

SUPPLEMENTARY TABLE I

A

Mutagenesis primers (F, forward primer; R, reverse primer)		
Primer	Sequence 5' -> 3'	
TMEM173_N154S_F	GGAATTTTCAGCGTGGCCCATGGGCTGGCAG	
TMEM173_N154S_R	ATGGGCCACGCTGAAATTCCCTTTTTCACACACTGCAG	
TMEM173_I200N_F	CGGCTGTATAATCTCCTCCCATTGGACTGTG	
TMEM173_I200N_R	TGGGAGGAGATTATACAGCCGCTGGCTCACT	
TMEM173_G207E_F	TTGGACTGTGAGGTGCCTGATAACCTGAGTATGGC	
TMEM173_G207E_R	ATCAGGCACCTCACAGTCCAATGGGAGGAGTTATATG	
TMEM173_H232R-F	CAGCAGACCGGTGACCGTGCTGGCATCAAGGATCGGG	
TMEM173_H232R-R	GATGCCAGCACGGTCACCGGTCTGCTGGGGCAGTTT	

Quantitative real-time PCR primers (F, forward primer ; R, reverse primer)		
Primer	Sequence 5' -> 3'	Gene
ASC_F	TTGGACCTCACCGACAAGC	apoptosis-associated speck like protein containing a CARD domain
ASC_R	ATGTGCGCAGCACGTTA	
B2M_F	GAGTATGCCTGCCGTGTGAA	beta-2 microglobulin (housekeeping)
B2M_R	TGCGGCATCTTCAAACCTCC	
CASP1_F	ATCCCACAATGGGCTCTGTTT	caspase-1
CASP1_R	CTCTTTCAGTGGTGGGCATCT	
IFIT2_F	GCCGAACAGCTGAGAATTGC	interferon induced protein with tetratricopeptide repeats 2
IFIT2_R	AGGCCAGTAGGTTGCACATTG	
IFNB1_F	GAGCTACAACCTTGCTTGGATTCC	interferon beta 1
IFNB1_R	CAAGCCTCCCATTCAATTGC	
IL1B_F	TGGCAATGAGGATGACTTGT	interleukin-1 beta
IL1B_R	GGAAAGAAGGTGCTCAGGTC	
IL18_F	TCAACTCTCTCCTGTGAGAACAAA	interleukin-18
IL18_R	GTCCTGGGACACTTCTCTGAAA	
MX1_F	CGAGATGTCCCGGATCTGACT	MX dynamin like GTPase 1
MX1_R	CACCACCAGGCTGATTGTCT	
NLRP3_F	CAACTGCAACCTCACGTCAC	NLR family pyrin domain containing 3
NLRP3_R	ACGGTCAGCTCAGGCTTTTC	
RPLP0_F	GAAATCCTGAGTGATGTGCAGC	ribosomal protein lateral stalk subunit P0 (housekeeping)
RPLP0_R	TCGAACACCTGCTGGATGAC	
TNF_F	TGCTGCACTTTGGAGTGATCG	tumor necrosis factor alpha
TNF_R	ATCTCTCAGCTCCACGCCATT	

B

SDM predictions on STING protein stability with C206Y and G207E patient mutations										
Mutation	PDB File	Residue 232	WT-RSA (%)	WT-DEPTH (Å)	WT-OSP	MUT-RSA (%)	MUT-DEPTH (Å)	MUT-OSP	Predicted pseudo $\Delta\Delta G$	Outcome
C206Y	4LOI	H	0.0	7.4	0.56	0.0	8.0	0.7	-1,27	Reduced stability
G207E	4LOI	H	57.1	4.4	0.35	49.8	3.5	0.27	-0,72	Reduced stability
C206Y	4KSY	R	0.0	6.7	0.53	0.1	7.0	0.64	-1,28	Reduced stability
G207E	4KSY	R	82.5	3.9	0.32	73.6	3.3	0.23	-0,63	Reduced stability

Percentage relative sidechain solvent accessibility (RSA) for wildtype (WT) and both mutant (MUT) residues at 206 and 207. Residue depth is presented for WT and MUT residues in angstrom units (Å). Residue occluded surface packing (OSP) is likewise presented for WT and MUT. Predicted pseudo $\Delta\Delta G$ and its effect on protein stability (outcome) are presented.