Supplementary Table S1. PCR amplification and sequencing primers for noncoding conserved sequences

Region	Genomic location (nt)**	Primer sequence	Novel nucleotide variation*
a	107,071,320- 107,071,430	F-CTTCCTAAATTCCTTAGGGAGTGAC R-GTTTCTTGAGGGCTAATCCTTATCT	
b	107,072,250- 107,072,850	F-CATAATTAAGATGCTGCACTCTGTG R-CTAAAGGTTGTTATTTGGGAGAAT	
		F-ATTATAATTTCTTTGGGTGGGAGAA R-ATTTAAGCTTCCCTTGACTCAATTT	
c	107,073,820- 107,073,970	F-AGACCTATTAGGACGCTATTGCTTT R-ATTGTGCACATGTACCCTAAAACTT	
d	107,080,160- 107,080,210	F-GTACCTCAGTTGGAAATGCAGAAAT R-GATCACACCACTGCACTCTAGC	
e	107,081,605- 107,081,635	F-AGCCTGGAACAATTTGATTTCTTA R-CAATCTTCGGAAGGAAGTCACTAT	
f	107,082,670- 107,082,730	F-TTCCCCTTTACAAGTGTCATTAAAA R-TCCTCAGTATATATGTGGCAACTGA	
g	107,084,175- 107,084,290	F-AAAACAAACAAACAAACACACACAC R-AGAGAATCCAACCATTAAAACATCA	
h	107,085,630- 107,086,150	F-ATAAATATGAGGCCAGGGTATAAGC R-ACCTTAGATTACTCACTTGGGCTTT	Heterozygous g.-3521A>T in *cis* with p.M1T in family 242, 4/110 normal control chromosomes
		F-AAGTGATGCATCTATTTCTTTGGAA R-AATAAGTCCTGCATGTATCTGGATG	Heterozygous g.-3247T>C in *cis* with p.L445W in families 142and 264, 5/78 normal control chromosomes
i	107,086,415- 107,086,435	F-GTTACTCTTTTGCCTCCTGTTGTTA R-ACAACTCTTTATTGAAGGCATTCTG	
j	107,086,835- 107,087,000	F-TTTTTGTCTAGTGAGGGAGAGAGAA R-CAACTCCACTACAACAGAGGAAAGT	Heterozygous g.-2393A>C in *cis* with p.M1T in family 242, 5/104 normal control chromosomes
k	107,087,263- 107,087,371	F-TCATTGTAGGATGTTTAGCAGCAT R-TCTCTGAAATGGTAGTCAGCATGT	Heterozygous g.-1952_-1951insT in *cis* with p.M1T in family 242, 5/110 normal control chromosomes
l	107,087,470- 107,087,600	F-CTCCCCTCTTCTCTGTATGTGAATA R-CTCTGTACATCAACCTTCCGTAATC	
m, n	107,087,850- 107,088,100	F-AGTTTTAACAAAGTTCATCCCAACA R-GGGACTCCTTAAAGAAGAGCAGAG	
o	107,089,050- 107,089,200	F-GTTTGGGGGAGATTTCAGAAC R-GAAGAGCGAGGAACAGAAAGAAC	
p	107,090,500- 107,090,850	F-TTTTTCTTTCATCTGTAGGTCACTG R-ACAAAGTTATGAACTGGATTCTGCT	
q	107,100,300- 107,100,700	F-GTGATCAATTTGACTCCATTTTTG R-TTCTTTCAATCAAAACCTCTTTCTG F-CAAGGTCTTTGAACCTACCATTTTA R-TATTTCAAGAGGATCATCGAGGTAG	
r	107,103,950- 107,104,350	F-ATGCCTCATTGGATTGTTAAATAAG R-TATGTGTACATGGCCTTACATTGTT F-TATTGGTGAAATGAAATGATTGGAG R-TGTTGACACGTTATTTTTGTATGGT	
s	107,119,750- 107,120,000	F-ATGTCCATTCTCCTGATGTTACCT R-AAGTTCCAACATAAGAGAAAACACG	
t	107,121-180- 107,121,400	F-ACTCAGACCTTTTGCACTAGACAGT R-CAGCCTGAAACAGTGACTATGG	
u	107,125,530- 107,125,600	F-CGTGAAAGCTCTATGCTTATCCTAT R-AACAGCCGTATTTTGGAATAAAAAG	
v	107,148,570- 107,148,880	F- CCTGGAAGTATTTGGTTGAGTAAGA R- GGCTATGAAAATAAAAATCACATCC	

*Polymorphisms from dbSNP are not included. **Nucleotide numbering was based upon the UCSC version hg18 (March 2006).

Supplementary Table S2. M0 twins.

Family #	213	219[a]	240	245	261
Zygosity[b]	MZ	DZ	DZ	MZ	DZ
Family history of twinning[b]	Maternal-DZ	Maternal-DZ	No	Maternal-DZ	Maternal-MZ
Assisted reproductive technology	None	None	Clomiphene citrate	None	*In vitro* fertilization
Paternal age (years) at conception	30	26	37	35	41
Gestational age (weeks) at birth	36	38	37	37	38
Birthweight[c] (lbs)	1: $5^{14/16}$ 2: $5^{10/16}$	1: $6^{9/16}$ 2: $5^{7/16}$	1: $6^{1/16}$ 2: $5^{6/16}$	1: $4^{15/16}$ 2: $4^{13/16}$	1: $6^{8/16}$ 2: $5^{11/16}$
Gender[c]	1: female 2: female	1: female 2: female	1: male 2: female	1: female 2: female	1: male 2: female
EVA laterality[c]	1: none 2: left	1: bilateral 2: right	1: none 2: bilateral	1: left 2: left	1: bilateral 2: none
Other health issues[c]	1: none 2: asthma	1: asthma, eczema 2: none	1: none 2: none	1: none 2: exercise-induced asthma	1: seasonal asthma 2: none

[a] Mother took Tegretol during pregnancy

[b] MZ, monozygotic; DZ, dizygotic

[c] 1, older twin; 2, younger twin