Supplementary File 1. Polymerase Chain Reaction (PCR) methodology for identification of lepra bacilli and amplification of drug resistance genes:

Sequences of primers used in the study:

Gene name	Primer sequence
folP	For- CTTGATCCTGACGATGCTGT
folP	Rev- CCACCAGACACATCGTTGAC
rpoB	For- GTCGAGGCGATCACGCCGCA
rpoB	Rev- CGACAA TGAACCGATCAGAC
gyrA	For- ATGGTCTCAAACCGGTACATC
gyrA	Rev- TACCCGGCGAACCGAAATTG

The target regions of the folp1, rpoB and gyrA genes were amplified in a thermal cycler (ABI, US) in 25ul volume containing genomic DNA, 12.5 µl Hot Start Taq polymerase PCR master mix (2X) (Qiagen), 1.25 of µl forward primer and reverse primer at final concentration 0.5µM. The final volume of reaction mix was made up with nuclease free water. The Primer sequences used in this study are listed in Table 1.

The reaction was cycled 40 times at 94ºC for 1 minute, 60^0C for 1 minute and 72ºC for 1 minute which was preceded by initial denaturation at 95ºC for 15 minute and ended by final extension at 72ºC for 10 minute.

Each reaction set-up contained one negative and one positive control. After detection of PCR product on a 2% agarose gel, amplicons were excised from the gel and were purified by using the Qiagen Gel extraction Kit. PCR products were sent for commercial sequencing. Sequence data were checked by blast at NCBI and analyzed using MEGA version 5.1 (http://megasoftware.net/).