Supplementary Table1 The frequency of genotypes and alleles of the tested SNPs in the First Stage (478 cases and 662 controls)

Nearest gene(s)	SNP	Genotype /Allele	Case	freq	Control	freq	P value	OR(95%CI)	Statistical Power
IL1A-IL1B	rs3783550	GG	212	0.446	293	0.446	0.991	1.001 (0.790-1.270)	
		GT	218	0.459	289	0.440	0.524	1.080 (0.852-1.369)	
		TT	45	0.095	75	0.114	0.295	0.812 (0.550-1.199)	
		G	642	0.676	875	0.666	0.622	1.046 (0.875-1.249)	0.867
RIPK2	rs2230801	CC	0	0.000	1	0.002	1	1.002 (0.999-1.005)	
		CT	15	0.031	21	0.032	0.965	0.985 (0.502-1.931)	
		TT	462	0.969	636	0.967	0.852	1.065 (0.547-2.076)	
		C	15	0.016	23	0.017	0.748	0.898 (0.466-1.730)	0.230
ADO-EGR2	rs1509966	AA	27	0.056	48	0.073	0.261	0.757 (0.465-1.232)	
		AG	167	0.349	254	0.388	0.186	0.848 (0.663-1.083)	
		GG	284	0.594	353	0.539	0.064	1.252 (0.987-1.590)	
		A	221	0.231	350	0.267	0.051	0.825 (0.679-1.001)	0.614
ADO-EGR2	rs7075773	CC	355	0.746	457	0.696	0.064	1.284 (0.985-1.673)	
		CT	111	0.233	181	0.275	0.108	0.800 (0.609-1.051)	
		TT	10	0.021	19	0.029	0.451	0.721 (0.332-1.564)	
		T	131	0.138	219	0.167	0.059	0.798 (0.631-1.009)	0.738
THADA	rs10176241	AA	201	0.421	310	0.473	0.087	0.813 (0.641-1.031)	
		AG	226	0.474	274	0.418	0.060	1.255 (0.990-1.592)	
		GG	50	0.105	72	0.110	0.791	0.950 (0.648-1.391)	

CPLX1	rs11248047	A	628	0.658	894	0.681	0.247	0.901 (0.754-1.075)	0.652
		GG	136	0.287	188	0.287	0.984	0.997 (0.768-1.295)	
		GA	233	0.492	311	0.476	0.595	1.066 (0.842-1.351)	
		AA	105	0.222	155	0.237	0.542	0.916 (0.691-1.214)	
INHBA	rs17705333	A	443	0.476	621	0.475	0.726	0.970 (0.821-1.147)	0.824
		AA	8	0.017	14	0.021	0.667	0.785 (0.327-1.886)	
		AG	120	0.252	167	0.254	0.932	0.988 (0.753-1.296)	
		GG	349	0.732	477	0.725	0.801	1.035 (0.794-1.349)	
IKZF1	rs9656588	A	136	0.143	195	0.148	0.708	0.956 (0.754-1.211)	0.426
		CC	86	0.180	118	0.180	0.995	1.001 (0.736-1.361)	
		CT	248	0.520	316	0.482	0.213	1.162 (0.917-1.471)	
		TT	143	0.300	221	0.337	0.181	0.841 (0.652-1.084)	
TNFSF8	rs911603	T	534	0.560	758	0.579	0.370	0.926 (0.782-1.096)	0.863
		CC	171	0.358	229	0.352	0.816	1.030 (0.805-1.318)	
		CA	229	0.480	303	0.465	0.626	1.061 (0.837-1.344)	
		AA	77	0.161	119	0.183	0.349	0.861 (0.628-1.179)	
IPMK-UBE2D1	rs28734985	A	383	0.401	541	0.416	0.503	0.944 (0.796-1.118)	0.673
		AA	393	0.824	556	0.842	0.407	0.875 (0.639-1.199)	
		AG	83	0.174	104	0.158	0.461	1.126 (0.821-1.545)	
		GG	1	0.002	0	0.000	0.420	0.998 (0.994-1.002)	
MAP3K11-RELA	rs10896027	G	85	0.089	104	0.079	0.379	0.613 (0.505-0.744)	0.544
		GG	23	0.048	39	0.060	0.414	1.144 (0.848-1.543)	
		GC	153	0.322	240	0.367	0.118	0.820 (0.639-1.052)	

		CC	299	0.629	375	0.573	0.058	1.264 (0.992-1.610)	
		G	199	0.209	318	0.243	0.060	0.825 (0.675-1.009)	0.536
MAP3K11-RELA	rs58950470	GG	385	0.821	514	0.786	0.148	1.248 (0.924-1.687)	
		GT	84	0.179	138	0.211	0.186	0.816 (0.603-1.103)	
		TT	0	0.000	2	0.003	0.231	1.003 (0.999-1.007)	
		T	84	0.090	142	0.109	0.140	0.808 (0.608-1.073)	0.465
ATP10A	rs4906762	TT	23	0.048	49	0.075	0.068	0.624 (0.375-1.039)	
		TC	188	0.392	230	0.351	0.154	1.194 (0.936-1.523)	
		CC	268	0.559	376	0.574	0.625	0.942 (0.743-1.195)	
		T	234	0.244	328	0.250	0.739	0.968 (0.798-1.174)	0.640
SOCS1-TNP2	rs3844576	CC	42	0.088	53	0.081	0.666	1.098 (0.719-1.676)	
		CA	185	0.387	262	0.399	0.689	0.952 (0.748-1.212)	
		AA	251	0.525	342	0.521	0.879	1.018 (0.804-1.289)	
		A	687	0.719	946	0.720	0.945	0.993 (0.825-1.196)	0.714
CKM-KLC3	rs1793978	CC	77	0.162	99	0.151	0.619	1.086 (0.785-1.502)	
		CT	216	0.454	331	0.505	0.091	0.816 (0.644-1.033)	
		TT	183	0.384	226	0.345	0.167	1.188 (0.930-1.518)	
		T	582	0.611	783	0.597	0.485	1.063 (0.896-1.261)	0.635
IL12A	rs2647935	CC	392	0.834	542	0.826	0.731	1.057 (0.771-1.450)	
		CT	76	0.162	114	0.174	0.594	0.917 (0.667-1.260)	
		TT	2	0.004	0	0.000	0.174	0.996 (0.990-1.002)	
		T	80	0.085	114	0.087	0.882	0.978 (0.725-1.318)	0.262
FUT2	rs1047781	AA	148	0.313	215	0.325	0.660	0.945 (0.733-1.217)	

		A/T	210	0.444	318	0.481	0.217	0.861 (0.680-1.092)	
		TT	115	0.243	128	0.194	0.045*	1.338 (1.006-1.779)	
		T	440	0.465	574	0.434	0.144	1.133 (0.958-1.340)	1
FUT2	rs601338	AA	0	0.000	1	0.002	1	1.002 (0.999-1.005)	
		AG	10	0.021	11	0.017	0.658	1.261 (0.531-2.995)	
		GG	467	0.979	647	0.982	0.828	0.866 (0.371-2.022)	
		A	10	0.010	13	0.010	1	1.063 (0.464-2.435)	0.204

SNP, single-nucleotide polymorphism; BD, Behcet’s disease; OR, odds ratio; 95 % CI, 95 % confidence interval; * : P< 0.05, Pc>0.05; Statistical power was estimated from effect size in the original Turkish data sets, allele frequency and sample size in the Chinese Han populatio

Supplementary Table 2 Main effects of SNPs identified in this study on clinical feature risk of BD

SNP	Clinical features	Genotype/ Allele	BD with	freq	BD without	Freq	P value	OR(95%CI)	Statistical Power
rs913678	Genital ulcer		n=685		n=551				
		CC	371	0.542	285	0.517	0.394	1.103 (0.881-1.381)	
		CT	262	0.382	221	0.401	0.505	0.925 (0.735-1.164)	
		TT	52	0.076	45	0.082	0.708	0.924 (0.609-1.400)	
		C	1004	0.733	791	0.718	0.404	1.079 (0.903-1.288)	0.134
	Arthritis		n=223		n=1013				
		CC	105	0.471	551	0.544	0.048*	0.746 (0.558-0.998)	
		CT	97	0.435	386	0.381	0.135	1.250 (0.932-1.677)	
		TT	21	0.094	76	0.075	0.336	0.282 (0.772-2.127)	
		C	307	0.688	1488	0.734	0.048*	0.799 (0.639-0.998)	0.505
	Skin lesions		n=926		n=310				
		CC	488	0.527	168	0.542	0.648	0.942 (0.728-1.219)	
		CT	366	0.395	117	0.377	0.578	1.078 (0.827-1.405)	
		TT	72	0.078	25	0.081	0.870	0.961 (0.598-1.544)	
		C	1342	0.725	453	0.731	0.771	0.970 (0.791-1.190)	0.059

	Positive pathergy test		n=47		n=1189				
		CC	21	0.447	635	0.534	0.240	0.705 (0.392-1.266)	
		CT	23	0.489	460	0.387	0.158	1.519 (0.847-2.723)	
		TT	3	0.064	94	0.079	0.703	0.794 (0.242-2.606)	
		C	65	0.691	1730	0.728	0.443	0.840 (0.537-1.313)	0.128
rs9316059	Genital ulcer		n=685		n=551				
		TT	32	0.047	31	0.056	0.448	0.822 (0.495-1.365)	
		TA	227	0.331	203	0.368	0.174	0.850 (0.672-1.075)	
		AA	426	0.622	317	0.575	0.096	1.214 (0.966-1.526)	
		T	291	0.212	265	0.240	0.097	0.852 (0.705-1.029)	0.382
	Arthritis		n=223		n=1013				
		TT	14	0.063	49	0.048	0.376	1.318 (0.714-2.431)	
		TA	64	0.287	366	0.361	0.035*	0.712 (0.518-0.977)	
		AA	145	0.650	598	0.590	0.098	1.290 (0.953-1.746)	
		T	92	0.206	464	0.229	0.298	0.875 (0.680-1.125)	0.174
	Skin lesions		n=931		n=305				
		TT	45	0.048	18	0.059	0.462	0.810 (0.461-1.421)	
		TA	326	0.350	104	0.341	0.770	1.041 (0.793-1.367)	

		AA	560	0.602	183	0.600	0.963	1.006 (0.773-1.310)	
		T	416	0.223	140	0.230	0.754	0.966 (0.777-1.201)	0.062
	Positive pathergy test		n=47		n=1189				
		TT	1	0.021	62	0.052	0.510	0.395 (0.054-2.913)	
		TA	16	0.340	414	0.348	0.913	0.966 (0.522-1.787)	
		AA	30	0.638	713	0.600	0.596	1.178 (0.643-2.160)	
		T	18	0.191	538	0.226	0.429	0.810 (0.480-1.366)	0.110
rs10094579	Genital ulcer		n=677		n=548				
		AA	47	0.069	40	0.073	0.809	0.947 (0.612-1.467)	
		CA	285	0.421	214	0.391	0.281	1.135 (0.902-1.428)	
		CC	5	0.510	294	0.536	0.349	0.898 (0.716-1.125)	
		A	906	0.280	294	0.268	0.520	1.060 (0.887-1.268)	0.097
	Arthritis		n=221		n=1004				
		AA	22	0.100	65	0.065	0.068	1.597 (0.962-2.652)	
		CA	75	0.339	424	0.422	0.023*	0.703 (0.518-0.954)	
		CC	124	0.561	515	0.513	0.195	1.214 (0.905-1.627)	
		A	119	0.269	554	0.276	0.776	0.967 (0.767-1.219)	0.058
	Skin lesions		n=925		n=300				

		AA	68	0.074	19	0.063	0.551	1.173 (0.693-1.986)	
		CA	374	0.404	125	0.417	0.705	0.950 (0.729-1.238)	
		CC	483	0.522	156	0.520	0.948	1.009 (0.777-1.309)	
		A	510	0.276	163	0.272	0.848	1.020 (0.830-1.255)	0.053
	Positive pathergy test		n=46		n=1179				
		AA	2	0.043	85	0.072	0.767	0.585 (0.139-2.455)	
		CA	19	0.413	480	0.407	0.936	1.025 (0.563-1.864)	
		CC	25	0.543	614	0.521	0.762	1.095 (0.606-1.979)	
		A	23	0.250	650	0.276	0.589	0.876 (0.542-1.416)	0.077
rs224127	Genital ulcer		n=686		n=552				
		GG	90	0.131	67	0.121	0.606	1.093 (0.779-1.533)	
		GA	321	0.468	262	0.475	0.814	0.973 (0.778-1.218)	
		AA	275	0.401	223	0.404	0.912	0.987 (0.785-1.241)	
		A	871	0.635	708	0.641	0.739	0.972 (0.825-1.147)	0.063
	Arthritis		n=223		n=1015				
		GG	29	0.130	128	0.126	0.873	1.036 (0.673-1.596)	
		GA	93	0.417	490	0.483	0.075	0.766 (0.572-1.028)	
		AA	101	0.453	397	0.391	0.088	1.289 (0.962-1.726)	
		A	295	0.661	1284	0.633	0.250	1.135 (0.915-1.409)	0.207

Skin lesions		n=931		n=307				
	GG	114	0.122	43	0.140	0.421	0.857 (0.587-1.249)	
	GA	437	0.469	146	0.476	0.851	0.976 (0.753-1.263)	
	AA	380	0.408	118	0.384	0.461	1.105 (0.848-1.439)	
	A	1197	0.643	382	0.622	0.355	1.093 (0.905-1.320)	0.153
Positive pathergy test		n=47		n=1191				
	GG	5	0.106	152	0.128	0.825	0.814 (0.317-2.089)	
	GA	28	0.596	555	0.466	0.080	1.689 (0.933-3.057)	
	AA	14	0.298	484	0.406	0.137	0.620 (0.328-1.170)	
	A	56	0.596	1523	0.639	0.388	0.831 (0.546-1.265)	0.144

OR, odds ratio; NS, not significant; 95 % CI, 95 % confidence interval; *: P< 0.05, Pc>0.05; Statistical power was estimated from effect size, allele frequency and sample size in this study.