Supplementary Table S2: Results of FBAT test among exposed and unexposed siblings and of FBAT homogeneity test in the EGEA and SLSJ samples for SNPs detected in EGEA with P≤5x10-3.

							EGEA						SLSJ						EGEA+SLSJ*					
							ETS exposed (1)		ETS unexposed (2)		FBAT-homogeneity test between (1) and (2)		ETS exposed (1)		ETS unexposed (2)		FBAT-homogeneity test between (1) and (2)		ETS exposed (1)		ETS unexposed (2)		FBAT-homogeneity test between (1) and (2)	
Chrom	SNP	Gene	location	position**	allele#	EAF##	Z	*P*	Z	*P*	c^2_{1df}	*P*	Z	*P*	Z	*P*	c^2_{1df}	*P*	Z	*P*	z	*P*	c^2_{1df}	*P*
1	rs10924249	KIF26B	flanking_3UTR	243837265	G/T	0.19	1.04	3.0E-01	-2.84	4.5E-03	8.15	4.3E-03	-0.70	4.8E-01	0.77	4.4E-01	1.07	3.0E-01	0.25	8.0E-01	-2.07	3.9E-02	3.58	5.9E-02
2	rs6736802	KIF5C	flanking_5UTR	149566980	A/C	0.56	2.70	6.9E-03	-1.64	1.0E-01	9.31	2.3E-03	-0.76	4.5E-01	0.69	4.9E-01	0.99	3.2E-01	1.60	1.1E-01	-1.18	2.4E-01	3.65	5.6E-02
2	rs6435220	KIF5C	flanking_5UTR	149569925	A/G	0.32	-2.84	4.5E-03	1.44	1.5E-01	8.77	3.1E-03	1.15	2.5E-01	0.32	7.5E-01	0.19	6.6E-01	-1.66	9.7E-02	1.40	1.6E-01	4.59	3.2E-02
4	rs1460354	ATP8A1	intron	42266423	C/T	0.78	-2.58	1.0E-02	1.96	5.0E-02	10.21	1.4E-03	-0.51	6.1E-01	1.59	1.1E-01	2.48	1.2E-01	-2.33	2.0E-02	2.52	1.2E-02	11.78	6.0E-04
4	rs13124088	ATP8A1	intron	42280405	A/G	0.80	-2.60	9.3E-03	1.43	1.5E-01	7.91	4.9E-03	0.00	1.0E+00	1.55	1.2E-01	1.46	2.3E-01	-2.00	4.5E-02	2.07	3.8E-02	8.29	4.0E-03
4	rs17448506	ATP8A1	intron	42343155	C/T	0.73	-3.99	6.6E-05	2.28	2.3E-02	18.51	1.7E-05	0.11	9.1E-01	1.93	5.3E-02	2.26	1.3E-01	-3.33	8.7E-04	2.94	3.3E-03	19.23	1.2E-05
6	rs160666	WRNIP1	flanking_3UTR	2719051	A/C	0.32	1.86	6.3E-02	-2.37	1.8E-02	9.01	2.7E-03	-0.28	7.8E-01	0.90	3.7E-01	0.71	4.0E-01	1.33	1.8E-01	-1.55	1.2E-01	4.17	4.1E-02
8	rs2279444	KIF13B	intron	29053769	A/G	0.16	2.24	2.5E-02	-1.80	7.3E-02	8.05	4.5E-03	0.73	4.7E-01	-0.45	6.5E-01	0.71	4.0E-01	2.26	2.4E-02	-1.62	1.0E-01	7.56	6.0E-03
9	rs2253304	ABCA1	intron	106658884	A/G	0.73	1.16	2.5E-01	-2.72	6.6E-03	8.09	4.5E-03	1.35	1.8E-01	-2.66	7.8E-03	8.65	3.3E-03	1.74	8.2E-02	-3.73	1.9E-04	16.06	6.1E-05
9	rs2253182	ABCA1	intron	106659945	C/G	0.27	-1.16	2.5E-01	2.72	6.6E-03	8.09	4.5E-03	-1.24	2.2E-01	2.55	1.1E-02	7.76	5.3E-03	-1.68	9.4E-02	3.65	2.6E-04	15.30	9.2E-05
9	rs2253175	ABCA1	intron	106660120	C/T	0.27	-1.16	2.5E-01	2.72	6.6E-03	8.09	4.5E-03	-1.24	2.2E-01	2.66	7.8E-03	8.28	4.0E-03	-1.68	9.4E-02	3.73	1.9E-04	15.75	7.2E-05
9	rs2253174	ABCA1	intron	106660153	A/G	0.73	1.16	2.5E-01	-2.72	6.6E-03	8.09	4.5E-03	1.24	2.2E-01	-2.66	7.8E-03	8.28	4.0E-03	1.68	9.4E-02	-3.73	1.9E-04	15.75	7.2E-05
9	rs2230805	ABCA1	coding	106663850	C/T	0.25	-0.91	3.6E-01	2.82	4.8E-03	7.99	4.7E-03	-1.71	8.8E-02	1.72	8.6E-02	5.67	1.7E-02	-1.78	7.6E-02	3.30	9.6E-04	13.84	2.0E-04
11	rs762667	MYO7A	coding	76546020	C/T	0.62	2.33	2.0E-02	-2.03	4.2E-02	9.32	2.3E-03	0.00	1.0E+00	-0.88	3.8E-01	0.58	4.5E-01	1.99	4.7E-02	-2.21	2.7E-02	8.79	3.0E-03
16	rs2914819	ATP2C2	intron	83026812	A/G	0.82	1.64	1.0E-01	-2.53	1.1E-02	8.99	2.7E-03	1.12	2.6E-01	-0.38	7.1E-01	0.86	3.5E-01	1.98	4.7E-02	-2.41	1.6E-02	9.75	1.8E-03
17	rs7225157	DNAH9	intron	11621510	A/G	0.17	2.09	3.7E-02	-2.66	7.9E-03	11.22	8.1E-04	1.48	1.4E-01	-1.53	1.3E-01	4.32	3.8E-02	2.56	1.0E-02	-3.05	2.3E-03	15.86	6.8E-05
18	rs12458154	ATP9B	intron	75187747	A/C	0.29	1.83	6.8E-02	-2.43	1.5E-02	9.17	2.5E-03	1.23	2.2E-01	0.05	9.6E-01	0.35	5.5E-01	2.18	3.0E-02	-1.88	6.0E-02	8.00	4.7E-03
20	rs6067867	ATP9A	intron	49698286	A/G	0.55	1.98	4.8E-02	-2.04	4.1E-02	8.02	4.6E-03	0.70	4.9E-01	-0.58	5.6E-01	0.78	3.8E-01	1.95	5.1E-02	-1.99	4.6E-02	7.68	5.6E-03
20	rs6067892	ATP9A	intron	49731315	A/G	0.47	-2.12	3.4E-02	2.20	2.8E-02	9.19	2.4E-03	-0.53	5.9E-01	0.63	5.3E-01	0.68	4.1E-01	-1.96	5.0E-02	2.18	3.0E-02	8.47	3.6E-03
20	rs1475670	ATP9A	intron	49777965	C/T	0.50	-1.73	8.4E-02	2.29	2.2E-02	8.19	4.2E-03	-0.78	4.3E-01	1.77	7.6E-02	3.59	5.8E-02	-1.81	7.0E-02	2.89	3.9E-03	11.48	7.0E-04

*: combined analysis by Stouffer's Z-score method

**: position in base pairs (dbSNP, build 37.1)

#: Baseline allele / Effect allele

##: Effect Allele frequency estimated in EGEA