Supplemental Material Table 1.

Primers used to resequence *NT5C3* and create expression constructs

Primer Name	Primer Sequence
F-5'-FR & Exon 1(NM_001002009.1)	GGTGCAAAACTGGATTCATAAAA
R-5'-FR & Exon 1(NM_001002009.1)	CTAGCGAGATCCCAGCCTGA
F-5'-FR & Exon 1(NM_016489.11)	GGACAGTAGAGAGAAAGCCGATA
R-5'-FR & Exon 1(NM_016489.11)	CCCTCAACCTGGAAAGAGACT
F-Exon 2	TGGCATAACAGGAAGAACCTG
R-Exon 2	TCTGAGAAGCACGACAATGTG
F-Exon R	ATGGTTGTATGTTGCACAGGAG
R-Exon R	ACCAATCCATTATGGTGAAAGC
F-Exon 3	GCTTGGTGTCCCACACTTTT
R-Exon 3	GGAAGCTGAGGAGGGAAAAC
F-Exon 4	TATAAAGGAACCGCATGAGAAAA
R-Exon 4	AAGAAAAAGCAGGTCTCCTCACT
F-Exon 5 & Exon 6	TCTCAGTGATGTAAGCGAGCA
R-Exon 5 & Exon 6	TCTGTTTGTTTGCAATACAGGT
F-Exon 7	GGAGGACTGGGAAACTCAGTAA
R-Exon 7	AGGTGGCATATTTTGGATATGG
F-Exon 8	ACAGCCCTCTTGGGCAGTAT
R-Exon 8R	GAGAAGGATGGAGTCCCACA
F-Exon 9 & Exon 10	AGCTATGGTGAATGTGATGGACT
R-Exon 9 & Exon 10	AGTGTGTTGAGAGAGGTGGAGAA

Site-directed mutagenesis, expression construct

F-Exon 2 (9)	ATGACTAA**C**CAAGAGTCTGCCGTACATGTGAA
R-Exon 2 (9)	TTCACATGTACGGCAGACTCTTG**G**TTAGTCAT
F-Exon 6 (276)	ACTAAAGGAAAAATA**T**TACGCTATTGAAGTTG
R-Exon 6 (276)	CAACTTCAATAGCGTA**A**TATTTTTCCTTTAGT
F-Exon 6 (306)	TGATCCTGTTCTTAC**C**GTAGAAGAGAAGTACC
R-Exon 6 (306)	GGTACTTCTCTTCTAC**G**GTAAGTTCAGGATCA
F-Exon 9 (959)	AGTGGCCAATGTTGA**A**CACATTCTGAAAATTG
R-Exon 9 (959)	CAATTTTCAGAATGTG**T**TCAACATTGGCCACT
F-Exon 10 (847)	ATTGTTTTAGTACAA**C**ATGAATCATTAGAAGT
R-Exon 10 (847)	ACTTCTAATGATTCAT**G**TTGTACTAAAACAAT

Bold, underlined letters are mutated bases in site-directed mutagenesis primers.

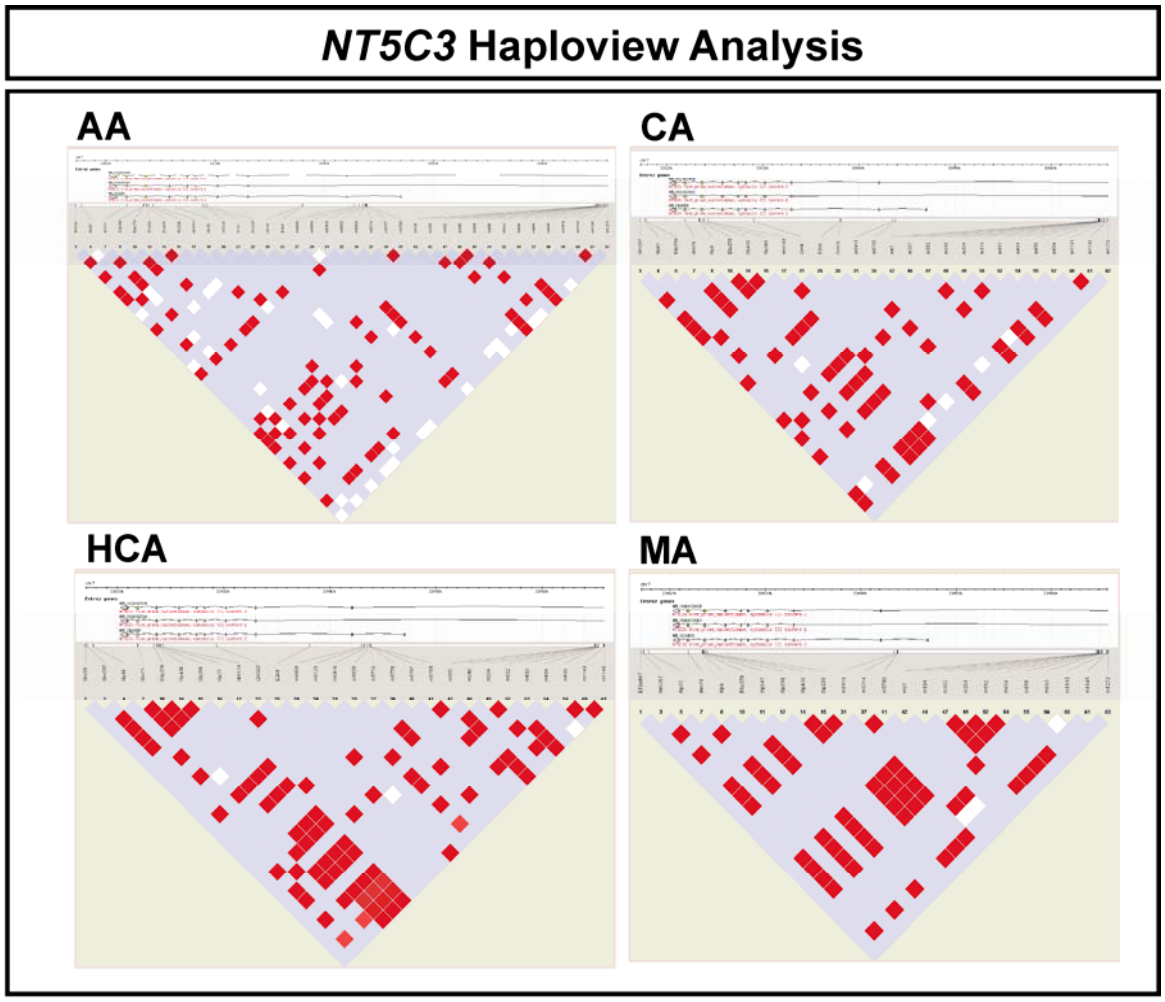
		Haplotype frequency																													
observed	allele	AA	CA	HCA	MA	(-1273)	(-1270)	(-1145)	(-1143)	(-1018)	(-944)	(-884)	(-693)	(-656)	(-654)	(-653)	(-552)	(-373)	(-354)	(-340)	(-302)	(-267)	(-258)	(-67)	(-5780)	(-5767)	(-5757)	(-5756)	(-5714)	(-5705)
o	*1A	0.200			0.167	A	T	T	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
o	*1B	0.158	0.289	0.192	0.433	A	T	G	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
o	*1C	0.150	0.292	0.300	0.133	A	T	T	A	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
o	*1D	0.083				A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
o	*1E	0.075				A	T	T	A	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
i	*1F	0.058				A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1G	0.058				C	T	T	G	T	T	D	C	C	G	T	C	C	T	T	G	D	D	T	C	A	A	T	A	C
i	*1H	0.050				A	T	T	A	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
i	*1I	0.033	0.008			A	T	T	G	T	T	I	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1J	0.025				A	T	T	G	T	T	D	C	C	G	T	C	C	C	G	G	D	I	T	C	A	A	T	A	C
i	*1K	0.017				A	T	G	G	T	T	D	C	C	A	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1L	0.008				A	T	G	G	C	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
i	*1M	0.008				A	T	T	G	T	T	D	C	C	G	T	C	C	C	G	G	D	D	T	C	A	A	T	A	C
i	*1N	0.008				A	T	T	G	T	T	D	C	C	G	T	C	C	T	T	G	D	D	T	G	A	A	T	G	C
i	*1O	0.008				C	T	T	G	T	C	D	C	C	G	T	C	C	T	T	G	D	D	T	C	A	A	T	A	C
i	*1P	0.009				C	T	T	G	T	T	D	C	C	G	T	C	C	T	T	G	D	D	T	G	A	T	T	A	C
i	*1Q	0.008				C	T	T	G	T	T	D	C	C	G	T	C	C	T	T	G	D	D	T	G	A	T	T	A	C
o	*1R		0.225	0.150*	0.117	A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
o	*1S		0,042*	0.083	0.067	A	T	T	G	T	T	D	C	C	A	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1T		0.036			A	T	G	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
i	*1U		0.019			A	T	G	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	C	C	A	A	T	A	C
i	*1V		0.017	0.008		A	T	T	G	T	T	D	C	C	G	T	C	C	C	G	G	D	D	T	C	A	A	T	A	C
i	*1W		0.017			A	T	T	G	T	T	D	C	T	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1X		0.008			A	C	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1Y		0.008			A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	A
i	*1Z		0.008			A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	I	D	T	C	A	A	T	A	C
i	*1AA		0.008			A	T	T	G	T	T	D	C	C	G	T	C	T	C	T	G	D	D	T	C	A	A	T	A	C
i	*1AB		0.008			A	T	T	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
o	*1AC			0.125	0.0167*	A	T	T	G	T	T	D	G	C	G	T	C	C	T	T	G	D	D	T	G	A	A	T	G	C
o	*1AD			0.083		A	T	T	G	T	T	D	C	C	A	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1AE			0.033		A	T	G	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	A	A	T	A	C
o	*1AF			0.025		A	T	G	G	T	T	D	C	C	G	T	G	C	T	T	A	D	D	T	C	T	A	T	A	C
i	*1AG			0.017		A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1AH			0.008		A	T	T	A	T	T	D	C	C	G	T	C	C	T	T	A	D	D	T	C	A	A	T	A	C
i	*1AJ			0.008		A	T	T	G	T	T	D	C	C	A	T	C	C	C	T	G	D	D	T	C	A	A	A	A	C
i	*1AK			0.008		A	T	T	G	T	T	D	C	C	G	C	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1AL			0.008		A	T	T	G	T	T	D	G	C	G	T	C	C	T	T	G	D	D	T	G	A	A	T	G	C
i	*1AM				0.008	A	T	T	G	T	T	D	C	C	A	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1AN				0.008	A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	C	C	A	A	T	A	C
i	*1AO				0.008	A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*1AP				0.008	A	T	T	G	T	T	D	C	C	G	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C
i	*2A				0.008	A	T	T	G	T	T	D	C	C	A	T	C	C	C	T	G	D	D	T	C	A	A	T	A	C

		Haplotype frequency																													
observed	allele	AA	CA	HCA	MA	(-5635)	(-5633)	(-5418)	(-5059)	(-4900)	(-4645)	E2(9)	I2(-237)	I2(-4)	I4(35)	I4(-114)	I5(77)	I5(266)	I5(430)	I5(548)	E6(276)	E6(306)	I6(9)	I6(71)	E9(759)	I9(52)	I9(61)	I9(-267)	I9(-38)	E10(847)
o	*1A	0.200			0.167	G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
o	*1B	0.158	0.289	0.192	0.433	G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
o	*1C	0.150	0.292	0.300	0.133	G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
o	*1D	0.083				G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	C	G	T	A	G	C	G
o	*1E	0.075				G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	C	A	C	G	T	A	A	C	G
i	*1F	0.058				G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1G	0.058				G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
i	*1H	0.050				G	A	G	A	G	G	T	G	T	T	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
i	*1I	0.033	0.008			G	A	A	G	G	G	T	G	G	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1J	0.025				G	A	A	G	G	G	C	G	T	C	A	C	A	A	A	T	T	A	C	G	T	G	G	C	G
i	*1K	0.017				G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1L	0.008				G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	C	A	C	G	T	A	A	C	G
i	*1M	0.008				G	G	A	G	G	T	C	G	T	C	G	C	A	A	A	T	T	A	C	G	T	A	G	C	G
i	*1N	0.008				G	A	G	G	G	G	T	G	T	C	G	C	A	A	A	T	C	A	C	G	T	A	A	C	G
i	*1O	0.008				G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	C	A	C	G	T	A	A	C	G
i	*1P	0.009				G	A	G	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	C	G	T	A	A	C	G
i	*1Q	0.008				G	A	G	G	G	G	T	A	T	C	G	C	A	A	A	T	T	A	C	G	T	A	A	C	G
o	*1R		0.225	0.150*	0.117	G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
o	*1S		0,042*	0.083	0.067	G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1T		0.036			G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	G	C	G	T	A	A	C	G
i	*1U		0.019			G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
i	*1V		0.017	0.008		G	A	A	G	G	G	C	G	T	C	A	C	A	A	A	T	T	A	C	G	T	G	G	C	G
i	*1W		0.017			G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1X		0.008			G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1Y		0.008			G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1Z		0.008			G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AA		0.008			G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AB		0.008			G	A	G	G	G	G	T	G	T	C	G	C	G	G	A	C	T	A	C	A	T	A	A	C	G
o	*1AC			0.125	0.0167*	G	A	G	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	C	G	T	A	A	C	G
o	*1AD			0.083		G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AE			0.033		G	A	G	G	A	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
o	*1AF			0.025		G	A	G	G	A	G	T	G	T	C	G	C	G	G	A	C	T	A	C	G	T	A	A	C	G
i	*1AG			0.017		A	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AH			0.008		G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AJ			0.008		G	A	A	G	G	G	T	G	T	C	G	G	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AK			0.008		G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AL			0.008		G	A	G	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	C	G	T	A	A	T	G
i	*1AM				0.008	G	A	A	G	G	G	T	G	T	C	G	C	A	A	T	T	T	A	T	G	T	A	G	C	G

i	*1AN				0.008	G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	G
i	*1AO				0.008	G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	A	A	G	C	G
i	*1AP				0.008	G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	G	T	G	T	A	G	C	G
i	*2A				0.008	G	A	A	G	G	G	T	G	T	C	G	C	A	A	A	T	T	A	T	G	T	A	G	C	C

Supplementary Table 2. Human *NT5C3* haplotypes. Variant nucleotides compared with the "reference sequence" (i.e., the most common sequence in African American subjects) are highlighted as white on black. Initial haplotype designations (*1 and *2) were made on the basis of amino acid sequence, with the WT allozyme designated *1. The *2 designation was used for the sequence that encoded His283. Subsequent assignments/letter designations were made based on descending allele frequencies, starting with haplotypes present in African-American subjects. The symbols I and D at 5'-FR locations (–884), (-267) and (-258) represent insertions and deletions, respectively. Polymorphisms at positions 5'FR(-496), 5'UTR(–194), 5'UTR(-134), I1(-5694), I1(-5654), I1(-5125), I1(-19), I2(-307), I3(103), I5(533) and I5(647) were excluded from this table because they were not represented in any of the haplotypes listed. We used a 1% frequency cutoff for inclusion in the table, but haplotypes containing synonymous or nonsynonymous SNP with frequencies lower than 1% were also included. o = observed data; i= inferred data.

Supplementary Figure 1. Human *NT5C3* linkage disequilibrium in AA, CA, HCA and MA subjects. D' values were calculated for each polymorphism pair. All values shown in color were statistically significant ($p<0.05$). Numbers identifying individual polymorphisms are those listed in **Table 1**.



Supplemental Figure 1