

Table S5 Candidate gene annotations of two major QTL *qPH-b_13* and *qPH-b_19-1* for plant height.

QTL	Gene ID (v2)	Expression pattern							large-effect SNPs and InDels					Arabidopsis ortholog	Descriptions
		Flower	Leaves	Shoot Apical Meristem	Stem	Pod	Root	Seed	Position	Type	ZP	ZH	Amino acid change		
<i>qPH-b_13</i>	Glyma.13G288100	0.00	0.00	0.00	0.00	0.68	0.13	11460.60	-	-	-	-	-	NA	NA
	Glyma.13G288200	10.39	9.31	8.41	11.14	11.95	11.62	16.96	-	-	-	-	-	AT4G27120.2	DDRKGK domain protein
	Glyma.13G288300	29.12	0.00	0.00	0.07	0.00	0.00	0.00	-	-	-	-	-	AT3G20580.1	COBRA-like protein 10 precursor
	Glyma.13G288400	7.44	11.1 , 1	9.17	15.36	16.44	30.52	13.23	-	-	-	-	-	AT4G27100.2	Ypt/Rab-GAP domain of gyp1p superfamily protein
	Glyma.13G288500	0.13	1.27	0.58	0.72	0.99	0.61	1.63	-	-	-	-	-	AT3G20570.1	Early nodulin-like protein 9
	Glyma.13G288600	0.06	0.04	0.12	0.43	0.26	0.13	0.19	-	-	-	-	-	AT4G27080.1	Protein disulfide isomerase
	Glyma.13G288700	0.02	0.04	0.03	0.20	0.05	0.19	0.15	-	-	-	-	-	AT5G54790.1	CTD small phosphatase-like protein

Glyma.13G288800	0.01	0.01	0.00	0.01	0.08	0.00	0.04	-	-	-	-	-	AT4G04890.1	Protodermal factor 2
Glyma.13G288900	0.00	0.00	0.24	0.00	0.00	0.00	0.00	-	-	-	-	-	AT1G29320.1	Transducin/WD40 repeat-like superfamily protein
Glyma.13G289000	0.02	0.00	0.16	0.86	0.20	0.00	2.07	-	-	-	-	-	AT5G54010.1	UDP-Glycosyltransferase superfamily protein
Glyma.13G289100	0.32	3.64	1.24	0.13	1.57	0.74	15.99	-	-	-	-	-	AT5G54010.1	UDP-Glycosyltransferase superfamily protein
Glyma.13G289200	0.00	0.00	0.01	0.00	0.01	35.97	1.20	-	-	-	-	-	AT5G54010.1	UDP-Glycosyltransferase superfamily protein
Glyma.13G289300	17.69	15.76	19.34	24.18	14.25	23.49	11.46	-	-	-	-	-	AT1G06400.1	Ras-related small GTP-binding family protein
Glyma.13G289400	11.66	11.76	1.05	4.42	1.52	94.40	0.94	-	-	-	-	-	AT3G58710.2	WRKY DNA-binding protein

Glyma.13G289500	0.10	0.11	0.62	0.95	0.09	2.03	0.15	-	-	-	-	-	AT2G42760.1	g protein 69 DUF1685 family protein DNAJ heat shock
Glyma.13G289600	97.40	89.32	4.88	9.97	9.04	4.24	18.40	-	-	-	-	-	AT2G42750.1	N-terminal domain-conta ining protein Ethylene responsive element binding factor 3 GSK3/SHAG
Glyma.13G289700	5.31	1.47	1.11	1.22	0.93	1.37	1.88	-	-	-	-	-	AT1G50640.1	GY-like protein kinase 1 Protein kinase superfamily protein Protein of unknown function (DUF1637)
Glyma.13G289800	3.89	2.83	11.81	9.08	12.88	2.63	26.88	-	-	-	-	-	AT1G06390.2	
Glyma.13G289900	3.34	1.50	14.03	4.12	6.39	4.05	26.71	-	-	-	-	-	AT3G58690.1	
Glyma.13G290000	7.10	5.00	3.55	8.26	8.17	5.88	4.12	-	-	-	-	-	AT2G42670.1	

Glyma.13G290100	0.00	0.00	0.00	0.03	0.00	3.92	0.06	-	-	-	-	-	AT2G38300.1	Myb-like HTH transcriptional regulator family protein
Glyma.13G290200	0.02	0.00	0.00	0.00	0.02	1.68	0.00	-	-	-	-	-	NA	NA Protein of unknown function
Glyma.13G290300	0.15	0.06	0.07	0.00	0.02	0.23	0.08	-	-	-	-	-	AT2G30990.2	(DUF688) Mitogen activated protein kinase kinase kinase-related
Glyma.13G290400	12.64	9.41	12.07	15.73	16.95	19.15	12.92	-	-	-	-	-	AT3G58640.2	Sequence-spe cific DNA binding transcription factors
Glyma.13G290500	2.10	2.67	1.44	2.12	1.90	1.78	1.58	-	-	-	-	-	AT3G58630.1	Protein of unknown function
Glyma.13G290600	1.68	0.28	9.49	72.21	3.93	1.00	1.01	-	-	-	-	-	AT2G42610.2	(DUF640)

Glyma.13G290700	3.27	11.29	10.43	5.07	3.88	0.62	0.78	-	-	-	-	-	AT2G42600.1	Phosphoenol pyruvate carboxylase 2
Glyma.13G290800	0.00	0.04	0.00	0.08	0.00	7.64	0.00	-	-	-	-	-	AT1G06330.1	Heavy metal transport/deto xification superfamily protein
Glyma.13G290900	104.60	99.18	103.26	185.47	123.21	206.19	130.86	-	-	-	-	-	AT2G42590.2	General regulatory factor 9
Glyma.13G291000	7.49	8.91	1.57	1.83	2.87	3.05	3.73	-	-	-	-	-	AT4G21470.1	Riboflavin kinase/FMN hydrolase
Glyma.13G291100	0.00	0.00	0.00	0.00	0.04	0.00	0.00	-	-	-	-	-	AT5G46230.1	Protein of unknown function(DU F538)
Glyma.13G291200	0.48	0.31	2.14	1.15	2.62	5.71	1.84	-	-	-	-	-	AT2G42580.1	Tetratricopeti de -repeat thioredoxin-li ke 3
Glyma.13G291300	25.93	60.41	62.27	54.58	62.46	36.74	190.42	-	-	-	-	-	AT3G58610.3	Ketol-acid reductoisome rase

Glyma.13G291400	6.67	1.05	2.30	1.78	2.03	18.66	1.83	-	-	-	-	-	AT1G68810.1	Basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Glyma.13G291500	7.03	6.89	8.23	13.45	14.86	15.31	8.57	-	-	-	-	-	AT3G58600.1	Adaptin ear-binding coat-associated protein 1
Glyma.13G291600	4.96	6.63	5.19	3.06	5.42	1.20	3.21	-	-	-	-	-	AT2G31130.1	Unknown protein
Glyma.13G291700	31.09	20.85	3.87	11.97	15.47	30.39	0.45	39187726	Missense	GG	CC	S261T	AT2G42570.1	Trichome birefringence-like39
Glyma.13G291800	0.54	0.01	0.01	0.00	0.00	0.46	21.39	-	-	-	-	-	AT2G42560.1	Late embryogenesis is abundant domain-containing protein
Glyma.13G291900	0.02	0.01	0.00	0.03	0.01	72.42	0.00	-	-	-	-	-	AT4G18540.1	Transmembrane protein
Glyma.13G292000	8.21	4.78	4.85	8.21	3.85	2.76	7.52	-	-	-	-	-	AT2G31090.1	Transmembrane protein
Glyma.13G292100	0.48	0.05	0.56	0.10	0.27	0.39	0.22	-	-	-	-	-	AT1G06240.1	Protein of unknown

														function
														DUF455
														Global
Glyma.13G292200	10.22	9.65	8.36	6.27	6.01	4.76	5.52	39210964	Missense	CC	TT	T63A	AT1G06230.3	transcription factor group
														E4
Glyma.13G292300	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	-	-	-	-	NA	NA
Glyma.13G292400	0.00	0.00	0.00	0.00	0.00	0.23	0.00	-	-	-	-	-	NA	NA
														TCP family
Glyma.13G292500	4.45	12.97	5.84	1.67	18.00	5.62	6.06	39248752	Missense	AA	GG	H343R	AT3G15030.3	transcription factor
														E3
Glyma.13G292600	1.03	1.14	4.76	0.68	0.67	5.99	0.00	39257706	Missense	GG	AA	T40A	AT2G42360.1	ubiquitin-protein ligase
								39257883	Missense	GG	AA	T99A		
								39258272	Missense	CC	GG	R228S		
														Plasmodesmata
Glyma.13G292700	1.16	6.65	4.85	2.18	2.18	1.94	2.39	-	-	-	-	-	AT3G58100.1	callose-binding protein 5
														Basic-leucine zipper (bZIP)
Glyma.13G292800	8.47	0.63	4.64	0.45	0.19	15.29	0.08	-	-	-	-	-	AT3G58120.1	transcription factor family
														protein
Glyma.13G292900	0.00	0.00	0.00	0.00	0.00	0.00	0.04	39289998	Missense	TT	GG	K175N	AT1G06260.1	Cysteine

qPH-b_19-1	Glyma.13G293000	0.11	0.35	0.97	1.47	1.21	0.23	0.52	39290887	Missense	AA	TT	D253E	AT1G06270.1	proteinases superfamily protein Pentatricopep tide repeat (PPR) superfamily protein
									39291113	Missense	TT	AA	L193F		
									39291549	Missense	CC	AA	S75A		
									39291636	Stop-gain	GG	AA	R - *		
	Glyma.13G293100	0.40	0.73	4.46	29.75	4.40	2.67	0.26	-	-	-	-	-	AT1G75840.1	RAC-like GTP binding protein 5
	Glyma.13G293200	1.11	2.85	4.00	19.61	13.23	27.32	0.90	-	-	-	-	-	AT5G60860.1	RAB GTPase homolog
	Glyma.13G293300	0.16	1.95	0.32	2.04	1.06	3.52	0.11	-	-	-	-	-	NA	A1F NA
	Glyma.13G293400	7.45	15.46	6.80	18.30	7.74	17.83	6.84	-	-	-	-	-	AT3G54680.1	Proteophosph oglycan-relat ed protein
	Glyma.19G194000	11.66	0.20	0.83	1.04	1.76	0.55	17.35	-	-	-	-	-	AT3G52780.1	Purple acid phosphatases superfamily protein
	Glyma.19G194100	0.18	0.00	1.61	0.71	1.28	0.52	1.75	45164521	Missense	TT	AA	H59L	AT3G52770.1	protein

Glyma.19G194200	7.43	7.24	4.46	8.32	6.93	5.71	7.22	-	-	-	-	-	AT3G52760.1	binding Integral membrane Yip1 family protein Phosphatidyl ethanolamine -binding protein
Glyma.19G194300	0.00	0.00	1.82	0.10	0.00	0.45	0.04	45183701	Missense	AA	TT	R166W	AT5G03840.1	
								45184804	Missense	CC	AA	R62S		
Glyma.19G194400	0.04	1.03	0.18	0.18	0.52	0.06	1.07	45200508	Missense	TT	AA	Q259L	AT2G36290.1	Alpha/beta-H ydrolases superfamily protein
Glyma.19G194500	0.27	0.03	0.42	1.35	0.23	0.37	4.95	45204441	Missense	CC	AA	T175	AT2G36270.1	Basic-leucine zipper (bZIP) transcription factor family protein
Glyma.19G194600	2.83	2.19	2.63	2.56	2.09	3.62	2.72	-	-	-	-	-	AT1G67190.2	F-box/RNI-li ke superfamily protein
Glyma.19G194700	7.90	6.53	4.41	5.38	3.78	10.39	2.92	45211466	Frameshift insertion	TT TG GA	T	N110F S	AT2G16710.2	Iron-sulphur cluster biosynthesis

										TT				family protein Tubulin/FtsZ
Glyma.19G194800	8.80	21.24	16.11	11.77	13.60	5.49	17.91	45216499	Missense	GG	AA	H29R	AT2G36250.2	family protein Unknown
Glyma.19G194900	4.41	13.36	3.13	1.90	3.10	1.01	1.02	-	-	-	-	-	AT3G52740.1	protein NA
Glyma.19G195000	0.03	0.00	0.69	0.25	0.06	0.60	0.35	45240320	Missense	AA	GG	V90I	NA	Probable small nuclear ribonucleopr oteins
Glyma.19G195100	54.95	60.67	96.53	73.40	61.06	95.77	78.28	-	-	-	-	-	AT2G23930.1	SAUR-like auxin-respon sive protein family
Glyma.19G195200	0.05	1.22	0.00	0.00	0.06	2.30	0.00	-	-	-	-	-	AT2G36210.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Glyma.19G195300	0.68	0.15	7.56	2.08	2.31	3.31	2.65	45258313	Missense	TT	CC	P851S	AT2G36200.1	Cell wall invertase 2
Glyma.19G195400	2.06	1.82	2.26	5.15	4.22	0.20	0.75	-	-	-	-	-	AT3G52600.1	Ubiquitin
Glyma.19G195500	87.31	177.34	247.45	259.79	144.21	309.88	285.39	-	-	-	-	-	AT3G52590.1	

															extension protein 1 Alpha/beta-H ydrolases superfamily protein
Glyma.19G195600	1.18	1.23	1.87	2.95	1.90	3.77	0.84	-	-	-	-	-	AT3G52570.1		
Glyma.19G195700	0.59	0.14	0.51	0.95	1.31	2.94	0.52	45278366	Frameshift insertion	CA	C	L47FS	AT3G15040.1	Protein of unknown function, DUF584	
								45278595	Missense	AA	GG	V124M			
Glyma.19G195800	0.45	2.59	0.02	0.00	0.08	0.07	0.02	45295210	Missense	GG	AA	Q72R	AT3G44350.2	NAC domain containing protein 61	
								45295211	Missense	CC	AA	Q72H			
Glyma.19G195900	29.51	22.27	15.61	22.80	14.10	35.07	16.13	-	-	-	-	-	AT3G11530.2	Vacuolar protein Sorting 55 (VPS55) family protein	
Glyma.19G196000	6.11	6.13	5.44	5.22	5.57	2.99	5.87	45317015	Missense	AA	GG	G61S	AT3G11540.1	Tetratricopep tide repeat (TPR)-like superfamily protein	

								45317378	Missense	CC	GG	E182Q		
								45329607	Missense	TT	AA	Q638L		
								45333287	Missense	TT	CC	S947L		
														Cyclophilin-like
Glyma.19G196100	1.99	3.21	10.45	4.99	5.58	5.02	8.48	-	-	-	-	-	AT2G36130.1	peptidyl-prolyl cis-trans isomerase family protein
Glyma.19G196200	0.02	0.04	0.40	0.11	0.10	0.07	0.19	-	-	-	-	-	AT5G06180.2	Protein of unknown function (DUF1022)
Glyma.19G196300	11.17	10.80	11.81	11.05	10.32	8.36	15.95	45344226 45374844	Missense Missense	GG CC	CC TT	I161M I4M	AT1G08370.1	Decapping 1
Glyma.19G196400	0.28	0.12	0.42	0.20	0.51	0.91	1.26	-	-	-	-	-	AT2G36090.1	F-box family protein
Glyma.19G196500	0.85	0.93	0.94	2.97	0.95	1.65	1.41	-	-	-	-	-	AT5G06240.1	Embryo defective 2735
Glyma.19G196600	1.23	0.03	0.83	0.36	0.34	2.80	0.21	45374259	Non frameshift insertion	GA AG	G	S199(in s F)	AT2G36080.1	AP2/B3-like transcriptional factor family protein

									45374844	Missense	CC	TT	I4M	
Glyma.19G196700	5.51	7.23	6.60	4.16	41.36	11.91	11.61	45384318	Missense	CC	TT	T415A	AT2G24280.1	Alpha/beta-H ydrolases superfamily protein
								45389589	Missense	TT	CC	S230N		

“-” represents no large-effect variation detected between ZP and ZP.