

Table S4. Linear mixed models of associations between height and 4 genes, which have an evidence of genome-wide significance ($P < 5 \times 10^{-8}$) in the replication sample.

Chr	Gene	SNP	MAF	Beta	SE	P
12	<i>NABP2</i>	rs77394186	0.110	-0.60	0.09	8.72E-12
12	<i>NABP2</i>	rs7311505	0.129	-0.52	0.08	8.69E-11
3	<i>RASA2</i>	rs295321	0.252	0.37	0.06	6.39E-09
3	<i>RASA2</i>	rs79147413	0.279	0.36	0.06	2.23E-09
12	<i>RNF41</i>	rs76280383	0.122	-0.57	0.08	1.15E-11
12	<i>SLC39A5</i>	rs11171781	0.116	-0.63	0.08	9.53E-14

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

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