

SUPPLEMENTARY DATA**Supplementary Table 1. CF patient cohort**

	CF cohort (n=442)
Gender (female/male)	218 / 224
Age (mean \pm SD)	21.4 \pm 12.6 yrs
FEV1 % of predicted (recent value) (mean \pm SD)	79.3 \pm 29.0 [#]
FEV1@20 years* (mean \pm SD)	80.1 \pm 24.2
CFTR Δ F508 (homozygous/heterozygous/others)	191 / 129 / 122
Positive <i>P. aeruginosa</i> microbiology	246 [§]

no FEV1 data at time of blood drawing available for 28 patients

§ no microbiological data available for 18 patients

Supplementary Table 2. RealTime Primer

Gene	Forward	Reverse
<i>β-actin</i>	CTCCGTGGCCTTAGCTGTG	TTTGGAGTACGCTGGATAGCCT
<i>CXCR1</i>	GAGCCCCGAATCTGACATT	AGCAGACACTGCAACACAC
<i>CXCR2</i>	ACAGCTACTTGGGAGGCTGA	TGCAGTGGTCACACCATT TT

Supplementary Table 3. MAF, minor allele frequencies of *CXCR1* and *CXCR2* SNPs in a healthy control population compared to the CF population studied.

CXCR1

SNP	Position	Location/ Function	Alleles	MAF KORA controls	MAF CF patients
rs2671222	-2668	Promoter	G/A	0.046	0.058
rs17838611	-2423	Promoter	G/A	0.019	0.016
rs16858841	-2329	Promoter	C/T	0.046	0.037
rs3138060	-1566	Intron	C/G	0.050	0.057
rs16858816	-143	Intron	C/T	0.045	0.038
rs16858811	92	Met/Arg	G/T	0.046	0.036
rs16858808	1003	Arg/Cys	C/T	0.045	0.035

CXCR2

SNP	Position	Location/ Function	Alleles	MAF KORA controls	MAF CF patients
rs3890158	-9203	Promoter	A/G	0.469	0.468
rs45493792	-9191	Promoter	-/T	0.472	0.368
rs3890157	-9185	Promoter	T/G	0.048	0.043
rs35231134	-9179	Promoter	-/T	0.492	0.502
rs4674258	-8909	Promoter	C/T	0.478	0.362
rs4674259	-8490	5'-UTR	A/G	0.468	0.368
rs17844697	-270	Intron	G/A	0.429	0.437
rs11574750	768	Val/Val	C/T	0.101	0.041
rs2230054	786	Leu/Leu	C/T	0.421	0.331
rs45606837	936	Leu/Leu	C/T	0.014	0.043
rs1126579	1209	3'-UTR	C/T	0.466	0.381
rs13306441	1420	3'-UTR	A/G	0.035	0.039
rs17844765	1437	3'-UTR	C/T	0	0.007
rs1126580	1441	3'-UTR	C/T	0.351	0.439

MAF, minor allele frequency; Note: no significant differences in the MAF SNP frequencies were found between control and CF individuals.

Supplementary Table 4. *CXCR1* and *CXCR2* tagging SNPs and haplotype combinations and their association with lung function (linear regression).*CXCR1*

SNP	B (95% CI)	Beta	P value
rs2671222	-5.58 (-13.52; 2.36)	-0.07	0.168
rs17838611	21.31 (6.40; 36.22)	0.142	0.005
rs16858841	20.73 (11.41; 30.06)	0.22	1.57 x 10 ⁻⁵
rs3138060	-5.28 (-13.23; 2.67)	-0.07	0.193
rs16858816	20.52 (11.21; 29.82)	0.22	1.86 x 10 ⁻⁵
rs16858811	21.72 (12.24; 31.20)	0.22	8.88 x 10 ⁻⁶
rs16858808	21.74 (12.09; 31.39)	0.22	1.24 x 10 ⁻⁵

CXCR2

SNP	B (95% CI)	Beta	P value
rx3890158	0.74 (-3.64; 5.13)	0.02	0.740
rs45493792	1.66 (-4.30; 7.63)	0.03	0.549
rs3890157	15.42 (7.29; 23.55)	0.19	2.22 x 10 ⁻⁴
rs35231134	2.88 (-1.10; 6.86)	0.07	0.156
rs4674258	-2.95 (-7.96; 2.06)	-0.06	0.247
rs4674259	0.80 (-3.78; 5.38)	0.02	0.731
rs17844697	-3.54 (-11.05; 3.98)	-0.07	0.354
rs11574750	20.34 (11.91; 28.76)	0.27	3.20 x 10 ⁻⁶
rs2230054	-2.03 (-7.97; 3.91)	-0.04	0.501
rs45606837	6.35 (-8.92; 21.63)	0.04	0.414
rs1126579	3.02 (-2.66; 8.71)	0.05	0.296
rs13306441	19.44 (10.24; 28.65)	0.21	4.06 x 10 ⁻⁵
rs17844765	-1.70 (-24.12; 20.72)	-0.01	0.882
rs1126580	1.90 (-3.95; 7.74)	0.04	0.524

Haplotypes

Haplotype	B (95% CI)	Beta	P value
<i>CXCR1</i> _Ha	21.51 (12.06; 30.97)	0.22	1.01 x 10 ⁻⁵
<i>CXCR2</i> _Ha	20.67 (10.77; 30.57)	0.21	4.98 x 10 ⁻⁵
<i>CXCR1-2</i> _Ha	19.86 (10.64; 29.09)	0.21	2.86 x 10 ⁻⁵

B, non-standardized regression coefficient B; 95% CI, 95% confidence interval.