

## Supplemental Data

### Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn's Disease

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**Table S1.** Most significant pathways (FDR<0.25) in the discovery cohort (WTCCC data set), with 25,000 permutations to estimate statistical significance. FDR: false discovery rate; FWER: family-wise error rate.

Pathway identifier	Pathway source	Description	Set size	Z-score	P-value	FDR	FWER
IL12Pathway	BioCarta	IL12 and Stat4 Dependent Signaling Pathway	20	3.814	0.00008	0.045	0.03851
tcrPathway	BioCarta	T Cell Receptor Signaling Pathway	41	3.562	0.00028	0.06	0.09827
hsa04660	KEGG	T cell receptor signaling pathway	88	3.339	0.00072	0.089	0.20394
hsa02010	KEGG	ABC transporters	42	3.317	0.00028	0.071	0.21671
GO0046982	GO	protein heterodimerization activity	126	3.315	0.0006	0.058	0.21815
TPOPathway	BioCarta	TPO Signaling Pathway	22	3.059	0.00124	0.114	0.43454
hsa05320	KEGG	Autoimmune thyroid disease	50	2.937	0.00426	0.143	0.55819
hsa04630	KEGG	Jak-STAT signaling pathway	146	2.881	0.00434	0.149	0.61815
hsa05330	KEGG	Allograft rejection	35	2.876	0.00345	0.134	0.62273
hsa04940	KEGG	Type I diabetes mellitus	41	2.78	0.00422	0.16	0.72197
GO0016050	GO	vesicle organization and biogenesis	36	2.695	0.00478	0.187	0.79916
GO0006691	GO	leukotriene metabolic process	21	2.575	0.00594	0.241	0.89036

**Table S2.** Test statistic for genes in the IL12/IL23 pathway in four GWAS data sets. For each gene, the top SNP, the test statistic (as chi2 values) and the P-value are shown. These values were also drawn in **Figure 1** in the main text for visual comparison of studies.

Gene	Locus	WTCCC			Ped-IBD			CDCC			CHOP-CD-AA		
		Top SNP	Chi2	P	Top SNP	Chi2	P	Top SNP	Chi2	P	Top SNP	Chi2	P
<i>IL12RB2</i>	1p31.1	rs7546245	38.27	6.17E-10	rs1495965	15.01	0.000107	rs1495965	25.13	5.36E-07	rs3790565	8.037	0.004583
<i>IL12B</i>	5q33.3	rs1363670	20.22	6.89E-06	rs6556412	10.59	0.00114	rs10045431	24.91	6.02E-07	rs1422878	6.234	0.01253
<i>IL12RB1</i>	19p13.11	rs374326	8.231	0.004117	rs12973060	2.25	0.1331	rs4808739	4.564	0.03264	rs375947	13.47	0.000242
<i>CD3D</i>	11q23.3	rs2276424	7.701	0.005519	rs2276424	1.162	0.2811	rs2276424	0.506	0.4769	rs2276424	6.284	0.01218
<i>CD3G</i>	11q23.3	rs2276424	7.701	0.005519	rs4938507	2.818	0.09324	rs17613576	1.447	0.229	rs2276424	6.284	0.01218
<i>CD247</i>	1q24.2	rs12061855	7.609	0.005806	rs1799704	5.147	0.02328	rs2988276	10.67	0.001088	rs870875	5.088	0.02409
<i>JUN</i>	1p32.1	rs2760484	7.555	0.005985	rs942123	11.36	0.000748	rs11207303	6.772	0.009258	rs6679571	4.416	0.03561
<i>CD3E</i>	11q23.3	rs4938499	7.52	0.0061	rs7937334	1.709	0.1911	rs2277289	0.8178	0.3658	rs12577841	5.579	0.01818
<i>IL18R1</i>	2q12.1	rs1035127	6.949	0.008388	rs13015714	11.89	0.000566	rs1035130	13.52	0.000237	rs11465597	2.011	0.1562
<i>JAK2</i>	9p24.1	rs7032169	6.368	0.01162	rs10974873	6.224	0.0126	rs10758669	17.74	2.54E-05	rs10815149	7.94	0.004834
<i>CCR5</i>	3p21.31	rs3918357	4.926	0.02645	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>MAPK14</i>	6p21.31	rs2237093	3.985	0.04591	rs2237094	2.386	0.1224	rs7757672	1.991	0.1582	rs7757672	7.296	0.006911
<i>IL18</i>	11q23.1	rs544354	3.158	0.07555	rs243908	1.47	0.2254	rs10891323	3.463	0.06275	rs10891323	2.269	0.132
<i>IFNG</i>	12q15	rs10492200	2.355	0.1249	rs12312186	10.6	0.001132	rs7967588	9.025	0.002664	rs12312186	5.147	0.02329
<i>MAP2K6</i>	17q24.3	rs10512573	2.244	0.1341	rs2716191	4.14	0.04189	rs11867183	6.252	0.01241	rs1121381	5.811	0.01593
<i>STAT4</i>	2q32.3	rs897200	2.22	0.1362	rs16833215	6.27	0.01228	rs2356352	4.354	0.03693	rs7574865	3.758	0.05255
<i>IL12A</i>	3q25.33	rs7643177	1.778	0.1824	rs10936194	3.829	0.05037	rs2561287	6.391	0.01147	rs7636840	3.074	0.07955
<i>TYK2</i>	19p13.2	rs3176768	1.378	0.2405	rs12720356	16.09	6.03E-05	rs281414	19.67	9.22E-06	rs280502	1.441	0.23
<i>ETV5</i>	3q27.2	rs1516728	0.9608	0.327	rs9867846	3.659	0.05576	rs6777779	2.191	0.1388	rs9820527	2.889	0.08917
<i>MAPK8</i>	10q11.22	rs17698002	0.4149	0.5195	rs1062225	4.405	0.03583	rs10857561	3.282	0.07003	rs11596599	5.121	0.02364

**Table S3.** Results from Barrett *et al* meta-analysis on CD for genes in the IL12/IL23 pathway.

Gene	Locus	SNP	Risk Allele	Non-risk Allele	Meta-Z	Meta-P
<i>IL12RB2</i>	1p31.1	rs7546245	C	T	8.45276	2.84E-17
<i>IL12B</i>	5q33.3	rs10045431	C	A	5.752226	8.81E-09
<i>IL12RB1</i>	19p13.11	rs374326	C	T	3.362568	0.000772
<i>CD3D</i>	11q23.3	rs3212262	G	T	1.942595	0.052065
<i>CD3G</i>	11q23.3	rs3212262	G	T	1.942595	0.052065
<i>CD247</i>	1q24.2	rs704853	G	T	2.566147	0.010284
<i>JUN</i>	1p32.1	rs6661505	C	T	3.545194	0.000392
<i>CD3E</i>	11q23.3	rs7937334	C	T	1.647788	0.099396
<i>IL18R1</i>	2q12.1	rs1035127	A	G	3.840931	0.000123
<i>JAK2</i>	9p24.1	rs10758669	C	A	4.966956	6.80E-07
<i>CCR5</i>	3p21.31					
<i>MAPK14</i>	6p21.31	rs2237093	C	T	1.266613	0.205294
<i>IL18</i>	11q23.1	rs11214108	A	G	2.46519	0.013694
<i>IFNG</i>	12q15	rs10878698	G	A	2.39998	0.016396
<i>MAP2K6</i>	17q24.3	rs2905443	C	T	2.400609	0.016368
<i>STAT4</i>	2q32.3	rs1584945	C	T	2.078147	0.037696
<i>IL12A</i>	3q25.33	rs6800657	G	A	2.012755	0.04414
<i>TYK2</i>	19p13.2	rs12720356	C	A	2.763306	0.005722
<i>ETV5</i>	3q27.2	rs9867846	A	G	2.231897	0.025622
<i>MAPK8</i>	10q11.22	rs17697885	C	T	1.870675	0.06139