

## Supplementary materials

**Table S1** Analysis of variance (ANOVA) of plant height in MT and ZM populations over three environments.

Population	Source	DF <sup>a</sup>	MS <sup>b</sup>	F <sup>c</sup>
MT	Genotype	288	2858.19	12.97**
	Environment	2	101597.76	461.15**
	Block within Environment	6	6579.24	29.86**
	Genotype × environment	573	360.94	1.64**
	Error	1651	220.31	
	ZM	Genotype	125	2118.32
Environment		2	44416.89	279.66**
Block within Environment		6	2009.65	12.65**
Genotype × environment		250	346.91	2.18**
Error		741	158.82	

\*\*  $P < 0.01$

<sup>a</sup> Degrees of freedom

<sup>b</sup> Mean square

<sup>c</sup> F value is used to determine significance

**Table S2 The candidate genes related with soybean plant height in stable QTL intervals**

<b>QTL</b>	<b>Gene name<sup>a</sup></b>	<b>Function annotation</b>
<i>qPH-6</i>	<i>Glyma06g40700</i> 、 <i>Glyma06g40730</i> 、 <i>Glyma06g40750</i> 、 <i>Glyma06g40810</i>	response to auxin stimulus
	<i>Glyma06g40800</i>	glycolysis
	<i>Glyma06g40860</i>	auxin homeostasis, response to auxin stimulus, auxin mediated signaling pathway
	<i>Glyma06g41520</i>	gibberellin biosynthetic process, gibberellic acid mediated signaling pathway
	<i>Glyma06g41530</i>	cell differentiation
	<i>Glyma06g41600</i>	cytokinesis by cell plate formation
	<i>Glyma06g41072</i>	auxin polar transport
	<i>qPH-17</i>	<i>Glyma17g37090</i>
<i>Glyma17g37120</i>		response to auxin stimulus, response to ethylene stimulus, positive regulation of auxin metabolic process
<i>Glyma17g37370</i>		positive regulation of auxin metabolic process, regulation of meristem growth, auxin polar transport, multidimensional cell growth
<i>Glyma17g37650</i>		tissue development
<i>Glyma17g37760</i>		cell tip growth, response to gibberellin stimulus
<i>Glyma17g37810</i>		response to ethylene stimulus
<i>Glyma17g38000</i>		regulation of unidimensional cell growth
<i>Glyma17g38150</i>		gibberellic acid mediated signaling pathway
<i>Glyma17g38210</i>		cell proliferation

<sup>a</sup>The gene were annotated in Wm82.a1 reference genome.

**Table S3 Summary genetic maps in ZM and MT populations**

Population	Chromosome	Bin numbers	Genetic distance of bin (cM)	
			Mean	Total
ZM	Gm01	117	1.05	122.1
	Gm02	144	1.11	158.7
	Gm03	117	0.82	94.8
	Gm04	120	1.07	127.1
	Gm05	109	0.92	99.3
	Gm06	158	1.06	166.6
	Gm07	135	0.93	124.1
	Gm08	185	1.02	187.3
	Gm09	131	0.98	128
	Gm10	137	0.98	133.3
	Gm11	123	1.17	143.2
	Gm12	83	1.26	103.3
	Gm13	158	1.14	178.5
	Gm14	106	1.11	116
	Gm15	126	0.98	123.1
	Gm16	113	1.04	116.4
	Gm17	119	1.15	135.9
	Gm18	165	0.79	130.4
	Gm19	114	1.18	133.9
	Gm20	140	0.78	108.4
	<b>Total</b>	<b>2600</b>	<b>1.01</b>	<b>2630.2</b>
MT	Gm01	157	0.63	102.4
	Gm02	174	0.84	148.5
	Gm03	200	0.55	109.8
	Gm04	171	0.7	119.1
	Gm05	152	0.74	112
	Gm06	223	0.54	123
	Gm07	200	0.63	125.7
	Gm08	224	0.78	174.6
	Gm09	195	0.6	119.1
	Gm10	159	0.87	137.8
	Gm11	154	0.91	145.8
	Gm12	134	0.74	102.3
	Gm13	225	0.59	140.9
	Gm14	168	0.65	112.7
	Gm15	173	0.59	101.7
	Gm16	167	0.57	96.4
	Gm17	153	0.77	116.5
	Gm18	226	0.49	114.7
	Gm19	183	0.65	140.4
	Gm20	160	0.66	108.2
	<b>Total</b>	<b>3598</b>	<b>0.68</b>	<b>2451.7</b>

