Supplemental Table 1. Association results in sample set 1

			Case[b]				Control[b]					
RS Number	Gene	Position and alleles[a]	11	12	22	HWE[c]	11	12	22	HWE[c]	$P_{allelic}$	$P_{genotypic}$
rs12656759		C131395509T	98	237	126	0.51	99	240	120	0.35	0.75	0.92
rs2073506		T131422637C	4	63	394	0.33	2	71	386	0.76	0.71	0.55
rs31481	IL3	A131425101G	13	107	339	0.19	12	120	325	0.86	0.45	0.59
rs11575022		C131429914A	2	43	416	0.33	7	42	410	0.0006	0.35	0.23
rs2069626	CSF2	G131438678A	0	15	446	1	0	9	450	1	0.22	
rs743564	CSF2	C131438778T	76	228	155	0.63	72	222	165	0.92	0.51	0.78
rs25882	CSF2	C131439359T	18	142	298	0.88	19	150	290	1	0.57	0.84
rs25887		C131443960A	83	232	146	0.64	87	223	149	0.85	0.96	0.86
rs25888		A131444345G	0	25	436	1	0	21	438	1	0.56	
rs31467		C131464737T	106	233	122	0.85	116	227	116	0.85	0.46	0.71
rs39897		C131464795T	96	235	130	0.64	93	239	127	0.35	0.96	0.95
rs154735		A131465431G	2	56	402	1	1	56	402	1	0.86	0.86
rs247008		A131475003G	42	198	221	0.91	41	213	205	0.20	0.47	0.56
rs156055		A131528076G	4	65	390	0.51	3	64	391	0.74	0.80	0.93
rs156033		T131555220C	12	126	323	1	11	131	317	0.74	0.82	0.91
rs2278398	P4HA2	G131558340A	100	244	117	0.23	97	229	132	0.93	0.40	0.49
rs156030	P4HA2	A131558816G	0	49	411	0.63	2	33	424	0.16	0.19	
rs152050		T131564725C	52	215	193	0.54	54	217	186	0.48	0.69	0.92
rs10520127	P4HA2	T131567154C	2	64	394	1	3	68	387	1	0.58	0.83
rs17618604	P4HA2	T131570083C	9	84	368	0.15	2	112	345	0.02	0.30	0.01
rs283763	P4HA2	T131581144A	14	159	288	0.19	16	162	281	0.26	0.65	0.89
rs7733814	P4HA2	T131584208C	2	59	400	1	1	55	401	1	0.60	0.81
rs157578	P4HA2	C131589221G	3	102	356	0.18	12	108	339	0.34	0.09	0.04
rs10036208		T131599222C	48	206	207	0.83	62	186	211	0.05	0.64	0.24
rs11749843		A131600397G	0	8	452	1	0	5	454	1	0.41	
rs2405271		C131601292G	11	151	299	0.13	19	138	302	0.55	0.82	0.26
rs334902		C131614458G	78	244	139	0.11	101	207	151	0.06	0.61	0.04
rs4594848		A131614497C	94	247	120	0.13	107	208	143	0.07	0.63	0.05
rs7727038		C131618156T	86	226	149	1	98	214	147	0.22	0.52	0.57
rs162881	PDLIM4	G131636693T	4	73	383	0.77	5	85	369	1	0.26	0.54
rs162896		T131640775C	0	33	427	1	0	20	439	1	0.07	
rs7737937		A131642880G	10	125	325	0.73	8	118	333	0.71	0.49	0.77
rs162899		G131643492A	26	175	260	0.71	25	178	254	0.45	0.87	0.95
rs272895		G131644273A	6	114	341	0.43	6	101	352	0.83	0.39	0.63
rs381870		T131650200A	11	146	304	0.21	18	142	299	0.77	0.52	0.41
rs162892		A131651149G	47	210	203	0.53	48	194	216	0.67	0.53	0.59
rs162889		T131652285C	18	191	252	0.02	22	177	260	0.31	0.78	0.59
rs2662314		T131653068C	7	115	338	0.56	7	107	344	0.84	0.61	0.85
rs157572		C131654011G	39	204	218	0.44	38	187	234	0.91	0.36	0.52
rs3792876	SLC22A4	T131665208C	4	62	394	0.32	3	60	396	0.72	0.73	0.92
rs3792884	SLC22A4	G131679160A	5	90	361	1	3	90	361	0.45	0.79	0.78
rs11739484	SLC22A4	G131684659A	0	25	436	1	0	23	436	1	0.78	
rs273912	SLC22A4	G131689248T	37	186	238	0.91	50	179	230	0.10	0.30	0.33
rs272879	SLC22A4	C131698445G	61	211	189	0.84	69	209	181	0.49	0.45	0.72

Supplemental Table 1 (continued)

			Case[b]				Control[b]					
RS Number	Gene	Position and alleles[a]	11	12	22	HWE[c]	11	12	22	HWE[c]	$P_{allelic}$	$P_{genotypic}$
rs11568506	SLC22A4	A131699359G	0	12	449	1	0	27	430	1	0.01	
rs17622208	SLC22A5	A131744949G	97	252	112	0.05	114	208	137	0.05	0.71	0.02
rs7731390	SLC22A5	G131749648C	0	47	413	0.62	1	38	420	0.59	0.45	
rs17689550	SLC22A5	T131750964C	5	86	370	1	6	96	356	1	0.35	0.64
rs35306350	SLC22A5	T131751187C	81	253	125	0.02	102	213	143	0.19	0.89	0.03
rs274549	SLC22A5	A131757017C	13	140	307	0.64	7	135	317	0.09	0.30	0.36
rs11739135		C131761296G	79	214	167	0.50	79	216	161	0.70	0.80	0.95
rs6596075		G131770127C	13	140	307	0.64	7	135	317	0.09	0.30	0.36
rs4705943	LOC441108	G131782903A	6	87	368	0.63	7	80	372	0.30	0.73	0.83
rs4705944	LOC441108	A131783163T	1	31	429	0.45	3	26	430	0.01	0.91	0.50
rs2285673	LOC441108	T131783868C	25	183	252	0.32	25	178	255	0.45	0.83	0.96
rs1004234	LOC441108	A131785000G	2	56	401	1	0	54	405	0.39	0.56	
rs11958162	LOC441108	A131799815T	8	105	348	1	3	107	349	0.13	0.60	0.31
rs4540166	LOC441108	T131807756C	19	164	277	0.50	22	158	279	1	0.96	0.85
rs7713818	LOC441108	T131816650C	45	201	213	0.91	46	216	197	0.25	0.40	0.56
rs10477741	LOC441108	G131823209T	7	94	358	0.82	5	95	359	0.82	0.83	0.85
rs6894249	LOC441108	G131825446A	64	231	166	0.28	59	230	169	0.20	0.68	0.89
rs2522051	LOC441108	C131825477T	81	241	136	0.16	108	208	143	0.06	0.35	0.04
rs10077785		T131829057C	20	164	277	0.59	19	163	277	0.50	0.90	0.99
rs2522057		G131829846C	79	237	145	0.34	79	222	157	1	0.56	0.62
rs2522064		A131834387G	10	147	304	0.12	20	148	290	0.89	0.19	0.16
rs17715481		G131843283A	1	67	393	0.50	0	77	382	0.06	0.47	
rs10072700		C131844802A	37	174	249	0.41	29	174	256	1	0.41	0.59
rs2070721	IRF1	G131853741T	98	219	144	0.40	90	227	141	1	0.80	0.78
rs2548997		G131863294A	58	195	207	0.25	47	208	203	0.60	0.70	0.45
rs4143832		T131890876G	12	102	345	0.17	17	126	316	0.33	0.03	0.10
rs4705959		C131893690T	26	179	253	0.54	32	159	268	0.21	0.65	0.33
rs2706399		A131895601G	104	232	124	0.85	103	242	107	0.16	0.46	0.50
rs739719		A131900764C	6	72	383	0.25	2	71	385	0.76	0.48	0.36
rs2069822	IL5	C131906781T	0	19	441	1	1	15	442	0.14	0.75	
rs2069812		A131907815G	40	216	205	0.13	43	194	220	1	0.50	0.41
rs2897443	RAD50	T131957493G	11	111	338	0.57	14	137	308	0.88	0.04	0.11
rs6884762	RAD50	T131966629C	0	15	446	1	0	34	424	1	0.01	
rs17772583	RAD50	G131981409A	27	180	253	0.54	30	163	266	0.45	0.57	0.52
rs2237060	RAD50	G131998784T	93	234	134	0.64	87	222	150	0.78	0.30	0.49
rs2158177	RAD50	G132011957A	8	112	339	0.85	12	133	314	0.74	0.06	0.17
rs1800925[d]		T132020708C	11	112	338	0.58	14	139	303	0.76	0.03	0.08
rs20541[d]	IL13	A132023863G	6	131	326	0.11	20	140	298	0.46	0.02	0.01
rs848[d]	IL13	A132024399C	6	132	323	0.08	19	145	294	0.88	0.01	0.01
rs1295683		A132026775G	3	78	380	1	6	70	383	0.24	0.89	0.49
rs2243297		A132027070T	0	26	435	1	2	34	423	0.18	0.12	
rs2243211		A132029321C	0	54	406	0.39	5	72	379	0.39	0.01	
rs762534		A132032655C	0	47	414	0.62	3	69	387	1	0.01	
rs2243248		G132036543T	3	50	408	0.23	1	71	387	0.34	0.11	0.08
rs2227282	IL4	C132041078G	18	173	270	0.15	45	162	251	0.02	0.02	0.00
rs2243263	IL4	C132041198G	3	84	373	0.60	9	90	360	0.26	0.17	0.17
rs12186803	KIF3A	A132067968G	4	103	353	0.38	15	110	333	0.15	0.04	0.02
rs10069772	KIF3A	A132068587G	4	90	362	0.81	11	105	343	0.43	0.04	0.08
rs17691077	KIF3A	C132071250A	9	102	349	0.68	7	97	355	0.83	0.54	0.81

[a] Positions according to genomic contig NT_034772.5 (Entrez Nucleotide). The minor allele is listed first, followed by the position in National Center for Biotechnology Information Genome Build 36.2 and then the major allele.

[b] Counts of genotype 11, 12 and 22.

[c] P-value from Hardy-Weinberg Equilibrium test.

[d] The data for these three SNPs were reported previously (21).

Supplemental Table 2. Minor allele frequencies and allele-based association of 5q31 SNPs with psoriasis

				Case[b]						Control[b]							
RS Number	Public	Position and alleles[a]	Study	11	12	22	Sum	MAF	HWE	11	12	22	Sum	MAF	HWE	P[c]	OR (95%CI)
rs11568506	SLC22A4	A131699359G	SS1	0	12	449	461	0.013	1	0	27	430	457	0.030	1	0.014	0.43 (0.21-0.86)
			SS2	2	18	473	493	0.022	0.02	0	16	474	490	0.016	1	0.34	1.37 (0.71-2.63)
			SS3	0	16	465	481	0.017	1	0	26	400	426	0.031	1	0.050	0.53 (0.28-1.00)
			All	2	46	1387	1435	0.017		0	69	1304	1373	0.025		0.043	0.68 (0.47-0.99)
rs4143832	LOC441108	T131890876G	SS1	12	102	345	459	0.137	0.17	17	126	316	459	0.174	0.33	0.029	0.75 (0.58-0.97)
			SS2	11	151	331	493	0.175	0.22	21	153	318	492	0.198	0.67	0.20	0.86 (0.68-1.08)
			SS3	15	129	337	481	0.165	0.51	15	117	294	426	0.173	0.40	0.68	0.94 (0.74-1.21)
			All	38	382	1013	1433	0.160		53	396	928	1377	0.182		0.026	0.85 (0.74-0.98)
rs2897443	RAD50	T131957493G	SS1	11	111	338	460	0.145	0.57	14	137	308	459	0.180	0.88	0.041	0.77 (0.60-0.98)
			SS2	9	161	323	493	0.182	0.03	22	154	316	492	0.201	0.57	0.27	0.88 (0.70-1.10)
			SS3	14	124	344	482	0.158	0.49	22	130	273	425	0.205	0.23	0.0092	0.72 (0.57-0.92)
			All	34	396	1005	1435	0.162		58	421	897	1376	0.195		0.0010	0.78 (0.69-0.91)
rs6884762	RAD50	T131966629C	SS1	0	15	446	461	0.016	1	0	34	424	458	0.037	1	0.0055	0.42 (0.23-0.79)
			SS2	0	30	463	493	0.030	1	0	30	462	492	0.030	1	0.96	0.99 (0.59-1.66)
			SS3	0	16	466	482	0.017	1	0	31	394	425	0.036	1	0.0078	0.44 (0.24-0.82)
			All	0	61	1375	1436	0.021		0	95	1280	1375	0.035		0.0025	0.61 (0.44-0.84)
rs1800925	IL13	T132020708C	SS1	11	112	338	461	0.145	0.58	14	139	303	456	0.183	0.76	0.029	0.76 (0.59-0.97)
			SS2	9	150	335	494	0.170	0.11	21	158	316	495	0.202	0.78	0.068	0.81 (0.64-1.02)
			SS3	16	119	345	480	0.157	0.17	21	131	272	424	0.204	0.37	0.010	0.73 (0.57-0.93)
			All	36	381	1018	1435	0.158		56	428	891	1375	0.196		0.00015	0.77 (0.67-0.88)
rs20541	IL13	A132023863G	SS1	6	131	326	463	0.154	0.11	20	140	298	458	0.197	0.46	0.018	0.75 (0.59-0.95)
			SS2	12	143	339	494	0.169	0.63	12	170	312	494	0.196	0.047	0.12	0.83 (0.66-1.05)
			SS3	8	131	341	480	0.153	0.38	12	138	272	422	0.192	0.35	0.029	0.76 (0.60-0.97)
			All	26	405	1006	1437	0.159		44	448	882	1374	0.195		0.00043	0.78 (0.68-0.90)
rs848	IL13	A132024399C	SS1	6	132	323	461	0.156	0.076	19	145	294	458	0.200	0.88	0.015	0.74 (0.58-0.94)
			SS2	12	144	338	494	0.170	0.53	13	171	308	492	0.200	0.067	0.085	0.82 (0.65-1.03)
			SS3	8	138	334	480	0.160	0.18	13	141	269	423	0.197	0.36	0.040	0.78 (0.61-0.99)
			All	26	414	995	1435	0.162		45	457	871	1373	0.199		0.00035	0.78 (0.68-0.89)
rs2243211		A132029321C	SS1	0	54	406	460	0.059	0.39	5	72	379	456	0.090	0.39	0.011	0.63 (0.44-0.90)
			SS2	0	51	441	492	0.052	0.63	3	67	420	490	0.074	0.74	0.039	0.67 (0.46-0.98)
			SS3	1	64	416	481	0.069	0.72	2	61	362	425	0.076	1	0.52	0.88 (0.62-1.26)
			All	1	169	1263	1433	0.060		10	200	1161	1371	0.080		0.0024	0.72 (0.58-0.89)
rs762534		A132032655C	SS1	0	47	414	461	0.051	0.62	3	69	387	459	0.082	1	0.0081	0.60 (0.41-0.87)
			SS2	1	54	437	492	0.057	1	4	67	420	491	0.076	0.51	0.084	0.72 (0.51-1.04)
			SS3	1	48	433	482	0.052	1	1	48	376	425	0.059	1	0.52	0.87 (0.58-1.31)
			All	2	149	1284	1435	0.053		8	184	1183	1375	0.073		0.0031	0.72 (0.58-0.89)
rs2227282	IL4	C132041078G	SS1	18	173	270	461	0.227	0.15	45	162	251	458	0.275	0.02	0.017	0.77 (0.62-0.95)
			SS2	27	188	279	494	0.245	0.63	34	193	265	492	0.265	1	0.30	0.89 (0.73-1.10)
			SS3	31	143	306	480	0.214	0.01	31	172	223	426	0.275	0.90	0.0024	0.71 (0.57-0.88)
			All	76	504	855	1435	0.229		110	527	739	1376	0.271		0.00022	0.79 (0.70-0.89)
rs12186803	KIF3A	A132067968G	SS1	4	103	353	460	0.121	0.38	15	110	333	458	0.153	0.15	0.045	0.76 (0.58-0.99)
			SS2	10	111	373	494	0.133	0.56	7	111	374	492	0.127	0.84	0.71	1.05 (0.80-1.36)
			SS3	7	86	389	482	0.104	0.33	12	94	320	426	0.138	0.15	0.023	0.71 (0.54-0.95)
			All	21	300	1115	1436	0.119		34	315	1027	1376	0.139		0.027	0.83 (0.71-0.98)
rs10069772	KIF3A	A132068587G	SS1	4	90	362	456	0.107	0.81	11	105	343	459	0.138	0.43	0.044	0.74 (0.56-0.99)
			SS2	10	99	381	490	0.121	0.29	11	120	359	490	0.145	0.72	0.13	0.81 (0.62-1.05)
			SS3	5	101	372	478	0.116	0.66	6	101	317	424	0.133	0.67	0.27	0.85 (0.64-1.13)
			All	19	290	1115	1424	0.115		28	326	1019	1373	0.139		0.0074	0.80 (0.68-0.94)

[a] Positions according to genomic contig NT_034772.5 (Entrez Nucleotide). The minor allele is listed first, followed by the position in National Center for Biotechnology Information Genome Build 36.2 and then the major allele.

[b] Counts for genotypes 11, 12 and 22; MAF: minor allele frequency: HWE: Hardy-Weinberg P-value

[c] P values and ORs are calculated by chi-square method for SS1, SS2 and SS3 and by Mantel-Haenszel method for the three sample sets combined (All); P-values for the three *IL13* markers in the combined sample sets are slightly different from our previous report which used Fisher's exact test (21).

Supplemental Table 3. LD measures of the twelve significant markers in controls of sample set 1

		D'											
		rs11568506	*rs4143832*	*rs2897443*	*rs6884762*	*rs1800925*	*rs20541*	*rs848*	*rs2243211*	*rs762534*	*rs2227282*	*rs12186803*	*rs10069772*
r^2	rs11568506		0.394	0.467	0.04	0.953	0.996	0.997	1	1	0.349	0.408	0.993
	rs4143832	0.001		0.721	0.918	0.747	0.296	0.3	0.378	0.465	0.349	0.24	0.097
	rs2897443	0.001	0.501		1	0.908	0.525	0.524	0.628	0.646	0.34	0.231	0.123
	rs6884762	0.001	0.154	0.177		1	0.56	0.556	0.549	0.555	0.557	0.987	0.505
	rs1800925	**0.006**	**0.517**	**0.801**	**0.174**		0.552	0.55	0.778	0.735	0.316	0.21	0.148
	rs20541	0.007	0.075	0.245	0.05	**0.278**		0.993	0.895	0.825	0.431	0.279	0.265
	rs848	0.008	0.076	0.241	0.048	**0.273**	0.979		0.913	0.826	0.441	0.3	0.271
	rs2243211	0.003	0.067	0.177	0.121	**0.263**	0.318	0.328		0.805	0.175	0.855	0.344
	rs762534	0.003	0.091	0.169	0.133	**0.212**	0.245	0.244	0.588		0.26	1	0.415
	rs2227282	0.01	0.067	0.066	0.031	**0.059**	0.12	0.128	0.008	0.016		0.956	0.849
	rs12186803	0.027	0.049	0.044	0.007	**0.035**	0.057	0.065	0.013	0.016	0.436		0.999
	rs10069772	0.005	0.007	0.011	0.061	**0.016**	0.046	0.047	0.074	0.096	0.305	0.029	

Supplemental Table 4. Chr5q31 markers in high LD (r^2>0.80) with rs1800925

Marker	Position (bp)	Gene Symbol	SNPType	r^2 with 1800925
rs12652920	131,913,139	IL5	putative TFBS[a]	0.895
rs2706338	131,923,748	RAD50	Intron	0.897
rs2244012	131,929,124	LOC441108	Intron	0.897
rs2299015	131,929,396	RAD50	Intron	0.877
rs2706347	131,933,016	RAD50	putative TFBS[a]	0.897
rs2706348	131,933,709	RAD50	Intron	0.897
rs17166050	131,943,112	RAD50	putative TFBS[a]	0.897
rs2522403	131,943,216	RAD50	Intron	0.897
rs2246176	131,945,249	RAD50	Intron	0.895
rs2252775	131,946,343	RAD50	Intron	0.897
rs10463893	131,955,938	RAD50	Intron	0.895
rs2897443	131,957,493	RAD50	putative TFBS[a]	0.897
rs2706370	131,960,915	RAD50	Intron	0.829
rs2706372	131,963,376	RAD50	Intron	0.89
rs12187537	131,967,803	RAD50	Intron	0.817
rs2522394	131,972,028	RAD50	Intron	0.897
rs10520114	131,976,790	RAD50	Intron	0.897
rs2301713	131,979,895	RAD50	Intron	0.892
rs6596086	131,980,121	RAD50	Intron	0.897
rs2106984	131,980,965	RAD50	Intron	0.897
rs7449456	131,981,326	RAD50	Intron	0.89
rs3798135	131,993,008	RAD50	Intron	0.897
rs3798134	131,993,078	RAD50	Intron	0.894
rs6596087	131,996,508	RAD50	Intron	0.881
rs6871536	131,997,773	RAD50	Intron	0.897
rs12653750	131,999,801	RAD50	Intron	0.897
rs2040703	132,000,157	RAD50	Intron	0.897
rs2040704	132,001,076	RAD50	putative TFBS[a]	0.897
rs2074369	132,001,562	RAD50	Intron	0.892
rs7737470	132,001,962	RAD50	Intron	0.897
rs2240032	132,005,026	RAD50	Intron	0.892
rs3091307	132,017,035		Intron	0.897

[a] Putative TFBS (transcription factor binding site).

Supplemental Table 5. Pairwise genotype counts for cases and controls

rs11568506	rs1800925	Cases N	Controls N
GG	CC	978	831
GG	CT	370	414
AG	CC	38	52
GG	TT	35	56
AG	CT	7	16
AA	CC	2	
AG	TT	1	