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Supplementary Table 1. Summary of candidate genes in the study associated with leprosy

SNP	Gene	Functional Consequence	MAF [a]	Molecular function for genes
rs76418789	*IL23R*	missense	0.011	IL23R was critical for optimal levels of pattern-recognition receptor-induced signaling and cytokines in human monocyte-derived macrophages[1]
rs146466242	*FLG*	stop gained	0.004	Encoded filaggrin, filaggrin plays a crucial role in the barrier function of epidermis[2]
rs2221593	*BATF3*	upstream	0.161	Plays a central role in the development of conventional dendritic cells, which in turn are critical for optimal priming of CD8+ T cells[3]
rs2058660	*IL18RAP/ IL18R1*	intron	0.694	Plays an important role in IFN-γ production[4]
rs73058713	*CDH18*	intron	0.178	Involves in neuronal development and govern metabolic processes in later life[5]

rs2275606	*RAB32*	ncRNA intronic	0.134	Key regulator of a host defense pathway that can restrict intracellular bacterial pathogens[6]
rs4720118	*BBS9*	intron	0.672	Involves in parathyroid hormone action in bones[7]
rs55894533	*CTSB*	intergenic	0.409	Associated with the migration ability of keratinocytes and unobstructed migration of keratinocytes[7]
rs6478108	*TNFSF15*	intron	0.715	Involved in mediating the switch from Th1 cells to Th2 cells[8]
rs10817758	*1-Dec*	intron	0.182	Acts as an accelerator in tumor progression[9]
rs780668	*SLC29A3*	missense	0.480	Encodes ENT3, a key role in maintaining T cell homeostasis by supporting the proliferation and survival of T cells[10]
rs663743	*CCDC88 B*	5 prime UTR variant	0.198	A key role for mobility and inflammatory functions of dendritic cells[11]
rs3764147	*LACC1*	missense	0.306	Associated with autoimmunity and granulomatous disease diseases[12]

rs142179458	*HIF1A*	missense	0.005	Plays a role in immune reactions and chaperone-mediated autophagy[13]
rs9302752	*NOD2*	upstream	0.500	pro-inflammatory[14]
rs149308743	*CARD9*	missense	<0.001	The adaptor CARD9 functions downstream of C-type lectin receptors for the sensing of microbial infection[15]
rs145562243	*NCKIPSD*	missense	<0.0001	involved in the Rho signaling pathway[16]

[a] Minor allele frequency (MAF) from the 1000 Genomes Project[17], variants with MAF <0.05 were regarded as rare.

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Supplementary table 2: Ethnicity distribution of the study groups

Ethnicity	Leprosy (n=1344)	Heredity-related Contacts (n=1908)	First-degree family members (n=1560)	Non-heredity-related Contacts (n=824)
Han	711(52.9)	1106(58.0)	872(55.9)	453(55.0)
Miao	169(12.6)	229(12.0)	197(12.6)	106(12.9)
Yi	144(10.7)	169(8.9)	141(9.0)	82(10.0)
Buyi	83(6.2)	52(2.7)	52(3.3)	26(3.2)
Tujia	35(2.6)	64(3.4)	42(2.7)	25(3.0)
Zhuang	34(2.5)	73(3.8)	61(3.9)	28(3.4)
Dai	39(2.9)	60(3.1)	54(3.5)	36(4.4)
Others	129(9.6)	155(8.1)	141(9.0)	68(8.3)

Supplementary table 3: Analysis of association between SNPs and leprosy[a]

SNP	Gene	Minor allele	F_A	F_U[b]	F_U[c]	F_U[d]	F_U[e]	OR (95% CI) [b]	P[b]	OR (95% CI) [c]	P[c]	OR (95% CI) [d]	P[d]	OR (95% CI) [e]	P[e]
rs2275606	*RAB32*	A	0.29	0.28	0.28	0.28	0.27	1.08(0.98 -1.20)	0.12	1.07 (0.96- 1.19)	0.24	1.05 (0.94- 1.18)	0.37	1.12 (0.98-1.29)	0.10
rs142179458	*HIF1A*	A	0.05	0.05	0.05	0.05	0.05	1.02(0.82 -1.26)	0.88	1.00 (0.80- 1.26)	0.98	0.97 (0.77- 1.24)	0.82	1.05 (0.79-1.41)	0.74
rs3764147	*LACC1*	G	0.41	0.34	0.36	0.37	0.30	1.362(1.24 -1.50)	1.62×10^{-10}	1.26(1.14- 1.40)	<0.0001	1.22(1.10- 1.36)	0.0002	1.26 (1.14-1.40)	<0.0001
rs55894533	*CTSB*	C	0.47	0.45	0.45	0.45	0.45	1.08(0.99 -1.19)	0.09	1.08 (0.98- 1.19)	0.13	1.08 (0.97- 1.20)	0.16	1.10 (0.97-1.24)	0.16
rs6478108	*TNFSF15*	T	0.40	0.43	0.43	0.42	0.44	0.89(0.81 -0.97)	0.01	0.90 (0.81- 0.99)	0.03	0.92 (0.83- 1.03)	0.13	0.87 (0.76-0.98)	0.02
rs73058713	*CDH18*	A	0.14	0.13	0.13	0.13	0.13	1.06(0.93 -1.22)	0.36	1.06 (0.92-1.22)	0.44	1.09 (0.94-1.27)	0.24	1.08 (0.90-1.29)	0.40
rs780668	*SLC29A3*	A	0.50	0.45	0.46	0.46	0.44	1.20(1.10 -1.32)	9.48×10^{-5}	1.17 (1.06-1.29)	0.002	1.15(1.04-1.28)	0.007	1.28 (1.13-1.45)	<0.0001
rs10817758	*DEC1*	T	0.44	0.46	0.46	0.46	0.45	0.94 (0.86 -1.04)	0.22	0.93 (0.84-1.02)	0.13	0.92 (0.83-1.02)	0.11	0.98 (0.87-1.11)	0.79
rs146466242	*FLG*	A	0.02	0.02	0.02	0.02	0.02	1.00(0.71 -1.40)	0.98	1.00 (0.69-1.44)	1.00	0.97 (0.66-1.41)	0.86	0.99 (0.63-1.55)	0.96
rs9302752	*NOD2*	C	0.27	0.24	0.25	0.25	0.22	1.18(1.06 -1.31)	0.002	1.11 (0.99-1.24)	0.07	1.12 (1.00-1.26)	0.06	1.35 (1.17-1.56)	<0.0001
rs2058660	*IL18RAP/IL18R1*	C	0.42	0.43	0.42	0.42	0.43	0.96 (0.88 -1.06)	0.45	0.98 (0.89-1.08)	0.69	1.00 (0.90-1.11)	1.00	0.93 (0.82-1.05)	0.25

rs4720118	*BBS9*	T	0.30	0.29	0.29	0.29	0.30	1.06(0.96-1.17)	0.27	1.07 (0.96-1.19)	0.23	1.09 (0.97-1.22)	0.14	1.04 (0.91-1.18)	0.61
rs663743	*CCDC88B*	A	0.23	0.21	0.21	0.22	0.21	1.13(1.01-1.26)	0.03	1.12 (0.99-1.26)	0.06	1.10 (0.97-1.24)	0.14	1.15 (0.99-1.34)	0.06
rs76418789	*IL23R*	A	0.05	0.04	0.04	0.04	0.03	1.14(0.91-1.44)	0.24	1.07 (0.84-1.36)	0.57	1.04 (0.81-1.34)	0.74	1.35 (0.98-1.87)	0.07

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in patients; F_U, minor allele frequency in control subjects; OR, odds ratio with respect to the minor allele; CI, confidence interval.

[a] Association tested with $\chi 2$ test or Fisher test.

[b] All HHCs as control subjects.

[c] Heredity-related Contacts as control subjects.

[d] First - degree family members as control subjects.

[e] non-Heredity-related Contacts as control subjects.

Supplementary table 4: Genotypic distributions of the study groups

SNP	Gene	Minor allele	aa/Aa/AA[a]				
			Cases (n=1344)	Controls[b] (n=2732)	Controls[c] (n=1908)	Controls[d] (n=1560)	Controls[e] (n=824)
rs2275606	*RAB32*	A	121/545/678	206/1098/1428	150/766/992	127/626/807	56/332/436
rs142179458	*HIF1A*	A	4/122/1218	10/240/2482	8/168/1732	7/141/1412	2/72/750
rs3764147	*LACC1*	G	225/665/454	315/1240/1177	249/875/784	208/730/622	66/365/393
rs55894533	*CTSB*	C	300/663/381	542/1374/816	382/956/570	313/782/465	160/418/246
rs6478108	*TNFSF15*	T	238/609/497	527/1311/894	367/908/633	299/722/539	160/403/261
rs73058713	*CDH18*	A	24/332/988	59/614/2059	38/438/1432	26/356/1178	21/176/627
rs780668	*SLC29A3*	A	339/655/350	522/1415/795	380/982/546	316/805/439	142/433/249
rs10817758	*DEC1*	T	252/682/410	563/1364/805	400/956/552	325/792/443	163/408/253
rs146466242	*FLG*	A	3/44/1297	3/96/2633	2/67/1839	2/56/1502	1/29/794
rs9302752	*NOD2*	C	103/524/717	154/1007/1571	119/721/1068	102/575/883	35/286/503
rs2058660	*IL18RAP/IL18R1*	C	225/670/449	523/1279/930	361/887/660	287/726/547	162/392/270
rs4720118	*BBS9*	T	124/571/649	234/1132/1366	154/802/952	124/647/789	80/330/414
rs663743	*CCDC88B*	A	70/482/792	140/870/1722	94/621/1193	80/511/969	46/249/529
rs76418789	*IL23R*	A	5/112/1227	6/206/2520	4/154/1750	3/130/1427	2/52/770

Abbreviations: SNP, single nucleotide polymorphism;

[a] aa/Aa/AA, the numbers of cases and controls with minor allele homozygote/heterozygote/major allele homozygote genotypes, respectively.

[b] All HHCs as control subjects.

[c] Heredity-related Contacts as control subjects.

[d] First - degree family members as control subjects.

[e] non-Heredity-related contacts as control subjects.

Supplementary table 5: Analysis of association between SNPs and leprosy onset early cases

SNP	Gene	Minor allele	aa/Aa/AA[a]		F_A	F_U	OR (95% CI) [b]	P[b]	Risk allele	OR (95% CI) [c]	P[c]
			Cases (n=44)	Controls (n=1300)							
rs2275606	*RAB32*	A	6/19/19	115/526/659	0.35	0.29	1.33 (0.85-2.07)	0.21	A	1.27 (0.81-1.97)	0.30
rs142179458	*HIF1A*	A	1/8/35	3/114/1183	0.11	0.05	2.65 (1.34-5.25)	0.004	A	2.31 (1.16-4.62)	0.02
rs3764147	*LACC1*	G	5/22/17	220/643/437	0.36	0.42	0.80 (0.51-1.24)	0.32	A	1.26 (0.81-1.98)	0.31
rs55894533	*CTSB*	C	8/23/13	292/640/368	0.44	0.47	0.89 (0.58-1.37)	0.61	A	1.13 (0.74-1.74)	0.56
rs6478108	*TNFSF15*	T	7/25/12	231/584/485	0.44	0.40	1.18 (0.77-1.81)	0.44	T	1.16 (0.76-1.75)	0.49
rs73058713	*CDH18*	A	0/13/31	24/319/957	0.15	0.14	1.06 (0.58-1.92)	0.86	A	1.09 (0.59-2.00)	0.79
rs780668	*SLC29A3*	A	14/21/9	325/634/341	0.56	0.49	1.29 (0.84-1.98)	0.25	A	1.26 (0.83-1.92)	0.28
rs10817758	*DEC1*	T	10/25/9	242/657/401	0.51	0.44	1.34 (0.87-2.05)	0.18	T	1.32 (0.85-2.04)	0.22
rs146466242	*FLG*	A	0/2/42	3/42/1255	0.02	0.02	1.24 (0.30-5.17)	0.77	A	1.27 (0.33-4.97)	0.73
rs9302752	*NOD2*	C	5/20/19	98/504/698	0.34	0.27	1.40 (0.90-2.20)	0.14	C	1.48 (0.95-2.33)	0.09
rs2058660	*IL18RAP/IL18R1*	C	10/19/15	215/651/434	0.44	0.42	1.12 (0.73-1.72)	0.61	C	1.14 (0.74-1.77)	0.55
rs4720118	*BBS9*	T	4/16/24	120/555/625	0.27	0.31	0.85 (0.53-1.37)	0.51	C	1.16 (0.72-1.88)	0.55
rs663743	*CCDC88B*	A	4/13/27	66/469/765	0.24	0.23	1.04 (0.63-1.72)	0.87	A	1.00 (0.61-1.65)	0.99
rs76418789	*IL23R*	A	0/2/42	5/110/1185	0.02	0.05	0.48 (0.12-1.98)	0.30	G	2.01 (0.49-8.27)	0.33

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in patients diagnosed at the age<14-year; F_U, minor allele frequency in patients diagnosed at the age≥14-year; OR, odds ratio with respect to the minor allele; CI,

confidence interval.

[a] aa/Aa/AA, the numbers of cases and controls with minor allele homozygote/heterozygote/major allele homozygote genotypes, respectively

[b] Association tested with $\chi 2$ test or Fisher test.

[c] Association tested with logistic regression model adjusted for sex and ethnicity.

Supplementary table 6: Analysis of association between SNPs and leprosy WHO classifications

SNP	Gene	Minor allele	aa/Aa/AA[a]		F_A	F_U	OR (95% CI)[b]	P[b]	Risk allele	OR (95% CI)[c]	P[c]
			Cases (n=173)	Controls (n=1171)							
rs2275606	*RAB32*	A	12/73/88	109/472/590	0.28	0.29	0.93 (0.73-1.199)	0.59	G	1.07 (0.83-1.37)	0.62
rs142179458	*HIF1A*	A	0/18/155	4/104/1063	0.05	0.05	1.09 (0.66-1.82)	0.73	A	1.13 (0.68-1.88)	0.64
rs3764147	*LACC1*	G	32/78/63	193/587/391	0.41	0.42	0.98 (0.78-1.23)	0.86	A	1.02 (0.81-1.28)	0.89
rs55894533	*CTSB*	C	39/86/48	261/577/333	0.47	0.47	1.02 (0.81-1.28)	0.87	C	1.02 (0.81-1.28)	0.88
rs6478108	*TNFSF15*	T	27/90/56	211/519/441	0.42	0.40	1.06 (0.84-1.34)	0.61	T	1.03 (0.83-1.29)	0.77
rs73058713	*CDH18*	A	2/48/123	22/284/865	0.15	0.14	1.09 (0.79-1.49)	0.61	A	1.10 (0.79-1.52)	0.57
rs780668	*SLC29A3*	A	41/88/44	298/567/306	0.49	0.50	0.98 (0.78-1.23)	0.86	A	1.01 (0.81-1.26)	0.93
rs10817758	*DEC1*	T	38/85/50	214/597/360	0.47	0.44	1.12 (0.89-1.40)	0.33	T	1.14 (0.90-1.44)	0.27
rs146466242	*FLG*	A	0/6/167	3/38/1130	0.02	0.02	0.92 (0.39-2.18)	0.85	A	1.06 (0.46-2.43)	0.89
rs9302752	*NOD2*	C	8/71/94	95/453/623	0.25	0.27	0.89 (0.68-1.15)	0.37	T	1.08 (0.83-1.40)	0.57
rs2058660	*IL18RAP/IL18R1*	C	36/82/55	189/588/394	0.45	0.41	1.14 (0.91-1.43)	0.25	C	1.15 (0.91-1.45)	0.24
rs4720118	*BBS9*	T	17/84/72	107/487/577	0.34	0.30	1.21 (0.95-1.54)	0.12	T	1.21 (0.95-1.54)	0.13
rs663743	*CCDC88B*	A	9/70/94	61/412/698	0.25	0.23	1.16 (0.90-1.50)	0.28	A	1.15 (0.88-1.50)	0.29
rs76418789	*IL23R*	A	0/10/163	5/102/1064	0.03	0.05	0.59 (0.31-1.14)	0.11	G	1.62 (0.84-3.11)	0.15

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in paucibacillary leprosy cases; F_U, minor allele frequency in multibacillary leprosy cases; OR, odds ratio with respect to the minor allele; CI, confidence interval.

[a] aa/Aa/AA, the numbers of cases and controls with minor allele

homozygote/heterozygote/major allele homozygote genotypes, respectively.

[b] Association tested with $\chi 2$ test or Fisher test.

[c] Association tested with logistic regression model adjusted for sex, ethnicity and age at diagnosis.

Supplementary table 7: Analysis of association between SNPs and leprosy subtypes

SNP	Gene	Minor allele	aa/Aa/AA[a]		F_A	F_U	OR (95% CI) [b]	P [b]	Risk allele	OR (95% CI)[c]	P[c]
			Cases (n=391)	Controls (n=841)							
rs76418789	*IL23R*	A	0/28/363	5/75/761	0.04	0.05	0.70(0.45-1.08)	0.10	G	1.37(0.89-2.11)	0.15
rs146466242	*FLG*	A	1/11/379	2/26/813	0.02	0.02	0.93(0.48-1.80)	0.83	A	1.06(0.57-1.98)	0.86
rs2058660	*IL18RAP/IL18R1*	C	79/184/128	132/426/283	0.44	0.41	1.12(0.94-1.33)	0.20	C	1.13(0.94-1.34)	0.19
rs73058713	*CDH18*	A	7/94/290	13/206/622	0.14	0.14	1.00(0.78-1.28)	0.99	A	1.01(0.78-1.29)	0.97
rs2275606	*RAB32*	A	25/166/200	82/333/426	0.28	0.30	0.91 (0.75-1.10)	0.33	G	1.09 (0.90-1.31)	0.39
rs4720118	*BBS9*	T	36/175/180	77/342/422	0.32	0.29	1.10(0.92-1.33)	0.29	T	1.10(0.92-1.32)	0.31
rs55894533	*CTSB*	C	77/216/98	199/395/247	0.47	0.47	1.01(0.85-1.19)	0.94	C	1.01(0.85-1.20)	0.91
rs6478108	*TNFSF15*	T	71/187/133	151/361/329	0.42	0.39	1.12(0.94-1.33)	0.21	T	1.09(0.92-1.29)	0.32
rs10817758	*1-Dec*	T	79/182/130	163/436/242	0.43	0.45	0.93(0.78-1.10)	0.40	C	1.07(0.90-1.27)	0.46
rs780668	*SLC29A3*	A	91/192/108	222/400/219	0.48	0.50	0.91(0.77-1.08)	0.28	G	1.07(0.91-1.27)	0.42
rs663743	*CCDC88B*	A	19/144/228	43/300/498	0.23	0.23	1.02(0.83-1.25)	0.86	A	1.01(0.82-1.24)	0.92

rs3764147	*LACC1*	G	51/174/166	161/435/245	0.35	0.45	0.67(0.56-0.79)	<0.0001	A	1.51(1.26-1.81)	<0.0001
rs142179458	*HIF1A*	A	3/40/348	1/71/769	0.06	0.04	1.38(0.94-2.01)	0.10	A	1.46(0.99-2.14)	0.05
rs9302752	*NOD2*	C	21/151/219	75/330/436	0.25	0.29	0.82(0.68-1.00)	<0.05	T	1.18(0.97-1.44)	0.09

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in tuberculoid cases (BT/TT); F_U, minor allele frequency in lepromatous cases (LL/BL); OR, odds ratio with respect to the minor allele; CI, confidence interval.

[a] aa/Aa/AA, the numbers of cases and controls with minor allele homozygote/heterozygote/major allele homozygote genotypes, respectively.

[b] Association tested with $\chi 2$ test or Fisher test.

[c] Association tested with logistic regression model adjusted for sex, ethnicity and age at diagnosis.

Supplementary table 8: Analysis of association between SNPs and reversal reaction in BB, BT and BL leprosy cases

SNP	Gene	Minor allele	aa/Aa/AA[a]		F_A	F_U	OR (95% CI)[b]	P[b]	Risk allele	OR (95% CI)[c]	P[c]
			Cases (n=54)	Controls (n=696)							
rs76418789	*IL23R*	A	1/3/50	2/62/632	0.05	0.05	0.98 (0.38-2.47)	0.96	G	1.02 (0.40-2.56)	0.97
rs146466242	*FLG*	A	0/1/53	2/24/670	0.009	0.02	0.46 (0.06-3.38)	0.43	T	1.95 (0.28-13.67)	0.50
rs2058660	*IL18RAP/IL18R1*	C	8/30/16	114/344/238	0.43	0.41	1.06 (0.72-1.58)	0.76	C	1.07 (0.71-1.60)	0.75
rs73058713	*CDH18*	A	3/17/34	13/167/516	0.21	0.14	1.68 (1.04-2.73)	0.03	A	1.69 (1.04-2.76)	0.03
rs2275606	*RAB32*	A	5/21/28	69/275/352	0.29	0.30	0.95 (0.62-1.47)	0.83	G	1.06 (0.69-1.62)	0.78
rs4720118	*BBS9*	T	6/20/28	61/297/338	0.30	0.30	0.98 (0.64-1.50)	0.92	C	1.03 (0.67-1.58)	0.91
rs55894533	*CTSB*	C	7/28/19	159/347/190	0.39	0.48	0.70 (0.47-1.04)	0.07	A	1.46 (0.97-2.18)	0.07
rs6478108	*TNFSF15*	T	13/22/19	117/314/265	0.44	0.39	1.23 (0.83-1.83)	0.30	T	1.21 (0.83-1.77)	0.33
rs10817758	*1-Dec*	T	7/31/16	135/335/226	0.42	0.43	0.93 (0.62-1.38)	0.72	C	1.09 (0.73-1.62)	0.69
rs780668	*SLC29A3*	A	13/29/12	176/331/189	0.51	0.49	1.08 (0.73-1.59)	0.71	A	1.07 (0.73-1.58)	0.72
rs663743	*CCDC88B*	A	3/17/34	39/248/409	0.21	0.23	0.88 (0.55-1.43)	0.61	G	1.13 (0.70-1.82)	0.61
rs3764147	*LACC1*	G	6/18/30	112/347/237	0.28	0.41	0.55	0.007	A	1.85	0.007

							(0.36-0.85)			(1.19-2.87)	
rs142179458	*HIF1A*	A	0/7/47	3/71/622	0.06	0.06	1.18 (0.53-2.63)	0.68	A	1.15 (0.52-2.55)	0.73
rs9302752	*NOD2*	C	5/17/32	46/257/393	0.25	0.25	1.00 (0.63-1.57)	0.99	C	1.04 (0.66-1.63)	0.87

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in reversal reaction in BB, BT and BL leprosy cases; F_U, minor allele frequency in BB, BT and BL leprosy cases free of reversal reaction; OR, odds ratio with respect to the minor allele; CI, confidence interval.

[a] aa/Aa/AA, the numbers of cases and controls with minor allele homozygote/heterozygote/major allele homozygote genotypes, respectively.

[b] Association tested with $\chi 2$ test or Fisher test.

[c] Association tested with logistic regression model adjusted for sex, ethnicity and age at diagnosis.

Supplementary table 9: Analysis of association between SNPs and erythema nodosum leprosum in LL and BL leprosy cases

SNP	Gene	Minor allele	aa/Aa/AA[a]		F_A	F_U	OR (95% CI)[b]	P[b]	Risk allele	OR (95% CI)[c]	P[c]
			Cases (n=75)	Controls (n=713)							
rs76418789	*IL23R*	A	0/9/66	4/62/647	0.06	0.05	1.20 (0.60-2.53)	0.56	A	1.23 (0.61-2.47)	0.57
rs146466242	*FLG*	A	0/4/71	2/21/690	0.03	0.02	1.54 (0.53-4.47)	0.43	A	1.49 (0.54-4.11)	0.44
rs2058660	*IL18RAP/IL18R1*	C	17/35/23	104/366/243	0.46	0.40	1.26 (0.90-1.77)	0.17	C	1.26 (0.89-1.79)	0.19
rs73058713	*CDH18*	A	0/22/53	12/171/530	0.15	0.14	1.09 (0.67-1.75)	0.74	A	1.08 (0.66-1.77)	0.75
rs2275606	*RAB32*	A	6/28/41	73/282/358	0.27	0.30	0.85 (0.58-1.24)	0.39	G	1.16 (0.80-1.68)	0.44
rs4720118	*BBS9*	T	7/30/38	63/295/355	0.29	0.30	0.99 (0.68-1.43)	0.96	C	1.02 (0.71-1.48)	0.91
rs55894533	*CTSB*	C	16/33/26	167/342/204	0.43	0.47	0.85 (0.60-1.19)	0.34	A	1.18 (0.84-1.65)	0.33
rs6478108	*TNFSF15*	T	19/31/25	122/302/289	0.46	0.38	1.37 (0.98-1.93)	0.07	T	1.31 (0.95-1.81)	0.10
rs10817758	*1-Dec*	T	13/44/18	143/359/211	0.47	0.45	1.06 (0.76-1.49)	0.74	T	1.09 (0.77-1.54)	0.64
rs780668	*SLC29A3*	G	15/38/22	190/338/185	0.45	0.50	0.82 (0.58-1.15)	0.24	A	1.23 (0.88-1.72)	0.23
rs663743	*CCDC88B*	A	5/24/46	36/258/419	0.23	0.23	0.97 (0.65-1.45)	0.90	G	1.01 (0.67-1.52)	0.96
rs3764147	*LACC1*	G	21/38/16	134/369/210	0.53	0.45	1.42	0.04	G	1.44	0.04

							(1.01-1.98)			(1.02-2.04)	
rs142179458	*HIF1A*	A	1/5/69	0/59/654	0.05	0.04	1.13 (0.51-2.53)	0.76	A	1.20 (0.53-2.71)	0.67
rs9302752	*NOD2*	C	6/33/36	62/280/371	0.30	0.28	1.08 (0.75-1.57)	0.67	C	1.10 (0.76-1.59)	0.60

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in erythema nodosum leprosum in LL and BL leprosy cases; F_U, minor allele frequency in LL and BL leprosy cases free of erythema nodosum leprosum; OR, odds ratio with respect to the minor allele; CI, confidence interval.

[a] aa/Aa/AA, the numbers of cases and controls with minor allele homozygote/heterozygote/major allele homozygote genotypes, respectively.

[b] Association tested with $\chi 2$ test or Fisher test.

[c] Association tested with logistic regression model adjusted for sex, ethnicity and age at diagnosis.

Supplementary table 10: Analysis of association between SNPs and leprosy reaction states

SNP	Gene	Minor allele	aa/Aa/AA[a]		F_A	F_U	OR (95% CI)[b]	P[b]	Risk allele	OR (95% CI)[c]	P[c]
			Cases (n=79)	Controls (n=67)							
rs76418789	*IL23R*	A	0/9/70	1/4/62	0.06	0.04	1.29 (0.45-3.718)	0.64	A	1.26 (0.45-3.52)	0.66
rs146466242	*FLG*	A	0/4/75	0/1/66	0.03	0.007	3.46 (0.38-31.29)	0.24	A	3.18 (0.34-29.58)	0.31
rs2058660	*IL18RAP/IL18R1*	C	17/39/23	11/36/20	0.46	0.43	1.13 (0.71-1.79)	0.62	C	1.12 (0.69-1.80)	0.65
rs73058713	*CDH18*	A	0/23/56	3/22/42	0.15	0.21	0.65 (0.35-1.18)	0.16	C	1.69 (0.89-3.23)	0.11
rs2275606	*RAB32*	A	6/29/44	7/27/33	0.26	0.31	0.79 (0.48-1.33)	0.38	G	1.20 (0.70-2.04)	0.51
rs4720118	*BBS9*	T	8/33/38	7/26/34	0.31	0.30	1.06 (0.64-1.74)	0.83	T	1.07 (0.65-1.75)	0.79
rs55894533	*CTSB*	C	17/35/27	10/34/23	0.44	0.40	1.15 (0.72-1.83)	0.56	C	1.12 (0.70-1.78)	0.64
rs6478108	*TNFSF15*	T	19/34/26	15/32/20	0.46	0.46	0.97 (0.61-1.54)	0.90	C	1.02 (0.64-1.62)	0.93
rs10817758	*1-Dec*	T	13/47/19	8/39/20	0.46	0.41	1.23 (0.77-1.96)	0.38	T	1.31 (0.77-2.21)	0.32
rs780668	*SLC29A3*	G	15/41/23	15/33/19	0.45	0.47	0.92 (0.58-1.46)	0.72	A	1.12 (0.70-1.80)	0.63
rs663743	*CCDC88B*	A	5/26/48	3/20/44	0.23	0.19	1.23 (0.70-2.16)	0.48	A	1.34 (0.74-2.40)	0.33
rs3764	*LACC1*	G	23/39/	7/26/34	0.54	0.30	2.74	<0.00	G	2.75	<

147			17				(1.69-4.44)	01		(1.65-4.59)	0.0001
rs1421 79458	*HIF1A*	A	1/6/72	0/8/59	0.05	0.06	0.84 (0.31-2.30)	0.73	G	1.15 (0.43-3.05)	0.78
rs9302 752	*NOD2*	C	7/36/36	6/24/37	0.32	0.27	1.26 (0.76-2.10)	0.37	C	1.32 (0.77-2.25)	0.31

Abbreviations: SNP, single nucleotide polymorphism; F_A, minor allele frequency in erythema nodosum leprosum cases; F_U, minor allele frequency in reversal reaction cases; OR, odds ratio with respect to the minor allele; CI, confidence interval.

[a] aa/Aa/AA, the numbers of cases and controls with minor allele homozygote/heterozygote/major allele homozygote genotypes, respectively.

[b] Association tested with $\chi 2$ test or Fisher test.

[c] Association tested with logistic regression model adjusted for sex, ethnicity and age at diagnosis.