Table S6

Disease	Chr.	Region (Mb)	Reference	SNP	PPAA	P-Value
CAD	9	22.01-22.12	[1–6]	rs9632884	0.64	2.53E-13
CD	1	67.38-67.46	[1, 4, 6, 7]	rs10489629	0.39	3.71E-12
CD	2	233.94-233.97	[1, 4, 6, 7]	rs6431654	0.30	7.37E-14
CD	3	49.43-49.87	[1, 4–7]	rs6784820	0.28	2.93E-05
CD	5	40.43-40.64	[1, 4–7]	rs10213846	0.37	3.84E-12
CD	6	32.82-32.84	[1, 4, 7]	rs7768538	0.13	2.24E-06
CD	**10**	**79.20-79.29**	**N/A**	**rs2579176**	**0.14**	**2.76E-04**
CD	10	101.26-101.28	[1, 4, 6, 7]	rs7081330	0.13	1.85E-06
CD	16	49.30-49.36	[4–7]	rs17221417	0.29	8.06E-12
HT	**14**	**45.46-45.66**	**N/A**	**rs762015**	**0.12**	**1.96E-03**
RA	1	114.02	[1, 4–6, 8, 9]	rs6679677	0.17	1.55E-26
RA	2	100.19	[10]	rs11694875	0.14	3.15E-04
RA	6	HLA	[1, 4–6, 8, 9]	rs6457617*	1.00	6.22E-79
RA	**17**	**4.10**	**N/A**	**rs9913077**	**0.14**	**1.29E-04**
T1D	1	113.80-114.15	[1, 4–6, 9, 11, 12]	rs1217396	0.39	1.62E-10
T1D	**2**	**206.67-206.85**	**N/A**	**rs4147713**	**0.22**	**1.82E-03**
T1D	**2**	**215.52-215.65**	**N/A**	**rs6737675**	**0.43**	**3.49E-04**
T1D	**3**	**12.51-12.58**	**N/A**	**rs1618545**	**0.19**	**3.11E-04**
T1D	3	46.26-46.37	[12]	rs1799865	0.33	4.89E-05
T1D	**3**	**82.74-82.82**	**N/A**	**rs1097157**	**0.25**	**2.33E-04**
T1D	**3**	**97.03-97.09**	**N/A**	**rs10934261**	**0.16**	**1.16E-04**
T1D	6	HLA	[1, 4–6, 9, 11, 12]	rs9273363*	1.00	0.00E+00
T1D	**6**	**120.74-120.84**	**N/A**	**rs12660882**	**0.16**	**3.50E-04**
T1D	12	109.82-111.40	[1, 4–6, 11, 12]	rs17696736	0.92	2.10E-15
T1D	**15**	**48.08-48.11**	**N/A**	**rs9302151**	**0.23**	**3.10E-03**
			N/A	**rs2414005**	**0.21**	**2.60E-03**
T1D	16	10.96-11.34	[1, 4, 6, 9, 11, 12]	rs243327	0.28	1.87E-04
T2D	**4**	**104.04-104.30**	**N/A**	**rs7698608**	**0.10**	**5.02E-04**
T2D	**5**	**153.62-153.63**	**N/A**	**rs11167666**	**0.06**	**3.99E-03**
T2D	10	114.74-114.80	[1, 4, 6, 11]	rs11196205	0.13	5.10E-11

Table of regions with at least two SNPs having PPAAs satisfying the 5% FWER threshold in the analysis of the WTCCC Data. Listed for all regions are the SNPs with the highest PPAA and their corresponding marginal p-values. The marginal p-values reported are found via linear regression and used as a direct comparison. The reference column gives literature sources that have previously suggested some level of association between a given region and disease. Rows listed in bold are those for which we did not find any sources that previously suggested association with that disease. These regions could potentially be novel. Note that some of the listed references [4, 11, 13] are works that utilize methods that consider pairwise interactions between SNPs. *Multiple SNPs in the HLA region are significant, so we choose the SNP with the lowest marginal p-value and report that as the most extreme.

References

[1] The Wellcome Trust Case Control Consortium. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, 447(7145):661–678, 2007. URL http://dx.doi.org/10.1038/nature05911.

[2] Daniela Zanetti, Robert Carreras-Torres, Esther Esteban, Marc Via, and Pedro Moral. Potential Signals of Natural Selection in the Top Risk Loci for Coronary Artery Disease: 9p21 and 10q11. *PLoS ONE*, 10(8):e0134840, 2015. doi: 10.1371/journal.pone.0134840. URL http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4529309/.

[3] Sonny Dandona, Alexandre F. R. Stewart, Li Chen, Kathryn Williams, Derek So, Ed O'Brien, Christopher Glover, Michel LeMay, Olivia Assogba, Lan Vo, Yan Qing Wang, Marino Labinaz, George A. Wells, Ruth McPherson, and Robert Roberts. Gene Dosage of the Common Variant 9p21 Predicts Severity of Coronary Artery Disease. *Journal of the American College of Cardiology*, 56(6):479–486, 2010. doi: http://dx.doi.org/10.1016/j.jacc.2009.10.092. URL http://www.sciencedirect.com/science/article/pii/S0735109710019583.

[4] Christoph Lippert, Jennifer Listgarten, Robert I. Davidson, Jeff Baxter, Hoifung Poon, Carl M. Kadie, and David Heckerman. An exhaustive epistatic SNP association analysis on expanded wellcome trust data. *Scientific Reports*, 3:1099 EP, 2013. URL http://dx.doi.org/10.1038/srep01099.

[5] Tao Feng and Xiaofeng Zhu. Genome-wide searching of rare genetic variants in WTCCC data. *Human Genetics*, 128(3):269–280, 2010. doi: 10.1007/s00439-010-0849-9. URL http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2922446/.

[6] Erich Dolejsi, Bernhard Bodenstorfer, and Florian Frommlet. Analyzing genome-wide association studies with an FDR controlling modification of the Bayesian information criterion. *PLoS ONE*, 9(7):e103322, 2014. URL http://dx.doi.org/10.1371%2Fjournal.pone.0103322.

[7] Andre Franke, Dermot P B McGovern, Jeffrey C Barrett, Kai Wang, Graham L Radford-Smith, Tariq Ahmad, Charlie W Lees, Tobias Balschun, James Lee, Rebecca Roberts, Carl A Anderson, Joshua C Bis, Suzanne Bumpstead, David Ellinghaus, Eleonora M Festen, Michel Georges, Todd Green, Talin Haritunians, Luke Jostins, Anna Latiano, Christopher G Mathew, Grant W Montgomery, Natalie J Prescott, Soumya Raychaudhuri, Jerome I Rotter, Philip Schumm, Yashoda Sharma, Lisa A Simms, Kent D Taylor, David Whiteman, Cisca Wijmenga, Robert N Baldassano, Murray Barclay, Theodore M Bayless, Stephan Brand, Carsten Buning, Albert Cohen, Jean-Frederick Colombel, Mario Cottone, Laura Stronati, Ted Denson, Martine De Vos, Renata D'Inca, Marla Dubinsky, Cathryn Edwards, Tim Florin, Denis Franchimont, Richard Gearry, Jurgen Glas, Andre Van Gossum, Stephen L Guthery, Jonas Halfvarson, Hein W Verspaget, Jean-Pierre Hugot, Amir Karban, Debby Laukens, Ian Lawrance, Marc Lemann, Arie Levine, Cecile Libioulle, Edouard Louis, Craig Mowat, William Newman, Julian Panes, Anne Phillips, Deborah D Proctor, Miguel Regueiro, Richard Russell, Paul Rutgeerts, Jeremy Sanderson, Miquel Sans, Frank Seibold, A Hillary Steinhart, Pieter C F Stokkers, Leif Torkvist, Gerd Kullak-Ublick, David Wilson, Thomas Walters, Stephan R Targan, Steven R Brant, John D Rioux, Mauro D'Amato, Rinse K Weersma, Subra Kugathasan, Anne M Griffiths, John C Mansfield, Severine Vermeire, Richard H Duerr, Mark S Silverberg, Jack Satsangi, Stefan Schreiber, Judy H Cho, Vito Annese, Hakon Hakonarson, Mark J Daly, and Miles Parkes. Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nat Genet*, 42(12):1118–1125, 2010. URL http://dx.doi.org/10.1038/ng.717.

[8] Ian C. Scott, Seth D. Seegobin, Sophia Steer, Rachael Tan, Paola Forabosco, Anne Hinks, Stephen Eyre, Ann W. Morgan, Anthony G. Wilson, Lynne J. Hocking, Paul Wordsworth, Anne Barton, Jane Worthington, Andrew P. Cope, and Cathryn M. Lewis. Predicting the Risk of Rheumatoid Arthritis and Its Age of Onset through Modelling Genetic Risk Variants with Smoking. *PLoS Genet*, 9(9):e1003808, 2013. URL http://dx.doi.org/10.1371%2Fjournal.pgen.1003808.

[9] Hariklia Eleftherohorinou, Victoria Wright, Clive Hoggart, Anna-Liisa Hartikainen, Marjo-Riitta Jarvelin, David Balding, Lachlan Coin, and Michael Levin. Pathway Analysis of GWAS Provides New Insights into Genetic Susceptibility to 3 Inflammatory Diseases. *PLoS ONE*, 4(11):e8068, 2009. URL http://dx.doi.org/10.1371%2Fjournal.pone.0008068.

[10] Eli A Stahl, Soumya Raychaudhuri, Elaine F Remmers, Gang Xie, Stephen Eyre, Brian P Thomson, Yonghong Li, Fina A S Kurreeman, Alexandra Zhernakova, Anne Hinks, Candace Guiducci, Robert Chen, Lars Alfredsson, Christopher I Amos, Kristin G Ardlie, Anne Barton, John Bowes, Elisabeth Brouwer, Noel P Burtt, Joseph J Catanese, Jonathan Coblyn, Marieke J H Coenen, Karen H Costenbader, Lindsey A Criswell, J Bart A Crusius, Jing Cui, Paul I W de Bakker, Philip L De Jager, Bo Ding, Paul Emery, Edward Flynn, Pille Harrison, Lynne J Hocking, Tom W J Huizinga, Daniel L Kastner, Xiayi Ke, Annette T Lee, Xiangdong Liu, Paul Martin, Ann W Morgan, Leonid Padyukov, Marcel D Posthumus, Timothy R D J Radstake, David M Reid, Mark Seielstad, Michael F Seldin, Nancy A Shadick, Sophia Steer, Paul P Tak, Wendy Thomson, Annette H M van der Helm-van Mil, Irene E van der Horst-Bruinsma, C Ellen van der Schoot, Piet L C M van Riel, Michael E Weinblatt, Anthony G Wilson, Gert Jan Wolbink, B Paul Wordsworth, Cisca Wijmenga, Elizabeth W Karlson, Rene E M Toes, Niek de Vries, Ann B Begovich, Jane Worthington, Katherine A Siminovitch, Peter K Gregersen, Lars Klareskog, and Robert M Plenge. Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. *Nature Genetics*, 42(6):508–514, 2010. URL http://dx.doi.org/10.1038/ng.582.

[11] Yu Zhang, Jing Zhang, and Jun S. Liu. Block-based Bayesian epistasis association mapping with application to WTCCC type 1 diabetes data. *Annals of Applied Statistics*, 5(3):2052–2077, 2011. doi: 10.1214/11-AOAS469. URL http://projecteuclid.org/euclid.aoas/1318514295.

[12] Jonathan P. Bradfield, Hui-Qi Qu, Kai Wang, Haitao Zhang, Patrick M. Sleiman, Cecilia E. Kim, Frank D. Mentch, Haijun Qiu, Joseph T. Glessner, Kelly A. Thomas, Edward C. Frackelton, Rosetta M. Chiavacci, Marcin Imielinski, Dimitri S. Monos, Rahul Pandey, Marina Bakay, Struan F. A. Grant, Constantin Polychronakos, and Hakon Hakonarson. A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. *PLoS Genet*, 7(9):e1002293, 2011. URL http://dx.doi.org/10.1371%2Fjournal.pgen.1002293.

[13] Min-Seok Kwon, Mira Park, and Taesung Park. IGENT: efficient entropy based algorithm for genome-wide gene-gene interaction analysis. *BMC Medical Genomics*, 7, 2014.