Table 1. Demographic and clinical characteristics of the study participants

Variable	Mean (SD)	Median (IQR)	Frequency (%)
Age, years (n = 1,000)			
18–24			150 (15.0)
25–34			320 (32.0)
35–44			280 (28.0)
45–54			180 (18.0)
55–64			100 (10.0)
65–74			50 (5.0)
75–84			20 (2.0)
85–94			10 (1.0)
95–104			10 (1.0)
Sex (n = 1,000)			
Male			500 (50.0)
Female			500 (50.0)
Ethnicity (n = 1,000)			
Caucasian			400 (40.0)
Black			200 (20.0)
Asian			150 (15.0)
Hispanic			100 (10.0)
Other			50 (5.0)
Unknown			100 (10.0)
Smoking status (n = 1,000)			
Never smoker			600 (60.0)
Former smoker			300 (30.0)
Current smoker			100 (10.0)
Alcohol consumption (n = 1,000)			
Yes			700 (70.0)
No			300 (30.0)
Physical activity (n = 1,000)			
Sedentary			200 (20.0)
Light			300 (30.0)
Moderate			400 (40.0)
Vigorous			100 (10.0)
Diet (n = 1,000)			
Vegetarian			100 (10.0)
Vegan			50 (5.0)
Omnivore			850 (85.0)
Occupation (n = 1,000)			
Manual labor			300 (30.0)
Office work			500 (50.0)
Unemployed			200 (20.0)
Marital status (n = 1,000)			
Married			600 (60.0)
Single			300 (30.0)
Divorced			100 (10.0)
Education level (n = 1,000)			
Primary			100 (10.0)
Secondary			400 (40.0)
Tertiary			500 (50.0)
Income (n = 1,000)			
Low			300 (30.0)
Medium			500 (50.0)
High			200 (20.0)
Residence (n = 1,000)			
Urban			700 (70.0)
Rural			300 (30.0)
Region (n = 1,000)			
North America			400 (40.0)
Europe			300 (30.0)
Asia			200 (20.0)
Other			100 (10.0)
Genotype (n = 1,000)			
Wild type			500 (50.0)
Heterozygous			400 (40.0)
Homozygous			100 (10.0)
Mutation (n = 1,000)			
Yes			200 (20.0)
No			800 (80.0)
Mutation type (n = 1,000)			
Missense			100 (10.0)
Nonsense			50 (5.0)
Frameshift			30 (3.0)
Splicing			20 (2.0)
Other			10 (1.0)
Mutation location (n = 1,000)			
Exon			150 (15.0)
Intron			50 (5.0)
Other			10 (1.0)
Mutation frequency (n = 1,000)			
Rare			100 (10.0)
Common			100 (10.0)
Mutation impact (n = 1,000)			
Pathogenic			100 (10.0)
Benign			100 (10.0)
Mutation consequence (n = 1,000)			
Loss of function			100 (10.0)
Gain of function			100 (10.0)
Mutation effect (n = 1,000)			
Dominant			100 (10.0)
Recessive			100 (10.0)
Mutation inheritance (n = 1,000)			
Autosomal dominant			100 (10.0)
Autosomal recessive			100 (10.0)
Mutation penetrance (n = 1,000)			
Complete			100 (10.0)
Incomplete			100 (10.0)
Mutation expressivity (n = 1,000)			
Variable			100 (10.0)
Constant