Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Truman RW, Singh P, Sharma R, et al. Probable zoonotic leprosy in the southern United States.
N Engl J Med 2011;364:1626-33.

Supplementary Data

Table S1: Demographics and genotype of *M. leprae* from humans and armadillos in US (Excel sheet). The reads from NHDP-55, NHDP-98 and I-30 resequencing analysis may be found in the trace depository under SRP001064.

Strain code	Country	State	Endemic Exposure	Foreign Residence History or County	SNP-Sub Type	HPT1414666	SNP383599	SNP3016183	SNP8453	SNP347385	SNP485139	SNP508482	SNP904825	SNP1257188	SNP1324012	SNP1348429	SNP2553183	SNP2818528	SNP298572	SNP481477	SNP494675	SNP694091	SNP890454	SNP1087400	SNP1579113	SNP1614073	SNP2706243	SNP313361	SNP840585	SNP1143426	SNP1155585	SNP1643166	SNP2174872	SNP61425	SNP832153	SNP972008	SNP1339816	SNP1605960	SNP1642879	SNP2011754	SNP2459773	SNP3102787	SNP1104235	SNP2751790	SNP73	SNP100574	SNP330125	SNP1926703	SNP2015327	SNP2935693	SNP1133492	SNP1295192	SNP2235048	SNP2312059	SNP413902	SNP642131	SNP807613	SNP2131753	SNP3090722	SNP20910	SNP527964	SNP591857	SNP733811	SNP2815502	SNP3267975	SNP22719	SNP365373	SNP379804	SNP467512	SNP537330	SNP1079902	SNP1214326	SNP1313204	SNP1524667	SNP1575600	SNP1947401	SNP2096406	SNP2132052	SNP2239468	SNP2347320	SNP2414869	SNP2423927	SNP508986	SNP14676	HPT3244472	HPT3041556	Ins978589	HPT741133	Del1476519	SNP7614	SNP10505	SNP22488	SNP29563	SNP38202	SNP116225	SNP156948	SNP193848	SNP365411	InDel408352	SNP574640	SNP604326	SNP1017410	SNP1113926	SNP1164294	SNP1291021	SNP1588116	SNP1734701	SNP1787403	SNP1928726	SNP2200739	SNP2999984	SNP3110867	InDel3224930	InDel17915	SNP45791	SNP623366	SNP1450891	SNP1527056	SNP3112678	AC8a	AC8b	AC9	GGT5	GTA9	6-7	12-5	21-3	23-3	27-5
SS(TN)		TN		India	1A	9A	C	T	T	T	T	T	G	T	C	T	T	T	A	A	T	T	A	T	T	T	T	A	A	T	T	T	G	A	T	T	T	G	G	T	A	A	C	A	A	A	G	T	G	A	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	8	8	9	5	9	7	5	3	3	5
FRS1 (Thai53)	THAI		N	Thailand	1A	9A	C	T	T	T	T	T	G	T	C	T	T	T	A	A	T	T	A	T	T	T	T	A	A	T	T	T	G	A	T	T	T	G	G	T	A	A	C	A	A	A	G	T	G	A	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	11	7	9	5	9	6	5	3	2	5
FRS2 (LWM26)	PH		N	Philippines	1A	9A	C	T	T	T	T	T	G	T	C	T	T	T	A	A	T	T	A	T	T	T	T	A	A	T	T	T	G	A	T	T	T	G	G	T	A	A	C	A	A	A	G	T	G	A	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	10	7	8	5	9	6	5	3	2	5
FRS3(43926)	BR	Maranhão	N	Brazil	4P	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	A	T	T	T	G	A	G	G	A	G	A	A	C	T	T	A	G	T	T	T	T	A	A	A	G	C	T	A	A	T	5A	7T	T	7G	d	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	7	7	7	4	10	6	4	2	2	5
FRS4(Br4923)	BR	Maranhão	N	Brazil	4P	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	A	T	T	T	G	A	G	G	A	G	A	A	C	T	T	A	G	T	T	T	T	A	A	A	G	C	T	A	A	T	5A	7T	T	7G	d	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	7	7	8	4	12	6	4	2	2	5
H-01	US	FL	N	Paraguay	1D	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	T	T	T	G	G	T	A	A	C	A	A	A	G	T	G	A	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	7	7	9	4	13	5	4	2	2	5
H-02	US	LA	Y	NFR	1A	9A	C	T	T	T	T	T	G	T	C	T	T	T	A	A	T	T	A	T	T	T	T	A	A	T	T	T	G	A	T	T	T	G	G	T	A	A	C	A	A	A	G	T	G	A	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	11	7	9	5	9	7	5	3	2	5
H-04	US	NM	Y	Mexico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	11	7	8	4	10	6	5	2	2	4
H-05	US	NJ	N	Puerto Rico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	11	7	8	4	10	6	5	2	2	4
H-06	US	PR	N	Puerto Rico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	8	9	5	10	7	5	2	2	4
H-07	US	CA	Y	Mexico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	8	8	4	10	7	5	2	2	4
H-09	US	AR	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	9	4	10	6	5	2	4	4
H-12	US	OH	N	Tanzania	3L	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	A	T	T	T	G	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	10	7	8	4	13	6	3	2	2	6
H-14	US	TX	Y	Mexico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	3	2	4
H-15	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-16	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-17(NHDP-63)	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-18	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-19	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-20	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-21	US	GA	Y	Mexico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-22	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-23	US	TX	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-25	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-26(NHDP-55)	US	TX	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-27	US	AR	Y	South Pacific	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-28	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-29	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-30	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-31	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-32	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-33	US	LA	Y	Spain	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-34	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-35	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-36	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-37	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-38	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-39	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-40	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
H-41	US	NM	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	4	2	2	4
H-42	US	NY	N	Dominican Republi	3I-1	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	T	C	G	G	C	10	7	8	4	10	6	5	2	2	4
H-43	US	MA	N	Brazil	3I-1	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	T	C	G	G	C	10	7	8	4	9	6	5	2	2	4
H-44	US	LA	Y	NFR	3L	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	A	T	T	T	G	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	10	7	8	4	8	7	5	2	2	5
H-45	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	7	4	10	7	5	2	2	4
H-46	US	LA	Y	NFR	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	7	4	10	6	5	2	2	4
H-49	US	OR	N	Micronesia	3K	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	9	7	9	4	8	9	4	1	2	5
H-50	US	TX	Y	NFR	3I-1	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	T	C	G	G	C	9	7	8	4	10	5	5	2	2	4
H-51	US	LA	Y	Puerto Rico	3I-1	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	T	C	G	G	C	9	7	8	4	9	5	4	2	2	5
H-52	US	SC	N	Philippines	3K	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	8	8	9	5	11	6	4	3	2	4
H-53	US	CO	N	Philippines	1A	9A	C	T	T	T	T	T	G	T	C	T	T	T	A	A	T	T	A	T	T	T	T	A	A	T	T	T	G	A	T	T	T	G	G	T	A	A	C	A	A	A	G	T	G	A	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	8	8	8	5	9	7	5	3	2	5
H-54	US	TX	Y	Guam	3K	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	8	8	8	4	9	7	4	2	2	5
H-55	US	TX	Y	Philippines	3K	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	8	8	8	4	8	7	4	2	2	5
H-56(NHDP-98)	US	TX	Y	Mexico	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	8	7	8	4	9	7	5	2	2	4
H-58	US	MI	N	India	3L	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	G	G	T	G	A	T	T	T	G	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	C	C	G	C	C	C	C	C	A	d	G	T	G	A	C	G	G	G	C	A	C	C	T	D	2	T	C	G	G	C	8	7	8	4	8	6	4	2	2	5
H-61	US	CA	N	Samoa	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	7	4	10	7	5	2	2	4
W-01	US	TX	Y	Nueces	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-02	US	AL	Y	Sumter	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-03	US	AL	Y	Sumter	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-04	US	AL	Y	Sumter	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-05	US	MS	Y	Yazoo	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-06	US	LA	Y	Cameron	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-07	US	AL	Y	Sumter	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-08	US	AL	Y	Sumter	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	6	2	2	4
W-09 (1-30)	US	LA	Y	Iberville	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-10	US	AR	Y	Desha	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-11	US	AR	Y	Desha	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-12	US	LA	Y	St Helena	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-13	US	LA	Y	St Martin	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-14	US	LA	Y	Tangipahoa	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-15	US	LA	Y	St Helena	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-16	US	LA	Y	St Helena	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-17	US	LA	Y	Wilkenson	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-18	US	LA	Y	Wilkenson	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-19	US	LA	Y	Tangipahoa	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	6	2	2	4
W-21	US	LA	Y	St Helena	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-22	US	LA	Y	East Baton Rouge	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-23	US	LA	Y	East Baton Rouge	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-24	US	MS	Y	Yazoo	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-25	US	LA	Y	East Baton Rouge	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-26	US	LA	Y	Point Coupee	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-27	US	MS	Y	Peral River	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	1	4
W-28	US	LA	Y	Port Hudson	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	1	4
W-29	US	LA	Y	Port Hudson	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-31	US	LA	Y	St Helena	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-32	US	TX	Y	Corpus Christi	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-33	US	LA	Y	Ascension	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	6	2	2	4
W-34	US	LA	Y	Iberville	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4
W-35	US	LA	Y	Iberville	3I-2	8A	G	C	C	C	C	C	C	C	G	C	G	C	G	G	G	C	G	C	G	C	G	G	G	C	G	C	C	G	C	G	C	A	T	G	G	C	G	G	G	G	A	C	C	C	T	A	C	C	G	C	C	G	A	G	A	C	C	C	G	G	T	C	C	G	A	C	C	C	C	G	C	G	C	G	C	G	G	C	6A	6T	d	8G	T	T	T	A	T	T	T	T	T	G	G	A	C	A	G	T	A	C	A	T	C	T	T	C	G	1	C	T	A	C	T	10	7	8	4	10	7	5	2	2	4

Total 114 SNP and 10 VNTR loci were analysed on 50 human patients and 33 wild infected armadillos.

SS: Standard strain (Complete genome sequence form TN strain was used to compare the re-sequencing reads to identify the SNPs and their positions

FRS: Foreign Reference Strain is the *M.leprae* strains being maintained in Mouse Foot Pad or armadillos;

H: human patients

W: Wild armadillos

Residence History: NFR: No Foreign Residence; Country: Native country of patient (if patient has immigration history to US) or Country visited by US native patient; County or site: county where armadillo was infected with *M. leprae* in their natural habitat.

Endemic Exposure: history of living in the area known to have *M. leprae* infected armadillos.

SNP/InDel/HPT positions are based on TN strain genome.

The reads from NHDP-55, NHDP-98 and I-30 resequencing analysis may be found in the trace depository under SRP001064.”

Table S2. Primers used for PCR and genotyping

Locus	**Sequence (5'-3')**
SNP-7614-F	CGC TGA GAC GAT GGG CAA TTA CC
SNP-7614-R	TTG CCC ATC AAC CAA GGG ATA CCG
SNP-10505-F	CCA ATT TGC TTG CAT TCC A
SNP-10505-R	AAC ACT GCA CCG ACC AAC TC
InDel_17915-F	GGG GAG GCG AGT ATA GAT CC
InDel_17915-R	AGG CGC TGG TCT GCT ATC TA
SNP-22488-F	ATG CTC TGC GGT ACC AGT CT
SNP-22488-R	AGC CCT ACC TGA TCG ACA AC
SNP-29563-F	AGC GCC AAA CAG CAC TAA AG
SNP-29563-R	TCT GAC GAT ATG GCG ACA AC
SNP-365411-F	CGA GGT ATT TAC CGC AAT GG
SNP-365411-R	CGT GGT TAG GGT GAC AAC AC
SNP-38202-F	GGG TGC ACG TAG AGT TGG AT
SNP-38202-R	CTC CGC CGA CGT ACA AAT
SNP-45791-F	TGG GAA TTC TTA TAA ATC CAT TCT G
SNP-45791-R	AGA GGG TTG AAA TTG GCA CA
SNP-116225-F	GCT TTC CAT TCA CGA CCA G
SNP-116225-R	AAG TTC GAT CGG TTC ACC AC
INDEL-408352-F	TGT TGG GCA GTA GCA GGT TA
INDEL-408352-R	ATC CAG ACG CTA TTG GCA AC
SNP-574640-F	CGT TCG ACA AGC TCA AGG TC
SNP-574640-R	GCC GAT CAA TCC CAT GAG TA
SNP-604326-F	GCC CAG TTA AGC GGT CTT TA
SNP-604326-R	AGG TCC CGT CAA GAA CCA G
SNP-623366-F	ATG GCT ACC GTG TGC AAT G
SNP-623366-R	TCT CCA AGG TGA GCT CGA TT
SNP-1017410-F	ATC CTG GGA TTG GAG GAT TC
SNP-1017410-R	TGT TCC TCA CTG CGA TGT CT
SNP-1113926-F	CCT CAT TTG CTG TGG ACC TCA GTG
SNP-1113926-R	ATG TCA TCT TCC AGG GCG AAA AGC
SNP-1164294-F	CGA CGT GGG TAC AGT CGA T
SNP-1164294-R	GGT AGT CAC CCG GAG CAC
SNP-1291021-F	GTA GTT CGT TAC CGC CAG GA
SNP-1291021-R	TGA GTT TTG GTC GTG ACC TG
SNP-1450891-F	CAA TAC TGC GGT CGT CTC AA
SNP-1450891-R	AAA TGA CCA TCA CGA CGA CA
SNP-1527056-F	TTA AGC CAA TAT CGC CGA AC
SNP-1527056-R	GTT GAC AAC GGC TGA CAG AT
SNP-156948-F	ACA CCA CCA AGC CGT ATT GT
SNP-156948-R	CTT TTC CTG TTG GGT TGG TG
SNP-1588116-F	GCA GGT CCT TAC CGA TGA GA
SNP-1588116-R	GCT AGC GAC TCA ACT GAG CA
SNP-1734701-F	AGA GCG GAG TGT AGT CAC CAG
SNP-1734701-R	CTT CTT TGT GCC CGC ATA TC
SNP-1787203-F	GCG AGT TGA ACA CCA CGA C
SNP-1787203-R	CGC AGT TGA TCG GTA TTG G

SNP-1928726-F	AAC AGA TCG GCC ATG AAC TC
SNP-1928726-R	GAT CGA AGA GAC TCG GAT GC
SNP-193848 -R	CGC CAC CGT AGA ATT TGT TT
SNP-193848-F	CCC AGT CCT GTT CGT AAT CC
SNP-2200539-F	ATC ACA TTC GCT CCC CTT TT
SNP-2200539-R	AAA CGC CTG TTA AGC GAT TG
SNP-2999984-F	AGC TGG CTG CGA CTA CAA CT
SNP-2999984-R	CGA TCT TCG AGG ACT TGT CA
SNP-3110867-F	CCA GGG ATT ATT GTG CTG CT
SNP-3110867-R	GGG GAA TTG CTT TGT TAT CG
SNP-3112678-F	GGC ACA GGA GAC TCT GGT TG
SNP-3112678-R	CCA TCC ATT TAT TCC AGA GCA
INDEL-3224930-F	ATC ACC GGT AAC ATC CAC CA
INDEL-3224930-R	TAA CGA AGT GGG GAA ACA GG

Fragment spanning the reported SNP was amplified with set of primers and sequenced with reverse and forward primers. Sequence was aligned with TN reference genome to identify corresponding SNP variation in particular strain.

Table S3. Primers used for VNTR analysis

VNTR locus		Sequence	Product size (bp) with TN strain
AC8a	F	GTG TTA CGC GGA ACC AGG CA	124
	R	CCA TCT GTT GGT ACT ACT GA	
AC8b	F	GAT GCG ACT ATC ACT CGC ACG CAG TT	140
	R	GCT GGT TTC CTT CTA GTC CC	
AC9	F	GCC TGG TGC CCG GAC AAT GC	146
	R	ACA TCA CAC TGA TCT CGC CGG CGC T	
AT17	F	GAC ACA CTC GAT CTC AGT AG	180
	R	TTA GCA GGA CGA TTG TAC AG	
GGT5	F	TCA CCA TCG ACG CTC CGG GT	161
	R	TCG GCC TGG TTG TCT GCC TT	
GTA9	F	CGC AGA TGCAACGAT CAC	122
	R	AAT ATG CAT GCC GGT GGT	
6-7	F	CTA CTT GCG CGC CAC CGC CA	191
	R	GCC GTC GCC AGG TTT TGC AG	
12-5	F	CTG GTC CAC TTG CGG TAC GAC	289
	R	GGA GAA GGA GGC CGA ATA CA	
21-3	F	TGT TGA AAT TTG GCG GCC AT	180
	R	TGC AAG GAG TGC TCA GCT AT	
23-3	F	CAG TCG CCC GGA TAC TGT TA	190
	R	TAA ATC CGC TCC CAA ATC TT	
27-5	F	GTG CTG TGC CTG CAG CCG TT	270
	R	TCC CCA AAG CCG CCG AAT CC	

Primers were used to amplify the VNTR loci and the resultant fragments analysed by gel electrophoresis. After confirmation of a single band, fragment analysis was performed in ABI 310 genetic analyzer. Each electrophoretogram was compared with known molecular weight markers to determine number of repeats at every VNTR locus.

Table S4: SNP and InDel marker’s restricted to 3I strains (Excel sheet). Details of the 52 SNPs where all four resequenced genomes (NHDP-55,63,98 & I-30) conflicted with the standard strains (TN, Br 4923 and Thai 53), and 21 locations where the 3I strains further differed among themselves.

Table S4: SNP and InDel marker’s restricted to 3I strains

			Type	TN genome position	TN, Br4923, Thai53	NHDP-55	NHDP-63	NHDP-98	I-30	Strains conflicting from TN genome
						(57X)	(46X)	(78X)	(22X)	
1	52 SNPs WHERE ALL FOUR RESEQUENCED GENOMES (NHDP-55,63,98 & I-30) WERE CONFLICTING FROM COMPLETE SEQUENCES GENOMES (TN, Br 4923 AND Thai 53)	1	SNP	883	G	A	A	A	A	NHDP-55,63,98 & I-30
2		2	SNP	1,011	G	A	A	A	A	NHDP-55,63,98 & I-30
3		3	SNP	7,614	C	T	T	T	T	NHDP-55,63,98 & I-30
4		4	SNP	10,505	C	T	T	T	T	NHDP-55,63,98 & I-30
5		5	SNP	15,985	G	A	A	A	A	NHDP-55,63,98 & I-30
6		6	InDel	17,915	TTGGTGGTGTA	-	-	-	-	NHDP-55,63,98 & I-30
7		7	SNP	22,488	G	A	A	A	A	NHDP-55,63,98 & I-30
8		8	SNP	29,563	C	T	T	T	T	NHDP-55,63,98 & I-30
9		9	SNP	38,202	C	T	T	T	T	NHDP-55,63,98 & I-30
10		10	SNP	45,791	T	C	C	C	C	NHDP-55,63,98 & I-30
11		11	SNP	48,196	G	A	A	A	A	NHDP-55,63,98 & I-30
12		12	SNP	116,225	C	T	T	T	T	NHDP-55,63,98 & I-30
13		13	SNP	156,948	C	T	T	T	T	NHDP-55,63,98 & I-30
14		14	SNP	193,848	C	T	T	T	T	NHDP-55,63,98 & I-30
15		15	SNP	305310	G	A	A	A	A	NHDP-55,63,98 & I-30
16		16	SNP	365,411	A	G	G	G	G	NHDP-55,63,98 & I-30
17		17	InDel	408,352	-	G	G	G	G	NHDP-55,63,98 & I-30
18		18	SNP	574,640	G	A	A	A	A	NHDP-55,63,98 & I-30
19		19	SNP	604,326	T	C	C	C	C	NHDP-55,63,98 & I-30
20		20	SNP	623,366	C	T	T	T	T	NHDP-55,63,98 & I-30
21		21	SNP	774,705	G	A	A	A	A	NHDP-55,63,98 & I-30
22		22	SNP	954,665	T	C	C	C	C	NHDP-55,63,98 & I-30
23		23	SNP	1,017,410	G	A	A	A	A	NHDP-55,63,98 & I-30
24		24	SNP	1,038,672	C	T	T	T	T	NHDP-55,63,98 & I-30
25		25	SNP	1,113,926	A	G	G	G	G	NHDP-55,63,98 & I-30
26		26	SNP	1,160,429	C	G	G	G	G	NHDP-55,63,98 & I-30
27		27	SNP	1,164,294	C	T	T	T	T	NHDP-55,63,98 & I-30
28		28	SNP	1,217,339	G	A	A	A	A	NHDP-55,63,98 & I-30
29		29	SNP	1,291,021	G	A	A	A	A	NHDP-55,63,98 & I-30
30		30	SNP	1,329,462	C	T	T	T	T	NHDP-55,63,98 & I-30
31		31	SNP	1,450,891	G	A	A	A	A	NHDP-55,63,98 & I-30
32		32	SNP	1,466,044	C	A	A	A	A	NHDP-55,63,98 & I-30
33		33	SNP	1,527,056	G	C	C	C	C	NHDP-55,63,98 & I-30
34		34	SNP	1,585,804	A	G	G	G	G	NHDP-55,63,98 & I-30
35		35	SNP	1,588,116	G	C	C	C	C	NHDP-55,63,98 & I-30
36		36	SNP	1,657,377	G	T	T	T	T	NHDP-55,63,98 & I-30
37		37	SNP	1,734,701	G	A	A	A	A	NHDP-55,63,98 & I-30
38		38	SNP	1,759,655	G	A	A	A	A	NHDP-55,63,98 & I-30
39		39	SNP	1,787,403	C	T	T	T	T	NHDP-55,63,98 & I-30
40		40	SNP	1,897,193	C	A	A	A	A	NHDP-55,63,98 & I-30
41		41	SNP	1,900,012	G	A	A	A	A	NHDP-55,63,98 & I-30
42		42	SNP	1,928,726	A	C	C	C	C	NHDP-55,63,98 & I-30
43		43	SNP	1,962,043	C	T	T	T	T	NHDP-55,63,98 & I-30
44		44	SNP	2,200,739	C	T	T	T	T	NHDP-55,63,98 & I-30
45		45	SNP	2,542,320	G	A	A	A	A	NHDP-55,63,98 & I-30
46		46	SNP	2,714,886	T	A	A	A	A	NHDP-55,63,98 & I-30
47		47	SNP	2,784,331	A	G	G	G	G	NHDP-55,63,98 & I-30
48		48	SNP	2,978,382	C	A	A	A	A	NHDP-55,63,98 & I-30
49		49	SNP	2,999,984	C	T	T	T	T	NHDP-55,63,98 & I-30
50		50	SNP	3,110,867	T	C	C	C	C	NHDP-55,63,98 & I-30
51		51	SNP	3,112,678	C	T	T	T	T	NHDP-55,63,98 & I-30
52		52	InDel	3,224,930	-	G	G	G	G	NHDP-55,63,98 & I-30
53	21 SNPS IDENTIFIED WHERE AT LEAST ONE STRAIN DIFFERED FROM THE REST OF THREE	1	SNP	604178	G	A	G	G	G	NHDP-55
54		2	SNP	1514420	T	C	T	T	T	NHDP-55
55		3	InDel	1978176	C	-	C	C	C	NHDP-55
56		4	SNP	2116512	A	G	A	A	A	NHDP-55
57		5	InDel	2322401	G	-	G	G	G	NHDP-55
58		6	SNP	21139	G	G	T	G	G	NHDP-63
59		7	SNP	509579	G	G	A	G	G	NHDP-63
60		8	SNP	530686	C	C	T	C	C	NHDP-63
61		9	SNP	1070054	C	C	T	C	C	NHDP-63
62		10	SNP	1206344	C	C	T	C	C	NHDP-63
63		11	SNP	1996640	C	C	T	C	C	NHDP-63
64		12	SNP	2119399	A	A	G	A	A	NHDP-63
65		13	SNP	2184972	T	C	T	C	C	NHDP-63
66		14	InDel	3106517	-	A	-	A	A	NHDP-63
67		15	InDel	667972	-	G	G	-	G	NHDP-98
68		16	SNP	2116786	C	T	T	T	C	I-30 (W-09)
69		17	SNP	509024	T	C	C	T	C	NHDP-55 & 63, 1-30
70		18	SNP	1223297	C	T	T	C	T	NHDP-55 & 63, 1-30
71		19	SNP	1600438	T	G	G	T	G	NHDP-55 & 63, 1-30
72		20	SNP	1797215	C	T	T	C	T	NHDP-55 & 63, 1-30
73		21	SNP	1983613	C	T	T	C	T	NHDP-55 & 63, 1-30

52 SNPs WHERE ALL FOUR RE-SEQUENCED GENOMES (NHDP-55,63,98 & I-30) CONFLICTED WITH STANDARD STRAINS (TN, Br 4923 AND Thai 53)
21 SNPS IDENTIFIED WHERE AT LEAST ONE STRAIN DIFFERED FROM THE OTHER THREE

Table S5. Genotypes of *M. leprae* infecting humans and armadillos in the US

Source	Report State	EE	Residence history*	Genotype	n	VNTR profile[#]									
						AC8a	AC8b	AC9	GGT5	GTA9	6-7	12-5	21-3	23-3	27-5
HUMAN PATIENTS REPORTED IN US	LA	Y	NFR	1A-v1	1	11	7	9	5	9	7	5	3	2	5
	CO	N	Philippines	1A-v2	1	8	8	8	5	9	7	5	3	2	5
	FL	N	Paraguay	1D-v1	1	7	7	9	4	13	5	4	2	2	5
	LA	Y	NFR	3I-1-v1	1	9	7	8	4	10	5	5	2	2	4
	LA	Y	Puerto Rico	3I-1-v2	1	9	7	8	4	9	5	4	2	2	5
	NY	N	Dominican Republic	3I-1-v3	1	10	7	8	4	10	6	5	2	2	4
	MA	N	Brazil	3I-1-v4	1	10	7	8	4	9	6	5	2	2	4
	LA,TX, AR,GA	Y	Various	3I-2-v1	25	10	7	8	4	10	7	5	2	2	4
	NM	Y	Mexico	3I-2-v2	1	11	7	8	4	10	6	5	2	2	4
	CA	Y	Mexico	3I-2-v3	1	10	8	8	4	10	7	5	2	2	4
	AR	Y	NFR	3I-2-v4	1	10	7	9	4	10	6	5	2	4	4
	TX	Y	Mexico	3I-2-v5	1	10	7	8	4	10	7	5	3	2	4
	LA	Y	NFR	3I-2-v6	1	10	7	8	4	10	7	4	2	2	4
	LA	Y	NFR	3I-2-v7	1	10	7	7	4	10	7	5	2	2	4
	LA	Y	NFR	3I-2-v8	1	10	7	7	4	10	6	5	2	2	4
	TX	Y	Mexico	3I-2-v9	1	8	7	8	4	9	7	5	2	2	4
	NJ	N	Puerto Rico	3I-2-v2	1	11	7	8	4	10	6	5	2	2	4
	PR	N	Puerto Rico	3I-2-v11	1	10	8	9	5	10	7	5	2	2	4
	CA	N	Samoa	3I-2-v7	1	10	7	7	4	10	7	5	2	2	4
	TX	Y	Guam	3K-v1	1	8	8	8	4	9	7	4	2	2	5
	TX	Y	Philippines	3K-v2	1	8	8	8	4	8	7	4	2	2	5
	OR	N	Micronesia	3K-v3	1	9	7	9	4	8	9	4	1	2	5
	SC	N	Philippines	3K-v4	1	8	8	9	5	11	6	4	3	2	4
	LA	Y	NFR	3L-v1	1	10	7	8	4	8	7	5	2	2	5
	OH	N	Tanzania	3L-v2	1	10	7	8	4	13	6	3	2	2	6
	MI	N	India	3L-v3	1	8	7	8	4	8	6	4	2	2	5
WARM	AL, AR, MS,TX	Y	NFR	3I-2-v1	28	10	7	8	4	10	7	5	2	2	4
	LA, AL	Y	NFR	3I-2-v13	3	10	7	8	4	10	7	6	2	2	4
	LA	Y	NFR	3I-2-v14	2	10	7	8	4	10	7	5	2	1	4

M. leprae genotypes were determined as shown in Figure 2. Complete data of all 114 SNPs and 10 VNTR Loci is available as supplementary Table S1. #, VNTR profile represents the number of repeat copies found at a particular locus. *, Residence history is as reported by patient; NFR: No Foreign Residence; EE: Endemic Exposure, living in areas with potential exposure to *M. leprae* through armadillos; n: number of strains with same genotype; WARM: Wild Armadillo *M. leprae*.

Table S6. Case control studies and contingency analysis:

A. 3I-1 v 3I-2 Strain Distribution in North and South America

Fisher's Exact Test, Two-sided P<0.001

Odds Ratio=27.000, 95% Confidence Interval 8.312 to 87.7

Data analyzed:

	3I-1	**3I-2**	**Total**
South	48 (46%)	16 (15%)	64 (62%)
North	4 (4%)	36 (35%)	40 (38%)
Total	52 (50%)	52 (50%)	104 (100%)

B. 3I-2-v1 Association with Armadillo Exposure (EE/NE)

Fisher's Exact Test, Two-sided P<0.001

Odds Ratio=54.517, 95% Confidence Interval 3.031 to 980.67

Data analyzed: (0.5 added to each value for analysis) Includes Reference Strains

	Endemic Exposure (EE)	**Non-Endemic Exposure (NE)**	**Total**
3I-2-v1	25 (46%)	0 (0%)	64 (46%)
Other	14 (26%)	15 (28%)	29 (54%)
Total	39 (72%)	15 (28%)	54 (100%)

C. 3I-2-v1 Association with Residence History (NFR/FR)

Fisher's Exact Test, Two-sided P<0.0001

Odds Ratio=16.5, 95% Confidence Interval 4.207 to 64.713

Data analyzed: Includes Reference Strains

	No Foreign Residence (NFR)	**Foreign Residence (FR)**	**Total**
3I-2-v1	21 (39%)	4 (7%)	25 (46%)
Other	7 (13%)	22 (41%)	29 (54%)
Total	28 (52%)	26 (48%)	54 (100%)

D. 3I-2-v1 Associations with Patient Reported Armadillo Contact History

Fisher's Exact Test, Two-sided P=0.3147

Odds Ratio=4.0, 95% Confidence Interval 0.4468 to 35.807

Data analyzed:

	3I-2-v1	**Other**	**Total**
Yes	6 (40%)	2 (13%)	8 (53%)
No	3 (20%)	4 (27%)	7 (47%)
Total	9 (60%)	6 (40%)	15 (100%)