

Supplementary materials

Materials and Methods

Bacterial strains and biopsy samples. The sources of purified DNA used in this study are listed in Table 1. Details of the biopsies and other tissue samples may be found in Tables 3 and S2. All human biopsies were obtained from studies, which had been approved by the appropriate IRB and after informed patient consent.

Comparative genomics and array analyses. High density membranes were prepared by spotting 1,741 PCR fragments, corresponding to the complete genome of the TN strain of *M. leprae*, using a QPIX gridding robot (Genetix, Hampshire, UK). Details of fragment locations in the genome may be found in Table S3. Genomic DNA (~1 μ g) was randomly labelled with [α^{33} P]dCTP using Prime-it II kits (Stratagene Systems, Kirkland, WA). Unincorporated nucleotides were removed by exclusion chromatography with the QIAquick Nucleotide Removal kit (Qiagen, Inc., Valencia, Calif). Membranes were hybridized overnight at 65°C with the labelled probe followed by six washing steps in 50 ml of 0.01 x SSPE, 0.2% SDS. The first three washes were done at room temperature for 3 min followed by three washes at 65°C for 20 min. Membranes were exposed and scanned on a STORM phosphorimager (Amersham Biosciences, Arlington Hights, IL). The hybridization signals of each spot obtained with the genomic DNA from various strains were compared to a control membrane hybridized with the TN reference strain using the Array vision software (Imaging Research Inc., Ontario, Canada). Typical comparative hybridization results are shown in Figure S1. Loci, corresponding to all hybridization spots that fell outside the limits established in Figure S1 (i.e. whose signal was >2X or <0.5 of that obtained with the control), were investigated further by locus-specific PCR analysis of the corresponding genomic DNA but no deletions were detected. Furthermore, owing to the use of partially overlapping capture probes, if deletions of >1kb had occurred they would likely have been detected by reduction in

signal with two consecutive capture probes. Fingerprinting and end-sequencing of cosmids from a second Indian strain of *M. leprae* were performed as described previously (19).

Real-time PCR. To test for variations in the copy number of dispersed repeats the following real-time PCR protocol was used. Primers were chosen using Primer 3 software available via (http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi). These targeted the repetitive sequences LEPRPT (five copies), LEPREP (eight copies), REPLEP (15 copies), RLEP (37 copies) and a single copy sequence was used as the control.

Quant_LEPRPT-F	5'-ACGCGATCGACGTATATTGA-3'
Quant_LEPRPT-R	5'-CAGGTGATGACCAGCAAGAC-3'
Quant_LEPREP-F	5'-CGCGGATCTGGCATAAGT-3'
Quant_LEPREP-R	5'-GGGTCGGTAACGAACTTGAA-3'
Quant_REPLEP-F	5'-CACAATTGTTCGGGACTGT-3'
Quant_REPLEP-R	5'-GCTGCGTACGGAGATAGACA-3'
Quant_RLEP-F	5'-GCGCTAACAACTATCCTCACA-3'
Quant_RLEP-R	5'-CCGCAGTGGACACGATTA-3'
Quant_Control-F	5'-CGTTAGTGTTCAGCGTCGTT-3'
Quant_Control-R	5'-AACCGATCTCGGAAAGCTA-3'

All amplification reactions were performed in a total volume of 25 μ l with an ABI Prism 7700 sequence detector (Applied Biosystems, Foster City, Ca) with 96 micowell plates (Microamp; Applied Biosystems). To optimize real-time PCR four concentrations of each primer were tested. After adjusting primer concentrations, serial dilutions of each strain DNA (62.5pg to 0.25pg) were tested with Quant_Control primers (200 nM). Each well (25 μ l) contained 5 μ l of diluted DNA, 12.5 μ l of SYBR Green I PCR Master Mix (Applied Biosystems), 5 μ l of diluted primers and 2.5 μ l distilled water. The reaction mixture was run using universal cycling parameters, 50°C for 2 min and 95°C for 10 min,

followed by 40 cycles at 95°C for 15 sec, 60°C for 1 min. Results were analysed according to the procedures recommended by Applied Biosystems.

SNP and Variable Number Tandem Repeat analysis. PCR fragments were generated from purified *M. leprae* genomic DNA, human biopsies or other tissue specimens, by standard procedures then sequenced using an AB3100 DNA sequencer (Applied Biosystems, Foster City, USA). The following primers were used for this purpose:

SNP-14676-F	AATGGAATGCTGGTGAGAGC	and	SNP-14676-R
CAATGCATGCTAGCCTTAATGA;			SNP-1642875-F
TGCTAGTTAACCGAGTACTGCTA		and	SNP-1642875-R
GTAGTAGTCTCCAAGTTGTGGTG;			SNP-2935685-F
ATCTGGTCCGGGTAGGAATC	and SNP-2935685-R	ACCGGTGAGCGCACTAAG.	

Briefly, PCR was carried out using 2.5 U of *Taq* DNA Polymerase (Invitrogen, life technologies) in a 50μl volume containing 250 pg of purified *M. leprae* DNA or 5μl of prepared biopsy samples, 200 nM of primers and reagents supplied by the manufacturer. The mixture was denatured at 94°C for 3 min followed by 45 PCR cycles (1 min at 94°C, 1 min at 55°C, extension at 72°C for 2 min) with a final extension at 72°C for 10 min in a thermocycler (PTC-100, MJ Research, Inc.). Primers were designed to amplify the DNA region flanking the target regions. As the primers used in sequencing were the same as for PCR, 10μl of PCR products were incubated with 5U of Exonuclease I (USB, Corp., Cleveland, Ohio) and 0.5U of Shrimp Alkaline Phosphatase (USB, Corp., Cleveland, Ohio) at 37°C for 30 min before enzyme inactivation at 80°C for 30 min. Then we added 4 μl of BigDye v3.1, 4 μl of BigDye v3.1 buffer (Applied Biosystems, Foster City, USA) and 200 nM of primer. The sequencing mixture was denatured at 96°C for 1 min followed by 40 cycles of denaturation at 96°C for 30 sec, annealing at 56°C for 15 sec and extension at 60°C for 4 min. Sequences were compiled and analysed using Gap4 and Artemis as described previously (5). In some instances, involving AT-rich regions, PCR products were purified using QIAquick PCR purification kit (Qiagen, Inc., Valencia, Calif.), and cloned into the pGEM®-T Easy Vector Systems (Promega, Woods Hollow Road, USA.) prior to sequencing. The complete results of SNP and VNTR analysis are summarized in Table S2.

Table S1. Sequenced loci from strain Br4923. Coding, non-coding and pseudogenes.

	Beginning	End	bp sequenced
PSEUDOGENE ML0035	42573	43595	1022
PSEUDOGENE ML0039	47405	48314	909
PSEUDOGENE ML0065	86913	87812	899
PSEUDOGENE ML0083	105675	106678	1003
PSEUDOGENE ML0090	111799	112698	899
PSEUDOGENE ML0148	209979	210981	1002
PSEUDOGENE ML0166	231829	232731	902
PSEUDOGENE ML0167	233549	234637	1088
PSEUDOGENE ML0194	260955	262011	1056
PSEUDOGENE ML0197	263403	264304	901
PSEUDOGENE ML0220	292337	293380	1043
PSEUDOGENE ML0259	338533	339574	1041
PSEUDOGENE ML0268	351994	352894	900
PSEUDOGENE ML0272	355524	356531	1007
PSEUDOGENE ML0305	390879	391785	906
PSEUDOGENE ML0326	416866	417879	1013
PSEUDOGENE ML0340	429666	430571	905
PSEUDOGENE ML0343	433786	434696	910
PSEUDOGENE ML0345	436510	437521	1011
PSEUDOGENE ML0360	454681	455719	1038
PSEUDOGENE ML0374	467080	467984	904
PSEUDOGENE ML0384	477537	478587	1050
PSEUDOGENE ML0401	499328	500348	1020
PSEUDOGENE ML0415	513508	514410	902
PSEUDOGENE ML0416	516501	517561	1060
PSEUDOGENE ML0433	533694	534705	1011
PSEUDOGENE ML0436	535944	536843	899
PSEUDOGENE ML0438	538750	539658	908
PSEUDOGENE ML0469	568533	569435	902
PSEUDOGENE ML0477	579093	580141	1048
PSEUDOGENE ML0504	612144	613197	1053
PSEUDOGENE ML0507	615666	616565	899
PSEUDOGENE ML0553	670224	671123	899
PSEUDOGENE ML0599	725692	726593	901
PSEUDOGENE ML0632	764582	765486	904
PSEUDOGENE ML0655	792524	793427	903
PSEUDOGENE ML0680	815103	816008	905
PSEUDOGENE ML0688	824253	825168	915
PSEUDOGENE ML0692	830062	830963	901
PSEUDOGENE ML0716	857280	858179	899
PSEUDOGENE ML0719	862196	863096	900
PSEUDOGENE ML0721	865034	866129	1095
PSEUDOGENE ML0744	886041	886940	899
PSEUDOGENE ML0767	909852	910755	903
PSEUDOGENE ML0789	932385	933287	902
PSEUDOGENE ML0795	940043	940945	902
PSEUDOGENE ML0822	973808	974710	902

PSEUDOGENE	ML0830	985162	986062	900
PSEUDOGENE	ML0856	1017548	1018450	902
PSEUDOGENE	ML0884	1049220	1050136	916
PSEUDOGENE	ML0931	1100926	1101989	1063
PSEUDOGENE	ML0943	1113138	1114037	899
PSEUDOGENE	ML0952	1120516	1121415	899
PSEUDOGENE	ML0991	1157966	1158872	906
PSEUDOGENE	ML1048	1214435	1215348	913
PSEUDOGENE	ML1062	1227288	1228193	905
PSEUDOGENE	ML1100	1271500	1272401	901
PSEUDOGENE	ML1104	1277904	1278807	903
PSEUDOGENE	ML1152	1346960	1347859	899
PSEUDOGENE	ML1154	1349865	1350767	902
PSEUDOGENE	ML1162	1360828	1361729	901
PSEUDOGENE	ML1184	1383768	1384671	903
PSEUDOGENE	ML1204	1421282	1422339	1057
PSEUDOGENE	ML1212	1433140	1434039	899
PSEUDOGENE	ML1235	1472257	1473156	899
PSEUDOGENE	ML1252	1497090	1497992	902
PSEUDOGENE	ML1281	1525036	1525938	902
PSEUDOGENE	ML1308	1560516	1561418	902
PSEUDOGENE	ML1345	1604209	1605109	900
PSEUDOGENE	ML1356	1616968	1617882	914
PSEUDOGENE	ML1378	1642236	1643151	915
PSEUDOGENE	ML1385	1657968	1658867	899
PSEUDOGENE	ML1416	1698012	1698918	906
PSEUDOGENE	ML1436	1725103	1726005	902
PSEUDOGENE	ML1449	1741841	1742884	1043
PSEUDOGENE	ML1456	1749686	1750588	902
PSEUDOGENE	ML1473	1774195	1775102	907
PSEUDOGENE	ML1490	1795417	1796316	899
PSEUDOGENE	ML1502	1811634	1812535	901
PSEUDOGENE	ML1528	1842964	1843863	899
PSEUDOGENE	ML1545	1868951	1869856	905
PSEUDOGENE	ML1563	1888184	1889094	910
PSEUDOGENE	ML1594	1919138	1920037	899
PSEUDOGENE	ML1620	1941683	1942588	905
PSEUDOGENE	ML1634	1968019	1968920	901
PSEUDOGENE	ML1665	2006707	2007609	902
PSEUDOGENE	ML1693	2039997	2040902	905
PSEUDOGENE	ML1732	2092145	2093045	900
PSEUDOGENE	ML1745	2106986	2107898	912
PSEUDOGENE	ML1766	2140808	2141716	908
PSEUDOGENE	ML1777	2153432	2154335	903
PSEUDOGENE	ML1852	2235763	2236832	1069
PSEUDOGENE	ML1869	2248965	2249864	899
PSEUDOGENE	ML1893	2278625	2279525	900
PSEUDOGENE	ML1984	2368175	2369091	916
PSEUDOGENE	ML2024	2415168	2416083	915

PSEUDOGENE	ML2036	2426837	2427738	901
PSEUDOGENE	ML2089	2484050	2484950	900
PSEUDOGENE	ML2097	2493319	2494223	904
PSEUDOGENE	ML2115	2515432	2516333	901
PSEUDOGENE	ML2132	2533999	2534913	914
PSEUDOGENE	ML2146	2549359	2550258	899
PSEUDOGENE	ML2149	2553224	2554292	1068
PSEUDOGENE	ML2208	2622864	2623780	916
PSEUDOGENE	ML2224	2640521	2641420	899
PSEUDOGENE	ML2238	2657091	2657992	901
PSEUDOGENE	ML2272	2696308	2697210	902
PSEUDOGENE	ML2287	2711245	2712161	916
PSEUDOGENE	ML2338	2772873	2773772	899
PSEUDOGENE	ML2361	2826668	2827753	1085
PSEUDOGENE	ML2364	2830114	2831017	903
PSEUDOGENE	ML2383	2854276	2855189	913
PSEUDOGENE	ML2408	2879084	2879988	904
PSEUDOGENE	ML2462	2935196	2936097	901
PSEUDOGENE	ML2520	3003092	3003991	899
PSEUDOGENE	ML2553	3045440	3046466	1026
PSEUDOGENE	ML2559	3051012	3051911	899
PSEUDOGENE	ML2585	3087409	3088311	902
PSEUDOGENE	ML2606	3110019	3110921	902
PSEUDOGENE	ML2645	3165562	3166581	1019
PSEUDOGENE	ML2658	3180406	3181306	900
PSEUDOGENE	ML2662	3188108	3189007	899
PSEUDOGENE	17-AT-F	2597586	2597904	318
PSEUDOGENE	18-AT-F	984395	984762	367
PSEUDOGENE	ML1353-int-F	1614220	1614068	152
TOTAL				114659
NON CODING	RNC-01	1103945	1103489	456
NON CODING	RNC-02	14721	14291	430
NON CODING	RNC-03	2013052	2012649	403
NON CODING	RNC-04	2801322	2800907	415
NON CODING	RNC-05	479589	479087	502
NON CODING	RNC-06	41494	41996	502
NON CODING	RNC-07	688101	688604	503
NON CODING	RNC-08	1376025	1376538	513
NON CODING	RNC-09	2299083	2299593	510
NON CODING	RNC-10	3138257	3138778	521
NON CODING	B1133-MIRU1	1691953	1692315	362
NON CODING	B1308-MIRU1	861747	862365	618
NON CODING	B1549-MIRU1	1371912	1371576	336
NON CODING	B1549-MIRU2	1368775	1368117	658
NON CODING	B1764-MIRU1	1194587	1195134	547
NON CODING	B1764-MIRU2	1206829	1207452	623
NON CODING	B2168-MIRU1	2917764	2918252	488
NON CODING	B2168-MIRU2	2883902	2884201	299
NON CODING	B2168-MIRU3	2915088	2915409	321

NON CODING	B2235-MIRU1	1164458	1164069	389
NON CODING	B2266-MIRU1	2617967	2617619	348
NON CODING	B2266-MIRU2	2613593	2613196	397
NON CODING	B2266-MIRU3	2611031	2610664	367
NON CODING	B937-MIRU1	648097	648641	544
NON CODING	L471-MIRU1	1328014	1327566	448
NON CODING	Miru01	153455	153872	417
NON CODING	Miru02	534495	534905	410
NON CODING	Miru05	876962	877380	418
NON CODING	Miru12	1629493	1629925	432
NON CODING	Miru13	1777631	1778077	446
NON CODING	Miru15	1915234	1915642	408
NON CODING	Miru16	2044072	2044505	433
NON CODING	TTC-F	2785574	2785374	200
NON CODING	15-AT-F	948757	949072	315
NON CODING	9-GTA-F	2583649	2583965	316
NON CODING	14-AT-F	308614	308914	300
	TOTAL			15595
CODING	murD	2379458	2379958	500
CODING	murD	2376152	2376652	500
CODING	ftsW	1082303	1083211	908
CODING	murG	1083002	1083996	994
CODING	murC	1083754	1084360	606
CODING	ML045	555472	555972	500
CODING	pgsA	552122	552622	500
CODING	ML1889	2270883	2271383	500
CODING	rpoC	2267526	2268026	500
CODING	ML2273	2698904	2699404	500
CODING	ML2274	2695552	2696052	500
CODING	HisS	602876	603376	500
CODING	HisS	599528	600028	500
CODING	ML0079	101929	102429	500
CODING	ML0081	98474	98974	500
CODING	ML1596	1923673	1924173	500
CODING	rpsB	1920378	1920878	500
CODING	rpoT	1190253	1190501	248
CODING	ML1180	1380201	1380701	500
CODING	ML1183	1382388	1382888	500
CODING	ML1053	1220074	1220574	500
CODING	ML1056	1221688	1222188	500
CODING	glnA	1094734	1094403	331
	TOTAL			12087
REPEAT	Rlep12	1093004	1097760	1000
REPEAT	Rlep5	279908	280964	1056
REPEAT	Rlep11	1018881	1019641	760
REPEAT	Rlep32	2308847	2309816	969
REPEAT	RLEP22	1650920	1652062	1142
	TOTAL			4927

Table S2. VNTR and SNP analysis of *M. leprae* from humans and animals.

Strain	Country of origin	Source	TTC	GTA	AT(14)	AT(15)	AT(17)	14676	1,642,875	2,935,685
Bra-01	Brazil	ILSL	11	8	14	12	13	C	T	C
Bra-03	Brazil	ILSL	11	9	13	21	12	C	T	C
Br4923	Brazil	CSU/NHDP	12	12	20	20	15	T	T	C
Bra-04	Brazil	ILSL	12	10	13	16	10	C	T	C
Bra-06	Brazil	ILSL	13	8	25	14	15	C	T	C
Bra-07	Brazil	ILSL	14	9	15	11	11	C	T	C
Bra-05	Brazil	ILSL	-	-	-	-	-	T	T	C
Bra-11	Brazil	ILSL	-	-	-	-	-	C	T	C
Bra-13	Brazil	ILSL	-	-	-	-	-	C	T	C
Bra-16	Brazil	ILSL	-	-	-	-	-	C	T	C
Bra-17	Brazil	ILSL	-	-	-	-	-	C	T	C
Bra-21	Brazil	ILSL	-	-	-	-	-	C	T	C
Bra-22	Brazil	ILSL	-	-	-	-	-	C	T	C
Bra-24	Brazil	ILSL	-	-	-	-	-	C	T	C
Ethiopia	Ethiopia	IP	29	8	14	19	13	C	T	A
Eth-3017	Ethiopia	CSU-NHDP	29	8	14	19	11	C	T	A
82073	France	IP	-	-	-	-	-	C	T	C
2310	France	HSL	-	-	-	-	-	C	T	C
89002	French West Indies	IP	12	7	22	14	10	T	T	C
89001	French West Indies	IP	13	8	10	21	11	C	G	A
81030	French West Indies	IP	14	9	14	15	12	T	T	C
89003	French West Indies	IP	14	11	13	13	14	T	T	C
85054	French West Indies	IP	14	8	9	13	13	C	T	C
86030	French West Indies	IP	15	9	14	15	11	T	T	C
1624	French West Indies	HSL	15	9	16	18	12	C	G	A
95015	French West Indies	IP	15	7	14	14	9	T	T	C
97011	French West Indies	IP	15	15	20	16	16	T	T	C
97016	French West Indies	IP	15	7	18	13	10	T	T	C
98007	French West Indies	IP	15	11	22	20	17	T	T	C
92002	French West Indies	IP	16	7	14	9	9	T	T	C
95034	French West Indies	IP	17	19	19	11	21	C	G	A
88056	French West Indies	IP	21	8	13	12	10	C	G	A
82007	French West Indies	IP	-	-	-	-	-	T	T	C

87038	French West Indies	IP	-	-	-	-	-	T	T	C
89033	French West Indies	IP	-	-	-	-	-	T	T	C
94030	French West Indies	IP	-	-	-	-	-	T	T	C
1261	French West Indies	HSL	-	-	-	-	-	C	T	C
2318	French West Indies	HSL	15	9	14	15	12	T	T	C
Guinea-C30	Guinea	CNAM	-	-	-	-	-	T	T	C
India-825	India	IP	12	8	11	21	13	C	G	A
India-823	India	IP	13	8	24	16	12	C	G	A
India2	India	IP	15	11	18	14	13	C	G	A
Tamil Nadu	India	IP	21	9	14	15	17	C	G	A
C-I-04	Ivory Coast	IP	12	8	13	14	15	T	T	C
C-I-06	Ivory Coast	IP	12	10	13	14	15	T	T	C
C-I-07	Ivory Coast	IP	12	10	13	14	16	T	T	C
C-I-02	Ivory Coast	IP	13	13	22	16	15	T	T	C
C-I-08	Ivory Coast	IP	-	-	-	-	-	T	T	C
C-I-09	Ivory Coast	IP	-	-	-	-	-	T	T	C
Korea-02	Korea	YU	16	8	19	18	14	C	T	C
Korea-03	Korea	YU	20	10	24	15	12	C	T	C
Korea-04	Korea	YU	22	11	14	15	13	C	G	A
Korea-05	Korea	YU	22	9	15	22	16	C	G	A
Korea-01	Korea	YU	-	-	-	-	-	C	G	A
B110	Madagascar	IPM	13	8	16	11	16	C	G	A
B137	Madagascar	IPM	13	12	14	14	13	C	G	A
B146	Madagascar	IPM	15	9	16	19	10	C	G	A
B172	Madagascar	IPM	17	10	24	19	11	C	G	A
B152	Madagascar	IPM	24	11	24	19	12	C	G	A
B107	Madagascar	IPM	-	-	-	-	-	C	G	A
Malawi-02	Malawi	ITD	13	8	-	-	-	C	G	A
Malawi-08	Malawi	ITD	10	9	-	-	-	C	G	A
Malawi-09	Malawi	ITD	10	9	-	-	-	C	G	A
Malawi-01	Malawi	ITD	21	8	-	-	-	C	T	A
Malawi-04	Malawi	ITD	16	8	-	-	-	C	T	A
Malawi-05	Malawi	ITD	13	9	-	-	-	C	T	A
Malawi-06	Malawi	ITD	11	9	-	-	-	C	T	A
Malawi-07	Malawi	ITD	10	9	-	-	-	C	T	A
Malawi-10	Malawi	ITD	10	9	-	-	-	C	T	A
Malawi-	Malawi	CSU/N	-	-	-	-	-	C	G	A

2936		HDP							
Mali-C39	Mali	CNAM	11	10	14	12	14	T	T
94004	Mali	CNAM	13	9	12	16	12	T	T
Mali-C22	Mali	CNAM	13	13	20	21	12	T	T
Mali-C13	Mali	CNAM	14	9	22	13	12	T	T
Mali-S14	Mali	CNAM	14	9	12	21	12	T	T
Mali-S31	Mali	CNAM	15	9	15	13	12	T	T
98004	Mali	CNAM	-	-	-	-	-	T	T
98011	Mali	CNAM	-	-	-	-	-	T	T
2508	Mali	CNAM	-	-	-	-	-	T	T
Mali-S27	Mali	CNAM	-	-	-	-	-	T	T
Mali-S29	Mali	CNAM	-	-	-	-	-	T	T
Mali-C39	Mali	CNAM	-	-	-	-	-	T	T
Bamako-01	Mali	CNAM	-	-	-	-	-	T	T
Bamako-02	Mali	CNAM	-	-	-	-	-	T	T
Bamako-04	Mali	CNAM	-	-	-	-	-	T	T
Bamako-05	Mali	CNAM	-	-	-	-	-	T	T
Bamako-06	Mali	CNAM	-	-	-	-	-	T	T
Bamako-07	Mali	CNAM	-	-	-	-	-	T	T
Bamako-08	Mali	CNAM	-	-	-	-	-	T	T
Bamako-09	Mali	CNAM	-	-	-	-	-	T	T
Bamako-10	Mali	CNAM	-	-	-	-	-	T	T
Bamako-11	Mali	CNAM	-	-	-	-	-	T	T
Bamako-13	Mali	CNAM	-	-	-	-	-	T	T
Bamako-14	Mali	CNAM	-	-	-	-	-	T	T
Bamako-15	Mali	CNAM	-	-	-	-	-	T	T
Bamako-16	Mali	CNAM	-	-	-	-	-	T	T
Bamako-17	Mali	CNAM	-	-	-	-	-	T	T
Bamako-18	Mali	CNAM	-	-	-	-	-	T	T
Bamako-19	Mali	CNAM	-	-	-	-	-	T	T
Bamako-20	Mali	CNAM	-	-	-	-	-	T	T
Mali-C10	Mali	CNAM	16	9	14	15	14	T	T
Mali-S41	Mali	CNAM	16	9	14	15	12	T	T
NHDP98	Mexico	CSU/N HDP	10	9	22	14	11	C	T
2704	Morocco	HSL	14	9	25	13	11	C	T

2804	Morocco	HSL	15	8	19	15	12	C	T	C
Nepal-27	Nepal/North -India	IP	9	10	12	12	13	C	G	A
Nepal-39	Nepal/North -India	IP	10	9	22	16	11	C	G	A
13766	Nepal/North -India	IP	16	10	14	26	13	C	G	A
Nepal-56	Nepal/North -India	IP	17	9	20	13	13	C	G	A
Nepal-34	Nepal/North -India	IP	19	8	13	14	10	C	G	A
Nepal-29	Nepal/North -India	IP	20	9	20	21	10	C	G	A
Nepal-26	Nepal/North -India	IP	13	8	14	10	14	C	T	A
Nepal-50	Nepal/North -India	IP	13	8	14	10	14	C	T	A
Nepal- 61B	Nepal/North -India	IP	12	11	12	10	11	C	T	A
Nepal-02	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal- 21A	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-32	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-38	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-40	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-44	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-45	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-49	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-57	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-60	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-63	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal-64	Nepal/North -India	IP	-	-	-	-	-	C	G	A
Nepal- 788	Nepal/North -India	IP	-	-	-	-	-	C	G	A
13786	Nepal/North -India	IP	-	-	-	-	-	C	G	A
13806	Nepal/North -India	IP	-	-	-	-	-	C	G	A
12389	Nepal/North -India	IP	-	-	-	-	-	C	G	A
9069	Nepal/North -India	IP	-	-	-	-	-	C	G	A
13784	Nepal/North -India	IP	-	-	-	-	-	C	T	A
13877	Nepal/North	IP	-	-	-	-	-	C	T	A

	-India								
97021	New-Caledonia	IP	11	9	11	18	10	C	G
96008	New-Caledonia	IP	14	10	22	12	15	C	T
95010	New-Caledonia	IP	15	10	21	11	15	C	T
94003	New-Caledonia	IP	29	9	15	14	15	C	G
82061	New-Caledonia	IP	-	-	-	-	-	C	G
92041	New-Caledonia	IP	-	-	-	-	-	C	T
99001	New-Caledonia	IP	27	9	21	21	14	C	T
Philippine s-08	Philippines	LWM	16	9	20	14	12	C	T
Philippine s-03	Philippines	LWM	19	9	17	15	16	C	G
Philippine s-04	Philippines	LWM	20	8	21	13	12	C	T
Philippine s-02	Philippines	LWM	25	9	14	14	15	C	G
Philippine s-05	Philippines	LWM	26	9	21	20	15	C	G
Philippine s-01	Philippines	LWM	27	10	19	14	17	C	G
Philippine s-06	Philippines	LWM	28	11	17	17	14	C	G
Philippine s-07	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-09	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-10	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-11	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-12	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-13	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-14	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-15	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-16	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-17	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-18	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-19	Philippines	LWM	-	-	-	-	-	C	G
Philippine s-20	Philippines	LWM	-	-	-	-	-	C	G
LWM26	Philippines	LWM	-	-	-	-	-	C	G

88063	Senegal	IP	18	10	11	19	14	T	T	C
2662	Senegal	HSL	13	10	24	22	10	T	T	C
Thai53	Thailand	IP	15	9	16	17	10	C	G	A
NHDP63	USA	CSU/N HDP	10	10	18	18	13	C	T	C
NHDP10	USA	NHDP	11	10	23	17	13	C	T	C
WARM1	USA	NHDP	11	10	26	16	14	C	T	C
*										
W260*	USA	NHDP	11	10	-	-	12	C	T	C
W415*	USA	NHDP	10	10	-	-	13	C	T	C
W508*	USA	NHDP	10	10	-	-	13	C	T	C
NHDP55	USA	NHDP	12	10	20	17	13	C	T	C
V-01	Venezuela	IBM	-	-	-	-	-	C	T	C
V-02	Venezuela	IBM	-	-	-	-	-	C	T	C
V-A	Venezuela	IBM	-	-	-	-	-	C	T	C
V-B	Venezuela	IBM	-	-	-	-	-	C	T	C
V-C	Venezuela	IBM	-	-	-	-	-	C	T	C

* Wild armadillo (natural infection)

- Not available

IP Institut Pasteur, Paris, France

IPM Institut Pasteur, Antananarivo, Madagascar

ILSL Instituto "Lauro de Souza Lima", Bauru, Sao Paulo, Brazil

NHDP National Hansen's Disease Program, Louisiana State University, USA

CSU Colorado State University, Fort Collins, Colorado, USA

HSL Hôpital Saint Louis, Paris, France

CNAM Centre National d'Appuis à la lutte Contre la Maladie, Bamako, Mali

YU Yonsei University, Seoul, Republic of Korea

ITD Karonga Prevention Study, Chilumba Malawi and London School of Hygiene and Tropical Medicine

LWM Leonard Wood Memorial Leprosy Research Center, Cebu, Philippines

IBM Instituto Biomedicina, Caracas, Venezuela

Table S3. Tiling path of PCR fragments used to construct the microarray. Names of clones and PCR fragments are given together with the genome coordinates.

Probes	Start	End	Probes	Start	End	Probes	Start	End
lep184e4	45	1683	lep71a10	1105877	1107538	lep59b5	2227495	2228974
lep98g12	681	2688	***Hole19	1107538	1108314	PCR17	2228962	2229657
lep204g11	1986	5434	lep362c10	1108314	1109799	lep283c4	2229571	2231015
lep143f5	4673	7019	lep360d3	1109808	1111357	lep189e1	2230995	2232669
lep114d3	6745	8888	lep23a6	1111356	1113471	lep125f4	2231800	2233990
lep128b12	8210	11178	lep213e08	1112886	1115576	lep22a1	2234205	2237104
lep109e3	10673	13040	lep16b6	1114734	1117220	lep236h12	2236344	2238825
lep163a1	12852	15091	lep122c12	1116374	1119856	lep209b5	2238270	2240276
lep125e7	14890	16952	lep131c9	1119514	1121943	PCR23	2240250	2241206
lep121a7	16116	18504	lep324g3	1121599	1124394	***Hole33	2241125	2241330
lep136h1	17111	19948	lep208h11	1124241	1126591	lep149e11	2241330	2244293
lep9b1	19173	21490	lep148c2	1126112	1128497	lep333b03	2243593	2246246
lep114g12	21222	23297	lep123f9	1127603	1130672	lep95c1	2245783	2248613
lep121h9	23297	25523	lep110d7	1130667	1132715	lep10b11	2247386	2250831
lep148h12	24634	27828	lep203b12	1132651	1135064	lep89f10	2250542	2252824
lep117f10	27210	29212	lep204d6	1134098	1137474	lep123a8	2251994	2254138
lep120g2	28700	31017	lep325c3	1136638	1139750	lep140c8	2254179	2256840
lep370h11	30172	31717	lep170d11	1139657	1141394	lep9g5	2256053	2259899
lep260d06	31179	33254	lep206b7	1140909	1143413	lep102h5	2259207	2262409
lep282a11	33214	34767	lep110c2	1143238	1146513	lep70e6	2261954	2263672
lep213f04	34701	37142	lep351c7	1146268	1148257	lep110e8	2262818	2265976
lep326d4	36920	39327	lep371a09	1147858	1149396	lep7g5	2265524	2268524
lep334e09	38606	40865	lep214a4	1149086	1151748	lep217a1	2268408	2270493
lep204b4	40801	43008	lep96b2	1151674	1154283	lep120f1	2270113	2272245
lep157g8	42855	44877	lep220c08	1153261	1156623	lep334b07	2271689	2274897
PCR24	44838	47875	lep34c10	1154981	1158394	lep119c9	2274226	2276808
lep145g11	47829	51050	lep109a7	1158033	1160138	lep110d10	2276217	2278710
lep336d10	50708	53446	lep116d6	1159838	1162380	lep155a7	2278440	2281422
lep119c8	52794	56485	lep123b10	1162278	1164730	lep19a8	2281068	2284194
lep215f01	55867	59190	lep107g7	1164148	1166880	lep220h05	2284098	2287140
lep230a8	58995	61540	lep20h9	1166329	1168484	lep201d7	2285561	2288826
lep121h10	61512	64391	lep261b09	1167908	1170398	lep208e8	2287990	2291989
lep20c8	64332	66623	lep29a10	1169665	1172664	lep142c2	2291479	2294391
lep126h6	66540	69509	lep44h10	1172153	1174499	lep116e10	2293949	2296688
lep121d6	69468	72181	lep254e06	1174271	1177559	lep215g07	2296166	2299261
lep334a09	71156	73649	lep223f3	1176701	1179846	lep113h3	2298694	2302025
lep109f5	72767	75089	lep103h12	1179204	1181321	lep117f11	2301840	2303970
lep228e02	74784	77395	lep120g4	1180220	1182715	lep128d7	2303372	2305641
lep220a02	76911	80845	lep109b8	1181821	1184630	lep15b9	2305225	2307777
lep113g10	80713	83196	lep157h1	1184394	1187535	lep127b4	2307743	2310370
PCR02	83125	85874	lep18c3	1186732	1189037	lep88a2	2309842	2311935
lep9e12	85778	88395	lep15b11	1187957	1190000	lep76d10	2311427	2313130
lep203e1	88047	90771	lep55c11	1189314	1190761	lep285a5	2312009	2313522
lep91e8	90081	93312	lep195g12	1190373	1191782	lep91c4	2313281	2315889
lep334e02	92906	95342	lep228e07	1191199	1193812	lep220c02	2315124	2317470
lep100f1	94553	97277	PCR13	1193771	1196720	lep223d4	2316972	2319732

lep11h8	96966	99518		lep139g6	1196623	1198820		lep105c6	2319082	2321380
lep322b2	99078	101816		lep21e11	1198560	1200874		lep209e2	2320964	2324010
lep116e3	101490	104223		lep201f12	1200609	1203193		lep324d3	2323798	2326417
lep44b8	104145	107676		lep102a12	1203010	1205393		lep32e11	2325508	2327887
lep119a2	107089	110240		lep191f12	1205145	1206612		lep395g11	2326167	2327970
lep201h7	109460	111832		lep259a05	1206302	1208742		lep333g02	2330006	2332175
lep333c11	111092	113294		lep44f6	1208285	1211239		lep250a08	2331780	2334077
lep152b11	113151	115339		lep30c9	1211067	1213212		lep140d9	2332884	2335964
lep130f10	114587	116646		lep219h9	1213079	1215561		lep234h7	2334882	2336961
lep284h12	116243	117987		lep315h12	1215257	1216809		lep215g04	2336896	2339000
lep362b08	117632	119070		lep42h5	1216072	1218969		lep123h11	2338274	2341638
lep60d4	119016	120660		lep321d1	1218254	1220317		lep216c06	2341611	2343728
lep22f10	120548	122659		***Hole20	1220317	1221302		lep128c8	2343951	2346153
lep36e12	121769	124862		lep220b11	1221302	1224074		lep203f10	2346046	2348062
lep228c03	123490	126037		lep9c7	1224063	1227331		lep206h7	2348008	2350877
lep334b11	125467	127545		lep189h4	1227099	1228814		lep254b05	2350641	2353175
lep44b2	127408	129841		lep125c1	1228716	1230998		lep336g11	2351481	2353771
lep324e11	129032	132195		lep42f1	1230568	1232753		***Hole34	2353771	2354146
lep106b9	131526	134913		lep309g8	1232562	1234225		lep259e04	2354146	2357148
lep71f8	134621	136472		lep152b3	1233940	1236267		lep148f2	2356469	2359355
lep76b10	135940	137409		lep123g7	1236012	1239320		lep333a08	2357633	2360882
lep351c11	137373	138873		lep254h08	1238607	1241841		lep118g8	2359891	2362005
lep372b09	138543	140213		lep121a8	1239857	1241977		lep104a10	2362028	2364280
lep333g03	140201	142428		lep376b1	1239867	1241459		lep221g11	2364218	2366510
lep223a4	141376	143546		***Hole21	1241459	1241990		lep86a8	2366251	2368313
lep109g1	142673	145395		lep220d11	1241990	1244889		lep152a11	2367745	2371342
lep195g3	143617	145362		lep145a4	1244694	1247699		lep265b3	2371157	2373305
***Hole1	145362	145512		lep293h12	1247214	1249015		lep108h10	2373143	2375213
lep218g1	145512	147751		lep87g5	1247911	1251074		lep370c03	2374238	2375857
lep145d5	146627	149231		lep127f8	1250866	1253066		lep372f08	2375737	2377348
lep349d6	149156	150688		lep71g8	1253009	1254783		lep139c10	2376801	2378853
lep365h7	150507	152370		lep211g10	1253095	1255454		lep227d12	2378838	2381049
lep212b6	151968	154446		lep15a8	1255364	1257539		lep121e7	2380695	2382785
lep369g12	154087	155787		lep364a07	1256499	1258183		lep95f6	2382529	2384609
PCR01	155760	157740		lep44b9	1257835	1260038		lep95d9	2384014	2386698
lep88g9	157774	159839		lep82d10	1259631	1261334		lep98g10	2386219	2388683
lep114h7	159835	161945		lep205h7	1261309	1263365		lep114e12	2387041	2389076
lep153a5	161390	163573		lep149d10	1262568	1264935		***Hole35	2389076	2389798
lep9h5	163289	165379		lep205f3	1264653	1266784		lep44c6	2389798	2392247
lep11g8	165179	168125		lep218h12	1266240	1269143		lep309b8	2391970	2393664
lep126f2	168068	170368		lep120c5	1268822	1271669		lep215f02	2393641	2396059
lep11a11	170126	173868		lep42e6	1271445	1274356		lep91h11	2395994	2398196
lep10d4	172637	175906		lep145e9	1272805	1275636		lep119g2	2397981	2401255
lep10g9	174331	177580		lep207d10	1275062	1278105		lep323c11	2400404	2403298
lep137f1	177556	180210		lep336c10	1277955	1281111		lep329b5	2402825	2405238
lep163h8	179155	181252		lep28h9	1280746	1283615		lep137b4	2404538	2406659
lep109g8	180218	182473		lep16f7	1283401	1285836		lep202h3	2405916	2408425
***Hole3	182473	182846		lep220g11	1285935	1288058		lep351b11	2408303	2409804
lep113f5	182846	185140		lep228f04	1286683	1289654		lep98d3	2409790	2412191

lep211a5	185027	187854		lep228c01	1288104	1291549		lep22e4	2411671	2413981
lep1b7	187442	189657		lep71e7	1291461	1293361		lep137a10	2413860	2415899
lep117d5	189561	192124		lep336g07	1292637	1294957		lep89d7	2414921	2417475
lep102d6	191596	194793		lep121d2	1293772	1297096		lep262c3	2416918	2418963
lep243e11	194545	197223		lep334a12	1296720	1298841		***Hole36	2418963	2419013
lep116h8	196797	198816		lep49b4	1298184	1299653		lep195h5	2419013	2420840
lep149d7	198764	200856		lep110g11	1299462	1301863		lep9d9	2420519	2423851
lep42f4	199412	202039		lep99c12	1301371	1303468		lep323d2	2423159	2425384
lep85h4	201215	203785		lep254f09	1303450	1305481		lep333c02	2425256	2427883
lep129g11	202863	205217		lep228d07	1304545	1306651		lep96d11	2427500	2429944
lep360f1	204095	205824		lep260b04	1306334	1308853		lep311f3	2430189	2431724
***Hole4	205824	206773		lep86d7	1308727	1311434		lep350g7	2431479	2433138
lep83b3	206773	208420		lep107e12	1310733	1313330		lep16d4	2432551	2435213
lep68h7	207821	209587		lep165a4	1313314	1315540		lep158d12	2434931	2437110
lep216d11	209251	211769		lep10e2	1315443	1317521		lep145b10	2436103	2438201
lep148b1	211218	213810		lep352e5	1317881	1319744		lep137b10	2437848	2440103
lep155a3	213317	216997		lep202d5	1318255	1321384		lep206b1	2440086	2442213
lep201h2	216080	219871		lep167d8	1320515	1323133		lep345f12	2441363	2443211
lep234a10	219302	221924		lep291c1	1322820	1324634		lep257b06	2442753	2445034
lep86e5	220419	224417		lep192h8	1323646	1325210		lep88g7	2444689	2446837
lep125f7	224128	226287		lep257d06	1324903	1326975		lep85b8	2446825	2449200
lep128e1	226086	228871		lep32e8	1326506	1328649		lep329c10	2449159	2452447
lep125e1	227566	230768		lep85b11	1328109	1330321		lep116d11	2452328	2454491
lep114a4	230573	232663		lep128b3	1330003	1332870		lep254f04	2454196	2456396
lep30c4	231394	234788		lep30g8	1332377	1334883		lep264g9	2456130	2458846
lep168h10	234610	237387		lep19c7	1333408	1336709		lep110c3	2458113	2460577
lep224f10	236673	238682		lep260a05	1336294	1339108		lep260f07	2459878	2462708
lep203a7	238367	241059		lep209h3	1338222	1340871		lep110f5	2461544	2463782
lep20b6	240162	242682		lep125h1	1339785	1341892		lep86a10	2463698	2466108
lep104c10	242639	245103		lep91d4	1341797	1344365		lep43h10	2466069	2468212
lep145b12	244851	246952		lep23h7	1343670	1346233		lep120f7	2467910	2469985
lep102h10	246750	248760		lep265f3	1345921	1349209		lep352f4	2469653	2471440
lep137b7	248751	250835		lep337h10	1348372	1350822		lep323e1	2470952	2473377
lep15b1	249843	253281		lep137g11	1350719	1353309		lep137e10	2471003	2473025
lep259c05	253119	255417		lep254f07	1353151	1355326		lep363e08	2471106	2472876
lep110a12	254105	256399		lep116g8	1355305	1358226		***Hole37	2472876	2474145
lep201f11	255550	258170		lep109c11	1357083	1360618		lep355c6	2474145	2475845
lep133a5	258076	260538		lep211c7	1360259	1362456		lep16f4	2475719	2478092
lep130f8	259258	261371		lep237c3	1361842	1364356		lep276g12	2477720	2479185
lep81a12	259478	261031		lep92f11	1363237	1365761		***Hole38	2479185	2479785
***Hole5	261031	261720		lep119a10	1365756	1368781		lep361c02	2479785	2481537
lep233f9	261720	263854		lep16b3	1367435	1370025		lep220e12	2481184	2483299
lep324d4	263624	266189		lep18c6	1369619	1372716		lep72d6	2482818	2484573
lep255e08	264414	267489		lep24g3	1372125	1374280		lep327d12	2483868	2487301
lep91f1	266197	268629		lep119e3	1373946	1376356		lep373a1	2486515	2488163
lep291g5	268114	269729		lep348g12	1376190	1377761		lep87d11	2488153	2490684
lep234d11	269658	272268		lep92b12	1377117	1379636		lep118e5	2489460	2492269
lep329b9	272159	274247		lep213e01	1378908	1381662		lep201g3	2491582	2493633
lep257d11	273716	275990		lep170h7	1381649	1383564		lep6c3	2493217	2495676

lep243h10	275984	278203		lep201a4	1383210	1385254		lep264a10	2494691	2497760
lep95b9	276432	279320		lep27h4	1385230	1387781		lep22f7	2497413	2500177
lep189g3	278809	280428		lep228f03	1386954	1389187		lep15a3	2500147	2502207
lep106h10	280354	282395		lep350e6	1389017	1390812		lep212a5	2501426	2503796
lep364b08	281720	283350		lep125g7	1390568	1393378		lep323c6	2503610	2506274
PCR03	283317	283679		lep44f8	1391634	1394405		lep337d10	2506197	2508229
lep219e12	283606	285919		lep167g11	1394316	1396809		lep27e11	2508122	2510630
lep324h8	285465	288805		lep237g9	1395850	1398866		PCR18	2510623	2514002
lep27f3	288451	291339		lep43h9	1397551	1400284		lep86f6	2513911	2515921
lep94f5	290258	293091		lep100e8	1397717	1399911		lep92g6	2515905	2518076
lep292b2	292494	294130		***Hole22	1399911	1400369		lep118c9	2516541	2520118
lep276f9	293478	294932		lep74e11	1400369	1402107		lep10d10	2519240	2522315
lep113c2	294736	296736		lep29b11	1400552	1403673		lep16a11	2520906	2523267
lep44e4	296297	299331		lep239h9	1402444	1404631		lep399h5	2521607	2523015
lep323d9	298310	301059		lep21h4	1403824	1406974		PCR19	2523024	2524167
lep88f8	300392	302514		lep294a7	1406348	1408123		lep375e2	2524070	2525538
lep315g9	301850	303369		lep30c8	1408078	1412005		lep43f8	2524642	2527538
lep114b9	303228	305820		lep133h12	1411197	1413249		lep259d06	2527224	2529517
lep113b12	305290	308063		PCR25	1413181	1415225		lep51g7	2528708	2530245
lep95g9	307072	309536		lep126g3	1415190	1417770		lep74f4	2529735	2531426
lep23c4	309335	311408		lep237h2	1417834	1420175		lep191h8	2531287	2533066
lep206c4	310319	312639		lep130e3	1418041	1420418		lep2g7	2532991	2534656
lep355h2	310409	312096		lep32a11	1419547	1422685		lep213e05	2533426	2536107
PCR04	311982	313079		PCR28	1422621	1424669		lep259h02	2536101	2538346
lep61g6	313070	314677		lep313c4	1424640	1426374		lep117d4	2537268	2540607
lep104h2	314481	316895		lep90a11	1425328	1428228		lep44h7	2540090	2543501
lep329e7	316760	320427		lep44d12	1427655	1429860		lep42f9	2542831	2545869
lep334c06	320249	322334		lep324e5	1429858	1432393		lep92f3	2545608	2548756
lep153d12	321791	324420		lep131b12	1432328	1435175		lep216a04	2547993	2550185
lep251d07	324075	326162		lep30g6	1434773	1437083		lep116b10	2549793	2551908
lep119d11	326153	328159		lep182f4	1436886	1438853		lep220h09	2551561	2553898
lep265a2	327851	330152		lep110b3	1437339	1440242		lep30h6	2553283	2556913
***Hole8	330152	331697		lep160f12	1439973	1442475		lep203h11	2555565	2557645
lep209g8	331697	333801		lep354a5	1441499	1443389		lep280a1	2555979	2557563
lep301g11	333522	335450		lep139h1	1443258	1446408		lep292a10	2556032	2557461
lep233a3	335051	337217		lep7h3	1445922	1448582		***Hole40	2557461	2558083
lep324a10	337029	339649		lep276f12	1446301	1447779		lep117e3	2558083	2561468
lep110h3	339594	341668		PCR14	1447728	1449320		lep167f10	2561389	2564063
lep157b6	341429	343587		lep195h1	1449285	1451054		lep217a8	2564014	2566375
lep30e12	343478	345562		PCR15	1451740	1453830		lep96a12	2565558	2568264
lep204a7	345431	347592		lep323g4	1453732	1456503		lep257b11	2568178	2570390
lep145g10	347589	351008		lep123c2	1456212	1459511		lep233d3	2570126	2572732
lep137f6	350194	352848		lep108h6	1458758	1461551		lep224b10	2571706	2574767
lep107a10	352028	354043		lep120c8	1461009	1463947		lep20e1	2574673	2576864
lep331c5	354020	356683		lep19d10	1463692	1466650		lep369a09	2576847	2578260
lep218g12	356407	359215		lep211e1	1465541	1467911		lep21h3	2578220	2580840
lep333f06	359250	362184		lep99a2	1467892	1470185		lep44a5	2579536	2582473
lep15b8	360489	364043		lep99a1	1469729	1473111		lep99c10	2582287	2584724
lep121h11	363563	365610		lep128e5	1472267	1475278		lep153d1	2583673	2586192

lep71g1	365501	367206		lep117b3	1474803	1477654		lep225f02	2586229	2588378
lep46e4	366172	367709		lep20f2	1477058	1479078		lep329d5	2588280	2590869
lep165a11	367454	369587		lep85d2	1478969	1481302		lep42f3	2590703	2593822
lep220g06	369354	371404		lep355e12	1481291	1482779		lep254h09	2592944	2596648
lep235g10	370129	373063		lep83d5	1482296	1484045		lep264h4	2596376	2599020
lep137f3	371841	374770		lep360f5	1483788	1485306		lep213f08	2598626	2601639
lep259f12	374592	376619		lep114e3	1486688	1488983		lep116b11	2601190	2604765
lep114h6	375413	378730		lep363a12	1488215	1489906		lep11d12	2604389	2606609
lep128c11	378642	381232		lep27e12	1489546	1491918		lep310a7	2606316	2607814
lep215h03	381202	384135		lep351h2	1491787	1493325		lep245f3	2607690	2611045
lep213c11	383858	386145		lep211b1	1493141	1495237		lep352a6	2610939	2612507
lep313b4	384943	386530		lep195a12	1493867	1495782		lep291a8	2612489	2614121
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lep208a3	386688	389649		lep34d9	1497228	1499624		lep333b09	2617376	2619435
lep220b09	388754	391640		lep56h1	1498215	1499803		lep113b1	2617835	2620164
lep18g12	391223	394139		***Hole24	1499803	1500657		lep240h9	2620086	2623086
lep108b4	393688	396166		lep301b4	1500657	1502196		lep283b12	2622830	2624456
lep136h5	396087	398918		lep95b7	1501594	1503853		lep308h5	2624417	2626028
lep22g12	398482	401069		lep230d12	1503020	1506029		lep182h5	2624772	2626602
lep76d8	400517	402285		lep220b10	1505441	1507781		lep44a4	2626779	2628899
lep209a7	401122	403243		lep116g7	1506707	1509465		lep207d6	2628721	2631034
lep208c12	402616	404765		lep127a8	1509283	1511535		lep23b8	2630341	2632531
lep213d05	404383	406512		lep126e3	1510883	1513140		lep334h02	2631833	2633926
lep70b3	406490	408321		lep289a12	1512913	1514518		lep9h8	2633382	2635641
lep10g1	408423	410871		lep124h7	1514303	1517070		lep129h7	2635125	2638559
lep212e2	410804	412850		lep115d7	1515885	1518060		lep137g10	2637505	2640225
lep44h11	412824	415697		lep209f11	1517355	1519804		lep250d03	2640161	2643169
lep189d10	415606	417261		lep211h3	1519724	1522180		lep149c5	2642268	2645173
lep116g4	416989	420443		lep264h7	1521784	1524148		lep211d10	2644159	2646532
lep82c3	419937	421791		lep143h4	1524129	1526687		lep121g8	2645390	2647462
lep136h7	421300	423492		lep22c1	1526216	1528269		lep239g11	2647113	2649483
lep225c11	422407	425777		lep297f12	1528096	1530030		lep355a4	2648455	2650018
lep167c9	425496	428472		lep118f7	1529894	1532015		lep130g11	2649783	2651848
lep89b1	427686	430068		lep250e10	1531161	1534041		lep19a11	2650825	2654272
lep251e08	429804	432270		lep20c12	1532780	1534940		lep9f11	2653535	2656368
lep23b4	431682	434388		lep143g5	1534347	1536538		lep140a6	2656211	2659082
lep109b5	434294	436558		lep122a3	1536304	1538445		lep149g10	2658399	2662025
lep32d8	434472	438408		lep219g7	1537653	1540511		lep23b5	2661474	2663917
lep44b11	437596	441228		lep149a7	1539754	1542306		lep88g5	2663030	2665312
lep123b2	441218	443647		lep92c3	1541335	1544500		lep389e5	2665181	2666654
lep30c3	442857	446030		lep262c4	1544047	1546835		lep265b5	2666335	2668681
lep220h01	445887	448110		lep110c4	1545910	1548387		lep324b12	2667590	2670392
lep216h06	447523	450453		lep292g5	1547954	1549658		lep125b2	2670234	2672383
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lep128c9	452311	455428		lep149g7	1551255	1554926		lep15a5	2673980	2677071
lep225d04	454465	457321		lep87c2	1552918	1556150		lep329e2	2676716	2678763
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lep5h10	461192	463757		lep89c10	1561024	1563111		lep122a6	2681947	2684944

lep119h7	463711	466061		lep117f9	1562926	1565752		lep9f8	2684555	2687569
lep114c2	464065	466338		lep324e12	1565537	1568247		lep329f6	2687109	2690476
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lep55h9	468026	469663		lep119a6	1572166	1574748		lep108b2	2693903	2696219
lep213h05	469417	471544		lep32d11	1574742	1577620		lep239c9	2696175	2698333
lep34d4	471458	473656		lep139a8	1577296	1580378		lep44f4	2698077	2701105
lep154b10	471783	475321		lep94f11	1580242	1582318		lep334e06	2699450	2702811
lep115e2	474502	477188		lep315c8	1582249	1583683		lep209h1	2702394	2705522
lep22d8	476282	478454		lep116f3	1583138	1586308		lep149h3	2704835	2707590
lep145e1	478305	480895		lep209g9	1584952	1588332		lep365c2	2707360	2709095
lep107c3	480314	482341		lep89d2	1588135	1590371		lep88e3	2708724	2710796
lep109g4	481913	483964		lep220c12	1590086	1592395		lep203a11	2709341	2712219
lep125h6	483263	486585		lep51e1	1592015	1593838		lep22h1	2712108	2714932
lep297h3	486473	487924		lep25a2	1592598	1594818		lep212b2	2714464	2717083
lep86g11	487709	491009		lep50g1	1594679	1596201		lep72e12	2716813	2718403
lep260e03	490639	493630		***Hole25	1596201	1596306		lep87d7	2717757	2720511
lep219b10	492667	495524		lep399f6	1596306	1597951		lep257a12	2718951	2722923
lep10a8	495482	497509		lep187h9	1597815	1599276		lep71d3	2721939	2723801
lep114c7	497141	499446		lep22b3	1599177	1601909		lep336c03	2723776	2726361
lep35f1	499353	501367		lep215g06	1600693	1604630		lep107g1	2725677	2728534
lep9h12	501215	504059		lep206d3	1604423	1606508		lep118d2	2728466	2731246
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lep206a12	505532	508947		lep362c01	1607901	1609443		lep98e2	2732153	2734344
lep97h6	507721	510722		lep390g2	1609111	1611037		lep130g3	2734071	2736675
lep311e3	510509	512266		lep94g6	1610084	1612682		lep216b04	2736557	2739458
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lep109h7	513760	516781		lep99e1	1613452	1616382		lep41b1	2742422	2744791
lep228d02	515336	518489		lep128g12	1615694	1617909		lep167b8	2744551	2746679
lep50f2	517727	519553		lep352d3	1617416	1618964		lep208e3	2745742	2748046
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lep99d2	521100	524168		lep30c10	1620969	1623400		lep15a12	2748944	2751577
lep160g7	523587	525980		lep324g8	1622553	1624712		lep73e5	2751355	2752921
lep110a11	525088	527126		lep240d7	1623823	1627256		lep259h08	2752205	2754366
lep203f11	526997	529254		lep324h9	1626139	1628200		lep336d01	2754069	2756744
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lep68f8	537364	538811		lep98e11	1637384	1639526		***Hole41	2763510	2763517
lep136h12	538779	541732		lep108f8	1639471	1641703		lep123a2	2763517	2766223
lep108d10	540684	542884		lep10f3	1641835	1644370		lep60e12	2766060	2767510
lep95c12	542672	544686		lep116b7	1642979	1645237		lep292b3	2767336	2768960
lep95f9	543989	547130		lep137g1	1644242	1646344		lep21h8	2768524	2772287
lep95h7	547113	549532		lep37a2	1646177	1648707		lep331d5	2772200	2774430
lep86d5	549164	551313		lep215b01	1648444	1650844		lep128c7	2774338	2776343
lep216d10	550238	553020		lep116d10	1650300	1652704		lep213a10	2776341	2778403
lep19b11	553019	555611		lep334d07	1652159	1654799		lep203e10	2777884	2780530
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lep117e1	556206	558223		lep209g7	1655280	1658345		lep18f10	2782233	2784325
lep107h11	558010	560057		lep91g3	1658215	1662212		lep30d5	2782427	2786215
lep18d7	560348	562374		lep137e2	1662076	1664369		lep328g10	2784917	2788319
lep104c9	561113	563579		lep204e4	1664135	1667114		lep122a10	2787342	2789432
lep65g11	563122	564562		lep114b4	1667060	1669530		lep201b8	2789069	2791257
lep98f4	563757	565828		lep230d9	1668205	1671456		lep102h7	2791218	2793353
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lep114h12	568352	571761		lep366b5	1672371	1673889		lep366h9	2793985	2795520
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lep35e12	573944	576189		lep94g12	1675087	1678097		lep191h6	2796539	2798348
lep107g5	575756	578394		lep223e4	1677998	1680214		lep228d10	2797868	2799892
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lep30d2	578856	581067		lep297e12	1683173	1684895	***Hole42	2799672	2800202	
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lep137f12	585372	588297		lep144g5	1689312	1692208		lep213d12	2803895	2806265
lep336h01	587957	590118		lep202e5	1692132	1695759		lep152h8	2805590	2808807
lep209f10	590032	592590		lep42e10	1694553	1698332		lep108f1	2807548	2810443
PCR27	592519	593748		lep90c2	1697590	1699610		lep331b1	2809943	2812519
lep325d1	593724	596576		lep15b3	1699271	1701629		lep255a06	2812443	2815040
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lep264a7	600339	602835		lep155g9	1704859	1707431		lep102a8	2818060	2820742
lep108b3	602145	604451		lep128g3	1706752	1708832		lep121f10	2819428	2821555
lep137f9	603938	606696		lep89d8	1708720	1710809		lep213d02	2820856	2824807
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lep73e12	609885	611518		lep216h11	1714080	1716144		lep236a10	2827262	2829699
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lep262d11	618384	621811		lep224a12	1723399	1725746		lep68b5	2836124	2837910
lep293a4	621330	622846		lep207g6	1725548	1727931		lep87a11	2837904	2840573
lep155b2	622755	624924		lep74h3	1727882	1729382		lep216b09	2839905	2841934
lep118h10	624908	627512		lep250g05	1728519	1731469		lep324b10	2841621	2844654
lep235e12	627154	629469		lep44c4	1731079	1734080		lep323d10	2844450	2847184
PCR05	629374	631716		lep125f2	1733913	1736031		lep311d5	2846980	2848496
lep336b07	631683	634742		lep277c9	1735806	1737229		lep324f2	2847708	2851304
lep239c7	633682	635798		lep324e8	1736937	1739426		lep70c1	2851197	2852981
lep9d8	635454	638151		lep373b10	1738727	1740413		lep233c2	2852386	2854507
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lep108d8	648596	650605		lep24f11	1749701	1752245		lep149c10	2864524	2868037
lep20f6	650333	653059		lep16d10	1751155	1753828		lep158g9	2867950	2870084
lep94e8	652685	655001		lep336b08	1753615	1756789		lep220a01	2868588	2870900
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lep127a1	673918	676113		lep92f2	1774155	1776505	***Hole43	2887019	2887469	
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lep220a05	676653	678843		lep208c9	1777676	1780969		lep145f1	2889507	2892148
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lep116e8	702231	704857		lep330c4	1802759	1805249	PCR21	2910972	2913631	
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lep213d11	706818	709220		lep32d1	1805786	1808153		lep384d08	2915695	2917467
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lep9b5	743253	746537		lep19a4	1844171	1846604		lep127b2	2956154	2958766
lep20c6	746152	748736		lep85b1	1846076	1848960		lep44c8	2958309	2961392

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lep123f8	750257	752693		lep105d3	1850712	1853357		lep34e1	2962763	2965074
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lep143g1	760003	762122		lep60e2	1858235	1859772		lep102h4	2968470	2971257
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lep108g5	782164	785278		lep114d10	1882642	1885013		lep23h1	2991851	2994472
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lep43f4	835607	838332		lep18d3	1934655	1936753		lep211d9	3036497	3038785
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lep87d6	840712	844346		lep121g11	1942404	1945224		lep257c06	3046135	3048698
lep18h2	843717	846271		lep167e11	1944653	1947534		lep265d6	3048827	3050894
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***Hole11	846700	846720	lep211e4	1948997	1951690	lep201c11	3051317	3053724
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lep262a4	848552	850645	lep42e8	1953485	1955851	lep19c1	3055635	3058082
lep105c2	850096	852425	lep85c5	1955451	1958925	lep212h1	3057425	3061156
lep286f11	852281	854079	lep35f2	1958092	1960131	lep217h5	3060319	3063651
lep117d12	853955	856341	lep254h01	1959307	1961964	lep107a12	3063088	3066080
lep363f06	856157	857772	lep127a2	1961776	1963916	lep103h1	3064237	3067648
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lep29b7	863730	866130	lep30g2	1968173	1970590	lep212h12	3073144	3075518
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lep257a11	872446	875005	lep90a10	1975529	1977628	lep110b7	3079493	3083089
lep297h6	874915	876468	lep110b11	1977303	1980445	lep213c04	3082820	3084965
lep223a1	876450	879423	lep336e07	1978168	1981922	lep220h02	3084083	3087688
lep155h7	878523	880711	lep245f4	1981009	1983103	lep5d9	3087466	3089508
lep118c11	879448	882210	lep86d9	1983034	1985729	lep116h2	3088320	3091567
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lep87d8	882940	885900	lep211g5	1988766	1990934	lep115d1	3092945	3095462
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lep389d2	889949	891446	lep19c10	1993428	1995703	lep148g7	3098673	3102091
PCR07	891362	893498	lep337b10	1994865	1997082	lep90b3	3101767	3104545
lep44b3	893499	895923	***Hole28	1997082	1997101	lep161g10	3104051	3106761
lep225g09	895510	898741	lep12h5	1997101	1999445	lep236g11	3106578	3109156
lep219g11	898592	901030	lep119b6	1998939	2000997	lep322a7	3108343	3111152
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lep148f11	901360	903431	lep76d7	2003009	2004719	***Hole44	3110997	3111363
lep153a9	903050	905660	***Hole29	2004719	2004732	lep369a07	3111363	3112946
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lep323d3	909276	911360	lep27e7	2007811	2011581	lep220f12	3116625	3119394
lep161f6	910778	912954	lep95e10	2011222	2014629	lep225h03	3118623	3120637
lep311c7	912404	914159	lep250a04	2013561	2015604	lep344b10	3120205	3122151
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lep90d12	944875	946883		lep154b6	2046644	2049099		lep94f9	3159465	3161787
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lep212a1	948025	950148		lep18h9	2050129	2053123		lep144h4	3162526	3164816
lep292c4	949877	951330		lep167h8	2052556	2055104		lep369a02	3164572	3166365
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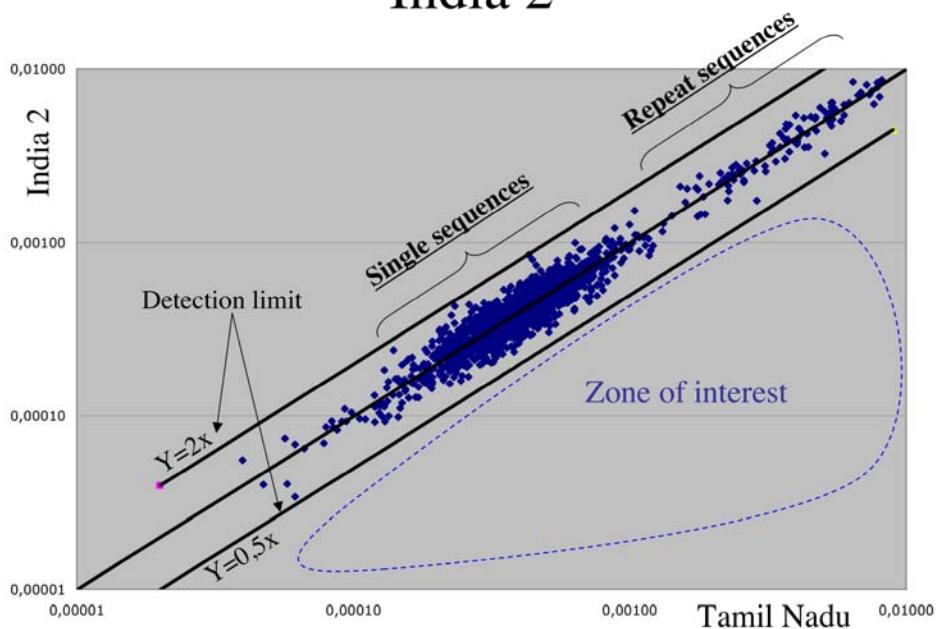
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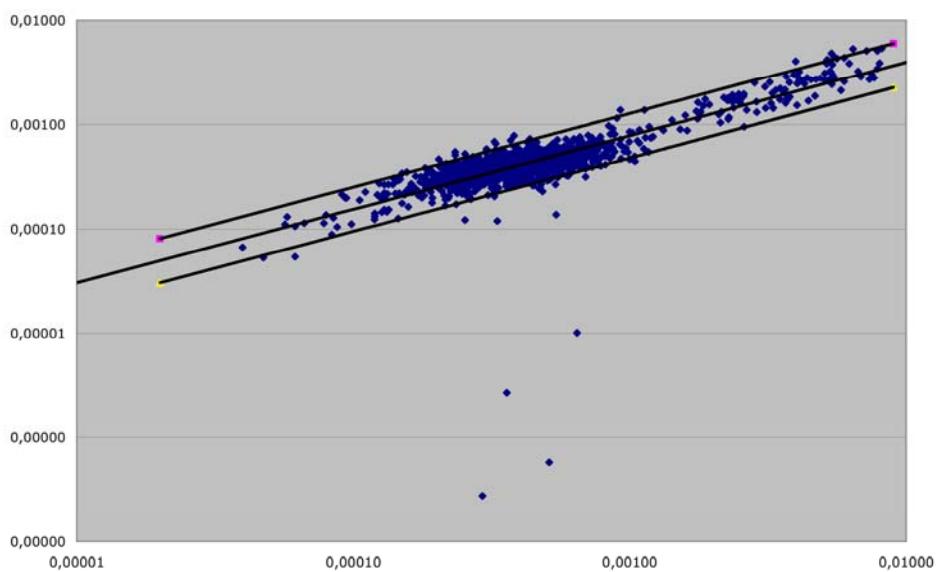
*** Hole : Gap in genome coverage

Figure S1. Microarray analysis and comparison of hybridization signals obtained from different strains of *M. leprae* using Array vision software. Five of the spots that repeatedly fell outside the limits were found in all experiments and probably represent spotting artifacts as the corresponding loci were present in all cases when PCR was performed.

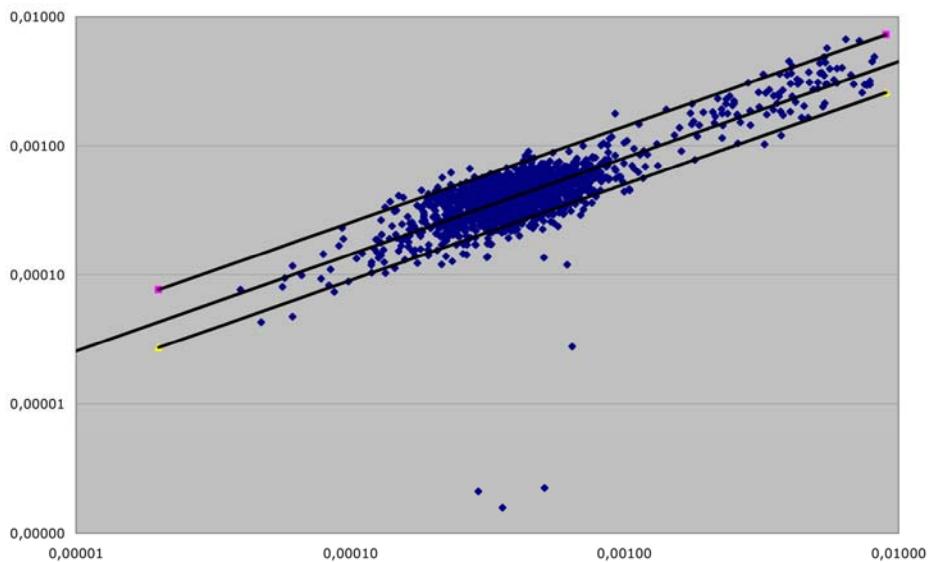
India 2



Thai-53 (Thailand)



Br4923 (Brazil)



NHDP98 (Mexico)

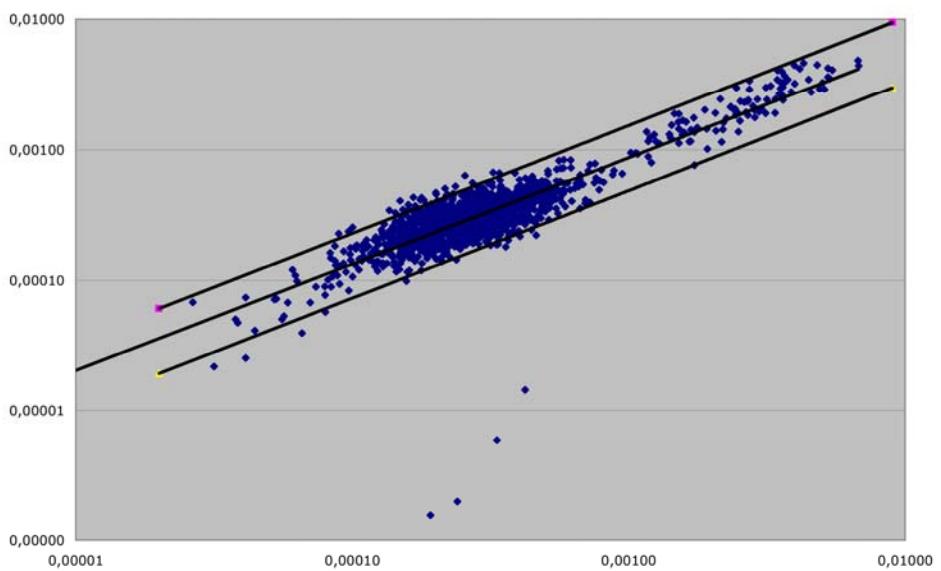


Figure S2. Q-PCR analysis of repetitive DNA.

	[Tamil Nadu]	[Africa]	[Br4923]	[Mex-NHDP98]	[Thai-53]
Lep rpt	5*	6	6	6	6
Lep rep	7*	7	8	5**	5**
Replep	15*	14	15	15	11
Rlep	37*	35	29	30	27

* Repeat Amplified in TN with our probes
 ** 7 copy found by PCR

