

Supporting Online Materials for:

Attempted replication of 50 reported asthma risk genes identifies a SNP in RAD50 as associated with childhood atopic asthma

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Table S-1. Associations between all assayed SNPs in candidate genes and childhood atopic asthma

Gene	Rank ^A	SNP	Assay ID ^B	Allele / Genotype	Cases		Controls		P-value		OR (95% CI) (overall)	
					N	%	N	%	(overall) ^C	(non-GWA) ^D	Comparison	Estimate
MUC5AC	1	rs2014486	C__1582230_10	G	104	51.5	492	51.4	0.97	0.67	A vs. G	0.99 (0.73-1.35)
				A	98	48.5	466	48.6				
				GG	24	23.8	135	28.2	0.25	0.91	AA vs. GG	0.97 (0.51-1.83)
				GA	56	55.4	222	46.3			GA vs. GG	1.42 (0.84-2.40)
PTPRD	2	rs10120501	C__8079074_20	T	84	41.6	431	44.3	0.47	0.49	C vs. T	1.12 (0.82-1.52)
				C	118	58.4	541	55.7				
				TT	16	15.8	92	18.9	0.74	0.23	CC vs. TT	1.29 (0.67-2.48)
				TC	52	51.5	247	50.8			TC vs. TT	1.21 (0.66-2.23)
PTPRD	2	rs7856322	C__29008083_20	G	184	91.1	798	81.6	0.0010 [†]	0.12	T vs. G	0.43 (0.26-0.72)
				T	18	8.90	180	18.4				
				GG	83	82.2	328	67.1	0.0051	0.29	TT vs. GG	NC
				GT	18	17.8	142	29.0			GT vs. GG	0.50 (0.29-0.87)
TNF	3	rs1800629	C__7514879_10	G	176	88.0	831	85.3	0.32	N/A	A vs. G	0.79 (0.50-1.26)
				A	24	12.0	143	14.7				
				GG	78	78.0	359	73.7	0.63	N/A	AA vs. GG	0.61 (0.14-2.74)
				GA	20	20.0	113	23.2			GA vs. GG	0.81 (0.48-1.39)
CTNNA3	4	rs1015484	C__32349527_10	C	183	92.4	926	94.9	0.17	0.33	T vs. C	1.52 (0.83-2.76)
				T	15	7.6	50	5.1				
				CC	84	84.8	439	90.0	0.27	0.61	TT vs. CC	NC
				CT	15	15.2	48	9.8			CT vs. CC	1.63 (0.87-3.05)
IL4R	7	rs1801275	C__2351160_20	A	128	64.6	712	74.2	0.0063*	N/A	G vs. A	1.57 (1.13-2.17)
				G	70	35.4	248	25.8				
				GG	45	45.5	263	54.8	0.0044*	N/A	AA vs. GG	3.02 (1.53-5.96)
				GA	38	38.4	186	38.8			GA vs. GG	1.19 (0.75-1.91)
AA	16	16.2	31	6.5								

Table S-1. Associations between all assayed SNPs in candidate genes and childhood atopic asthma (continued)

Gene	Rank ^A	SNP (type)	Assay ID	Allele / Genotype		Cases		Controls		P-value		OR (95% CI) (overall)	
				N	%	N	%	(overall) ^D	(non-GWA) ^E	Comparison	Estimate		
IL4R	7	rs1805010	C__2769554_10	A	105	52.5	520	53.7	0.75	N/A	G vs. A	1.05 (0.77-1.42)	
				G	95	47.5	448	46.3					
				AA	28	28.0	142	29.3	0.95	N/A	GG vs. AA	1.10 (0.60-2.02)	
				AG	49	49.0	236	48.8			AG vs. AA	1.05 (0.63-1.75)	
				GG	23	23.0	106	21.9					
ZFR	8	rs889318	C__7508162_20	C	114	57.6	547	57.2	0.93	0.27	T vs. C	0.99 (0.72-1.34)	
				T	84	42.4	409	42.8					
				CC	35	35.4	165	34.5	0.98	0.30	TT vs. CC	0.98 (0.54-1.80)	
				CT	44	44.4	217	45.4			CT vs. CC	0.96 (0.59-1.56)	
				TT	20	20.2	96	20.1					
DAP3	10	rs821551	C__1463658_10	C	96	48.0	567	59.7	0.0024 [†]	0.17	A vs. C	1.60 (1.18-2.18)	
				A	104	52.0	383	40.3					
				CC	28	28.0	183	38.5	0.011 [†]	0.26	AA vs. CC	2.30 (1.30-4.05)	
				CA	40	40.0	201	42.3			CA vs. CC	1.30 (0.77-2.19)	
				AA	32	32.0	91	19.2					
IL13	11	rs20541	C__2259921_20	G	158	80.6	773	80.4	0.93	0.37	A vs. G	0.98 (0.67-1.45)	
				A	38	19.4	189	19.6					
				GG	63	64.3	315	65.5	0.68	0.42	AA vs. GG	0.65 (0.19-2.40)	
				GA	32	32.7	143	29.7			GA vs. GG	1.12 (0.7-1.79)	
				AA	3	3.1	23	4.8					
RAD50	12	rs2706347	C__16274080_10	G	121	60.5	736	75.1	0.000024 ^{**}	0.038 [*]	T vs. G	1.97 (1.43-2.71)	
				T	79	39.5	244	24.9					
				GG	43	43.0	287	58.6	0.00011 ^{**}	0.071	TT vs. GG	3.58 (1.95-6.59)	
				GT	35	35.0	162	33.1			GT vs. GG	1.44 (0.89-2.34)	
				TT	22	22.0	41	8.4					
ADAM33	13	rs2280090	C__15969380_10	G	167	83.5	817	84.8	0.66	N/A	A vs. G	1.10 (0.73-1.66)	
				A	33	16.5	147	15.2					
				GG	71	71.0	351	72.8	0.91	N/A	AA vs. GG	1.24 (0.40-3.81)	
				GA	25	25.0	115	23.9			GA vs. GG	1.07 (0.65-1.78)	
				AA	4	4.0	16	3.3					
TGFB1	13	rs1800469	C__8708473_10	G	128	64.0	664	68.7	0.19	N/A	A vs. G	1.24 (0.90-1.70)	
				A	72	36.0	302	31.3					
				GG	40	40.0	226	46.8	0.41	N/A	AA vs. GG	1.51 (0.73-3.10)	
				GA	48	48.0	212	43.9			GA vs. GG	1.28 (0.81-2.03)	
				AA	12	12.0	45	9.3					

Table S-1. Associations between all assayed SNPs in candidate genes and childhood atopic asthma (continued)

Gene	Rank ^A	SNP (type)	Assay ID	Allele / Genotype	Cases		Controls		P-value		OR (95% CI) (overall)	
					N	%	N	%	(overall) ^D	(non-GWA) ^E	Comparison	Estimate
ADRB2	14	rs1042713	C__2084764_20	G	117	59.1	578	60.1	0.80	N/A	A vs. G	1.04 (0.76-1.42)
				A	81	40.9	384	39.9				
				GG	36	36.4	172	35.8	0.77	N/A	AA vs. GG	1.15 (0.61-2.15)
				GA	45	45.5	234	48.6			GA vs. GG	0.92 (0.57-1.49)
GSTP1	15	rs1695	C__3237198_20	A	132	66.0	633	65.7	0.93	0.80	G vs. A	0.99 (0.71-1.36)
				G	68	34.0	331	34.3				
				AA	41	41.0	209	43.4	0.52	0.65	GG vs. AA	0.79 (0.36-1.72)
				AG	50	50.0	215	44.6			AG vs. AA	1.19 (0.75-1.87)
				GG	9	9.0	58	12.0				
AOAH	16	rs2251949	C__15921708_10	C	164	82.0	803	82.6	0.84	0.11	T vs. C	1.04 (0.70-1.55)
				T	36	18.0	169	17.4				
				CC	70	70.0	330	67.9	0.15	0.21	TT vs. CC	2.18 (0.80-5.92)
				CT	24	24.0	143	29.4			CT vs. CC	0.79 (0.48-1.31)
TT	6	6.0	13	2.7								
MS4A2	17	rs569108	C__900116_10	A	191	95.5	937	96.4	0.54	N/A	G vs. A	1.26 (0.60-2.67)
				G	9	4.5	35	3.6				
				AA	91	91.0	452	93.0	0.67	N/A	GG vs. AA	NC
				AG	9	9.0	33	6.8			AG vs. AA	1.35 (0.63-2.93)
GG	0	0.0	1	0.2								
PTPRE	19	rs10830196	C__2009016_10	C	124	62.6	706	72.0	0.0081*	0.26	T vs. C	1.54 (1.12-2.12)
				T	74	37.4	274	28.0				
				CC	32	32.3	264	53.9	0.000039**	0.038*	TT vs. CC	1.20 (0.50-2.88)
				CT	60	60.6	178	36.3			CT vs. CC	2.78 (1.74-4.45)
TT	7	7.1	48	9.8								
MEFV	22	rs2741919	C__1388036_10	T	102	51.0	567	58.5	0.052	0.10	C vs. T	1.35 (1.0-1.83)
				C	98	49.0	403	41.5				
				TT	22	22.0	169	34.8	0.042	0.20	CC vs. TT	1.77 (0.91-3.41)
				TC	58	58.0	229	47.2			TC vs. TT	1.95 (1.15-3.30)
CC	20	20.0	87	17.9								
HAVCR2	23	rs11741184	C__30832167_10	G	154	78.6	725	74.9	0.28	0.14	C vs. G	0.81 (0.56-1.18)
				C	42	21.4	243	25.1				
				GG	62	63.3	263	54.3	0.14	0.30	CC vs. GG	1.16 (0.45-2.97)
				GC	30	30.6	199	41.1			GC vs. GG	0.64 (0.40-1.03)
CC	6	6.1	22	4.5								
HAVCR2	23	rs10515746	C__2082054_20	C	159	79.5	768	79.2	0.92	0.32	A vs. C	0.98 (0.67-1.43)
				A	41	20.5	202	20.8				
				CC	63	63.0	297	61.2	0.75	0.49	AA vs. CC	1.35 (0.43-4.23)
				CA	33	33.0	174	35.9			CA vs. CC	0.89 (0.56-1.42)
AA	4	4.0	14	2.9								

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Gene	Rank ^A	SNP (type)	Assay ID	Allele / Genotype	Cases		Controls		P-value		OR (95% CI) (overall)	
					N	%	N	%	(overall) ^D	(non-GWA) ^E	Comparison	Estimate
NOS1	24	rs7977109	C__3141919_10	G	73	35.8	447	46.9	0.0039 [†]	0.28	A vs. G	1.58 (1.16-2.16)
				A	131	64.2	507	53.1				
				GG	13	12.7	105	22.0	0.016 [†]	0.48	AA vs. GG	2.51 (1.28-4.92)
				GA	47	46.1	237	49.7			GA vs. GG	1.60 (0.83-3.09)
DPP10	26	rs7606549	C__29021725_10	A	81	40.5	468	49.1	0.028 [†]	0.17	G vs. A	1.41 (1.04-1.93)
				G	119	59.5	486	50.9				
				AA	18	18.0	118	24.7	0.084	0.39	GG vs. AA	1.91 (1.03-3.54)
				AG	45	45.0	232	48.6			AG vs. AA	1.27 (0.70-2.29)
TCRB1	27	rs17291	C__2483960_10	G	122	61.0	642	66.0	0.17	0.39	A vs. G	1.24 (0.91-1.70)
				A	78	39.0	330	34.0				
				GG	37	37.0	212	43.6	0.39	0.64	AA vs. GG	1.53 (0.79-2.99)
				GA	48	48.0	218	44.9			GA vs. GG	1.26 (0.79-2.02)
FYN	28	rs9374283	C_29828201_10	T	197	98.5	944	96.1	0.095	0.73	C vs. T	0.38 (0.12-1.24)
				C	3	1.5	38	3.9				
				TT	97	97.0	454	92.5	0.25	0.93	CC vs. TT	NC
				TC	3	3.0	36	7.3			TC vs. TT	0.39 (0.12-1.29)
IL16	29	rs4128766	C__26994392_10	G	137	69.2	749	77.9	0.0089 [†]	0.46	A vs. G	1.57 (1.12-2.20)
				A	61	30.8	213	22.1				
				GG	49	49.5	294	61.1	0.032 [†]	0.63	AA vs. GG	2.54 (1.18-5.47)
				GA	39	39.4	161	33.5			GA vs. GG	1.45 (0.92-2.31)
IFNGR2	30	rs9978166	C__26795977_10	A	159	81.1	822	84.7	0.21	0.0089	G vs. A	1.29 (0.87-1.92)
				G	37	18.9	148	15.3				
				AA	65	66.3	346	71.3	0.31	0.03	GG vs. AA	2.37 (0.71-7.91)
				AG	29	29.6	130	26.8			AG vs. AA	1.19 (0.73-1.92)
ORMDL3	31	rs7216389	C__29062108_10	C	80	40.0	437	45.0	0.20	N/A	T vs. C	1.23 (0.90-1.67)
				T	120	60.0	535	55.0				
				CC	19	19.0	97	20.0	0.20	N/A	TT vs. CC	1.36 (0.74-2.50)
				CT	42	42.0	243	50.0			CT vs. CC	0.88 (0.49-1.59)
IL10	33	rs1800896	C__1747360_10	C	85	43.4	415	42.8	0.88	N/A	T vs. C	0.98 (0.72-1.33)
				T	111	56.6	555	57.2				
				CC	19	19.4	90	18.6	0.98	N/A	TT vs. CC	0.95 (0.51-1.77)
				CT	47	48.0	235	48.5			CT vs. CC	0.95 (0.53-1.70)
TT	32	32.7	160	33.0								

Table S-1. Associations between all assayed SNPs in candidate genes and childhood atopic asthma (continued)

Gene	Rank ^A	SNP (type)	Assay ID	Allele / Genotype	Cases		Controls		P-value		OR (95% CI) (overall)	
					N	%	N	%	(overall) ^D	(non-GWA) ^E	Comparison	Estimate
SCGB1A1	33	rs3741240	C__25473445_10	G	135	67.5	646	66.3	0.75	N/A	A vs. G	0.95 (0.69-1.31)
				A	65	32.5	328	33.7				
				GG	42	42.0	224	46.0	0.078	N/A	AA vs. GG	0.57 (0.25-1.34)
				GA	51	51.0	198	40.7			GA vs. GG	1.37 (0.88-2.16)
AA	7	7.0	65	13.3								
NOS2	36	rs6505524	C__2593752_10	C	117	59.1	516	53.6	0.16	0.95	A vs. C	0.80 (0.59-1.09)
				A	81	40.9	446	46.4				
				CC	30	30.3	140	29.1	0.080	0.97	AA vs. CC	0.53 (0.26-1.09)
				CA	57	57.6	236	49.1			CA vs. CC	1.13 (0.69-1.84)
AA	12	12.1	105	21.8								
IL8RA	37	rs2671222	Custom	C	178	89.9	893	92.3	0.27	0.00064	T vs. C	1.34 (0.80-2.25)
				T	20	10.1	75	7.7				
				CC	80	80.8	413	85.3	0.52	0.0035	TT vs. CC	1.29 (0.14-11.7)
				CT	18	18.2	67	13.8			CT vs. CC	1.39 (0.78-2.46)
TT	1	1.0	4	0.8								
CTTN	39	rs583397	C__590420_10	C	164	82.8	762	78.9	0.21	0.62	A vs. C	0.77 (0.52-1.16)
				A	34	17.2	204	21.1				
				CC	69	69.7	299	61.9	0.32	0.88	AA vs. CC	0.87 (0.29-2.62)
				CA	26	26.3	164	34.0			CA vs. CC	0.69 (0.42-1.12)
AA	4	4.0	20	4.1								
CCL5	39	rs2280788	C__15874396_20	G	197	98.5	939	97.4	0.36	N/A	C vs. G	0.57 (0.17-1.91)
				C	3	1.5	25	2.6				
				GG	98	98.0	457	94.8	0.017*	N/A	CC vs. GG	NC
				GC	1	1.0	25	5.2			GC vs. GG	0.19 (0.02-1.39)
CC	1	1.0	0	0.0								
IL1RN	39	rs447713	C__8737974_10	A	157	78.5	732	75.8	0.41	N/A	G vs. A	0.86 (0.59-1.24)
				G	43	21.5	234	24.2				
				AA	61	61.0	280	58.0	0.62	N/A	GG vs. AA	0.59 (0.20-1.74)
				AG	35	35.0	172	35.6			AG vs. AA	0.93 (0.59-1.48)
GG	4	4.0	31	6.4								
PTGDR	39	rs11157907	C__3226996_10	T	172	86.9	811	84.3	0.36	N/A	C vs. T	0.81 (0.52-1.27)
				C	26	13.1	151	15.7				
				TT	73	73.7	345	71.7	0.20	N/A	CC vs. TT	NC
				TC	26	26.3	121	25.2			TC vs. TT	1.02 (0.62-1.66)
CC	0	0.0	15	3.1								
STAT6	39	rs324015	C__620398_10	C	166	83.0	735	77.5	0.087	N/A	T vs. C	0.71 (0.47-1.05)
				T	34	17.0	213	22.5				
				CC	68	68.0	287	60.5	0.20	N/A	TT vs. CC	0.32 (0.08-1.40)
				CT	30	30.0	161	34.0			CT vs. CC	0.79 (0.49-1.26)
TT	2	2.0	26	5.5								

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Gene	Rank ^A	SNP (type)	Assay ID	Allele / Genotype	Cases		Controls		P-value		OR (95% CI) (overall)	
					N	%	N	%	(overall) ^D	(non-GWA) ^E	Comparison	Estimate
TBX21	39	rs4794067	C__11626504_10	T	159	79.5	701	73.6	0.083	N/A	C vs. T	0.72 (0.50-1.05)
				C	41	20.5	251	26.4				
				TT	63	63.0	264	55.5	0.22	N/A	CC vs. TT	0.43 (0.15-1.25)
				TC	33	33.0	173	36.3			TC vs. TT	0.80 (0.50-1.27)
				CC	4	4.0	39	8.2				
TBXA2R	39	rs4523	C__2576299_10	G	143	71.5	622	64.0	0.042*	N/A	A vs. G	0.71 (0.51-0.99)
				A	57	28.5	350	36.0				
				GG	54	54.0	200	41.2	0.060	N/A	AA vs. GG	0.64 (0.31-1.29)
				GA	35	35.0	222	45.7			AG vs. GG	0.58 (0.37-0.93)
				AA	11	11.0	64	13.2				
OPN3	42	rs1053230	C__8856260_10	C	154	78.6	772	80.2	0.59	0.53	T vs. C	1.11 (0.76-1.61)
				T	42	21.4	190	19.8				
				CC	63	64.3	307	63.8	0.18	0.78	TT vs. CC	2.13 (0.84-5.40)
				CT	28	28.6	158	32.8			CT vs. CC	0.86 (0.53-1.40)
				TT	7	7.1	16	3.3				
IL33	44	rs16924243	C__34291163_10	T	179	89.5	919	94.7	0.0050 [†]	0.28	C vs. T	2.11 (1.24-3.60)
				C	21	10.5	51	5.3				
				TT	80	80.0	437	90.1	0.016 [†]	0.38	CC vs. TT	1.82 (0.19-17.73)
				TC	19	19.0	45	9.3			TC vs. TT	2.31 (1.28-4.15)
				CC	1	1.0	3	0.6				
AFM234TB10	45	rs6489058	C__2599062_10	G	155	78.3	703	72.9	0.12	0.35	T vs. G	0.75 (0.52-1.08)
				T	43	21.7	261	27.1				
				GG	61	61.6	258	53.5	0.30	0.23	TT vs. GG	0.57 (0.22-1.51)
				GT	33	33.3	187	38.8			GT vs. GG	0.75 (0.47-1.19)
				TT	5	5.1	37	7.7				
PDGFRA	46	rs7656613	C__128991_10	T	161	80.5	699	72.1	0.014 [†]	0.38	C vs. T	0.62 (0.43-0.91)
				C	39	19.5	271	27.9				
				TT	66	66.0	262	54.0	0.064	0.68	CC vs. TT	0.41 (0.16-1.08)
				TC	29	29.0	175	36.1			TC vs. TT	0.66 (0.41-1.06)
				CC	5	5.0	48	9.9				
CCL11	48	rs3744508	Custom	G	173	85.6	816	85.0	0.82	1.00	A vs. G	0.95 (0.62-1.46)
				A	29	14.4	144	15.0				
				GG	75	74.3	346	72.1	0.72	0.66	AA vs. GG	1.38 (0.37-5.15)
				GA	23	22.8	124	25.8			GA vs. GG	0.86 (0.51-1.43)
				AA	3	3.0	10	2.1				

Table S-1 footer note:

A: Position in list of 251 genes identified to be associated with asthma, ranked from highest to lowest gene ranking score. Genes may have the same rank if they had identical gene ranking scores. **B:** Applied Biosystems catalogue number of the pre-made TaqMan assay for this SNP. “Custom” indicates that this assay used custom primers. **C:** Two-tailed chi-square P-values among all samples (n=103 cases and n=499 controls assayed; actual genotype counts are lower due to absent uncalled samples). **D:** Two-tailed chi-square P-values only among samples that were not previously genotyped in the PRAM GWAS (n=38 cases and n=457 controls assayed). This value was not applicable (N/A) if there was no prior evidence for these genes in the PRAM GWA (i.e., such genes were not selected due to prior evidence already present in the whole sample set). *: $0.0011 < P\text{-value} < 0.05$ and the gene for this SNP was not selected due to prior evidence in the PRAM GWAS. **: $P\text{-value} < 0.0011$ (Bonferroni-corrected value of $\alpha=0.05$ for 44 SNP comparisons) . †: $P\text{-value} < 0.05$ in the overall sample, but no independent replication of association was observed in the non-GWAS samples. All SNPs listed had a call rate $> 95\%$ among cases and controls and a chi-square HWE test $P\text{-value} > 0.00096$ among controls. NC indicates that an odds ratio could not be calculated for this comparison due to a zero cell count.

Table S-2. Prior evidence measures of all candidate asthma risk genes.

Name	Chromo- some	Prior evidence measures			References ^E	Assayed in current study? ^F	
		Rank ^A	Overall score ^B	GWAS score ^C			Publication score ^D
MUC5AC	11	1	48.87	47.87	1	[1]	Yes
PTPRD	9	2	47.84	46.84	1	[2]	Yes
TNF	6	3	31.00	0.00	31	[3-33]	Yes
CTNNA3	10	4	29.85	28.85	1	[34]	Yes
PDE4D	5	5	25.05	24.05	1	[35]	Yes
ADAMTS12	5	6	24.76	23.76	1	[36]	Yes
IL4R	16	7	23.00	0.00	23	[32,37-58]	Yes
ZFR	5	8	19.82	18.82	1	[36]	Yes
IL4	5	9	18.00	0.00	18	[37,38,46,49,54,59-71]	Yes
DAP3	1	10	15.71	14.71	1	[72]	Yes
GSTM1	1	11	15.00	0.00	15	[73-87]	No, deletion
IL13	5	11	15.00	0.00	15	[39,41,44,62,65,71,88-96]	Yes
RAD50	5	12	14.37	12.37	2	[92,97]	Yes
ADAM33	20	13	13.00	0.00	13	[98-110]	Yes
HLA-DRB1	6	13	13.00	0.00	13	[28,29,111-121]	No, HLA polymorphism
TGFB1	19	13	13.00	0.00	13	[7,23,51,122-131]	Yes
ADRB2	5	14	12.00	0.00	12	[132-143]	Yes
GSTP1	11	15	11.00	0.00	11	[77,80,84,144-151]	Yes
AOAH	7	16	10.98	9.98	1	[152]	Yes
MS4A2	11	17	10.00	0.00	10	[138,153-161]	Yes
NPSR1	7	18	9.50	1.50	8	[88,162-168]	No, assay design failure for identified SNP
PTPRE	10	19	9.15	8.15	1	[169]	Yes
CD14	5	20	9.00	0.00	9	[39,122,170-176]	Yes
GSTT1	22	21	8.00	0.00	8	[73,78,79,84,85,87,177,178]	No, deletion
HLA-DQB1	6	21	8.00	0.00	8	[92,112,115,116,118,179-181]	No, HLA polymorphism
LTA	6	21	8.00	0.00	8	[3,26-28,31,117,182,183]	No, RFLP polymorphism
MEFV	16	22	7.71	6.71	1	[184]	Yes
HAVCR2	5	23	7.07	4.07	3	[185-187]	Yes
NOS1	12	24	7.03	3.03	4	[188-191]	Yes
FLG	1	25	7.00	0.00	7	[192-198]	No, multiple loss of function polymorphisms
IFNG	12	25	7.00	0.00	7	[32,199-204]	No, repeat polymorphism
DPP10	2	26	6.84	1.84	5	[98,131,205-207]	Yes
TCRB	7	27	6.77	5.77	1	[208]	Yes
FYN	6	28	6.61	5.61	1	[209]	Yes
IL16	15	29	6.18	5.18	1	[210]	Yes
IFNGR2	21	30	6.07	5.07	1	[88]	Yes
ACE	17	31	6.00	0.00	6	[211-216]	No, deletion
ORMDL3	17	31	6.00	0.00	6	[217-222]	Yes
STAT4	2	32	5.76	4.76	1	[201]	Yes
HLA-DPB1	6	33	5.00	0.00	5	[112,120,223-225]	No, HLA polymorphism
IL10	1	33	5.00	0.00	5	[33,126,226-228]	Yes
SCGB1A1	11	33	5.00	0.00	5	[229-233]	Yes
HLA-DQA1	6	34	4.89	1.89	3	[116,179,180]	No, HLA polymorphism
PTGER3	1	35	4.84	2.84	2	[234,235]	Yes
NOS2	17	36	4.63	1.63	3	[236-238]	Yes

IL8RA	2	37	4.58	3.58	1	[239]	Yes
MYLK	3	38	4.21	2.21	2	[240,241]	Yes
CTTN	11	39	3.97	2.97	1	[242]	Yes
CCL5	17	39	4.00	0.00	4	[243-246]	Yes
CCR5	3	39	4.00	0.00	4	[247-250]	No, gene increased in rank order while study in progress
CYSLTR1	X	39	4.00	0.00	4	[251-254]	Yes
IL18	11	39	4.00	0.00	4	[255-258]	No, assay design failure
IL1RL1	2	39	4.00	0.00	4	[131,226,259,260]	No, gene increased in rank order while study in progress
IL1RN	2	39	4.00	0.00	4	[25,261-263]	Yes
IRF1	5	39	4.00	0.00	4	[203,204,264,265]	No, repeat polymorphism
LTC4S	5	39	4.00	0.00	4	[252,266-268]	Yes
NAT2	8	39	4.00	0.00	4	[269-272]	No, gene increased in rank order while study in progress
PTGDR	14	39	4.00	0.00	4	[273-276]	Yes
SERPINE1	17	39	4.00	0.00	4	[170,277-279]	No, assay design failure
STAT6	12	39	4.00	0.00	4	[88,191,280,281]	Yes
TBX21	17	39	4.00	0.00	4	[282-285]	Yes
TBXA2R	19	39	4.00	0.00	4	[234,286-288]	Yes
VDR	12	40	4.00	0.00	4	[88,289-291]	No, gene increased in rank order while study in progress
ALOX5AP	13	41	3.89	0.89	3	[292-294]	No, gene increased in rank order while study in progress
OPN3	1	42	3.83	2.83	1	[295]	Yes
CHI3L1	1	43	3.82	1.82	2	[296,297]	No, gene increased in rank order while study in progress
IL33	9	44	3.48	2.48	1	[260]	Yes
AFM234TB10	12	45	3.23	1.23	2	[298,299]	Yes
PDGFRA	4	46	3.07	2.07	1	[300]	Yes
TGFB2	1	47	3.02	2.02	1	[301]	No, gene increased in rank order while study in progress
AICDA	12	48	3.00	0.00	3	[42,302,303]	No, gene increased in rank order while study in progress
C3	19	48	3.00	0.00	3	[304-306]	No, gene increased in rank order while study in progress
CCL11	17	48	3.00	0.00	3	[307-309]	Yes
CCL24	7	48	3.00	0.00	3	[310-312]	No – gene count reached
CCL26	7	48	3.00	0.00	3	[310,311,313]	No – gene count reached
CSF2	5	48	3.00	0.00	3	[314-316]	No – gene count reached
CTLA4	2	48	3.00	0.00	3	[317-319]	No – gene count reached
CYBA	16	48	3.00	0.00	3	[320-322]	No – gene count reached
EDN1	6	48	3.00	0.00	3	[88,323,324]	No – gene count reached
GSDMB	17	48	3.00	0.00	3	[222,325,326]	No – gene count reached
HAVCR1	5	48	3.00	0.00	3	[186,327,328]	No – gene count reached
IL12B	5	48	3.00	0.00	3	[32,329,330]	No – gene count reached
IL5	5	48	3.00	0.00	3	[63,331,332]	No – gene count reached
NOD1	7	48	3.00	0.00	3	[333-335]	No – gene count reached

NOS3	7	48	3.00	0.00	3	[336-338]	No – gene count reached
PHF11	13	48	3.00	0.00	3	[163,339,340]	No – gene count reached
TLR10	4	48	3.00	0.00	3	[88,341,342]	No – gene count reached
TLR2	4	48	3.00	0.00	3	[174,343,344]	No – gene count reached
HLA-DRA	6	49	2.97	1.97	1	[92]	No – gene count reached
SFRS8	12	50	2.93	1.93	1	[345]	No – gene count reached
TNC	9	51	2.90	0.90	2	[167,346]	No – gene count reached
IKBKAP	9	52	2.88	1.88	1	[347]	No – gene count reached
IL17A	6	53	2.80	1.80	1	[348]	No – gene count reached
IRAK3	12	54	2.67	1.67	1	[349]	No – gene count reached
IL18R1	2	55	2.68	0.68	2	[131,350]	No – gene count reached
SOCS1	16	56	2.67	0.67	2	[334,351]	No – gene count reached
CCL2	17	57	2.65	0.65	2	[352,353]	No – gene count reached
LEPR	1	58	2.45	1.45	1	[354]	No – gene count reached
CYP2J2	1	59	2.43	1.43	1	[355]	No – gene count reached
CXCL12	10	60	2.42	1.42	1	[314]	No – gene count reached
DEFB1	8	61	2.35	0.35	2	[356,357]	No – gene count reached
IL5RA	3	62	2.31	1.31	1	[358]	No – gene count reached
CHIA	1	63	2.27	0.27	2	[359,360]	No – gene count reached
DAF	1	64	2.20	1.20	1	[361]	No – gene count reached
5-LO	10	65	2.00	0.00	2	[362,363]	No – gene count reached
AFM302WD9	12	65	2.00	0.00	2	[298,364]	No – gene count reached
AFM312WB5	7	65	2.00	0.00	2	[208,364]	No – gene count reached
AFM351TB9	12	65	2.00	0.00	2	[299,365]	No – gene count reached
ARG2	14	65	2.00	0.00	2	[366,367]	No – gene count reached
CCR2	3	65	2.00	0.00	2	[247,368]	No – gene count reached
CD86	3	65	2.00	0.00	2	[226,369]	No – gene count reached
CFTR	7	65	2.00	0.00	2	[370,371]	No – gene count reached
COX2	1	65	2.00	0.00	2	[372,373]	No – gene count reached
CYFIP2	5	65	2.00	0.00	2	[131,374]	No – gene count reached
GPR44	11	65	2.00	0.00	2	[375,376]	No – gene count reached
HLA-B	6	65	2.00	0.00	2	[377,378]	No – gene count reached
HNMT	2	65	2.00	0.00	2	[379,380]	No – gene count reached
ICAM1	19	65	2.00	0.00	2	[381,382]	No – gene count reached
IL1B	2	65	2.00	0.00	2	[25,383]	No – gene count reached
IL1R2	2	65	2.00	0.00	2	[32,384]	No – gene count reached
IL2	4	65	2.00	0.00	2	[126,385]	No – gene count reached
IL3	5	65	2.00	0.00	2	[253,386]	No – gene count reached
IL6	7	65	2.00	0.00	2	[32,263]	No – gene count reached
IL8	4	65	2.00	0.00	2	[387,388]	No – gene count reached
IL9	5	65	2.00	0.00	2	[69,389]	No – gene count reached
LTA4H	12	65	2.00	0.00	2	[292,294]	No – gene count reached
MBL2	10	65	2.00	0.00	2	[390,391]	No – gene count reached
MMP9	20	65	2.00	0.00	2	[392,393]	No – gene count reached
MUC7	4	65	2.00	0.00	2	[394,395]	No – gene count reached
NQO1	16	65	2.00	0.00	2	[18,74]	No – gene count reached
PTGER2	14	65	2.00	0.00	2	[234,396]	No – gene count reached
PTGER4	5	65	2.00	0.00	2	[36,234]	No – gene count reached
SPINK5	5	65	2.00	0.00	2	[397,398]	No – gene count reached
TAP1	6	65	2.00	0.00	2	[399,400]	No – gene count reached
TIMD4	5	65	2.00	0.00	2	[401,402]	No – gene count reached
TLR4	9	65	2.00	0.00	2	[59,403]	No – gene count reached
TLR6	4	65	2.00	0.00	2	[341,404]	No – gene count reached
TLR9	3	65	2.00	0.00	2	[171,405]	No – gene count reached
CX3CR1	3	66	1.69	0.69	1	[406]	No – gene count reached
LY86	6	67	1.64	0.64	1	[407]	No – gene count reached

hCLCA1	1	68	1.64	0.64	1	[408]	No – gene count reached
A1PI	14	70	1.46	0.46	1	[409]	No – gene count reached
HLA-DQA2	6	71	1.43	0.43	1	[92]	No – gene count reached
15-LO	17	72	1.00	0.00	1	[410]	No – gene count reached
ADH5	4	72	1.00	0.00	1	[411]	No – gene count reached
ADORA1	1	72	1.00	0.00	1	[412]	No – gene count reached
ADORA2A	22	72	1.00	0.00	1	[412]	No – gene count reached
ADRA1B	5	72	1.00	0.00	1	[206]	No – gene count reached
AFM042XD12	5	72	1.00	0.00	1	[69]	No – gene count reached
AFM058XD6	13	72	1.00	0.00	1	[413]	No – gene count reached
AFM161YF6	4	72	1.00	0.00	1	[414]	No – gene count reached
AFM197XG5	8	72	1.00	0.00	1	[415]	No – gene count reached
AFM198WE11	5	72	1.00	0.00	1	[416]	No – gene count reached
AFM203YG7	6	72	1.00	0.00	1	[364]	No – gene count reached
AFM205ZH4	5	72	1.00	0.00	1	[298]	No – gene count reached
AFM207VE1	12	72	1.00	0.00	1	[415]	No – gene count reached
AFM211YC7	5	72	1.00	0.00	1	[298]	No – gene count reached
AFM263WG5	5	72	1.00	0.00	1	[153]	No – gene count reached
AFM288VA9	5	72	1.00	0.00	1	[298]	No – gene count reached
AFM294ZE9	12	72	1.00	0.00	1	[299]	No – gene count reached
AFMA136XA5	9	72	1.00	0.00	1	[364]	No – gene count reached
AFMB026XG9	5	72	1.00	0.00	1	[416]	No – gene count reached
AFMB330YF1	2	72	1.00	0.00	1	[364]	No – gene count reached
AGT	1	72	1.00	0.00	1	[417]	No – gene count reached
ARG1	6	72	1.00	0.00	1	[367]	No – gene count reached
ATA33B03	11	72	1.00	0.00	1	[298]	No – gene count reached
ATA41E04	16	72	1.00	0.00	1	[414]	No – gene count reached
BDNF	11	72	1.00	0.00	1	[418]	No – gene count reached
C3AR1	12	72	1.00	0.00	1	[305]	No – gene count reached
C5	9	72	1.00	0.00	1	[305]	No – gene count reached
CAT	11	72	1.00	0.00	1	[419]	No – gene count reached
CCR3	3	72	1.00	0.00	1	[247]	No – gene count reached
CHLC.ATA27A06	12	72	1.00	0.00	1	[414]	No – gene count reached
CHLC.GATA89B07	6	72	1.00	0.00	1	[298]	No – gene count reached
CHML	1	72	1.00	0.00	1	[295]	No – gene count reached
CHRM1	11	72	1.00	0.00	1	[420]	No – gene count reached
CMA1	14	72	1.00	0.00	1	[421]	No – gene count reached
CXCR3	X	72	1.00	0.00	1	[422]	No – gene count reached
CYP1B1	2	72	1.00	0.00	1	[423]	No – gene count reached
CYP24A1	20	72	1.00	0.00	1	[226]	No – gene count reached
CYP2R1	11	72	1.00	0.00	1	[226]	No – gene count reached
CYSLTR2	13	72	1.00	0.00	1	[424]	No – gene count reached
DARC	1	72	1.00	0.00	1	[425]	No – gene count reached
DENND1B	1	72	1.00	0.00	1	[426]	No – gene count reached
EPHX1	1	72	1.00	0.00	1	[151]	No – gene count reached
F3	1	72	1.00	0.00	1	[427]	No – gene count reached
FCGR3A	1	72	1.00	0.00	1	[428]	No – gene count reached
GATA62A04	5	72	1.00	0.00	1	[414]	No – gene count reached
GCLM	1	72	1.00	0.00	1	[429]	No – gene count reached
GPX1	3	72	1.00	0.00	1	[430]	No – gene count reached
GTAT1H06	6	72	1.00	0.00	1	[298]	No – gene count reached
HLA-C	6	72	1.00	0.00	1	[116]	No – gene count reached
HLA-DMB	6	72	1.00	0.00	1	[431]	No – gene count reached
HLA-G	6	72	1.00	0.00	1	[432]	No – gene count reached
HLX	1	72	1.00	0.00	1	[433]	No – gene count reached
HMOX1	22	72	1.00	0.00	1	[434]	No – gene count reached

IDO1	8	72	1.00	0.00	1	[384]	No – gene count reached
IFNA1	9	72	1.00	0.00	1	[435]	No – gene count reached
IGHG2	14	72	1.00	0.00	1	[436]	No – gene count reached
IKZF3	17	72	1.00	0.00	1	[326]	No – gene count reached
IL12A	3	72	1.00	0.00	1	[126]	No – gene count reached
IL12RB1	19	72	1.00	0.00	1	[437]	No – gene count reached
IL17F	6	72	1.00	0.00	1	[438]	No – gene count reached
IL17RB	3	72	1.00	0.00	1	[439]	No – gene count reached
IL1A	2	72	1.00	0.00	1	[25]	No – gene count reached
IL21	4	72	1.00	0.00	1	[440]	No – gene count reached
IL7R	5	72	1.00	0.00	1	[36]	No – gene count reached
IL9R	X	72	1.00	0.00	1	[441]	No – gene count reached
INPP4A	2	72	1.00	0.00	1	[442]	No – gene count reached
IRAK1	X	72	1.00	0.00	1	[334]	No – gene count reached
ITGB3	17	72	1.00	0.00	1	[443]	No – gene count reached
LIFR	5	72	1.00	0.00	1	[36]	No – gene count reached
MAP3K7IP1	22	72	1.00	0.00	1	[334]	No – gene count reached
MICB	6	72	1.00	0.00	1	[444]	No – gene count reached
MIF	22	72	1.00	0.00	1	[445]	No – gene count reached
MPO	17	72	1.00	0.00	1	[446]	No – gene count reached
MRC1	10	72	1.00	0.00	1	[447]	No – gene count reached
MTHFR	11	72	1.00	0.00	1	[448]	No – gene count reached
MUC2	11	72	1.00	0.00	1	[449]	No – gene count reached
MYB	6	72	1.00	0.00	1	[260]	No – gene count reached
NAT1	8	72	1.00	0.00	1	[86]	No – gene count reached
NPPA	1	72	1.00	0.00	1	[450]	No – gene count reached
PAFAH	17	72	1.00	0.00	1	[451]	No – gene count reached
PARP1	1	72	1.00	0.00	1	[452]	No – gene count reached
PGDS	4	72	1.00	0.00	1	[453]	No – gene count reached
PIM2	X	72	1.00	0.00	1	[454]	No – gene count reached
PLAU	10	72	1.00	0.00	1	[455]	No – gene count reached
PLAUR	19	72	1.00	0.00	1	[456]	No – gene count reached
PON1	7	72	1.00	0.00	1	[423]	No – gene count reached
PPARG	3	72	1.00	0.00	1	[457]	No – gene count reached
PRLR	5	72	1.00	0.00	1	[36]	No – gene count reached
PRNP	20	72	1.00	0.00	1	[206]	No – gene count reached
PTGIR	19	72	1.00	0.00	1	[234]	No – gene count reached
PTGS2	1	72	1.00	0.00	1	[458]	No – gene count reached
SELE	1	72	1.00	0.00	1	[459]	No – gene count reached
SERPINA3	14	72	1.00	0.00	1	[460]	No – gene count reached
SIGLEC8	19	72	1.00	0.00	1	[461]	No – gene count reached
SLC6A4	17	72	1.00	0.00	1	[462]	No – gene count reached
SOD2	6	72	1.00	0.00	1	[463]	No – gene count reached
STAT2	12	72	1.00	0.00	1	[464]	No – gene count reached
TIMP1	X	72	1.00	0.00	1	[465]	No – gene count reached
TLE4		72	1.00	0.00	1	[466]	No – gene count reached
TLR1	4	72	1.00	0.00	1	[341]	No – gene count reached
TLR7	X	72	1.00	0.00	1	[467]	No – gene count reached
TLR8	X	72	1.00	0.00	1	[467]	No – gene count reached
TOP2A	17	72	1.00	0.00	1	[220]	No – gene count reached
TSLP	5	72	1.00	0.00	1	[468]	No – gene count reached
UGT1A6	2	72	1.00	0.00	1	[423]	No – gene count reached
WDR36	5	72	1.00	0.00	1	[260]	No – gene count reached
Xp21.2	X	72	1.00	0.00	1	[469]	No – gene count reached
ZPBP2	17	72	1.00	0.00	1	[326]	No – gene count reached

Table S-2 footer note:

A: Position in list of 251 genes identified to be associated with asthma, ranked from highest to lowest gene ranking scores. Genes may have the same rank if they had identical gene ranking scores. **B:** Gene ranking score, equal to the sum of the GWAS score and the publication score. **C:** Sum of the smallest of F-exact $-\log(P)$ allelic or genotypic values for all SNPs with $P < 0.05$ in each gene, scaled to the density of SNPs in that gene, within the PRAM GWAS. **D:** Number of prior publications reporting a significant association between this gene and asthma. **E:** Reference list of prior publications associated with each gene. Note that reference numbering is different from that of the main manuscript document. **F:** A gene was not assayed if it met one or more of the following criteria: 1) citations for the gene only reported non-SNP polymorphisms (e.g., deletions or repeats) as factors associated with asthma and there were no significant SNPs in the GWAS, 2) the gene was in the HLA superlocus, 3) a TaqMan genotyping assay could not be designed for the selected SNPs in a gene; or 4) 50 genes had already been selected for genotyping when proceeding down the ranked list (“gene count reached”).

Supplemental references for Table S-2:

Note that reference numbering is different from that of the main manuscript document.

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Table S-3. Association statistics and minor allele frequencies for significant SNPs, using the PRAM and HapMap CEU control groups.

Gene	SNP	Chi-square P-values		Minor Allele Frequencies		
		PRAM control (n=499)	HapMap CEU (n=113)	PRAM case (n=103)	PRAM control	HapMap CEU
RAD50	rs2706347	0.000024 (allelic)	0.000015 (n=113) (allelic)	0.395	0.249	0.204
PTPRE	rs10830196	0.0081 (allelic)	0.0026 (n=113) (allelic)	0.374	0.280	0.239
IL4R	rs1801275	0.0063 (allelic)	0.00036 (n=113) (allelic)	0.353	0.258	0.185
CCL5	rs2280788	0.017 (genotypic)	0.69 (n=54) (genotypic)	0.015	0.026	0.009
TBXA2R	rs4523	0.042 (allelic)	0.059 (n=107) (allelic)	0.285	0.360	0.371

Table S-4A. RAD50 (rs2706347) associations stratified by race.

Race	Allele / genotype	Cases		Controls		P-value (overall)
		N	%	N	%	
White	G	60	31.82	579	77.82	0.0427
	T	28	68.18	165	22.18	
	GG	23	52.27	229	61.56	0.0449
	GT	14	31.82	121	32.53	
	TT	7	15.91	22	5.91	
African-American	G	9	37.50	25	40.32	0.8102
	T	15	62.50	37	59.68	
	GG	3	25.00	7	22.58	0.8021
	GT	3	25.00	11	35.48	
	TT	6	50.00	13	41.94	
Hispanic	G	29	64.04	69	84.15	0.0068
	T	17	36.96	13	15.85	
	GG	9	39.13	29	70.73	0.0299
	GT	11	47.83	11	26.83	
	TT	3	13.04	1	2.44	
Other or Biracial	G	23	54.76	63	68.48	0.1245
	T	19	45.24	29	31.52	
	GG	8	47.83	22	38.1	0.1927
	GT	7	41.30	19	33.33	
	TT	6	10.87	5	28.57	

Table S-4B. PTPRE (rs10830196) associations stratified by race.

Race	Allele / genotype	Cases		Controls		P-value (overall)
		N	%	N	%	
White	C	63	71.59	570	76.41	0.3177
	T	25	28.41	176	23.59	
	CC	20	45.45	222	59.52	0.0419
	CT	23	52.27	126	33.78	
	TT	1	2.27	25	6.70	
African-American	C	14	58.33	27	42.19	0.1763
	T	10	41.67	37	57.81	
	CC	3	25.00	6	18.75	0.2242
	CT	8	66.67	15	46.88	
	TT	1	8.33	11	34.38	
Hispanic	C	25	54.35	49	59.76	0.5522
	T	21	45.65	33	40.24	
	CC	4	17.39	15	36.59	0.1025
	CT	17	73.91	19	46.34	
	TT	2	8.70	7	17.07	
Other or Biracial	C	22	55.00	60	68.18	0.1497
	T	18	45.00	28	31.82	
	CC	5	25.00	21	47.73	0.2273
	CT	12	60.00	18	40.91	
	TT	3	15.00	5	11.36	

Table S-4C. IL4R (rs1801275) associations stratified by race.

Race	Allele / genotype	Cases		Controls		P-value (overall)
		N	%	N	%	
White	A	72	83.72	584	79.35	0.3391
	G	14	16.28	152	20.65	
	AA	30	69.77	227	61.68	0.5846
	AG	12	27.91	130	35.33	
	GG	1	2.33	11	2.99	
African-American	A	7	29.17	23	41.07	0.3135
	G	17	70.83	33	58.93	
	AA	0	0.00	4	14.29	0.3741
	AG	7	58.33	15	53.57	
	GG	5	41.67	9	32.14	
Hispanic	A	23	50.00	53	64.63	0.1058
	G	23	50.00	29	35.37	
	AA	7	30.43	16	39.02	0.1093
	AG	9	39.13	21	51.22	
	GG	7	30.43	4	9.76	
Other or Biracial	A	26	61.90	52	60.47	0.8754
	G	16	38.10	34	39.53	
	AA	8	38.10	16	37.21	0.9790
	AG	10	47.62	20	46.51	
	GG	3	14.29	7	16.28	

Table S-4D. TBXA2R (rs4523) associations stratified by race.

Race	Allele / genotype	Cases		Controls		P-value (overall)
		N	%	N	%	
White	G	63	73.26	464	62.87	0.0577
	A	23	26.74	274	37.13	
	GG	23	53.49	150	40.65	0.1788
	GA	17	39.53	164	44.44	
	AA	3	6.98	55	14.91	
African-American	G	23	95.83	47	75.81	0.0323
	A	1	4.17	15	24.19	
	GG	11	91.67	18	58.06	0.1050
	GA	1	8.33	11	35.48	
	AA	0	0.00	2	6.45	
Hispanic	G	31	64.58	48	60.00	0.6055
	A	17	35.42	32	40.00	
	GG	12	50.00	11	27.50	0.0185
	GA	7	29.17	26	65.00	
	AA	5	20.83	3	7.50	
Other or Biracial	G	26	61.90	63	68.48	0.4548
	A	16	38.10	29	31.52	
	GG	8	38.10	21	45.65	0.7285
	GA	10	47.62	21	45.65	
	AA	3	14.29	4	8.70	

Table S-4E. CCL5 (rs2280788) associations stratified by race.

Race	Allele / genotype	Cases		Controls		P-value (overall)
		N	%	N	%	
White	G	85	96.59	714	97.28	0.7130
	C	3	3.41	20	2.72	
	GG	42	95.45	347	94.55	0.0105
	GC	1	2.27	20	5.45	
	CC	1	2.27	0	0.00	
African-American	G	24	100.00	61	98.39	0.5314
	C	0	0.00	1	1.61	
	GG	12	100.00	30	96.77	0.5290
	GC	0	0.00	1	3.23	
	CC	0	0.00	0	0.00	
Hispanic	G	46	100.00	77	96.25	0.1837
	C	0	0.00	3	3.75	
	GG	23	100.00	37	92.5	0.1784
	GC	0	0.00	3	7.50	
	CC	0	0.00	0	0.00	
Other or Biracial	G	42	100.00	87	98.86	0.4880
	C	0	0.00	1	1.14	
	GG	21	100.00	43	97.73	0.4863
	GC	0	0.00	1	2.27	
	CC	0	0.00	0	0.00	

Table S-5. Power analysis by disease allele frequency and effect estimate, for P-value < 0.0011.

OR	Disease allele frequency					
	0.05	0.10	0.20	0.30	0.40	0.50
1.25	1%	5%	13%	20%	22%	21%
1.50	1%	5%	13%	20%	22%	21%
1.75	4%	16%	39%	49%	51%	46%
2.00	11%	37%	67%	74%	73%	67%
2.50	37%	78%	94%	95%	93%	88%
3.00	69%	96%	99%	99%	98%	95%
3.50	89%	99%	100%	100%	99%	98%
4.00	97%	100%	100%	100%	100%	99%

Percentages are probability that the test will reject a false null hypothesis of no association. Calculated for n=103 cases, n=499 controls, disease prevalence = 10%, using an additive genetic model. Calculations performed using the CaTS Power Calculator for Two Stage Association Studies (<http://www.sph.umich.edu/csg/abecasis/cats/index.html>).