The American Journal of Human Genetics, Volume *92*

Supplemental Data

Common Genetic Risk Factors for Venous Thrombosis in the Chinese Population

Liang Tang, Hua-Fang Wang, Xuan Lu, Xiao-Rong Jian, Bi Jin, Hong Zheng, Yi-Qing Li, Qing-Yun Wang, Tang-Chun Wu, Huan Guo, Hui Liu, Tao Guo, Jian-Ming Yu, Rui Yang, Yan Yang, and Yu Hu

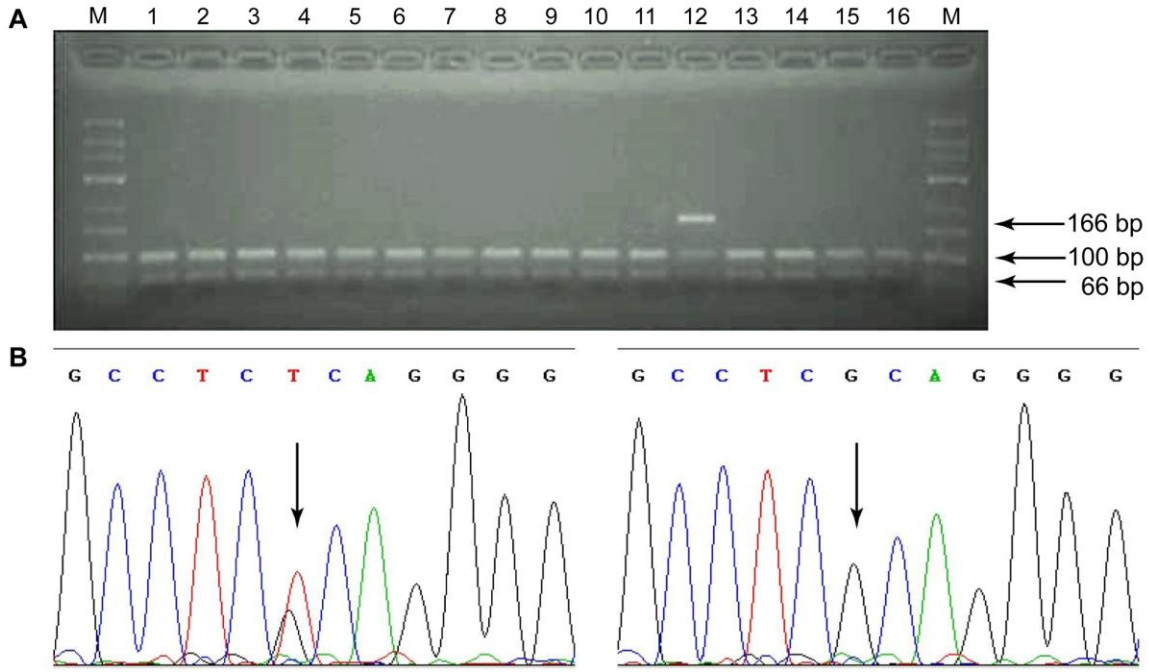

Figure S1. ***THBD*** **c.−151G>T Variant Detection by PCR-RFLP and Direct Sequencing**

(A) Electrophoretic patterns following Mwo I digestion. The PCR products were 178 bp. The amplicons from the wild-type allele had two restriction sites, yielding three bands of 100 bp, 66 bp and 12 bp after digestion. In contrast, the amplified products from the mutant allele lacked one recognition site, generating two fragments of 166 bp and 12 bp. The 12-bp fragment could not be observed. M, DNA marker with a 50-bp ladder. Lanes 1-11 and 13-16, normal individuals. Lane 12, heterozygous individual for the variant. (B) Chromatograms obtained by sequencing. Left, G/T heterozygote; Right, G/G wild-type.

Table S1. Primers for PCR and Sequencing Used in This Study

Region	Forward Primer (5'–3')	Reverse Primer (5'–3')	AT (°C)	Product (bp)
Genomic amplification				
g.4011-4640	AAACCTCCTTAGCCGACCC	CAAGGAAAGCCTGGATTGC	58	630
g.4493-5042	TAGGCAGGTCCTCCCAAAG	CAGACACTTCTTGCCGCTG	58	550
g.4873-5510	GAGAACCCAGCAATCCGAGTAT	GTGTTGTTGTCTCCCGTAACCC	58	638
g.5287-5903	GCGACCTTCCTCAATGCCA	TCCACGCTGCAGTCCCAAG	58	617
g.5727-6281	CTCGATCACCTACGGCACCC	CAGTTGGCTCTGAAGCACGG	58	555
g.6205-6731	TGCCACTGCTACCCTAACTACG	GCGATGGAGATGCCTATGAG	58	527
g.6586-7189	ATTGGCACCGACTGTGACTC	CAATAACGCTCACCCTCCTG	58	604
Genotyping	GCACTTCCTTCCTTTTCCCGA	CAGAGGGGCACAGGACGC	60	178
Plasmid construction	GCCGGTACCGTTACAGGGGTGCTG GCCTT	CCGAAGCTTGGAGCAGAGGGGCAC AGGAC	64	356

The amplification regions were designated according to the genomic sequences of *THBD*.