Supplementary Table 1: GWAS loci with functional outside variants

Lead SNP	Gene Target	Regulatory Circuitry
rs10201872	SP100	PreSTIGE
rs10488631	IRF5	Hi-C
rs1077667	C3	Super
rs1077667	GPR108	Super
rs10892279	TRAPPC4	Hi-C
rs10892279	UPK2	Hi-C
rs10995271	ADO	Hi-C
rs11150589	SEPHS2	Super
rs11175593	LRRK2	PreSTIGE
rs11203203	RSPH1	Hi-C, Super
rs11203203	TMPRSS3	Hi-C, Super
rs11755724	RREB1	Hi-C
rs11860650	ITGAD	PreSTIGE
rs12025416	ATP1A1OS	PreSTIGE
rs12456021	ALPK2	Super
rs12531711	IRF5	Hi-C
rs12711490	IRF8	Super
rs12928822	RMI2	Super
rs13239597	IRF5	Hi-C
rs13277113	FAM167A	Super
rs13333054	IRF8	Super
rs1335532	ATP1A1OS	PreSTIGE
rs13428812	DNMT3A	Super
rs16940202	IRF8	PreSTIGE
rs1738074	RSPH3	Hi-C
rs17445836	IRF8	Super
rs17810546	IL12A	Hi-C
rs2176082	PXK	Super
rs2283792	YPEL1	Super
rs2284553	IL10RB	Hi-C
rs2297441	C20orf195	Super
rs2300747	ATP1A1OS	PreSTIGE
rs2413583	PDGFB	Super
rs2413583	SYNGR1	Super
rs2425752	NCOA5	Hi-C, Super
rs2431697	C5orf54	Super
rs2762051	DLEU1	Hi-C
rs290986	SYK	PreSTIGE, Hi-C, Super
rs3024493	DYRK3	Hi-C
rs3024493	FAIM3	Hi-C
rs3024493	IL19	PreSTIGE, Hi-C, Super
rs3024505	DYRK3	Hi-C
rs3024505	IL19	PreSTIGE, Hi-C, Super
rs354033	ZNF767	Super
rs4308217	ILDR1	Super
rs4656940	CD244	PreSTIGE, Hi-C
rs4656940	CD48	Super
rs4656940	LY9	PreSTIGE, Hi-C, Super
rs4656940	SLAMF7	PreSTIGE, Super
rs4680534	IL12A	Hi-C
rs4780355	RMI2	Super
rs4781011	CLEC16A	Hi-C
rs4781011	DEXI	Super
rs4781011	FAM18A	PreSTIGE
rs4810485	CD40	Super
rs4810485	NCOA5	Hi-C
rs4953911	MGAT5	Super
rs6074022	CD40	Super
rs6074022	NCOA5	Hi-C
rs615672	HLA-DQA1	Super
rs615672	HLA-DQB1	Super
rs615672	HLA-DRB1	Super
rs630923	TRAPPC4	Hi-C
rs630923	UPK2	Hi-C
rs6445975	PXK	Super
rs6498169	CIITA	Super
rs6498169	DEXI	Super
rs660895	HLA-DQA1	PreSTIGE, Super
rs660895	HLA-DQB1	Super
rs660895	HLA-DRB5	PreSTIGE, Super
rs660895	HLA-DRB6	PreSTIGE, Super
rs6716753	SP100	PreSTIGE
rs7155603	FLVCR2	Super
rs7172677	C15orf39	Super
rs7200786	SOCS1	Super
rs7238078	ALPK2	Super
rs7238078	MALT1	PreSTIGE, Hi-C, Super
rs7253363	ELOF1	Super
rs7423615	SP100	PreSTIGE
rs7923837	KIF11	Super
rs806321	DLEU1	Hi-C
rs874040	C4orf52	Hi-C
rs907611	SYT8	Super
rs9596270	DLEU1	Hi-C
rs960709	ANXA6	Hi-C, Super
rs960709	GM2A	Hi-C
rs9888739	ITGAD	PreSTIGE

Supplementary Table 2: Outside variant loci evaluated in luciferase reporter assays

Enhancer region (hg18)	Gene Target(s)	Functional Outside Variants	Primer sequences	
chr9:92,597,336-92,599,537	SYK	rs10993693, rs290997	FWD	**GGAGACAU**GATCTTGGTATGAGAAAAACCATCT
			REV	**GGGAAAGU**GCGCAGATTTAGATCTTCATTCA
chr16:84,546,145-84,547,502	IRF8	rs7199472	FWD	**GGAGACAU**GGAGGTGACTTCTGCATTGA
			REV	**GGGAAAGU**CGGTACAAAGGCCTGAGGT
chr1:159,025,419-159,027,509	SLAMF7, LY9	rs1333065, rs12405457	FWD	**GGAGACAU**CAGAACCTGTCCCCTCATCA
			REV	**GGGAAAGU**GCTGAACTGAACTTAAGGCTGA
chr18:54,380,385-54,381,923	MALT1	rs8090585	FWD	**GGAGACAU**GGAGGTGACTTCTGCATTGA
			REV	**GGGAAAGU**CGGTACAAAGGCCTGAGGT
chr2:230,891,662-230,892,865	SP100	rs11679076	FWD	**GGAGACAU**CAGGATTCGATACCATCACTCA
			REV	**GGGAAAGU**GAAAACTCATCCATCTCATCTGC
chr6:32,683,356-32,684,808	HLA-DQA1	rs646984	FWD	**GGAGACAU**CCCATCGTCTAAAACATGCAC
			REV	**GGGAAAGU**CCAAAACTTGCCCTTTTTAATG
chr12:38,848,086-38,849,374	LRRK2	rs728624, rs728623, rs2708489, rs1948380	FWD	**GGAGACAU**TTGTGTCAGTAATCATTTATCTGCAT
			REV	**GGGAAAGU**TGAGATATGAAAAATAGTTTCAGCAAA

Supplementary Table 3: Summary of candidate “third SNPs” evaluated

			"3rd" SNPs with effects: Independent effect on expression, no additional variance explained by GWAS or outside variant			"3rd" SNP with effects that are imputed on GWAS panel		
Gene	**Candidate "3rd" SNPs per gene**	**Number tests per gene**	**P<7.5E-8 (uncorrected)**	**P<0.05 (corrected)**	**P<5E-3 (uncorrected)**	**P<7.5E-8 (uncorrected)**	**P<0.05 (corrected)**	**P<5E-3 (uncorrected)**
ADO	3094	5638	16	61	116	8	20	50
ALPK2	3489	7275	0	0	15	NA	NA	15
ATP1A1OS	2396	3806	0	1	1	NA	1	1
C20orf195	4680	8976	0	0	14	NA	NA	6
C3	4823	9289	0	0	47	NA	NA	5
C4orf52	3064	5928	15	15	15	15	15	15
CD244	3359	6147	11	11	11	11	11	11
CD40	3292	6160	0	0	20	NA	NA	3
CD48	2897	5245	0	3	29	NA	3	29
CIITA	3827	7729	0	0	11	NA	NA	10
CLEC16A	4115	8417	0	0	55	NA	NA	49
DEXI	4101	8387	2	30	121	2	30	121
DLEU1	3113	5821	0	80	89	NA	80	89
DNMT3A	2859	5307	0	0	26	NA	NA	5
DYRK3	1771	3143	0	0	15	NA	NA	14
ELOF1	3546	6010	0	0	49	NA	NA	21
FAIM3	2352	4416	0	0	3	NA	NA	1
FAM18A	3829	7553	0	0	36	NA	NA	5
FLVCR2	2783	5221	0	0	3	NA	NA	*
GPR108	4875	9459	12	15	116	12	15	111
HLA-DQA1	22081	53643	30	30	30	30	30	30
HLA-DQB1	22346	54378	0	0	0	NA	NA	NA
HLA-DRB1	21533	52289	0	0	0	NA	NA	NA
HLA-DRB5	20633	49967	237	390	1377	111	214	668
HLA-DRB6	20865	50545	10	10	10	10	10	10
IL10RB	2735	5805	0	1	51	NA	1	45
IL12A	2703	4451	32	33	33	32	33	33
IL19	2286	4304	0	0	0	NA	NA	NA
ILDR1	2951	5931	0	0	13	NA	NA	3
IRF5	3305	6393	13	18	20	13	18	20
IRF8	4764	9180	0	0	13	NA	NA	8
KIF11	2579	4495	0	0	144	NA	NA	11
LRRK2	3431	6717	0	1	60	NA	1	54
LY9	3060	5556	0	10	11	NA	10	11
MALT1	3473	7217	0	0	6	NA	NA	5
MGAT5	3212	6454	0	0	41	NA	NA	2
NCOA5	3230	5904	0	0	12	NA	NA	7
PDGFB	3300	6724	10	32	32	10	32	32
RMI2	4124	8710	0	0	0	NA	NA	NA

Supplementary Table 3: Summary of candidate “third SNPs” evaluated (continued)

			"3rd" SNPs with effects: Independent effect on expression, no additional variance explained by GWAS or outside variant			"3rd" SNP with effects that are imputed on GWAS panel		
Gene	**Candidate "3rd" SNPs per gene**	**Number tests per gene**	**P<7.5E-8 (uncorrected)**	**P<0.05 (corrected)**	**P<5E-3 (uncorrected)**	**P<7.5E-8 (uncorrected)**	**P<0.05 (corrected)**	**P<5E-3 (uncorrected)**
RREB1	4184	8352	0	0	9	NA	NA	2
RSPH1	4852	9082	0	0	0	NA	NA	NA
RSPH3	3806	7802	143	171	204	125	150	166
SEPHS2	1291	2363	0	6	8	NA	6	8
SLAMF7	3053	5595	4	8	8	4	8	8
SOCS1	3990	8212	0	0	31	NA	NA	31
SP100	3425	7299	0	0	6	NA	NA	3
SYK	3953	7381	0	0	0	NA	NA	NA
SYNGR1	3172	6404	0	0	0	NA	NA	NA
SYT8	4991	10399	0	0	15	NA	NA	14
TMPRSS3	4898	9394	0	0	25	NA	NA	15
TRAPPC4	2488	5352	36	36	36	36	36	36
UPK2	2415	5133	0	0	0	NA	NA	NA
YPEL1	2986	5942	0	0	78	NA	NA	6
ZNF767	3676	7272	0	14	15	NA	7	7
ANXA6	3595	7191	0	0	0	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac
C15orf39	2018	3906	0	43	61	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac
C5orf54	3451	6671	0	0	24	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac
FAM167A	4904	10348	59	59	59	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac
GM2A	3627	7237	8	8	8	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac
ITGAD	2129	4297	2	6	11	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac
PXK	2847	5551	0	1	140	Lupus or Celiac	Lupus or Celiac	Lupus or Celiac

* gene excluded from percentage calculations

NOTE: only loci associated with RA, MS, UC and CD were evaluated for impact on clinical risk