

Supplemental Table I. Study Population for Large Airway Epithelial Gene Expression¹

Parameter	Large airway gene expression	
	Nonsmoker	Smoker
n	20	31
Sex (male/female)	14/6	21/10
Age (yr)	40 ± 8	44 ± 7
Race (Af/H/E/As/AH) ²	8/3/7/1/1	20/5/6/0/0
Smoking-related		
Pack-yr	NA	28 ± 18
Urine nicotine (ng/ml)	0	1059 ± 1088
Urine cotinine (ng/ml)	0	1099 ± 1091
Pulmonary function³		
FVC (% predicted)	107 ± 13	112 ± 11
FEV1(% predicted)	103 ± 28	110 ± 12
FEV1/FVC (% observed)	82 ± 5	82 ± 7
TLC (% predicted)	100 ± 14	103 ± 12
DLCO (% predicted)	101 ± 16	96 ± 12

¹ Biological samples from a total of 51 research subjects were used to assess large airway gene expression; where mean values are provided, the error indicates the standard deviation.

² Race is indicated as African (Af), Hispanic (H), European (E), Asian(As), African/Hispanic (AH).

³ Pulmonary function: tests included forced vital capacity (FVC), forced expiratory volume in 1 sec (FEV1), total lung capacity (TLC), and diffusion capacity for carbon monoxide (DLCO).