

Table S1. Linear mixed models of associations between height and 39 genotyped SNPs, which have an evidence of genome-wide significance ($P < 5 \times 10^{-8}$) in the discovery sample.

Gene	Chr	SNP	A1	A2	Region	MAF	BETA	SE	P	Previous reports
<i>CEP250</i>	20	rs224363	T	C	Intron	0.289	0.44	0.08	3.17×10^{-8}	
		rs2236164	C	T	Intron	0.290	0.43	0.08	3.68×10^{-8}	He et al. (2014)
		rs4911503	T	C	Intron	0.289	0.43	0.08	4.50×10^{-8}	
		rs6060438	C	T	Intron	0.290	0.43	0.08	4.14×10^{-8}	
<i>CS</i>	12	rs3816804	T	C	Intron	0.168	-0.60	0.09	1.53×10^{-12}	Hao et al. (2013)
<i>DCAF16</i>	4	rs10489037	A	G	Non-coding transcript	0.140	-0.61	0.09	8.52×10^{-11}	
		rs7672919	T	G	Intron	0.285	-0.55	0.07	8.27×10^{-14}	
		rs7678436	A	G	Intron	0.357	-0.43	0.07	9.51×10^{-10}	Okada et al. (2010); He et al. (2014); Wojcik et al. (2019)
<i>DCAF16-NCAPG</i>	4	rs7667864	A	C	2KB upstream	0.435	0.45	0.07	3.77×10^{-11}	
		rs1395371	C	T	2KB upstream	0.450	0.46	0.07	9.09×10^{-12}	
<i>EFEMP1</i>	2	rs3791679	A	G	Intron	0.233	0.50	0.08	5.42×10^{-10}	Gudbjartsson et al. (2008); Okada et al. (2010); Berndt et al. (2013); Wood et al. (2014); Tachmazidou et al. (2017); Wojcik et al. (2019)
		rs17047290	C	T	Intron	0.136	0.59	0.09	5.40×10^{-10}	

Gene	Chr	SNP	A1	A2	Region	MAF	BETA	SE	P	Previous reports
		rs3791675	C	T	Intron	0.236	0.48	0.08	1.02 x10 ⁻⁹	Weedon et al. (2008); Cho et al. (2009); Kim et al. (2010); Allen et al. (2010); Liu et al. (2010); He et al. (2014); Wojcik et al. (2019)
<i>IGF1</i>	12	rs5742657	G	A	Intron	0.287	-0.44	0.08	3.72 x10 ⁻⁸	
<i>LCORL</i>	4	rs6842303	T	G	Intron	0.446	0.48	0.07	1.91 x10 ⁻¹²	
		rs16895917	C	T	Intron	0.148	-0.63	0.09	8.54 x10 ⁻¹²	
		rs925098	G	A	Intron	0.434	0.49	0.09	2.26 x10 ⁻⁸	Carty et al. (2011); Wojcik et al. (2019)
		rs724577	A	C	Intron	0.440	0.46	0.07	1.19 x10 ⁻¹¹	N'Diaye et al. (2011); Wojcik et al. (2019)
<i>RASA2</i>*	3	rs295321	C	T	Intron	0.250	0.45	0.08	3.57 x10 ⁻⁸	
<i>UQCCI</i>	20	rs6060369	C	T	Intron	0.275	0.46	0.08	1.05 x10 ⁻⁸	Lettre et al. (2008); Sanna et al. (2008); He et al. (2014); Wojcik et al. (2019)
		rs6088791	C	T	Intron	0.275	0.46	0.08	6.68 x10 ⁻⁹	
		rs6060373	G	A	Intron	0.281	0.44	0.08	2.95 x10 ⁻⁸	Weedon et al. (2008); Wojcik et al. (2019)
		rs6141546	T	C	Intron	0.283	0.47	0.08	3.82 x10 ⁻⁹	
		rs4911493	A	G	Intron	0.283	0.46	0.08	6.59 x10 ⁻⁹	

Gene	Chr	SNP	A1	A2	Region	MAF	BETA	SE	P	Previous reports
		rs4911494	C	T	Missense	0.284	0.46	0.08	5.29 x10 ⁻⁹	
		rs6087705	G	A	2KB upstream	0.284	0.46	0.08	8.88 x10 ⁻⁹	
		rs4911495	C	A	Intron	0.175	0.50	0.09	2.72 x10 ⁻⁸	
		rs6088813	C	A	Intron	0.284	0.46	0.08	5.02 x10 ⁻⁹	Soranzo et al. (2009); Wojcik et al. (2019)
<i>ZBTB38</i>	3	rs7613516	G	A	Intron	0.491	0.45	0.07	2.65 x10 ⁻⁹	
		rs6440003	A	T	Intron	0.305	0.50	0.08	3.42 x10 ⁻¹¹	Weedon et al. (2008); N'Diaye et al. (2011); Wojcik et al. (2019)
		rs6764769	G	G	5' UTR	0.324	0.52	0.08	4.13 x10 ⁻¹²	
		rs6763931	A	A	Intron	0.328	0.53	0.08	2.59 x10 ⁻¹²	Gudbjartsson et al. (2008); Soranzo et al. (2009); He et al. (2014); Wojcik et al. (2019)
		rs724016	G	A	Intron	0.325	0.55	0.08	5.04 x10 ⁻¹³	Lettre et al. (2008); Sanna et al. (2008); Allen et al. (2010); Wood et al. (2014); Tachmazidou et al. (2017); Wojcik et al. (2019)
		rs76983194	C	A	Intron	0.276	0.49	0.08	2.60 x10 ⁻¹⁰	
		rs6762722	G	A	Intron	0.225	0.47	0.08	1.87 x10 ⁻⁸	
		rs6762826	G	A	Intron	0.278	0.49	0.08	3.99 x10 ⁻¹⁰	
		rs56339671	A	G	Intron	0.277	0.49	0.08	4.31 x10 ⁻¹⁰	
		rs4683404	G	A	Intron	0.282	0.53	0.08	1.12 x10 ⁻¹¹	
		rs7626871	G	A	Intron	0.249	0.48	0.08	5.02 x10 ⁻⁹	

A1 = minor allele in the present Taiwanese population, A2 = major allele in the present Taiwanese population, Chr = chromosome,

BETA = Beta coefficients, MAF = minor allele frequency, SE = standard error.

* denotes a novel gene.

Analysis was obtained after adjustment for covariates including age, gender, ancestry representative principle components, and a polygenic effect due to genetic relatedness.