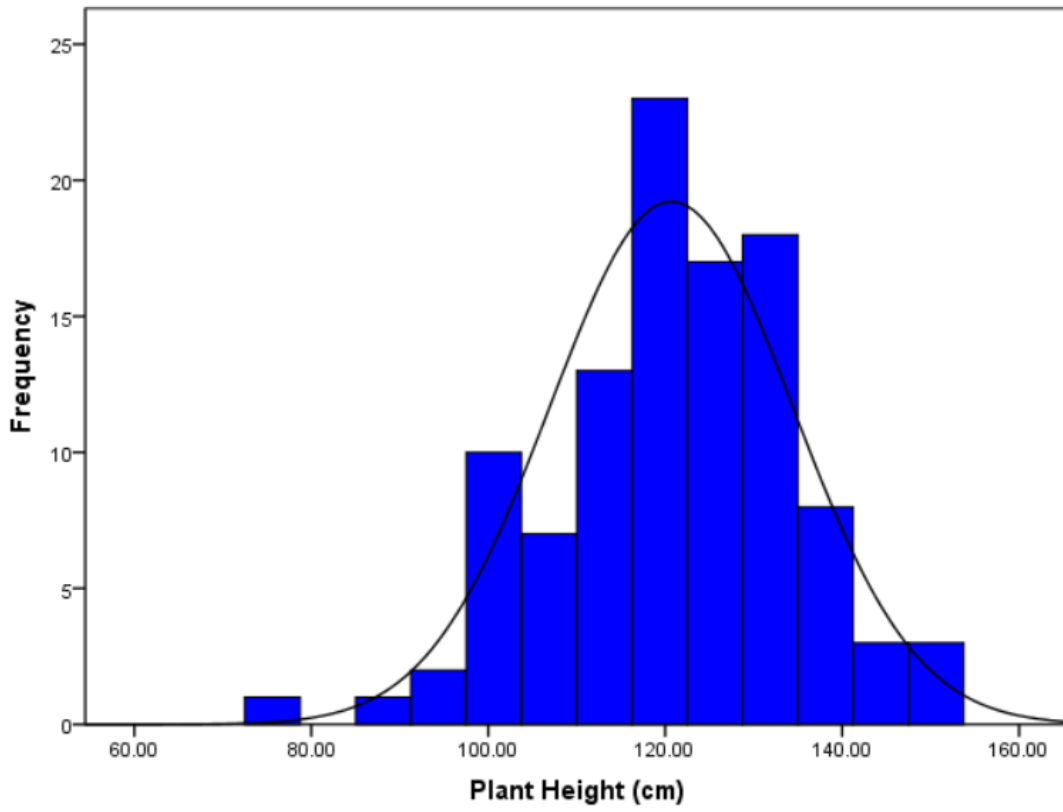
E13



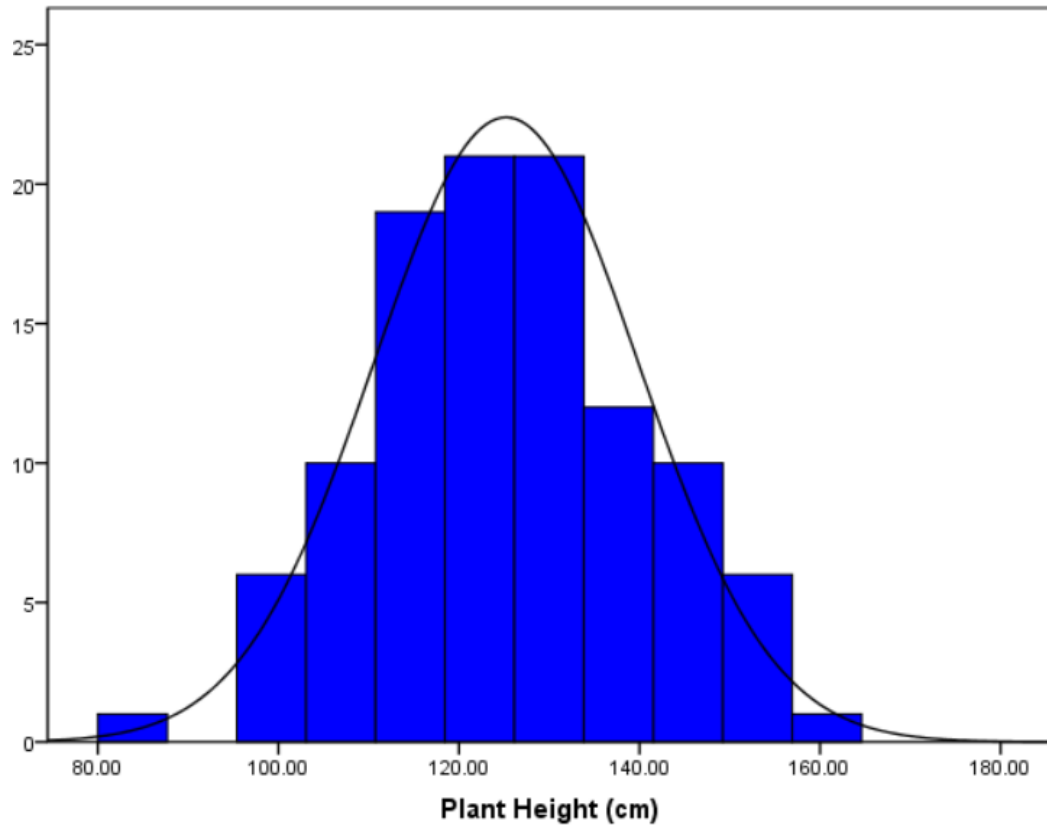
E14



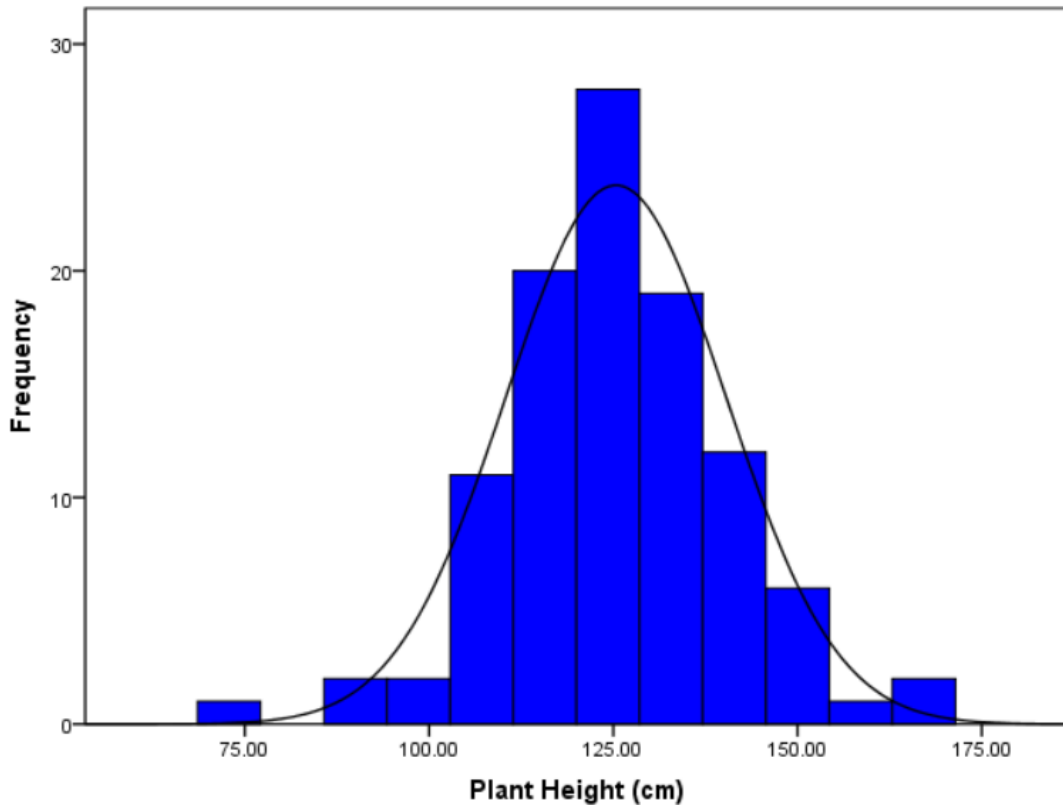
E15



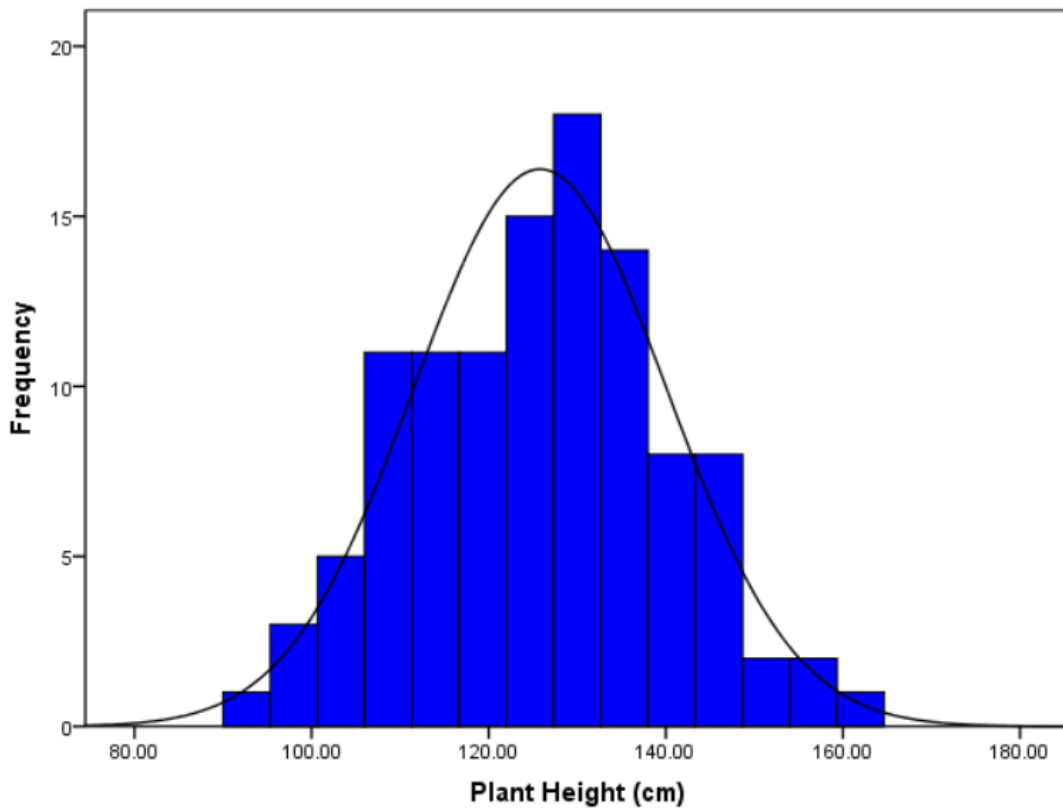
E16

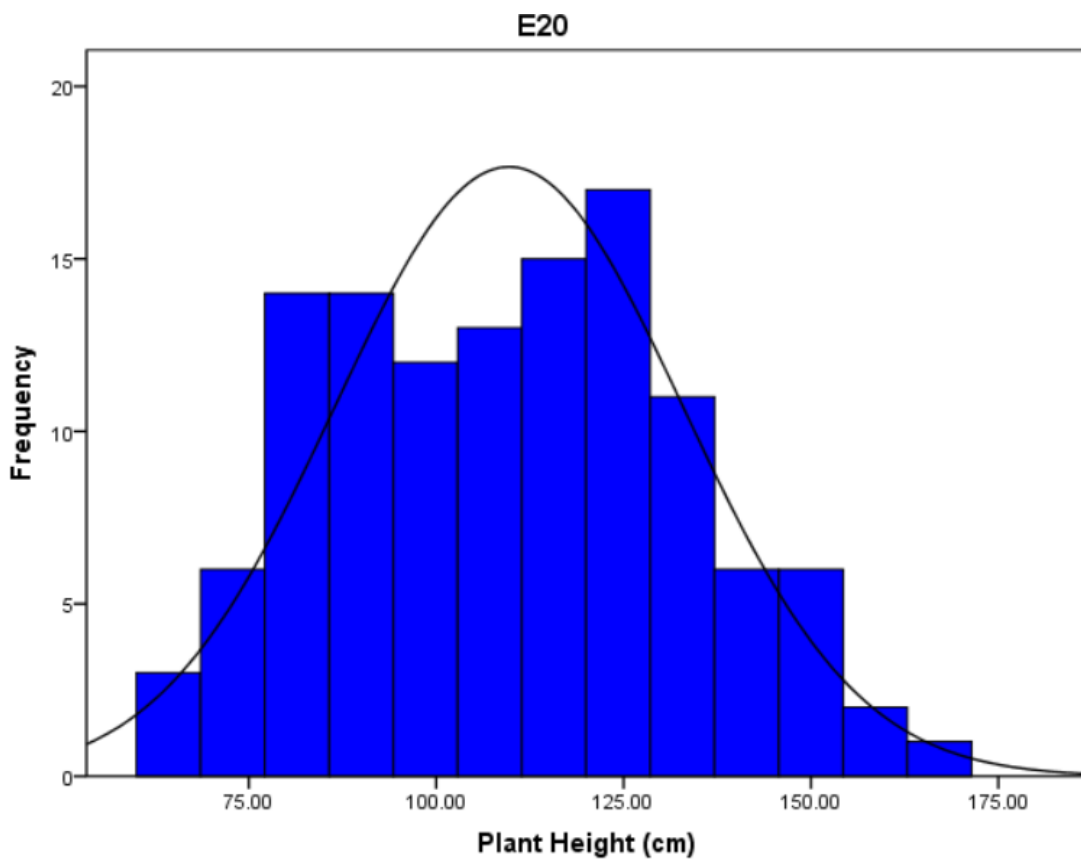
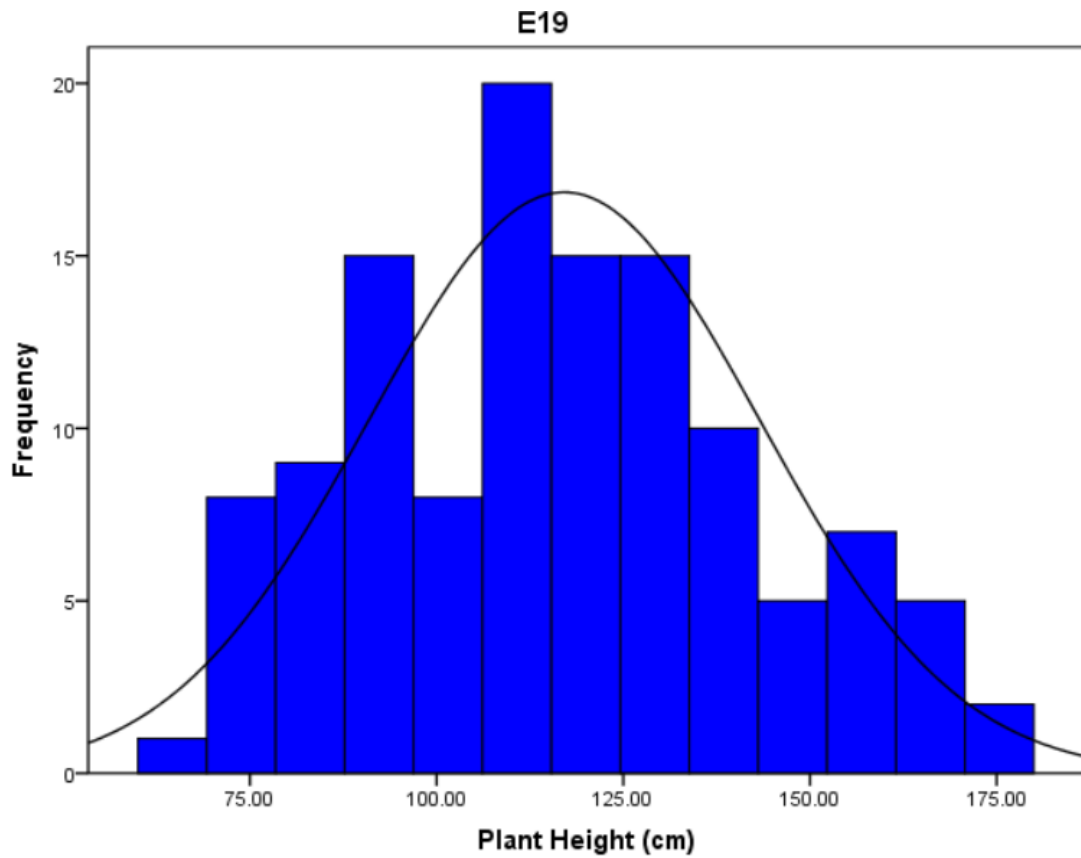


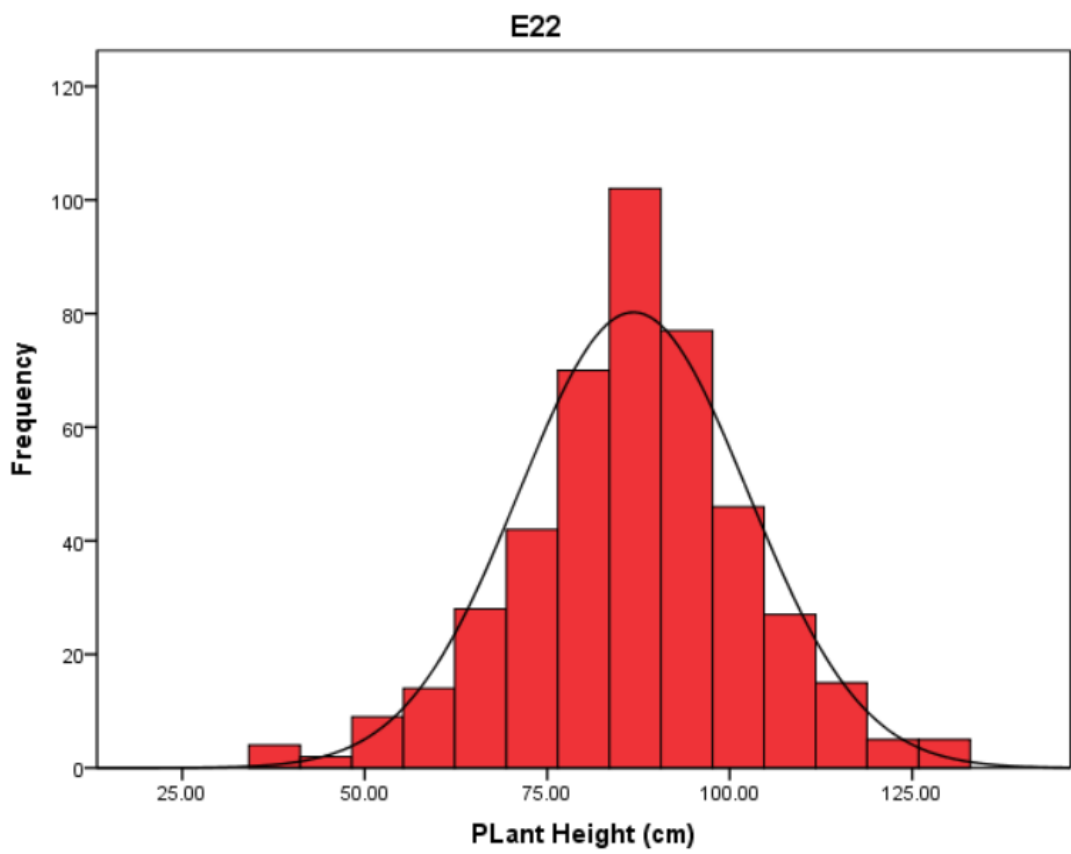
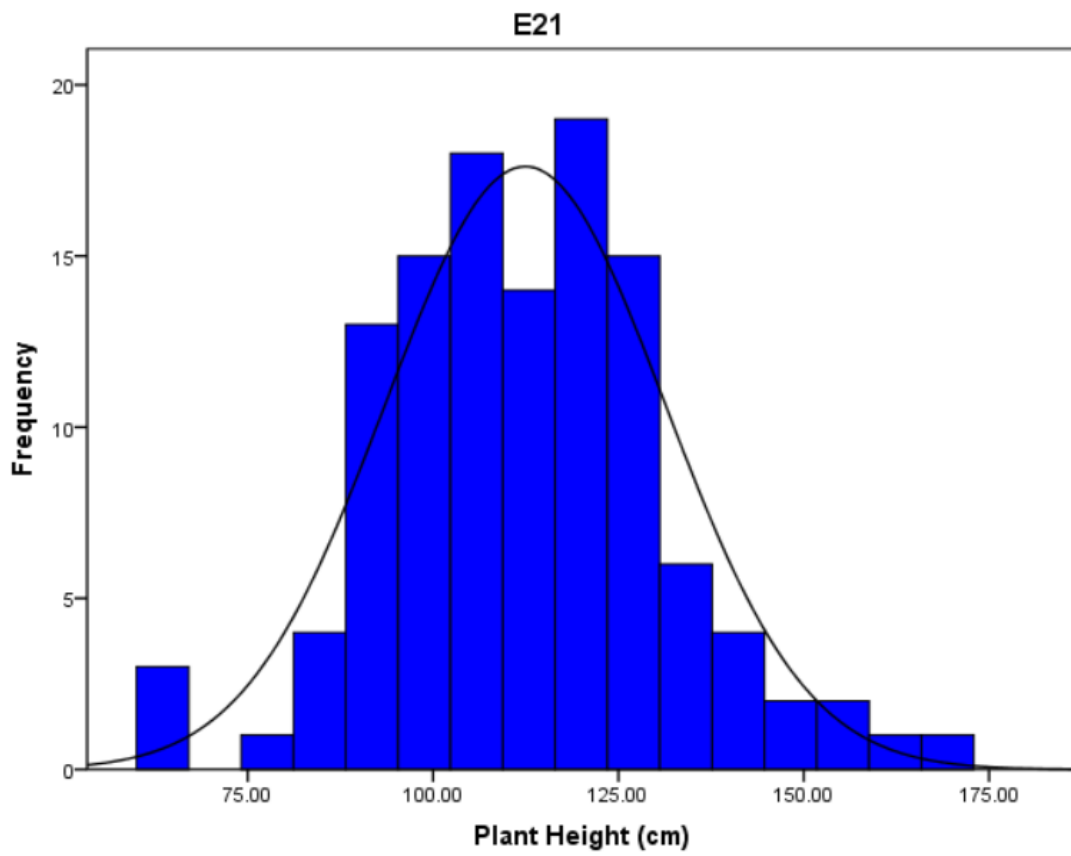
E17

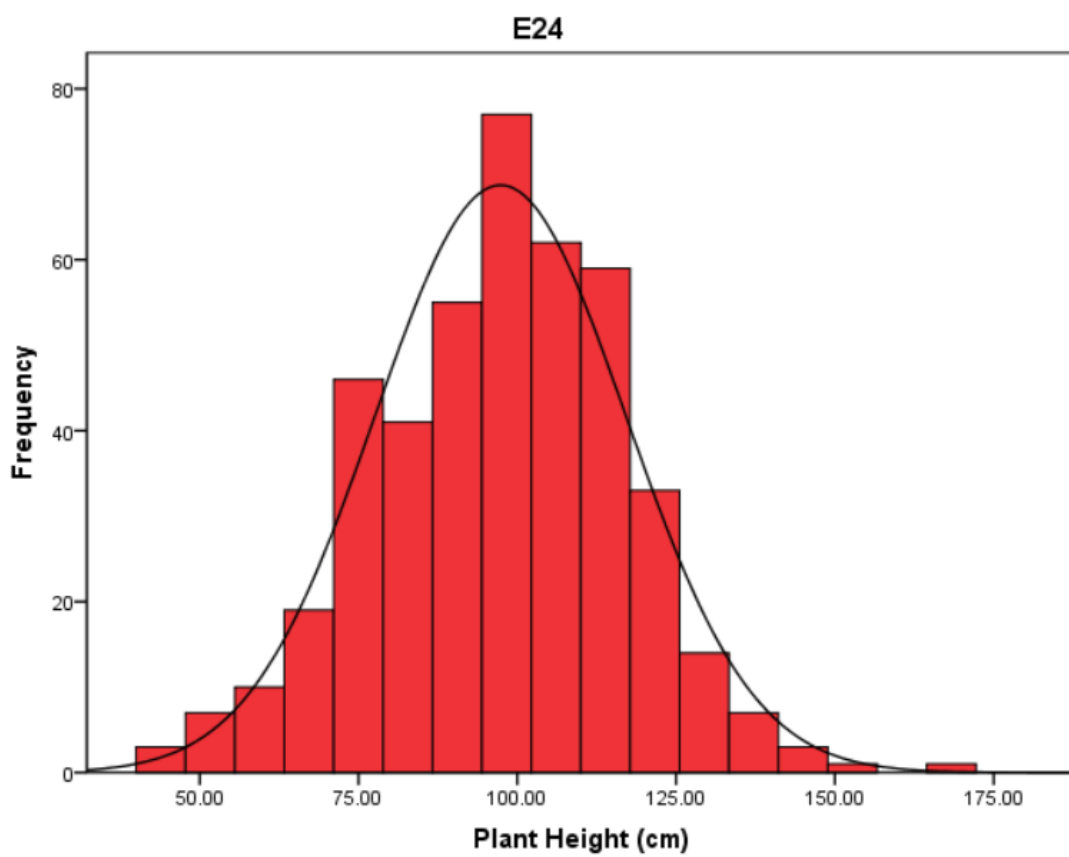
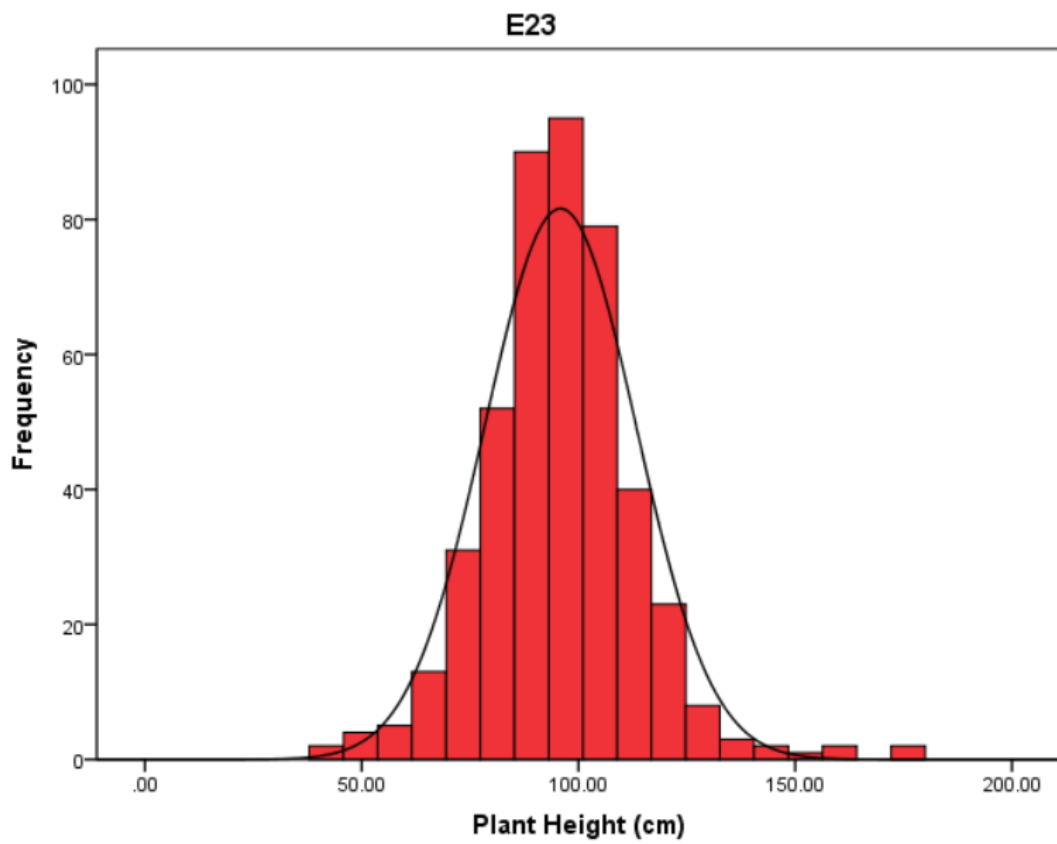


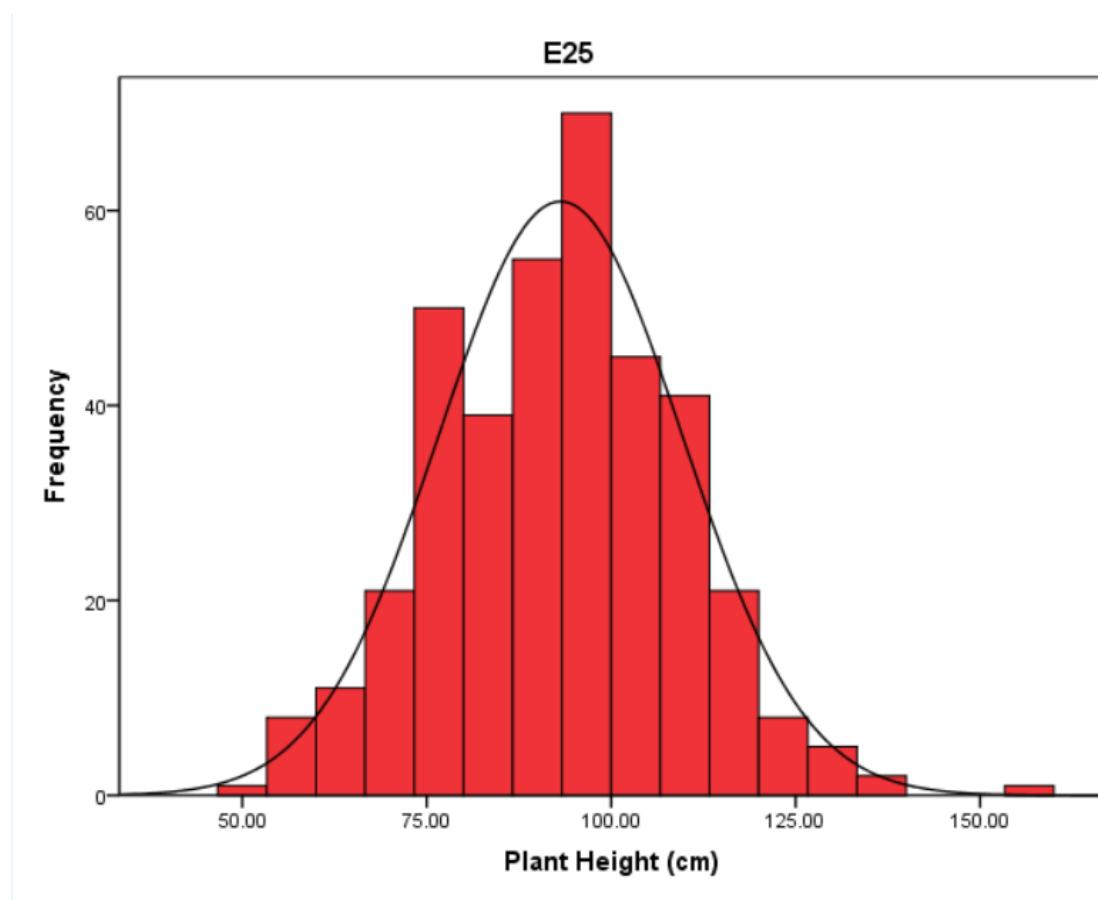
E18





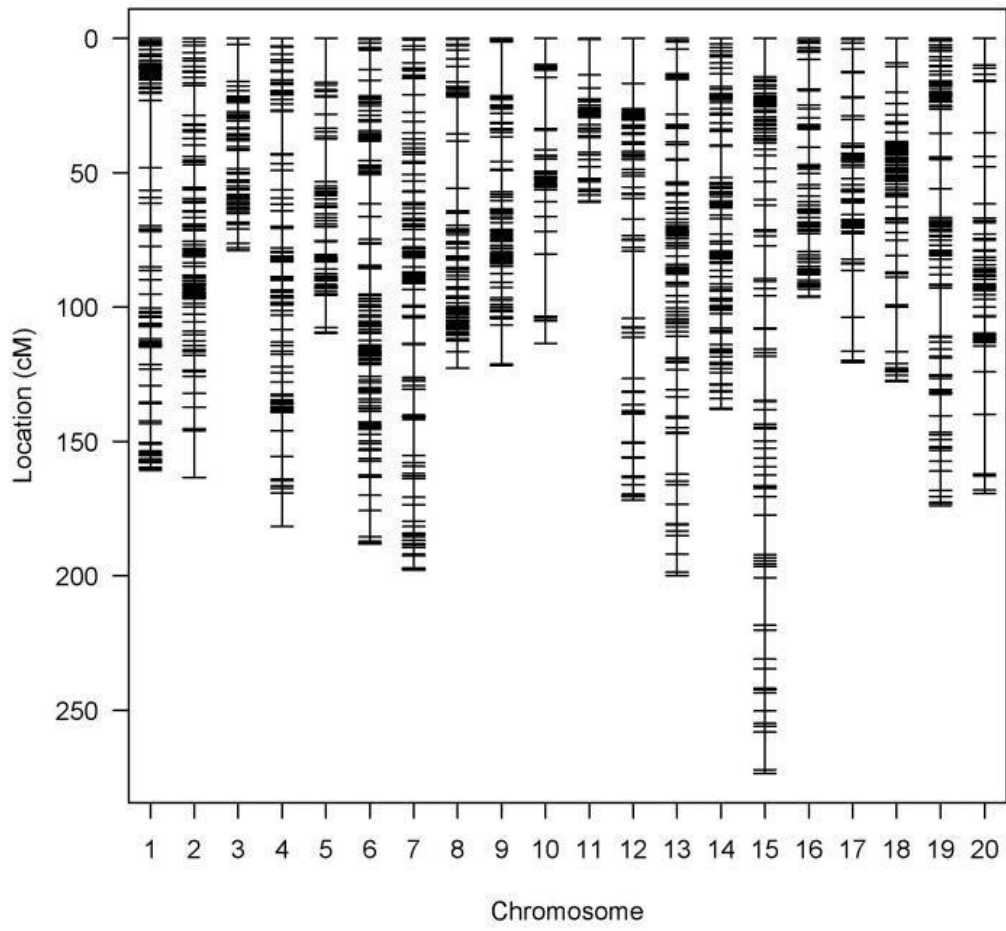




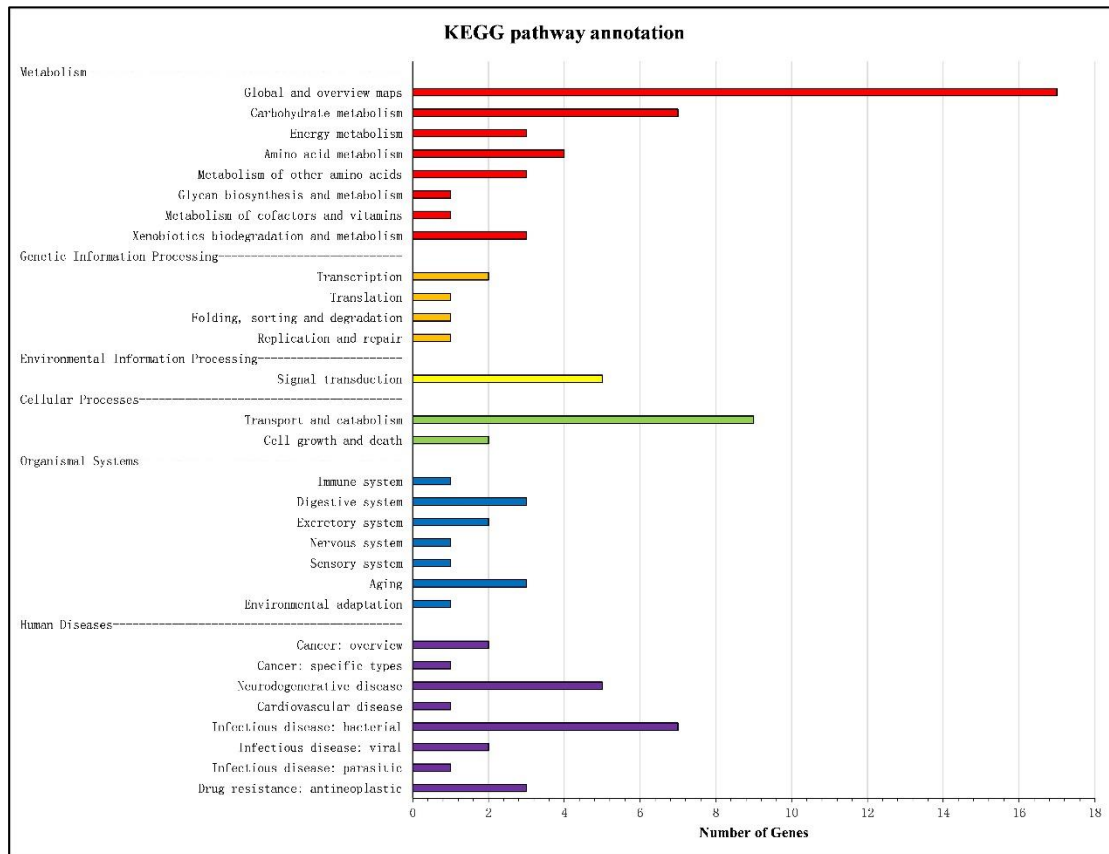


Supplementary Figure S1. Frequency histograms of plant height in RIL 3613 population in 21 environments and in the gremlasm panel in 4 environments.

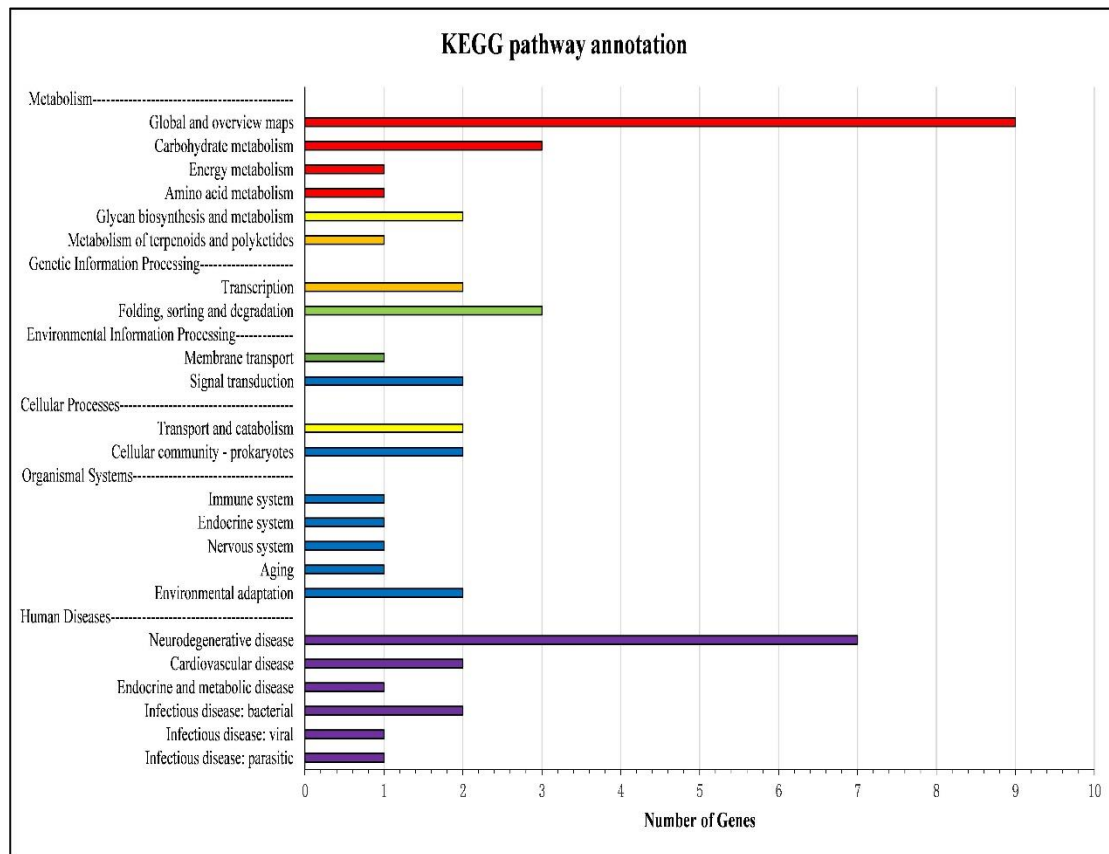
High-density bin map



Supplementary Figure S2. The high-density bin map of RIL3613.



Supplementary Figure S3. KEGG pathway annotation for 140 candidate genes of 6 QTLs.



Supplementary Figure S4. KEGG pathway annotation for 80 candidate genes of 14 QTNs.

Table S1. Summary of planting conditions of 25 environments.

Environment	Location	Group type	Experimental treatment			Sowing date
			Density ($\times 10^5$ plant/hm ²)	Plant space (cm)	N/P ₂ O ₅ /K ₂ O Fertilizer (kg/hm ²)	
E1	Harbin	RIL3613	28	5.4	18/46/30	2015.05.10
E2	Harbin	RIL3613	32	4.8	18/46/30	2015.05.10
E3	Keshan	RIL3613	28	5.4	18/46/30	2013.05.15
E4	Harbin	RIL3613	22	6.8	18/46/30	2014.05.10
E5	Keshan	RIL3613	28	5.4	18/46/30	2015.05.10
E6	Keshan	RIL3613	32	4.8	18/46/30	2015.05.10
E7	Acheng	RIL3613	22	6.8	18/46/30	2016.05.15
E8	Acheng	RIL3613	22	6.8	18/46/30	2016.05.05
E9	Acheng	RIL3613	25	6.0	18/46/30	2016.05.05
E10	Acheng	RIL3613	22	6.8	36/92/60	2016.05.05
E11	Shuangcheng	RIL3613	22	6.8	18/46/30	2016.05.15
E12	Shuangcheng	RIL3613	22	6.8	18/46/30	2016.05.10
E13	Shuangcheng	RIL3613	25	6.0	18/46/30	2016.05.10
E14	Shuangcheng	RIL3613	22	6.8	36/92/60	2016.05.10
E15	Harbin	RIL3613	22	6.8	18/46/30	2016.05.17
E16	Harbin	RIL3613	22	6.8	18/46/30	2016.05.07
E17	Harbin	RIL3613	25	6.0	18/46/30	2016.05.07
E18	Harbin	RIL3613	22	6.8	36/92/60	2016.05.07
E19	Shuangcheng	RIL3613	22	6.8	18/46/30	2017.05.10
E20	Harbin	RIL3613	22	6.8	18/46/30	2018.05.10
E21	Harbin	RIL3613	22	6.8	18/46/30	2019.05.10
E22	Shuangyashan	Germplasm	22	6.8	18/46/30	2018.05.10
E23	Shuangyashan	Germplasm	22	6.8	18/46/30	2019.05.10
E24	Harbin	Germplasm	22	6.8	18/46/30	2018.05.10
E25	Harbin	Germplasm	22	6.8	18/46/30	2019.05.10

Table S2. Primer sequences used for qPCR analysis of eight differentially expressed genes.

Primers name	Sequence
05G066200-Q-F	GGCATGGATTCTCGATGAG
05G066200-Q-R	CCCTGGATGATAAATGTGTGA
06G306300-Q-F	ACTTCCTCGATTCTCTTCTCT
06G306300-Q-R	CTCTTCTCTGCCCTTTCAA
16G143600-Q-F	CGAGAGTGTTCAACCATCT
16G143600-Q-R	CTCAGTAGTGCTAGGAAAGT
18G044400-Q-F	CAGTGGGACCTTTACACTTT
18G044400-Q-R	TCAGACTATCAAGCTCAACAA
18G045100-Q-F	AATTGTGAGAGCTATATGTTAGAG
18G045100-Q-R	CTACTGAGCACCAACAAAT
06G185500-Q-F	CCATTCCATTGCTTTGCTG
06G185500-Q-R	ATATGTTGTGGCAATGTGAG
06G187000-Q-F	TGCATCAGTTTCTCATCCA
06G187000-Q-R	AACGCAAATTACATCAGAGG
06G186400-Q-F	GAACAAATCAAACTCCAGGA
06G186400-Q-R	TGCTGATGGGTGAATGTAA
FBOX-Q-F	TTGTTTATCAGAGTTGCACG
FBOX-Q-R	TCAATCCCATCCAGAATCAA

Table S3. Descriptive statistics for soybean plant height of RIL3613 and germplasm population under different environments.

Parents:P1,female cultivar"Dongnong L13";P2,male cultivar"Heihe36". Range,Difference between maximum and minimum value. Mean±standard deviation of the observed values.

Env.	Parents(cm)		RIL3613 and germplasm						
	P1	P2	Min(cm)	Max(cm)	Range(cm)	Mean±STD(cm)	Skew	Kurt	GCV(%)
E1	-	-	80.00	177.00	97	127.97±17.27	0.31	0.10	13.50
E2	-	-	73.00	166.00	93	115.10±18.44	0.18	-0.29	16.02
E3	-	-	94.00	133.00	39	111.13±9.10	0.46	-0.48	8.19
E4	-	-	75.80	145.00	69.2	115.02±12.84	-0.42	0.45	11.16
E5	83.40	135.40	77.00	149.20	72.2	117.4±14.16	0.11	-0.19	12.06
E6	82.60	135.80	78.00	147.60	69.6	117.00±13.95	-0.03	-0.07	11.93
E7	91.00	86.00	58.50	139.50	81	103.15±17.30	-0.37	-0.20	16.77
E8	93.00	96.33	59.50	143.67	84.17	108.94±15.52	-0.18	0.48	14.25
E9	94.50	106.00	67.00	153.50	86.5	103.95±17.79	0.40	0.32	17.11
E10	109.33	97.50	73.33	175.00	101.67	113.09±15.40	0.22	1.78	13.62
E11	110.00	101.33	88.00	149.67	61.67	120.99±12.56	-0.09	-0.13	10.38
E12	124.67	104.33	82.50	160.00	77.5	120.70±11.96	-0.15	1.15	9.91
E13	116.00	107.33	91.33	163.50	72.17	126.43±14.27	0.04	0.06	11.29
E14	142.00	118.00	95.33	160.67	65.34	127.33±14.06	0.14	-0.17	11.04
E15	120.00	115.00	75.50	150.50	75	120.68±13.75	-0.38	0.32	11.40
E16	122.00	115.00	87.00	160.00	73	125.22±14.66	0.07	-0.40	11.71
E17	120.00	120.50	75.50	166.00	90.5	125.36±14.96	-0.05	1.03	11.93
E18	126.00	110.50	95.00	163.00	68	125.8±14.28	0.01	-0.27	11.35
E19	162.50	85.67	67.33	179.00	111.67	117.10±26.23	0.30	-0.58	22.40
E20	-	-	63.67	164.00	100.33	109.70±23.22	0.09	-0.77	21.17
E21	-	-	66.00	166.67	100.67	112.43±18.86	0.15	0.36	16.78
E22	-	-	37.00	131.00	94	86.82±15.65	-0.19	0.54	18.03
E23	-	-	38.33	176.67	138.34	95.83±17.44	0.48	2.40	18.20
E24	-	-	40.00	168.67	128.67	97.35±19.77	-0.10	0.08	20.31
E25	-	-	47.00	158.00	111	93.13±16.50	0.12	0.22	17.71

Table S4. Detailed information of 39 QTLs identified from linkage analysis.

LOD,logarithm of odds. PVE,phenotypic variation explained by QTL. ADD,contribution of parents to the additive effect.

QTL	Env.	Chr.	Maker Intrerval	LOD	PVE (%)	ADD	Physical Region (Mb)	Method
<i>qPH-3-1</i>	E5	3	36c03078-36c03080	2.71	1.13	-6.40	42.76-43.23	IM
<i>qPH-3-2</i>	E5	3	36c03070-36c03078	2.55	1.11	-6.80	42.08-42.92	IM
<i>qPH-3-3</i>	E12	3	36c03068-36c03077	2.52	7.75	3.87	41.96-42.76	IM
<i>qPH-3-4</i>	E13/E13	3	36c03040-36c03061	3.12/3.22	11.50/11.58	6.55/6.32	33.71-38.61	IM/ICIM
<i>qPH-3-5</i>	E8	3	36c03058-36c03059	2.69	8.47	-4.67	36.79-38.09	ICIM
<i>qPH-4-1</i>	E16/E16	4	36c04095-36c04061	4.03/4.72	6.66/4.39	40.85/39.02	17.49-52.38	IM/ICIM
<i>qPH-5-1</i>	E5/E6	5	36c05022-36c05024	3.80/3.79	1.53/2.59	1.02	6.04-6.51	IM/IM
<i>qPH-5-2</i>	E5/E6/E5/E6	5	36c05023-36c05027	4.90/4.62/5.53/4.62	2.25/3.61/15.59/17.42	0.01	6.20-27.82	IM/IM/ICIM/ICIM
<i>qPH-6-3</i>	E4	6	36c06067-36c06098	2.62	9.12	12.52	13.90-40.48	IM
<i>qPH-6-1</i>	E5	6	36c06014-36c06015	2.68	1.18	-4.63	2.08-3.08	IM
<i>qPH-6-2</i>	E5/E6/E5	6	36c06023-36c06024	4.31/3.12/4.77	1.77/2.19/11.54	-0.22	4.22-4.34	IM/IM/ICIM
<i>qPH-6-5</i>	E5/E6	6	36c06136-36c06141	3.31/2.95	1.99/3.12	1.05	49.81-50.29	IM/IM
<i>qPH-6-4</i>	E5/E6	6	36c06129-36c06130	3.23/3.13	1.32/2.17	1.04	49.30-49.54	IM/IM
<i>qPH-6-6</i>	E16	6	36c06117-36c06128	4.43	4.39	39.02	47.35-49.30	ICIM
<i>qPH-7-1</i>	E5/E6	7	36c07006-36c07021	3.16/3.05	1.31/2.27	1.06	1.70-5.61	IM/IM
<i>qPH-7-3</i>	E4	7	36c07018-36c07020	2.71	7.65	3.94	4.57-5.11	ICIM
<i>qPH-7-2</i>	E5	7	36c07016-36c07017	2.82	6.55	4.08	4.24-4.57	ICIM
<i>qPH-9-1</i>	E5/E6	9	36c09041-36c09045	3.07/3.00	1.25/2.08	1.03	5.96-6.96	IM/IM
<i>qPH-9-2</i>	E5/E6	9	36c09123-36c09138	2.70/2.55	1.16/1.85	1.04	46.39-48.49	IM/IM
<i>qPH-10-1</i>	E5/E6	10	36c10074-36c10075	3.74/3.43	1.52/2.36	1.06	43.35-44.32	IM/IM
<i>qPH-12-1</i>	E5/E6	12	36c12013-36c12078	3.21/2.93	1.32/2.07	1.06	3.44-39.34	IM/IM
<i>qPH-12-2</i>	E5/E6	12	36c12075-36c12080	2.99/2.62	2.62/3.70	1.06	38.95-39.60	IM/IM

<i>qPH-13-2</i>	E13/E13	13	36c13143-36c13146	2.51/2.61	9.36/9.28	4.38/4.20	42.15-42.60	IM/ICIM
<i>qPH-13-1</i>	E16/E16	13	36c13032-36c13076	3.68/4.38	6.65/4.39	40.78/38.99	15.01-28.07	IM/ICIM
<i>qPH-15-2</i>	E5/E6	15	36c15015-36c15092	3.20/3.12	1.31/2.16	1.03	4.38-19.51	IM/IM
<i>qPH-15-1</i>	E6	15	36c15008-36c15013	2.76	2.26	-4.91	2.74-4.30	IM
<i>qPH-15-3</i>	E9	15	36c15147-36c15148	2.53	9.52	-10.31	46.24-46.82	ICIM
<i>qPH-16-2</i>	E8	16	36c16050-36c16052	2.64	8.32	-6.05	26.75-27.01	IM
<i>qPH-16-5</i>	E8/E9/E8	16	36c16064-36c16067	3.04/5.33/3.69	9.08/18.99/11.60	-0.10	30.33-30.91	IM/IM/ICIM
<i>qPH-16-3</i>	E12/E18/E12	16	36c16063-36c16064	3.40/3.71/3.40	10.36/14.45/12.90	-0.16	30.17-30.42	IM/IM/ICIM
<i>qPH-16-1</i>	E14	16	36c16032-36c16087	3.70	13.98	-30.15	9.76-34.46	IM
<i>qPH-16-4</i>	E16/E16	16	36c16063-36c16065	4.41/4.41	5.08/3.67	1.00	30.17-30.71	IM/ICIM
<i>qPH-17-1</i>	E16	17	36c17075-36c17076	2.61	3.12	-5.68	37.51-37.67	IM
<i>qPH-18-1</i>	E1/E1	18	36c18003-36c18004	2.56/2.56	9.55/9.55	1.00	0.42-0.70	IM/ICIM
<i>qPH-18-3</i>	E4/E4	18	36c18021-36c18023	2.90/5.02	5.71/14.90	0.78	5.13-5.37	IM/ICIM
<i>qPH-18-2</i>	E5/E6	18	36c18015-36c18016	3.25/3.13	1.33/2.18	1.04	3.73-4.03	IM/IM
<i>qPH-20-1</i>	E5/E6	20	36c20018-36c20058	2.67/2.55	1.22/2.03	1.04	8.41-40.49	IM/IM
<i>qPH-20-2</i>	E5	20	36c20026-36c20064	2.66	1.30	-6.38	27.71-42.18	IM
<i>qPH-20-3</i>	E19/E19	20	36c20052-36c20053	2.59/2.59	9.50/9.50	1.00	38.39-40.07	IM/ICIM

Table S5. Detailed information of 62 QTNs identified from GWAS.

Env.	Method	QTN name	Chromosome	Marker Position (bp)	QTN effect	LOD score	r ² (%)	Genotype for code 1
E1	pKWmEB	AX-90379562	3	8737078	-3.37	3.98	3.50	CC
E1	ISIS EM-BLASSO	AX-90340071	4	41370162	-2.36	3.98	2.17	GG
E1	pLARmEB	AX-90340537	4	46076527	2.24	3.04	1.41	CC
E1	ISIS EM-BLASSO	AX-90340537	4	46076527	2.66	3.53	1.98	CC
E1	pKWmEB	AX-90345308	4	46149902	-1.79	3.21	2.81	CC
E1	ISIS EM-BLASSO	AX-90394421	4	48094662	-2.74	4.57	2.36	AA
E1	ISIS EM-BLASSO	AX-90484715	5	41589098	-5.79	4.32	3.43	TT
E1	mrMLM	AX-90517857	7	8683811	3.77	10.45	5.47	AA
E1	FASTmrMLM	AX-90517857	7	8683811	2.72	4.42	2.96	AA
E1	pKWmEB	AX-90517857	7	8683811	2.63	3.58	4.39	AA
E1	ISIS EM-BLASSO	AX-90490091	8	16160043	2.30	3.14	1.92	GG
E1	FASTmrEMMA	AX-90406988	9	43611311	-3.95	3.13	1.40	CC
E1	mrMLM	AX-90413941	10	3454273	5.82	4.34	5.11	TT
E1	mrMLM	AX-90408071	12	4688133	-2.73	3.11	2.75	CC
E1	ISIS EM-BLASSO	AX-90422072	12	11591717	-2.90	3.59	1.62	TT
E1	pLARmEB	AX-90464777	13	36427433	3.79	4.53	2.77	TT
E1	pKWmEB	AX-90464777	13	36427433	4.07	5.03	5.33	TT
E1	FASTmrEMMA	AX-90349538	14	4050895	-6.88	6.06	3.96	GG
E1	pLARmEB	AX-90349538	14	4050895	-2.63	3.89	2.35	GG
E1	pKWmEB	AX-90349538	14	4050895	-2.88	4.28	4.22	GG
E1	ISIS EM-BLASSO	AX-90349538	14	4050895	-2.65	3.96	2.37	GG
E1	pKWmEB	AX-90509379	17	41270817	-3.20	3.35	3.74	TT
E2	ISIS EM-BLASSO	AX-90432429	2	49629311	-5.04	3.31	1.55	GG
E2	FASTmrMLM	AX-90348734	3	30282653	-4.22	3.67	1.80	TT
E2	mrMLM	AX-90396409	3	39646963	-5.21	3.44	3.44	GG

E2	FASTmrMLM	AX-90396409	3	39646963	-4.58	4.85	2.79	GG
E2	pLARmEB	AX-90396409	3	39646963	-3.33	3.26	1.23	GG
E2	ISIS EM-BLASSO	AX-90366905	3	39730335	-3.73	5.57	3.12	TT
E2	mrMLM	AX-90501415	3	45475385	-4.27	4.34	3.65	GG
E2	FASTmrMLM	AX-90501415	3	45475385	-4.62	7.28	4.49	GG
E2	pKWmEB	AX-90501415	3	45475385	-3.12	3.36	2.53	GG
E2	ISIS EM-BLASSO	AX-90501415	3	45475385	-5.14	8.77	5.53	GG
E2	pKWmEB	AX-90417410	6	16237961	3.39	5.43	3.50	TT
E2	mrMLM	AX-90512501	6	16287356	4.17	3.76	3.48	CC
E2	FASTmrMLM	AX-90512501	6	16287356	3.42	4.29	2.46	CC
E2	FASTmrMLM	AX-90464100	7	7199711	-3.74	4.98	3.08	AA
E2	mrMLM	AX-90337523	9	4554050	-5.70	3.68	3.80	CC
E2	pLARmEB	AX-90337523	9	4554050	-4.59	4.04	2.16	CC
E2	ISIS EM-BLASSO	AX-90337523	9	4554050	-4.05	3.20	2.00	CC
E2	FASTmrMLM	AX-90326100	9	4594345	2.83	3.77	1.81	TT
E2	pKWmEB	AX-90326100	9	4594345	2.25	3.12	2.32	TT
E2	pLARmEB	AX-90328574	9	37051323	-2.74	3.10	1.12	GG
E2	pKWmEB	AX-90525331	9	42687919	-2.76	4.06	3.52	CC
E2	pKWmEB	AX-90305533	9	45948280	2.33	3.05	2.09	AA
E2	ISIS EM-BLASSO	AX-90369694	9	45972880	-3.08	4.40	2.13	TT
E2	pKWmEB	AX-90358981	12	698006	-6.76	3.74	3.82	GG
E2	pKWmEB	AX-90476230	13	28419527	6.21	6.17	8.65	CC
E2	pKWmEB	AX-90329811	13	30727565	-4.06	3.02	3.46	AA
E2	pLARmEB	AX-90405334	14	13576817	-3.60	3.28	2.46	NN
E2	mrMLM	AX-90427310	15	40106135	-4.64	4.11	3.87	AA
E2	pLARmEB	AX-90446407	15	40806859	3.90	4.70	2.55	TC
E2	mrMLM	AX-90391827	15	43843097	4.86	3.97	4.84	TT
E2	pLARmEB	AX-90391827	15	43843097	3.33	4.20	1.99	TT

E2	pLARmEB	AX-90517408	18	2443523	-5.67	4.04	2.22	TT
E2	pKWmEB	AX-90517408	18	2443523	-4.32	3.51	3.16	TT
E2	FASTmrMLM	AX-90489138	18	57797391	-2.60	3.44	1.52	TC
E3	mrMLM	AX-90467085	2	30172805	-13.21	3.58	13.12	TT
E3	mrMLM	AX-90436869	2	49671843	-11.36	5.57	5.29	AA
E3	pKWmEB	AX-90436869	2	49671843	-6.79	3.50	3.22	AA
E3	ISIS EM-BLASSO	AX-90436869	2	49671843	-6.98	3.46	2.32	AA
E3	pKWmEB	AX-90497688	3	3534464	-4.10	3.89	3.79	GG
E3	ISIS EM-BLASSO	AX-90497688	3	3534464	-5.44	5.54	3.50	GG
E3	mrMLM	AX-90381345	5	27499073	-4.67	3.84	3.17	TT
E3	pLARmEB	AX-90475130	6	16085818	4.63	5.31	3.27	CC
E3	pKWmEB	AX-90475130	6	16085818	3.48	3.22	3.25	CC
E3	pLARmEB	AX-90514879	9	37095768	-4.33	4.08	2.30	CC
E3	pKWmEB	AX-90514879	9	37095768	-3.83	3.97	3.54	CC
E3	ISIS EM-BLASSO	AX-90514879	9	37095768	-3.98	3.76	2.12	CC
E3	pKWmEB	AX-90395513	9	45995160	-3.34	3.04	3.72	CC
E3	ISIS EM-BLASSO	AX-90395513	9	45995160	-3.75	3.39	2.16	CC
E3	mrMLM	AX-90307995	10	39996072	4.91	3.83	3.50	AA
E3	pKWmEB	AX-90307995	10	39996072	2.71	3.36	2.01	AA
E3	pKWmEB	AX-90498700	14	13044908	6.85	3.45	3.40	AA
E3	ISIS EM-BLASSO	AX-90498700	14	13044908	7.87	3.69	2.30	AA
E3	mrMLM	AX-90452177	15	42966910	5.89	4.31	3.08	TT
E3	pKWmEB	AX-90452177	15	42966910	3.22	3.27	2.11	TT
E3	mrMLM	AX-90501849	15	49193510	-5.70	4.11	3.29	GG
E3	FASTmrMLM	AX-90424485	16	18622183	-5.86	4.17	4.44	AA
E3	pKWmEB	AX-90424485	16	18622183	-6.33	5.49	6.62	AA
E3	ISIS EM-BLASSO	AX-90424485	16	18622183	-5.07	3.35	3.32	AA
E3	pLARmEB	AX-90477703	19	38794633	-6.44	3.74	4.22	GG

E4	mrMLM	AX-90510322	1	2325529	-5.16	3.54	5.05	CC
E4	pKWmEB	AX-90510322	1	2325529	-3.74	3.67	5.76	CC
E4	ISIS EM-BLASSO	AX-90510322	1	2325529	-3.29	3.10	2.21	CC
E4	FASTmrMLM	AX-90487494	2	5051558	-2.52	3.22	2.34	TT
E4	mrMLM	AX-90488156	3	37229944	-6.74	4.11	5.06	CC
E4	pLARmEB	AX-90488156	3	37229944	-4.52	3.81	2.46	CC
E4	pKWmEB	AX-90488156	3	37229944	-4.39	3.88	2.47	CC
E4	ISIS EM-BLASSO	AX-90488156	3	37229944	-4.03	3.08	1.95	CC
E4	pKWmEB	AX-90381430	4	40732113	-4.15	3.56	3.38	GG
E4	pLARmEB	AX-90408496	6	3316834	2.21	3.10	1.52	AA
E4	mrMLM	AX-90478413	6	48951836	3.97	3.72	4.16	GG
E4	pLARmEB	AX-90478413	6	48951836	3.08	4.09	2.69	AG
E4	ISIS EM-BLASSO	AX-90478413	6	48951836	2.94	3.99	2.46	AG
E4	mrMLM	AX-90446838	13	146394	-4.82	3.70	4.73	TT
E4	pLARmEB	AX-90446838	13	146394	-3.48	3.82	2.66	TT
E4	pKWmEB	AX-90446838	13	146394	-3.96	4.95	4.90	TT
E4	ISIS EM-BLASSO	AX-90446838	13	146394	-3.88	4.52	3.31	TT
E4	pKWmEB	AX-90472359	13	10844802	3.31	4.76	6.00	GG
E4	pLARmEB	AX-90484138	13	11886622	2.83	3.39	2.30	CC
E4	ISIS EM-BLASSO	AX-90484138	13	11886622	3.02	3.59	2.63	CC
E4	mrMLM	AX-90437138	16	31681528	3.56	3.75	4.32	TT
E4	ISIS EM-BLASSO	AX-90437138	16	31681528	2.20	3.54	1.77	TT
E4	ISIS EM-BLASSO	AX-90309282	18	17190316	2.70	3.33	1.90	TT

Table S6. Detailed information of 46 candidate genes in 6 QTLs genome regions annotated by KEGG database.

Bold font indicates genes that we propose correlate with plant height in soybean.

Gene name	Chromosome	Position	KO number	Annotation
<i>Glyma.05G063500.1</i>	Chr05	6132703..6134032	K09286	EREBP; EREBP-like factor
<i>Glyma.05G063600.1</i>	Chr05	6176576..6178197	K09286	EREBP; EREBP-like factor
<i>Glyma.05G063800.1</i>	Chr05	6195994..6204815	K05609	UCHL3, YUH1; ubiquitin carboxyl-terminal hydrolase L3 [EC:3.4.19.12]
<i>Glyma.05G063900.1</i>	Chr05	6208653..6212478	K05607	AUH; methylglutaconyl-CoA hydratase [EC:4.2.1.18]
<i>Glyma.05G064300.1</i>	Chr05	6280527..6284133	K07874	RAB1A; Ras-related protein Rab-1A
<i>Glyma.05G064500.1</i>	Chr05	6314575..6317826	K13783	SLC37A1_2; MFS transporter, OPA family, solute carrier family 37 (glycerol-3-phosphate transporter), member 1/2
<i>Glyma.05G064700.1</i>	Chr05	6339518..6342630	K21889	TMBIM6, BII, TEGT; Bax inhibitor 1
<i>Glyma.05G065900.1</i>	Chr05	6460756..6468689	K01358	clpP, CLPP; ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
<i>Glyma.05G066200.1</i>	Chr05	6482196..6486368	K00261	GLUD1_2, gdhA; glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
<i>Glyma.06G056200.1</i>	Chr06	4236012..4237969	K02221	yggT; YggT family protein
<i>Glyma.06G056300.1</i>	Chr06	4240910..4249727	K17686	copA, ctpA, ATP7; P-type Cu ⁺ transporter [EC:7.2.2.8]
<i>Glyma.06G056400.1</i>	Chr06	4255938..4263871	K20718	ER; LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]
<i>Glyma.06G056500.1</i>	Chr06	4266559..4287629	K10357	MYO5; myosin V
<i>Glyma.06G056800.1</i>	Chr06	4298002..4301634	K02905	RP-L29e, RPL29; large subunit ribosomal protein L29e
<i>Glyma.06G057000.1</i>	Chr06	4306103..4312215	K19729	GNAT3; guanine nucleotide-binding protein G(t) subunit alpha 3
<i>Glyma.06G057400.1</i>	Chr06	4330457..4331415	K14686	SLC31A1, CTR1; solute carrier family 31 (copper transporter), member 1
<i>Glyma.06G303700.1</i>	Chr06	49315918..49324382	K09338	HD-ZIP; homeobox-leucine zipper protein
<i>Glyma.06G304900.1</i>	Chr06	49394949..49398871	K07976	RAB; Rab family, other
<i>Glyma.06G305000.1</i>	Chr06	49400897..49406873	K05387	GRIP; glutamate receptor, ionotropic, plant
<i>Glyma.06G305700.1</i>	Chr06	49451501..49461369	K01681	ACO, acnA; aconitate hydratase [EC:4.2.1.3]
<i>Glyma.06G305800.1</i>	Chr06	49468768..49475099	K04532	NAE1, APPBP1; NEDD8-activating enzyme E1 regulatory subunit
<i>Glyma.06G305900.1</i>	Chr06	49475669..49484007	K12951	ctpD; cobalt/nickel-transporting P-type ATPase D [EC:7.2.2.-]

<i>Glyma.06G306000.1</i>	Chr06	49495126..49500468	K20855	B3GALT1S; beta-1,3-galactosyltransferase 1/2/3/4/5/7/8 [EC:2.4.1.-]
<i>Glyma.06G306300.1</i>	Chr06	49529272..49531512	K08341	GABARAP, ATG8, LC3; GABA(A) receptor-associated protein
<i>Glyma.06G309800.1</i>	Chr06	49817964..49819907	K03132	TAF7; transcription initiation factor TFIID subunit 7
<i>Glyma.06G310200.1</i>	Chr06	49870537..49873394	K13280	SEC11, sipW; signal peptidase I [EC:3.4.21.89]
<i>Glyma.06G310400.1</i>	Chr06	49880338..49884322	K11271	DSCC1, DCC1; sister chromatid cohesion protein DCC1
<i>Glyma.06G310500.1</i>	Chr06	49885349..49910175	K10742	DNA2; DNA replication ATP-dependent helicase Dna2 [EC:3.6.4.12]
<i>Glyma.06G311000.1</i>	Chr06	49960875..49965249	K13457	RPM1, RPS3; disease resistance protein RPM1
<i>Glyma.06G311100.1</i>	Chr06	49969809..49984031	K13457	RPM1, RPS3; disease resistance protein RPM1
<i>Glyma.06G311200.1</i>	Chr06	49978178..49982087	K13457	RPM1, RPS3; disease resistance protein RPM1
<i>Glyma.06G311400.1</i>	Chr06	49984980..49989498	K21752	DRAP1, NC2-alpha; Dr1-associated corepressor
<i>Glyma.06G312200.1</i>	Chr06	50060597..50070632	K11292	SUPT6H, SPT6; transcription elongation factor SPT6
<i>Glyma.06G312800.1</i>	Chr06	50130854..50136972	K18466	VPS26; vacuolar protein sorting-associated protein 26
<i>Glyma.06G312900.1</i>	Chr06	50144641..50149944	K09422	MYBP; transcription factor MYB, plant
<i>Glyma.06G313200.1</i>	Chr06	50178962..50180179	K13154	ZCRB1; U11/U12 small nuclear ribonucleoprotein 31 kDa protein
<i>Glyma.16G143600.1</i>	Chr16	30379885..30382483	K02716	psbO; photosystem II oxygen-evolving enhancer protein 1
<i>Glyma.18G043700.1</i>	Chr18	3734876..3739321	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
<i>Glyma.18G044400.1</i>	Chr18	3836270..3837813	K00963	UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
<i>Glyma.18G044900.1</i>	Chr18	3881382..3884162	K23618	AAE11_12; acyl-activating enzyme 11/12 [EC:6.2.1.2 6.2.1.-]
<i>Glyma.18G045000.1</i>	Chr18	3889384..3895138	K07889	RAB5C; Ras-related protein Rab-5C
<i>Glyma.18G045100.1</i>	Chr18	3897921..3904561	K17839	PAO4, PAO3, PAO2; polyamine oxidase [EC:1.5.3.17 1.5.3.-]
<i>Glyma.18G045400.1</i>	Chr18	3935899..3937220	K18172	CMC2; COX assembly mitochondrial protein 2
<i>Glyma.18G045800.1</i>	Chr18	3960056..3964823	K12864	CTNBL1; beta-catenin-like protein 1
<i>Glyma.18G045900.1</i>	Chr18	3971126..3974924	K18881	DJ1D; D-lactate dehydratase [EC:4.2.1.130]
<i>Glyma.18G046000.1</i>	Chr18	3971126..3974924	K18881	DJ1D; D-lactate dehydratase [EC:4.2.1.130]

Table S7. Detailed information of 37 candidate genes in 14 QTNs genome regions annotated by KEGG database.

Bold font indicates genes that we propose correlate with plant height in soybean.

Gene name	Chromosome	Position	KO number	Annotation
<i>Glyma.03G156700.1</i>	Chr03	37189825..37198694	K17471	SULTR3; sulfate transporter 3
<i>Glyma.03G156800.1</i>	Chr03	37217752..37225871	K08857	NEK1_4_5; NIMA (never in mitosis gene a)-related kinase 1/4/5 [EC:2.7.11.1]
<i>Glyma.03G157300.1</i>	Chr03	37267895..37271586	K09419	HSFF; heat shock transcription factor, other eukaryote
<i>Glyma.04G163900.1</i>	Chr04	40730419..40731291	K16297	SCPL-II; serine carboxypeptidase-like clade II [EC:3.4.16.-]
<i>Glyma.04G165500.1</i>	Chr04	41393620..41396114	K03263	EIF5A; translation initiation factor 5A
<i>Glyma.04G189600.1</i>	Chr04	46047721..46051704	K08287	E2.7.12.1; dual-specificity kinase [EC:2.7.12.1]
<i>Glyma.04G189900.1</i>	Chr04	46066906..46071217	K16280	RGLG; E3 ubiquitin-protein ligase RGLG [EC:2.3.2.27]
<i>Glyma.04G190100.1</i>	Chr04	46083382..46086444	K11294	NCL, NSR1; nucleolin
<i>Glyma.04G190200.1</i>	Chr04	46086785..46089618	K00573	E2.1.1.77, pcm; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]
<i>Glyma.04G190500.1</i>	Chr04	46131920..46135591	K01076	ABHD17; abhydrolase domain-containing protein 17 [EC:3.1.2.22]
<i>Glyma.04G190700.1</i>	Chr04	46143583..46146881	K16292	CEP, CYSEP; KDEL-tailed cysteine endopeptidase [EC:3.4.22.-]
<i>Glyma.04G190800.1</i>	Chr04	46145464..46147709	K07304	msrA; peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]
<i>Glyma.04G191100.1</i>	Chr04	46174420..46176838	K01728	pel; pectate lyase [EC:4.2.2.2]
<i>Glyma.04G208600.1</i>	Chr04	48101018..48102540	K11097	SNRPE, SME; small nuclear ribonucleoprotein E
<i>Glyma.04G209000.1</i>	Chr04	48117080..48122942	K05546	GANAB; mannosyl-oligosaccharide alpha-1,3-glucosidase [EC:3.2.1.207]
<i>Glyma.04G190100.1</i>	Chr04	48117080..48122942	K11294	NCL, NSR1; nucleolin
<i>Glyma.06G185000.1</i>	Chr06	16072529..16076159	K09377	CSRP; cysteine and glycine-rich protein
<i>Glyma.06G185500.1</i>	Chr06	16114111..16119696	K05954	FNTB; protein farnesyltransferase subunit beta [EC:2.5.1.58]
<i>Glyma.06G185600.1</i>	Chr06	16120283..16123534	K03946	NDUFA2; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 2
<i>Glyma.06G186100.1</i>	Chr06	16201252..16204650	K01205	NAGLU; alpha-N-acetylglucosaminidase [EC:3.2.1.50]
<i>Glyma.06G186300.1</i>	Chr06	16211217..16217224	K00130	betB, gbsA; betaine-aldehyde dehydrogenase [EC:1.2.1.8]
<i>Glyma.06G186400.1</i>	Chr06	16225061..16230826	K00966	GMPP; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
<i>Glyma.06G186800.1</i>	Chr06	16242993..16252777	K09391	E2F7_8; transcription factor E2F7/8
<i>Glyma.06G187000.1</i>	Chr06	16265397..16267777	K14492	ARR-A; two-component response regulator ARR-A family
<i>Glyma.06G187200.1</i>	Chr06	16286588..16290289	K18875	EDS1; enhanced disease susceptibility 1 protein
<i>Glyma.06G187300.1</i>	Chr06	16309938..16313286	K18875	EDS1; enhanced disease susceptibility 1 protein
<i>Glyma.12G063400.1</i>	Chr12	4648141..4651679	K10355	ACTF; actin, other eukaryote
<i>Glyma.12G064000.1</i>	Chr12	4707197..4709987	K03283	HSPA1s; heat shock 70kDa protein 1/2/6/8
<i>Glyma.12G064100.1</i>	Chr12	4713945..4723793	K03217	yidC, spoIIIJ, OXA1, ccfA; YidC/Oxa1 family membrane protein insertase

<i>Glyma.12G115800.1</i>	Chr12	11598507..11605137	K20098	ERCC6L2; DNA excision repair protein ERCC-6-like 2 [EC:3.6.4.-]
<i>Glyma.12G116000.1</i>	Chr12	11609351..11616101	K17560	URII; unconventional prefoldin RPB5 interactor 1
<i>Glyma.12G116100.1</i>	Chr12	11628133..11638543	K23788	TUL1, FLY1_2; transmembrane E3 ubiquitin-protein ligase [EC:2.3.2.27]
<i>Glyma.16G096600.1</i>	Chr16	18621149..18647713	K20715	PHOT; phototropin [EC:2.7.11.1]
<i>Glyma.16G156600.1</i>	Chr16	31673196..31676637	K22145	TMEM18; transmembrane protein 18
<i>Glyma.16G156800.1</i>	Chr16	31700335..31703734	K15378	SLC45A1_2_4; solute carrier family 45, member 1/2/4
<i>Glyma.16G156900.1</i>	Chr16	31709625..31711896	K15378	SLC45A1_2_4; solute carrier family 45, member 1/2/4
<i>Glyma.16G157000.1</i>	Chr16	31722232..31724487	K15378	SLC45A1_2_4; solute carrier family 45, member 1/2/4

Table S8. Comparison of QTL detected in multiple environments with those in previous studies.

QTL	Env.	Chr.	Maker Interval	QTL of Previous Studies	Reference
<i>qPH-5-1</i>	E5/E6	5	36c05022-36c05024	Plant height 26-5	(Sun <i>et al.</i> 2006)
<i>qPH-5-2</i>	E5/E6	5	36c05023-36c05027	Plant height 26-2/Plant height 17-2	(Kabelka <i>et al.</i> 2004; Sun <i>et al.</i> 2006)
<i>qPH-6-2</i>	E5/E6	6	36c06023-36c06024	Plant height 25-4	(Guzman <i>et al.</i> 2007)
<i>qPH-6-5</i>	E5/E6	6	36c06136-36c06141	Plant height 27-1	(Josie <i>et al.</i> 2007)
<i>qPH-6-4</i>	E5/E6	6	36c06129-36c06130	Plant height 20-3	(Gai <i>et al.</i> 2007)
<i>qPH-7-1</i>	E5/E6	7	36c07006-36c07021	Plant height 2-4/Plant height 8-2/Plant height 13-9	(Mansur <i>et al.</i> 1993; Orf <i>et al.</i> 1999; Specht <i>et al.</i> 2001)
<i>qPH-9-1</i>	E5/E6	9	36c09041-36c09045	mqPlant height-009/Plant height 17-4/Plant height 18-1	(Kabelka <i>et al.</i> 2004; Wang <i>et al.</i> 2004; Pathan <i>et al.</i> 2013)
<i>qPH-9-2</i>	E5/E6	9	36c09123-36c09138	Plant height 30-3/Plant height 35-3	(Palomeque <i>et al.</i> 2009; Rossi <i>et al.</i> 2013)
<i>qPH-10-1</i>	E5/E6	10	36c10074-36c10075	Plant height 19-2/Plant height 11-1	(Mian <i>et al.</i> 1998; Wang <i>et al.</i> 2004)
<i>qPH-12-1</i>	E5/E6	12	36c12013-36c12078	Plant height 4-1/Plant height 13-4/Plant height 36-1	(Lee <i>et al.</i> 1996; Specht <i>et al.</i> 2001; Eskandari <i>et al.</i> 2013)
<i>qPH-12-2</i>	E5/E6	12	36c12075-36c12080	Plant height 4-1	(Lee <i>et al.</i> 1996)
<i>qPH-15-2</i>	E5/E6	15	36c15015-36c15092	Plant height 26-10/Plant height 29-4	(Sun <i>et al.</i> 2006; Liu <i>et al.</i> 2011)
<i>qPH-16-5</i>	E8/E9	16	36c16064-36c16067		
<i>qPH-16-3</i>	E12/E18	16	36c16063-36c16064		
<i>qPH-18-2</i>	E5/E6	18	36c18015-36c18016	mqPlant height-007	(Pathan <i>et al.</i> 2013)
<i>qPH-20-1</i>	E5/E6	20	36c20018-36c20058	Plant height 25-2/Plant height 12-1/Plant height 16-1	(Sebolt <i>et al.</i> 2000; Chapman <i>et al.</i> 2003; Guzman <i>et al.</i> 2007)