Supplementary Table

Supp Table 1. SNPs chromosomal localization and variant allele frequency (VAF) within all subjects and according to database (dbGaP VAF).

SNP	Chromosome localization	ref/ref		ref/var var/var		VAF		dbGaP VAF
rs1356229	3:4087317 intron	CC	536 (96.2%)	CT TT	21 (3.8%) 0 (0.0%)	C T	0.98 0.02	0.97 0.03
rs308739	3:4334346 intron	CC	484 (87.1%)	CA AA	72 (12.9%) 0 (0.0%)	C A	0.94 0.06	0.94 0.06
rs4685744	3:4361853 intron/utr3	CC	152 (27.3%)	CT TT	260 (46.7%) 145 (26.0%)	C T	0.51 0.49	0.50 0.50
rs2819562	3:4361930 intron/utr3	CC	123 (22.1%)	CT TT	256 (46.0%) 177 (31.8%)	C T	0.45 0.55	0.45 0.55
rs2819561	3:4362083 intron/utr3	AA	123 (22.1%)	AG GG	257 (46.2%) 176 (31.7%)	A G	0.45 0.55	0.45 0.55
rs2633852	3:4362153 intron/cds-syn	AA	121 (21.8%)	AG GG	255 (46.0%) 178 (32.1%)	A G	0.45 0.55	0.42 0.58
rs11915920	3:4368850 intron/utr3	CC	154 (27.7%)	CT TT	261 (46.9%) 141 (25.4%)	C T	0,51 0.49	0.50 0.50
rs807785	3:4379029 intron	CC	50 (9.0%)	CT TT	234 (42.0%) 273 (49.0%)	C T	0.30 0.70	0.30 0.70
rs3864051	3:4390432 Intron	CC	297 (53.5%)	CT TT	245 (44.1%) 13 (2.3%)	C T	0.76 0.24	0.67 0.34
rs794187	3:4394488 Intron	CC	231 (41.5%)	CT TT	260 (46.8%) 65 (11.7%)	C T	0.65 0.35	0.66 0.34
rs794185	3:4395674 Intron	TT	166 (29.8%)	TC CC	287 (51.5%) 104 (18.7%)	T C	0.56 0.44	0.58 0.42
rs2322683	3:4426914 intron	CC	73 (13.1%)	CT TT	237 (42.6%) 246 (44.2%)	C T	0.34 0.66	0.33 0.67
rs793391	3:4427508 intron	TT	255 (45.8%)	TG GG	239 (42.9%) 63 (11.3%)	T G	0.67 0.33	0.70 0.30
rs12634249	3:4444619 intron	CC	321 (57.6%)	CA AA	203 (36.4%) 33 (5.9%)	C A	0.76 0.24	0.77 0.23
rs2819590	3:4467058 missense	CC	283 (51.1%)	CT TT	222 (40.1%) 49 (8.8%)	C T	0.71 0.29	0.71 0.29
rs304092	3:4477309 unknown	GG	277 (49.8%)	GA AA	229 (41.2) 50 (9.0%)	G A	0.70 0.30	0.71 0.29

SNPs are sorted according to chromosome localization (chromosome localization is from GRCh 38.p12).

dbGaPVAF is from ALFA Allele Frequency project (ethnical origin: European), release version: 20201027095038