

Supplementary Table 1. Data for 74 SNPs (from a total of 112 SNPs) that were used in genetic risk score model. SNPs were ranged according to their p-value. Our data was compared to the data of the reference study (Jostins L, Ripke S, Weersma RK et al. . Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease *Nature*. 2012;491:119-124). RAF_IC and OR_IC are from the reference study.

#	Chr	SNP	Pos_hg19(Mb)	Key Genes (+N additional in locus)	P value	RAF	RAF_IC	RA	OR	95% CI	OR_IC
1	5	rs11741861	150.02-150.52	TNIP1,IRGM,ZNF300 P1,(8)	0,005	0,081	0,093	G	2,193	1,261-3,817	1,249
2	1	rs11209026	67.4-67.95**	IL23R,IL12RB2,(4)	0,008	0,962	0,933	G	3,236	1,309-8,000	2,013
3	2	rs3749171	218.89-219.39	GPR35,(12)	0,009	0,159	0,167	T	1,730	1,153-2,597	1,135
4	6	rs12663356	21.17-21.67	(3)	0,011	0,546	0,533	C	1,465	1,093-1,965	1,095
5	10	rs11010067	35.04-35.55	CREM,(3)	0,018	0,346	0,346	G	1,456	1,071-1,980	1,115
6	5	rs2188962	130.36-132.01*	IRF1,IL13,CSF2,SLC22 A4,IL4,IL3,IL5,PDLIM 4,SLC22A5,ACSL6,(8)	0,021	0,445	0,425	T	1,416	1,056-1,897	1,158
7	22	rs2266959	21.67-22.17	MAPK1,YDJC,UBE2L3 ,RIMBP3,CCDC116,(8)	0,022	0,212	0,186	T	1,524	1,066-2,179	1,105
8	9	rs10758669	4.73-5.23	JAK2,(4)	0,023	0,399	0,349	C	1,422	1,056-1,916	1,174
9	1	rs670523	114.05-114.55	UBQLN4,RIT1,MSTO1 ,(28)	0,057	0,329	0,324	A	1,366	1,002-1,863	1,06
10	6	rs1819333	167.12-167.62	CCR6,RPS6KA2,RNAS ET2,(3)	0,062	0,564	0,523	T	1,333	0,993-1,789	1,081
11	5	rs11742570	40.02-40.74**	PTGER4,(1)	0,067	0,622	0,605	C	1,329	0,983-1,796	1,198

12	19	rs516246	48.95-49.45	DBP,SPHK2,IZUMO1, FUT2,(22)	0,069	0,407	0,483	T	1,323	0,983-1,780	1,107
13	2	rs925255	60.95-61.45	FOSL2,BRE,(1)	0,077	0,635	0,557	C	1,323	0,978-1,792	1,092
14	17	rs2945412	25.59-26.09	LGALS9,NOS2,(3)	0,080	0,617	0,587	A	1,311	0,971-1,773	1,137
15	2	rs12994997	62.3-62.8	ATG16L1, INPP5D, (7)	0,088	0,537	0,523	A	1,292	0,964-1,730	1,233
16	15	rs17293632	67.18-67.68	SMAD3,(2)	0,090	0,260	0,235	T	1,335	0,958-1,862	1,067
17	1	rs3024505	206.68-207.18	IL10,IL20,IL19,IL24,PI GR,MAPKAPK2,FAIM 3,RASSF5,(3)	0,091	0,171	0,16	A	1,416	0,962-2,084	1,208
18	20	rs913678	48.7-49.2	CEBPB,(5)	0,104	0,706	0,662	T	1,319	0,956-1,818	1,056
19	5	rs11739663	0.34-0.84	SLC9A3,(8)	0,111	0,838	0,76	T	1,391	0,931-2,075	1,071
20	20	rs259964	57.57-58.07	ZNF831,CTS,(5)	0,119	0,471	0,464	A	1,265	0,945-1,694	1,085
21	1	rs4656958	160.6-161.1	CD48,SLAMF1,ITLN1, CD244,F11R,USF1,SLA MF7,ARHGAP30,(8)	0,121	0,712	0,686	G	1,302	0,943-1,799	1,061
22	2	rs2382817	162.85-163.35	SLC11A1,CXCR2,CXC R1,PNKD,ARPC2,TM BIM1,CTDSP1,(8)	0,122	0,405	0,408	A	1,279	0,951-1,720	1,073
23	11	rs2155219	76.04-76.54	(5)	0,138	0,537	0,509	T	1,250	0,933-1,675	1,151
24	15	rs28374715	41.29-41.81	ITPKA,NDUFAF1,NU SAP1,(8)	0,143	0,709	0,738	A	1,276	0,924-1,762	1,082
25	17	rs12942547	40.28-40.78	STAT3,STAT5B,STAT5 A,(13)	0,145	0,631	0,58	A	1,255	0,927-1,699	1,103
26	11	rs561722	114.13-114.63	FAM55A,FAM55D,(5)	0,147	0,618	0,663	C	1,256	0,929-1,697	1,12

27	16	rs26528	28.26-28.93	RABEP2,IL27,EIF3C,S ULT1A1,SULT1A2,NU PR1,(9)	0,157	0,533	0,451	C	1,245	0,93-1,668	1,099
28	10	rs12722515	5.83-6.33	IL2RA,IL15RA,(6)	0,160	0,865	0,849	C	1,383	0,896-2,132	1,102
29	1	rs17391694	78.37-78.87	(5)	0,190	0,914	0,889	C	1,146	0,859-2,482	1,134
30	1	rs4845604	151.54-152.04	RORC,(14)	0,209	0,856	0,857	G	1,316	0,865-2,000	1,144
31	2	rs7608910	65.42-65.92	REL,C2orf74,KIAA184 1,AHSA2,(6)	0,231	0,434	0,394	G	1,202	0,896-1,610	1,138
32	1	rs7554511	155.22-156.12	KIF21B,(6)	0,239	0,788	0,725	C	1,258	0,879-1,802	1,164
33	2	rs6740462	230.84-231.34	SPRED2,(1)	0,256	0,767	0,739	A	1,238	0,876-1,750	1,081
34	6	rs13204742	127.99-128.49	(2)	0,295	0,116	0,124	T	1,282	0,813-2,020	1,173
35	10	rs1250546	80.78-81.28	(5)	0,309	0,661	0,604	A	1,188	0,873-1,617	1,096
36	9	rs10781499	138.99-139.64*	CARD9,PMPCA,SDC CAG3,INPP5E,(19)	0,327	0,415	0,412	A	1,166	0,868-1,566	1,188
37	10	rs1042058	30.47-30.97	MAP3K8,(3)	0,327	0,593	0,592	C	1,168	0,869-1,572	1,075
38	12	rs11564258	40.5-41.03*	LRRK2,MUC19	0,381	0,017	0,0252	A	1,847	0,581-5,875	1,334
39	19	rs4802307	46.6-47.1†	(9)	0,403	0,732	0,706	G	1,161	0,834-1,614	1,099
40	21	rs2284553	34.52-35.02	IFNGR2,IFNAR1,IFN AR2,IL10RB,GART,T MEM50B,(6)	0,486	0,643	0,599	G	1,125	0,830-1,524	1,123
41	12	rs7134599	68.24-68.74	IFNG,IL26,IL22,(1)	0,487	0,361	0,378	A	1,118	0,826-1,513	1,096
42	10	rs10761659	64.12-64.89**	(3)	0,493	0,611	0,543	G	1,120	0,831-1,511	1,166
43	5	rs254560	134.19-134.69	(6)	0,501	0,431	0,397	A	1,110	0,827-1,488	1,056
44	7	rs864745	27.92-28.42	CREB5,JAZF1,(1)	0,503	0,536	0,497	T	1,109	0,827-1,486	1,087

45	3	rs3197999	28.36-28.86	MST1,PFKFB4,MST1R, UCN2,GPX1,IP6K2,BS N,IP6K1,USP4,(56)	0,510	0,283	0,296	A	1,122	0,813-1,549	1,18
46	5	rs10065637	102.61-103.11	IL6ST,IL31RA,(1)	0,513	0,807	0,773	C	1,138	0,786-1,646	1,123
47	21	rs2823286	16.56-17.06	(0)	0,514	0,710	0,708	G	1,120	0,812-1,546	1,157
48	19	rs17694108	33.48-33.98	CEBPG,(8)	0,520	0,310	0,282	A	1,118	0,816-1,531	1,1
49	7	rs10486483	26.63-27.13†	(2)	0,528	0,220	0,247	A	1,134	0,797-1,612	1,089
50	6	rs1847472	90.71-91.21	(1)	0,530	0,668	0,655	C	1,107	0,812-1,508	1,060
51	9	rs4246905	117.3-117.89**	TNFSF8,TNFSF15,TN C,(2)	0,557	0,278	0,709	C	1,116	0,804-1,548	1,142
52	1	rs12568930	22.45-22.95	(3)	0,578	0,874	0,821	T	1,163	0,749-1,805	1,095
53	16	rs1728785	68.33-68.83	ZFP90,(6)	0,583	0,795	0,767	C	1,110	0,773-1,595	1,075
54	14	rs194749	69.02-69.52	ZFP36L1,(4)	0,593	0,225	0,226	C	1,116	0,788-1,580	1,075
55	2	rs1517352	233.87-234.42	STAT1,STAT4,(2)	0,603	0,542	0,6	C	1,092	0,815-1,462	1,077
56	15	rs7495132	90.92-91.42	CRTC3,(3)	0,618	0,903	0,891	C	1,157	0,705-1,898	1,134
57	6	rs212388	159.24-159.74	TAGAP,(5)	0,693	0,332	0,41	C	1,068	0,784-1,455	1,105
58	1	rs1801274	161.22-161.72	FCGR2A,FCGR2B,FC GR3A,HSPA6,FCGR3 B,FCRLA,(9)	0,709	0,561	0,509	A	1,065	0,794-1,427	1,124
59	10	rs2790216	59.74-60.24	CISD1,IPMK,(2)	0,735	0,742	0,778	G	1,067	0,765-1,488	1,066
60	8	rs6651252	129.31-129.81	(0)	0,736	0,875	0,865	T	1,101	0,707-1,715	1,185
61	7	rs1456896	49.94-50.55*	ZPBP,IKZF1,(4)	0,738	0,731	0,688	T	1,066	0,767-1,481	1,088
62	6	rs3851228	111.55-112.09	TRAF3IP2,FYN,REV3L ,(2)	0,799	0,095	0,073	T	1,074	0,653-1,770	1,153

63	11	rs11230563	60.52-61.02	CD6,CD5,PTGDR2,(12)	0,810	0,687	0,654	C	1,054	0,769-1,444	1,085
64	3	rs9847710	18.51-19.01	PRKCD,ITIH4,(8)	0,814	0,339	0,416	C	1,048	0,771-1,425	1,064
65	5	rs6871626	158.53-159.07**	IL12B,(3)	0,818	0,365	0,337	A	1,037	0,767-1,402	1,181
66	10	rs4409764	101.03-101.53	NKX2-3,(6)	0,824	0,488	0,491	T	1,043	0,779-1,395	1,182
67	21	rs2836878	40.21-40.71	(3)	0,868	0,727	0,733	G	1,040	0,749-1,443	1,18
68	21	rs7282490	45.37-45.87	ICOSLG,(9)	0,880	0,400	0,391	G	1,026	0,762-1,380	1,105
69	6	rs6920220	137.75-138.25	TNFAIP3,(1)	0,923	0,182	0,206	A	1,022	0,700-1,493	1,102
70	1	rs2488389	197.33-197.87	C1orf53,(2)	0,930	0,234	0,22	A	1,016	0,719-1,435	1,115
71	1	rs2651244	70.74-71.24	(3)	1,000	0,568	0,599	G	1,004	0,749-1,348	1,015
72	13	rs17085007	27.27-27.77	(2)	1,000	0,225	0,183	C	1,001	0,706-1,418	1,106
73	18	rs1893217	12.55-13.05	(6)	1,000	0,156	0,157	G	1,006	0,673-1,502	1,171
74	19	rs2024092	0.87-1.37	GPX4,HMHA1,(20)	1,000	0,280	0,215	A	1,005	0,726-1,392	1,156

Supplementary table 2. Data for 38 SNPs (from a total of 112 SNPs) that were not included in the genetic risk score model due to opposite allele direction compared to the reference study (Jostins L, Ripke S, Weersma RK et al.. Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease *Nature*. 2012;491:119-124). RAF_IC and OR_IC are from the reference study.

#	Chr	SNP	Pos_hg19(Mb)	Key Genes (+N additional in locus)	P value	RAF	RAF_IC	RA	RA_IC	OR	95% CI	OR_IC
1	1	rs2816958	199.84-200.34	(3)	0,530	0,096	0,887	T	G	1,170	0,714-1,916	1,230
2	1	rs6426833	19.88-20.42**	9	0,656	0,484	0,539	G	A	1,074	0,696-1,246	1,010
3	1	rs6679677	19.88-20.42**	PTPN22,DCLRE1B,(7)	0,406	0,078	0,907	A	C	1,271	0,740-2,183	1,196
4	2	rs10495903	200.62-201.12	(5)	0,830	0,862	0,130	C	T	1,051	0,688-1,605	1,086
5	2	rs10865331	43.56-44.06	(3)	0,593	0,623	0,396	G	A	1,094	0,810-1,477	1,098
8	2	rs17229285	191.67-192.17	(0)	0,824	0,483	0,496	T	C	1,037	0,775-1,387	1,117
6	2	rs2111485	199.27-200.12*	IFIH1,(5)	0,168	0,630	0,404	G	A	1,239	0,917-1,678	1,066
7	2	rs6716753	241.31-241.83*	SP140,(5)	0,264	0,806	0,196	T	C	1,239	0,856-1,795	1,134
9	3	rs4256159	47.96-49.96**	(0)	0,912	0,870	0,140	C	T	1,044	0,677-1,611	1,107
10	4	rs13126505	52.8-53.3	(1)	0,401	0,925	0,096	G	A	1,318	0,751-2,309	1,172
11	5	rs1363907	95.99-96.49	ERAP2,ERAP1,LNPEP ,(2)	0,169	0,613	0,411	G	A	1,241	0,917-1,675	1,068
12	5	rs2930047	10.44-10.94	DAP,(2)	0,149	0,613	0,382	T	C	1,255	0,929-1,692	1,065
13	5	rs6863411	141.26-141.76	SPRY4,NDFIP1,(5)	0,817	0,364	0,630	A	T	1,044	0,771-1,412	1,089
14	6	rs12199775	143.65-144.15	PHACTR2,(5)	0,002	0,085	0,929	G	A	2,353	1,359-4,082	1,129
15	6	rs17119	14.46-14.96	(0)	0,925	0,191	0,786	C	A	1,031	0,712-1,493	1,071

16	6	rs9264942	31.02-31.52	HLA- C,PSORS1C1,NFKBIL1 ,MICB,(18)	0,823	0,562	0,378	T	C	1,037	0,773-1,391	1,145
17	6	rs9358372	20.47-21.06*	(2)	0,491	0,624	0,379	A	G	1,113	0,824-1,504	1,089
18	7	rs38904	116.64-117.14	(6)	0,654	0,440	0,532	C	T	1,071	0,799-1,436	1,054
19	7	rs4722672	26.97-27.47‡	(14)	0,421	0,781	0,183	T	C	1,163	0,817-1,656	1,091
20	7	rs9297145	98.5-99	SMURF1,(6)	0,421	0,780	0,265	A	C	1,163	0,817-1,656	1,082
21	8	rs921720	126.28-126.78	TRIB1,(1)	0,022	0,386	0,609	A	G	1,421	1,053-1,919	1,081
22	9	rs4743820	93.67-94.17	NFIL3,(2)	0,410	0,284	0,702	C	T	1,157	0,838-1,596	1,056
23	11	rs483905	95.77-96.27	JRKL,MAML2,(2)	0,108	0,696	0,292	C	A	1,307	0,951-1,796	1,056
24	11	rs559928	63.85-64.39	CCDC88B,RPS6KA4,T RPT1,FLRT1,(20)	0,611	0,157	0,821	T	C	1,119	0,751-1,667	1,101
25	12	rs11168249	47.95-48.45	VDR,(8)	0,501	0,565	0,467	T	C	1,110	0,827-1,488	1,054
26	13	rs3764147	44.2-44.7	LACC1,(3)	0,431	0,769	0,248	A	G	1,153	0,815-1,630	1,155
27	14	rs8005161	88.22-88.72	GPR65,GALC,(1)	0,689	0,917	0,089	C	T	1,146	0,675-1,946	1,153
28	15	rs16967103	38.64-39.14	RASGRP1,SPRED1,(2)	1,000	0,796	0,203	T	C	1,016	0,708-1,458	1,088
29	16	rs11150589	30.22-30.72	ITGAL,(20)	0,371	0,547	0,463	C	T	1,150	0,858-1,541	1,090
30	16	rs7404095	23.61-24.11	PRKCB,(5)	0,499	0,428	0,572	T	C	1,119	0,834-1,502	1,060
31	17	rs1292053	57.71-58.21	TUBD1,RPS6KB1,(9)	0,653	0,569	0,446	A	G	1,078	0,803-1,445	1,076
32	17	rs12946510	37.66-38.16	IKZF3,ZPBP2,GSDMB, ORMDL3,GSDMA,(12)	0,328	0,580	0,465	C	T	1,168	0,869-1,570	1,157
33	18	rs7240004	46.14-46.64	SMAD7,(2)	0,256	0,407	0,616	G	A	1,195	0,889-1,608	1,057
34	18	rs727088	67.28-67.78	CD226,(2)	0,941	0,519	0,484	A	G	1,021	0,763-1,366	1,077
35	19	rs11879191	10.22-10.76*	TYK2,PPAN- P2RY11,ICAM1,(25)	1,000	0,180	0,797	A	G	1,012	0,693-1,478	1,136

36	20	rs6017342	42.81-43.31	ADA,HNF4A,(9)	0,335	0,481	0,530	A	C	1,160	0,867-1,553	1,228
37	20	rs6088765	33.55-34.05	PROCR,UQCC,CEP25 0,(8)	0,656	0,526	0,437	T	G	1,073	0,802-1,437	1,079
38	22	rs2413583	39.4-39.97*	ATF4,TAB1,APOBEC3 G,(16)	0,675	0,147	0,833	G	C	1,100	0,730-1,659	1,209