TABLE S1. PRIMERS FOR PCR AMPLIFICATION

SNP*	Primer†	Genbank	Nucleotide Sequence (5'→3')	Annealing Temperature	Length
	1840.5	Y14768	CTAAGTGTGTATGGAGTGAATG	57°C	296 bp
+691g ins/del	2135.3	Y14768	CCCTGAGGTGTCTGGTTTTC		
	196.5	Y14768	GAAGCAAAGGAGAAGCTGAGA	56°C	948 bp
-851c/t, -308g/a, and *-238g/a*	1143.3	Y14768	TCTGGAGGAAGCGGTAGTGG		

*SNP nomenclature according Herrmann et al. (1998) *Eur J Clin Invest* 28:59-66.

† The number preceding the decimal point refers to the nucleotide position of the Genbank DNA sequence of the specified accession number given in the neighboring column, which also corresponds to the 5' nucleotide of the oligonucleotide. The annotation '.5' refers to a forward primer and '.3' refers to a reverse primer. The annealing temperature for amplification and the length of the obtained PCR products are also given.

TABLE S2. SINGLE NUCLEOTIDE PRIMER EXTENSION OLIGONUCLEOTIDES

TNFα SNP*	Primer†	Genbank	Nucleotide Sequence (5'→3') ‡
+691g ins/del	1939.5	Y14768	AAAAGTGTGAGAAGAGAGATGGGG
-851c/t	394.3	Y14768	$(AAA)_{11}$ ACTCTACATGGCCCTGTCTTC ‡
-308g/a	943.5	Y14768	$(AAA)_{9}$ ACAATAGGTTTTGAGGGGCATG
-238g/a	1013.5	Y14768	$(AAA)_{13}$ AGAAGACCCCCCTCGGAATC

* SNP nomenclature according to Herrmann et al. (1998) *Eur J Clin Invest* 28:59-66.

† The number refers to the polymorphic nucleotide position of the Genbank DNA sequence of the specified accession number given in the neighbouring column. The annotation '.5' refers to a forward primer and '.3' refers to a reverse primer.

‡ The length of the oligonucleotide may be increased through addition of an A-tail; $(AAA)_n$ means 3 x n A nucleotides.

‡A reverse oligonucleotide is used.

TABLE S3. DISTRIBUTION OF ALLELES AND GENOTYPES OF SNPS IN TNFα IN CF PATIENTS AND CONTROLS

TNFα SNP	Genotype and Allele Frequency	Cystic Fibrosis Patients*			Control Subjects*		
		Czech	Belgian	Total	Czech	Belgian	Total
+691g ins/del	*ins/ins* n(%)	106(89.8)	48(85.7)	154(88.5)	96(94.1)	79(92.9)	175(93.6)
	ins/del n(%)	12(10.2)	8(14.3)	20((11.5)	6(5.9)	6(7.1)	12(6.4)
	del/del n(%)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)	0(0.0)
	ins n(%)	224(94.9)	104(92.9)	328(94.3)	198(97.1)	164(96.5)	362(96.8)
	del n(%)	12(5.1)	8(7.1)	20(5.7)	6(2.9)	6(3.5)	12(3.2)
-851c/t	*cc* n(%)	87(75.7)	42(77.8)	129(76.3)	87(74.3)	64(78.1)	151(75.9)
	ct n(%)	27(23.5)	11(20.4)	38(22.5)	27(23.1)	17(20.7)	44(22.1)
	tt n(%)	1(0.9)	1(1.85)	2(1.2)	3(2.6)	1(1.2)	4(2.0)
	c n(%)	201(87.4)	95(88.0)	296(87.6)	201(85.9)	145(88.4)	346(86.9)
	t n(%)	29(12.6)	13(12.0)	42(12.4)	33(14.1)	19(11.6)	52(13.1)
-308g/a	*gg* n(%)	88(76.5)	42(76.4)	129(75.9)	92(78.0)	63(76.8)	155(77.5)
	ga n(%)	23(20.0)	13(23.6)	37(21.8)	23(19.5)	18(22.0)	41(20.5)
	aa n(%)	4(3.5)	0(0.0)	4(2.4)	3(2.5)	1(1.2)	4(2.0)
	g n(%)	199(86.5)	97(88.2)	295(86.8)	207(87.7)	144(87.8)	351(87.8)
	a n(%)	33(14.2)	13(11.8)	45(13.2)	29(12.3)	20(12.2)	49(12.2)
-238g/a†	*gg* n(%)	103(89.6)	47(85.5)	150(88.2)	106(90.6)	73(89.0)	179(90.0)
	ga n(%)	10(8.7)	8(14.6)	18(10.6)	11(9.4)	9(11.0)	20(10.0)
	aa n(%)	2(1.7)	0(0.0)	2(1.2)	0(0.0)	0(0.0)	0(0.0)
	g n(%)	216(93.9)	102(92.7)	318(93.5)	223(95.3)	155(94.5)	378(95.0)
	a n(%)	14(6.1)	8(7.3)	22(6.5)	11(4.7)	9(5.5)	20(5.0)

*For each genotype/allele, the number of individuals/alleles is given; the percentage is given between brackets. The distribution of alleles/genotypes in the Belgian controls, Czech controls, Belgian CF patients, Czech CF patients and total patient and control populations were not significantly different as tested by likelihood χ^2 ratio or by the Fisher exact probability test when more than 20% of the cells had an expected count of less than 5.

There may be a difference in number of genotypes/alleles typed for the different SNPs, since that gap-filling of data could not always be successfully completed.

† Czech patients were not in Hardy Weinberg equilibrium for this SNP, all other groups were in Hardy Weinberg equilibrium.

TABLE S4. DISTRIBUTION OF MEAN BMI ACCORDING TO TNFα GENOTYPES

TNFα SNP	Mean (SD) BMI [kg/m^2]*		Mean Difference	95%CI	p-value
	ins/ins (n=100)	ins/del (n=13)			
+691g ins/del	16.2 (2.1)	17.2 (1.8)	1.0	-0.2 to 2.1	0.11
	cc (n=81)	ct+tt (n=30)			
-851c/t	16.3 (2.1)	16.4 (1.9)	0.1	-1.0 to 0.8	0.85
	gg (n=90)	ga+aa (n=22)			
-308g/a	16.3 (2.1)	16.1(1.8)	0.2	-1.2 to 0.8	0.66
	gg (n=101)	ga+aa (n=11)			
-238g/a	16.3 (2.1)	16.4 (2.4)	0.1	-1.2 to 1.4	0.87

*The analysis was performed by a two-sample t-test. There may be a difference in number of genotypes/alleles typed for the different SNPs, since that gap-filling of data could not always be successfully completed.