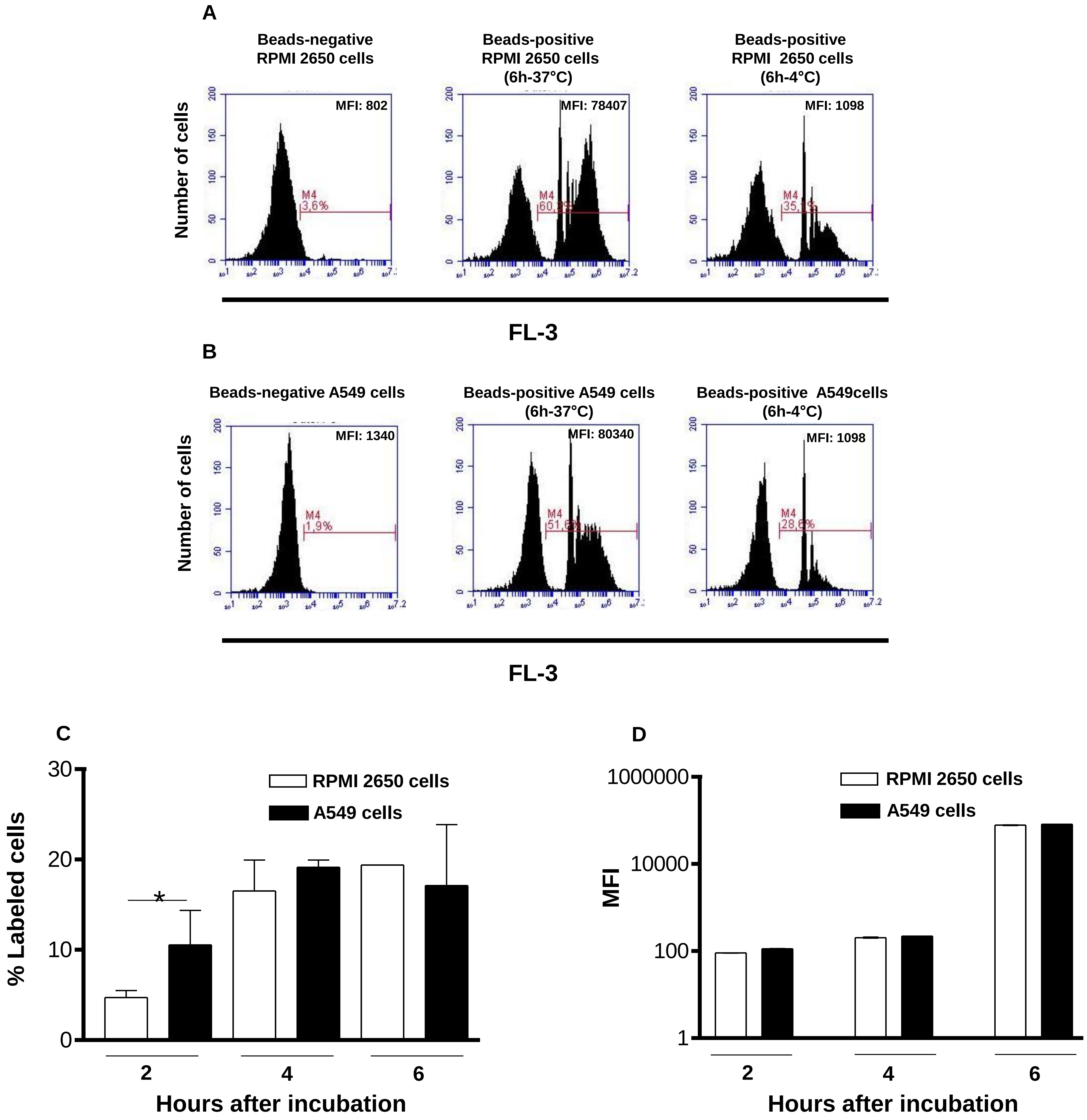

**Supplementary Figure 1: Nasal and alveolar epithelial cells show a similar capacity to uptake inert particles.** Monolayers of epithelial cells were incubated with fluorescent beads at 37°C or at 4°C at different time points and detached and analyzed by flow cytometry. (A, B) Representative histograms showing the positive RPMI 2650 (A) and A549 (B) cells after 6 h of incubation with fluorescent beads at 37°C or at 4°C. (C) The percentage of cells with internalized beads was determined, as follows: % cells with internalized beads = bead-positive cells (37°C) – bead-positive cells (4°C). (D) Median fluorescence intensity (MFI) of cells with internalized beads was calculated, as follows: MFI of cells with internalized beads = MFI (37°C) – MFI (4°C). The data represent the mean values ± SD of two experiments performed in duplicate. * $P < 0.05$ was considered statistically significant.

## TABLE S1: Cell surface proteins simultaneously identified in crude and NaOH-treated *M. leprae*

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML0072c | *Soda* | Probable superoxide dismutase SodA | 0 | Cyt./Memb./Cw | 18.8 [a]/19.3[b] | Rv3846 |
| ML0317 | *groEL2* | Heat shock protein Hsp65 family | 0 | Cyt./Memb./Cw | 51.6[a]/54.9[b] | Rv0440 |
| ML0380 | *groES* | 10 kDa chaperonin GroEs | 0 | Cyt./Memb. | 73[a]/58[b] | Rv3418c |
| ML0381 | *groEL1* | 60 kDa chaperonin 1 GroEL1 | 0 | Cyt./Memb. | 25.5[a]/53.6[b] | Rv3417 |
| ML1623 | *htpG* | Heat shock protein Hsp90 family | 0 | Cw | 9.9[a]/28.4[b] | Rv2299c |
| ML1795 | *hsp18* | Antigen 18kDa Hsp18 | 0 | Cyt./Memb./Cw | 37.8[a]/25.7[b] | - |
| ML2042 | *ahpC* | Alkyl hidroperoxide reductase | 0 | Cyt./Memb. | 51.8[a]/73.3[b] | Rv2428 |
| ML2254 | *otsA* | Probable trehalose phosphate synthase | 0 | N.d. | 13.7[a]/6.8[b] | Rv3490 |
| ML2490c | *clpB* | Heat Shock protein | 0 | Cw | 6.4[a]/13.9[b] | Rv0384c |
| ML2496c | *dnaK* | Probable chaperone protein DnaK | 0 | Cyt./Memb. | 24.8[a]/41.6[b] | Rv0350 |
| ML0101 | *pks13* | Polyketide synthase | 1 | N.d. | 16.4[a]/3.1[b] | Rv3800c |
| ML0138c | *fadD28* | Probable fatty-acid-CoA synthetase | 1 | Memb./Cw | 20.3[a]/21.6[b] | Rv2941 |
| ML0139 | *Mas* | Mycocerosic acid synthase | 1 | Memb. /Cw | 13.4[a]/11.2[b] | Rv2940c |
| ML0660c | *fadE23* | Probable acyl-CoA dehydrogenase | 1 | N.d. | 12.4[a]/10.8[b] | Rv3140 |
| ML0737 | *fadE25* | Probable acyl-CoA dehydrogenase | 1 | N.d. | 6.7[a]/6.7[b] | Rv3274c |
| ML0887c | *fadD15* | Probable long-chain-fatty-acid-CoA ligase | 1 | N.d. | 10.3[a]/10.5[b] | Rv2187 |
| ML1229 | *pks4* | Polyketide beta-ketoacyl synthase | 1 | Cw | 2.2[a]/3.1[b] | Rv1180 |
| ML1654 | acpM | Involved in meromycolate extension | 1 | Cyt. | 42.6[a]/33.9[b] | Rv2244 |
| ML2028 | fbpB | Secreted antigen 85B | 1 | Cyt./Memb./Cw | 14.1[a]/10.7[b] | Rv1886c |
| ML2161c | *fadB* | Probable fatty oxidation | 1 | Cyt./Memb. | 25.2[a]/46.2[b] | Rv0860 |
| ML2162c | *fadA* | Acyl –CoA Thiolase | 1 | Memb. | 11.2[a]/45.9[b] | Rv0859 |
| ML2353c | *ppsE* | Probable polyketide beta-ketoacyl synthase | 1 | Memb./Cw | 16.4[a]/8.1[b] | Rv2935 |
| ML2354c | *ppsD* | Phenolpthiocerol synthesis type-I polyketide synthase | 1 | N.d. | 2[a]/22.6[b] | Rv2934 |
| ML2402 | *echA8* | Probable enoyl-coa hydratase | 1 | Cw. | 10.1[a]/22.6 [b] | Rv1070c |
| ML2426 | *cmaA2* | Cyclopropane-fatty-acyl-phospholipid synthase | 1 | N.d. | 22.1[a]/36[b] | Rv0503c |
| ML2461c | *fadB2* | Probable 3-hydroxybutyryl-coa dehydrogenase | 1 | Memb. | 12.5[a]/47.7[b] | Rv0468 |
| ML2546c | *fadD2* | Probable fatty-acid-coA ligase | 1 | N.d. | 10.3[a]/9.5 [b] | Rv0270 |
| ML2563 | *fadE5* | Probable acyl-CoA dehydrogenase | 1 | Cyt./Memb. | 12.4[a]/16.2[b] | Rv0244c |
| ML2565 | *fabG4* | Oxoacyl-reductase | 1 | Memb./Cw | 19.2[a]/47.4[b] | Rv0242c |

## TABLE S1: (continued)

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML0778 | *ml0778* | Conserved hypothetical protein | 2 | N.d. | 10.5[a]/25.3[b] | Rv3241c |
| ML0854 | *gpsI* | RNA degradation | 2 | Memb..Cw | 10.3[a]/18.6[b] | Rv2783c |
| ML1014c | *sigB* | Sigma factor from RNA polymerase | 2 | N.d. | 7.8[a]/6.0[b] | Rv2710 |
| ML1132 | *rho* | Probable transcripition termination factor | 2 | N.d. | 3.9[a]/5.8[b] | Rv1297 |
| ML1382 | *rpsA* | Probable ribosomal protein | 2 | Cyt./Memb. | 5.6[a]/8.5[b] | Rv1630 |
| ML1394 | *infC* | Initiation factor-3 | 2 | N.d. | 18.3[a]/43.1[b] | Rv1641 |
| ML1597c | *tsf* | Elongation factor | 2 | N.d. | 14.1[a]/24.3[b] | Rv2889c |
| ML1598c | *rpsB* | 30s ribosomal protein | 2 | Memb. | 20.6[a]/18.4[b] | Rv2890c |
| ML1683c | *hupB* | Probable DNA-binding protein | 2 | Memb./Cw | 14[a]/39[b] | Rv2986c |
| ML1877c | *tuf* | Iron-regulated elongation factor | 2 | Cyt./Memb./Cw | 36.9[a]/38.9 [b] | Rv0685 |
| ML1878c | fusA1 | Probable elongation factor | 2 | N.d. | 5.7[a]/20.8[b] | Rv0684 |
| ML1890c | *rpoC* | RNA polymerase | 2 | Cyt./Memb./Cw | 19.5[a]/18.5[b] | Rv0668 |
| ML1891c | *rpoB* | RNA polymerase | 2 | Cyt./Memb./Cw | 11.5[a]/30.1[b] | Rv0667 |
| ML1905c | *rplK* | Probable 50s ribosomal protein | 2 | N.d. | 16.9[a]/31[b] | Rv0640 |
| ML1906c | *nusG* | Probable transcription antitermination | 2 | Cyt. | 16.2[a]/26.3[b] | Rv0639 |
| ML1957c | *rpoA* | Putative RNA polymerase | 2 | Memb. | 35.2[a]/54.2[b] | Rv3457c |
| ML1958c | *rpsD* | 30s ribosomal protein | 2 | Cw | 39.3[a]/13.4[b] | Rv3458c |
| ML0235 | *clpC* | Probable ATP-dependent Clp protease | 3 | N.d. | 4.5[a]/17.6[b] | Rv3596c |
| ML0644 | *ml0644* | Probable conserved transmembrane protein | 3 | Memb./Cw | 24.2[a]/42.7[b] | Rv3193c |
| ML0841 | *mmpI* | Major Memb. protein | 3 | Memb. | 38.4[a]/42.7 [b] | - |
| ML0922 | *wag31* | unknown | 3 | N.d. | 15.4[a]/11.7[b] | Rv2145c |
| ML1839c | *sppa* | Possible protease | 3 | Memb. | 16.4[a]/30.7 [b] | Rv0724 |
| ML1892c | *mkl* | Active transport of ribonucleotide | 3 | Nd | 13.3[a]/13[b] | Rv0655 |
| ML2489c | *ml2489c* | Unknown | 3 | Nd | 13.3[a]/8.4[b] | Rv0383c |
| ML0127 | *ml0127* | Possible methyltransferase | 7 | Memb./Cw | 21[a]/23.6[b] | Rv2959c |
| ML0130c | *ml0130* | Probable methyltransferase | 7 | Memb. | 28.1 a) / 8.9[b] | Rv2952 |
| ML0131 | *ml0131* | Possible oxidoreductase | 7 | Memb. | 27.5[a]/51.6[b] | Rv2951c |
| ML0161 | *purH* | Purine biosynthesis | 7 | Memb. | 4[a]/11.6[b] | Rv0957 |
| ML0183 | *moeA1* | Probable molybdopterin biosynthesis | 7 | Cw. | 8[a]/7.3[b] | Rv0994 |

## TABLE S1: (continued)

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML0315c | *ml0315c* | Oxidoreductase | 7 | Cyt./Memb. | 29.6$^{a}$/51.6 $^{b}$ | Rv0068 |
| ML0387 | guaB2 | Inosine-5'-monophosphate dehydrogenase | 7 | N.d. | 6.2$^{a}$/13.2$^{b}$ | Rv3411c |
| ML0418 | ml0418 | Possible oxidoreductase | 7 | Cw | 11$^{a}$/22.4$^{b}$ | Rv3368c |
| ML0485c | *gabT* | Probable 4-aminobutyrate aminotransferase | 7 | Cw | 6.7$^{a}$/28.9$^{b}$ | Rv2589 |
| ML0544 | *metK* | S-adenosylmethionine synthase | 7 | Cyt./Memb. | 14.1$^{a}$ /8.7$^{b}$ | Rv1392 |
| ML0570 | *gap* | Probable glyceraldehyde 3-phosphate dehydrogenase | 7 | Memb. | 10.9$^{a}$/14.7$^{b}$ | Rv1436 |
| ML0578 | *ppc* | Phosphoenolpyruvate carboxylase | 7 | N.d. | 7.4$^{a}$/7.4$^{b}$ | - |
| ML0582c | *tal* | Transaldolase | 7 | N.d. | 10.1$^{a}$/8.3$^{b}$ | Rv1448c |
| ML0583c | *tkt* | Probable transketolase | 7 | N.d. | 6.4$^{a}$/11.2$^{b}$ | Rv1449c |
| ML0674 | *folD* | Involved in purine biosynthesis | 7 | Cyt. | 9.6$^{a}$/5.3$^{b}$ | Rv3356c |
| ML0697c | *sdhA* | Succinate dehydrogenase | 7 | N.d. | 6.7$^{a}$/ 14.7$^{b}$ | Rv3318 |
| ML0771 | *sahH* | Putative S-adenosyl-L-homocysteine hydrolase | 7 | Cyt. | 8.7$^{a}$/32.3 $^{b}$ | Rv3248c |
| ML0842 | *csd1* | Probable cysteine desulfurase | 7 | Memb. | 5.6 $^{a}$/12.1$^{b}$ | - |
| ML0861c | *sucB* | Dihydrolipoamide succinyltransferase | 7 | Cyt. | 13.6$^{a}$/12.5$^{b}$ | Rv2215 |
| ML0873 | *adk* | Probable adenosine kinase | 7 | Cyt. | 15.1$^{a}$/16.7$^{b}$ | Rv2202c |
| ML0925 | *glnA* | Glutamine synthetase | 7 | Memb. | 2.9$^{a}$/18$^{b}$ | Rv2220 |
| ML0961c | *metE* | Probable methyltransferase | 7 | Cyt./Cw | 7.8$^{a}$/23.9$^{b}$ | Rv1133c |
| ML1091 | *mdh* | Malate dehydrogenase | 7 | Cyt | 17.6$^{a}$/16.7$^{b}$ | Rv1240 |
| ML1095c | *sucA* | 2-oxoglutarate dehydrogenase | 7 | Memb. | 6.3$^{a}$/5.5$^{b}$ | Rv1248c |
| ML1129 | *thrA* | Homoserine dehydrogenase | 7 | Memb. | 7$^{a}$/7$^{b}$ | Rv1294 |
| ML1143 | *atpA* | Probable atp synthase alpha chain | 7 | Cyt. | 7.5$^{a}$/19.4$^{b}$ | Rv1308 |
| ML1144 | *atpG* | ATP synthase | 7 | Memb./Cw | 16.1$^{a}$/20.5 $^{b}$ | Rv1309 |
| ML1145 | atpD | ATP synthase | 7 | Cyt./ Memb. | 12.6 $^{a}$/48$^{b}$ | Rv1310 |
| ML1159 | ml1159 | Thioredoxin | 7 | N.d. | 11a/48.5b | Rv1324 |
| ML1323 | prcA | Proteasome | 7 | Memb. | 18.5$^{a}$/29.8$^{b}$ | Rv2109c |
| ML1412 | argG | Probable Argininosuccinate synthase | 7 | N.d. | 6.8$^{a}$/9.5$^{b}$ | Rv1658 |
| ML1458c | proA | Phosphate reductase protein | 7 | N.d. | 8.3$^{a}$/19.1$^{b}$ | Rv2427c |
| ML1480c | clpP1 | ATP-dependent Clp protease | 7 | Cyt. | 15$^{a}$/37$^{b}$ | Rv2461c |
| ML1692c | serA1 | phosphoglycerate dehydrogenase | 7 | N.d. | 10.8$^{a}$/6.6$^{b}$ | Rv2996c |
| ML1694c | ilvC | Probable ketol-acid reductoisomerase | 7 | Cyt. | 12.3$^{a}$/31.2$^{b}$ | Rv3001c |
| ML1711c | fixB | Probable electron transfer flavoprotein | 7 | Cyt./Memb. | 15$^{a}$/17 $^{b}$ | Rv3028c |

## TABLE S1: (continued)

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML1751c | moeY | Possible molybdopterin biosynthesis protein | 7 | N.d. | 12.6[a]/10.8[b] | Rv1355c |
| ML1794 | ml1794 | Probable amidotransferase | 7 | N.d. | 7[a]/9.7[b] | Rv2294 |
| ML1814 | acn | Aconitate hydratase | 7 | N.d. | 6.1[a]/16.5[b] | Rv1475c |
| ML1947 | fum | Fumarase | 7 | N.d. | 10.1[a]/19.6[b] | Rv1098c |
| ML1953c | glyA1 | Serine hydroxymethyltransferase | 7 | N.d. | 4.5[a]/26.1[b] | Rv1093 |
| ML1985c | aceA | Isocitrate lyase | 7 | Memb./Cw | 5[a]/13.3[b] | Rv1916 |
| ML2046 | lldD2 | L-lactate dehydrogenase | 7 | Memb. | 17.6[a]/7.7[b] | Rv1872c |
| ML2069 | glcB | Malate synthase | 7 | Cyt./Cw | 10.1[a]/23.9[b] | Rv1837c |
| ML2130c | gltA2 | Probable citrate synthase | 7 | Cyt./Memb. | 11.6[a]/33.4[b] | Rv0896 |
| ML2263c | menB | Probable naphthoate synthase | 7 | N.d. | 11.7[a]/18.7[b] | Rv0548c |
| ML2277 | grcC1 | Probable polyprenyl-diphosphate synthase | 7 | N.d. | 12.4[a]/17.3[b] | Rv0562 |
| ML2502 | aspC | Probable aspartate aminotransferase | 7 | N.d. | 4.1[a]/6.4[b] | Rv0337c |
| ML2608c | ilvD | Involved in valine and isoleucine biosynthesis | 7 | N.d. | 6.9[a]/8.5[b] | Rv0189c |
| ML2634c | pntB | Transhydrogenase | 7 | N.d. | 6.8[a]/7.2[b] | Rv0157 |
| ML2636c | pntAa | Transhydrogenase | 7 | N.d. | 6.8[a]/17.2[b] | Rv0155 |
| ML2639c | ml2639c | Probable aldehyde dehydrogenase | 7 | N.d. | 10.6[a]/7.4 [b] | Rv0147 |
| ML2672c | icd2 | Probable isocitrate dehydrogenase | 7 | Memb. | 9.7[a]/10.7[b] | Rv0066c |
| ML0773 | mtrA | Transcriptional activator, part of a two component regulatory system. | 9 | Memb./Cw | 12.4[a]/24.9[b] | Rv3246c |
| ML1810c | moxR1 | Transcriptional regulatory protein | 9 | Memb | 18.6[a]/34.2[b] | Rv1479 |
| ML0055c | ml0055c | Conserved hypothetical protein | 10 | N.d. | 4.9[a]/9.6[b] | Rv3868 |
| ML0129c | ml0129 | Conserved hypothetical protein | 10 | Memb. | 38.5[a]/31.6 [b] | Rv2953 |
| ML0860c | ml0860c | Conserved hypothetical protein | 10 | N.d. | 10.1[a]/26.4[b] | Rv2216 |
| ML1444 | *ml1444* | Conserved hypothetical protein | 10 | Memb. | 10.3[a]/13.8[b] | Rv2054 |
| ML1898 | ml1898 | Conserved hypothetical protein | 10 | N.d. | 9.6[a]/6.7[b] | Rv0647c |
| ML2346c | ml2346 | Conserved hypothetical protein | 10 | N.d. | 16.3 [a]/11.3[b] | - |
| ML2465 | Ml2465 | Conserved hypothetical protein | 10 | Memb. | 27.7[a]/27.1[b] | Rv0464c |

N.d- Not determined

The confidence interval was of 100% to all identified proteins.

*The leproma identification (ID) and the functional category (FC) were obtained from Leproma ( http://genolist.pasteur.fr/Leproma/).

**The subcellular localization was obtained from data previously described in the literature (1; 2; 3; 4; 5 and 6). The abbreviations Cyt, Cw and Memb mean, respectively, cytosolic, cell wall and membrane fractions.

[a] Peptide sequence coverage (%) obtained in NaOH-treated *M. leprae*.

[b] Peptide sequence coverage (%) obtained in crude *M. leprae*

## TABLE S2: Cell surface-exposed proteins identified only in crude *M. leprae*

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML0625 | *dnaJ2* | Probable chaperone protein DnaJ2 | 0 | N.d. | 6.3 | Rv2373c |
| ML0862 | *ephD* | Putative oxidoreductase | 0 | Memb. | 5.9 | Rv2214c |
| ML2015c | *cinA* | Probable cinA-like protein | 0 | N.d. | 12.9 | Rv1901c |
| ML1158 | *fadA4* | Probable acetyl-coa acetyltransferase | 1 | N.d. | 9.2 | Rv1323 |
| ML2185 | *desA1* | Putative acyl-desaturase | 1 | N.d. | 14.2 | Rv0824c |
| ML2498 | *ml2498* | Possible enoyl-Coa hydratase | 1 | N.d. | 18.3 | - |
| ML0002 | *dnaN* | Probable DNA polymerase | 2 | N.d. | 8.8 | Rv0002 |
| ML0155 | *sucC* | Succinyl-CoA-synthetase | 2 | N.d. | 9.7 | Rv0951 |
| ML0826 | *glyS* | Probable t-rna synthesase | 2 | Memb. | 17.5 | Rv2357c |
| ML1174 | *rphA* | Probable ribonuclease | 2 | Cyt. | 15.8 | Rv1340 |
| ML1553 | *proS* | Probable prolyl tRNA synthetase | 2 | Memb./Cw | 12.1 | - |
| ML1556c | *infB* | Translation initiation factor | 2 | N.d. | 9.2 | Rv2839c |
| ML1688c | *gltS* | Probable glutamyl-trna synthetase | 2 | N.d. | 9.0 | Rv2992c |
| ML1700c | *gatB* | Putative glutamyl-tRNA synthetase | 2 | N.d. | 5.78 | Rv3009c |
| ML1731c | *nrdF* | Involved in the dna replication pathway | 2 | N.d. | 14.8 | Rv3048c |
| ML1860c | *rplB* | Probable 50s ribosomal protein | 2 | Memb. | 21.8 | Rv0704 |
| ML2697c | *pcnA* | Putative polymerase | 2 | N.d. | 9.5 | Rv3907c |
| ML1316 | *mpa* | Probable proteassome | 3 | N.d. | 14.8 | Rv2115c |
| ML1367 | *ml1367* | Putative initiation inhibitor protein | 3 | N.d. | 13.8 | Rv1708 |
| ML1481c | *tig* | Trigger factor protein | 3 | N.d. | 15.4 | Rv2462c |
| ML1622c | *ffh* | Export of extra-cytoplasmic proteins | 3 | Memb. | 9.0 | Rv2916c |
| ML1633c | *ml1633c* | Exported protease | 3 | Memb. | 7.9 | Rv2224c |
| ML2082c | *secA2* | Putative ATPase | 3 | N.d. | 7.1 | Rv1821 |
| ML2188 | *phoY2* | Probable phosphate transport system | 3 | N.d. | 25.2 | Rv0821c |
| ML2352c | *drrA* | Antibiotic resistance | 3 | N.d. | 21.5 | Rv2936 |
| ML2706c | *parB* | Probable chromosome partitioning protein | 3 | N.d. | 7.8 | Rv3917c |
| ML0210c | *ppa* | Inorganic pyrophosphate | 7 | Memb. | 21.6 | Rv3628 |
| ML0255 | *eno* | Probable enolase | 7 | Memb. | 9.3 | Rv1023 |
| ML0269c | *fdg1* | Probable F420-dependent glucose-6-phosphate dehydrogenase | 7 | Cyt. | 25.9 | Rv0407 |
| ML0286c | *fba* | Probable fructose biphosphate aldolase | 7 | Cyt. | 20 | Rv0363c |

**TABLE S2: (continued)**

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML0348 | *ml0348* | Possible coenzyme F420-dependent oxidoreductase | 7 | Cyt./Memb. | 26 | Rv3520c |
| ML0551c | *ml0551c* | Methyltransferase | 7 | Cyt. | 14.6 | Rv1405c |
| ML0572 | *tpi* | Possible Triosephospate | 7 | Cyt. | 22.2 | Rv1438 |
| ML0611 | *lepA* | GTP binding protein | 7 | N.d. | 7.6 | Rv2404c |
| ML0839c | *cysK* | Probable cysteine synthase | 7 | Cyt./Memb | 19.4 | Rv2334 |
| ML0866 | *ilvE* | Probable branched-chain amino acid transaminase | 7 | N.d. | 21.2 | Rv2210c |
| ML0875 | *ctaC* | Transmemb cytochrome c oxidase | 7 | N.d. | 13.6 | Rv2200c |
| ML0896 | *aroG* | Play a role in chorismate biosynthesis | 7 | N.d. | 10.2 | Rv2178c |
| ML0996 | *dapF* | Diaminopimelate epimerase | 7 | N.d. | 13.2 | Rv2726c |
| ML1023c | *ppgK* | Polyphosphate glucokinase | 7 | N.d. | 9.9 | Rv2702 |
| ML1130 | *thrC* | Threonine synthase | 7 | Cyt. | 25.8 | Rv1295 |
| ML1272 | *trpB* | Tryptophan synthase | 7 | N.d. | 10.6 | Rv1612 |
| ML1273 | *trpA* | Tryptophan synthase | 7 | N.d. | 18.5 | Rv1613 |
| ML1310 | *hisG* | ATP phosphoribosyltransferase | 7 | N.d. | 23.7 | Rv2121c |
| ML1322 | *prcB* | Proteassome | 7 | Memb. | 17.2 | Rv2110c |
| ML1363 | *pyrG* | CTP synthase | 7 | N.d. | 8.5 | Rv1699 |
| ML1479c | *clpP2* | Putative protease | 7 | Cw | 18.7 | Rv2460c |
| ML1532 | *ald* | L-alanine dehydrogenase | 7 | N.d. | 10 | Rv2780 |
| ML1651 | *aceE* | pyruvate dehydrogenase | 7 | N.d. | 4.2 | Rv2241 |
| ML1701c | *pfkA* | phosphofructokinase | 7 | N.d. | 29.2 | Rv3010c |
| ML1832c | *kad* | Possible adenylate synthase | 7 | Cyt. | 18.8 | Rv0733 |
| ML2038c | *bfrA* | Bacterioferritin | 7 | Cyt./Memb. | 28.9 | Rv1876 |
| ML2053c | *adhA* | Probable alcohol dehydrogenase | 7 | N.d. | 19.6 | Rv1862 |
| ML2059 | *ml2059* | Possible oxodoreductase | 7 | Cw | 30.4 | Rv1856c |
| ML2065 | *gnd1* | Probable 6-phosphogluconate dehydrogenase | 7 | N.d. | 9.7 | Rv1844c |
| ML2136 | *serC* | Phosphoserine aminotransferase | 7 | N.d. | 9.0 | Rv0884c |
| ML2167 | *pdc* | Indole-3-pyruvate decarboxylase | 7 | Cyt. | 23.4 | Rv0853c |
| ML2226c | *ptrB* | Probable protease | 7 | Cw | 11.5 | Rv0781/Rv0782 |
| ML2387 | *lpd* | Dihydrolipoamide dehydrogenase | 7 | Memb. | 27.8 | Rv0462 |
| ML2394c | *metB* | Methionine biosynthesis | 7 | Memb. | 18.3 | Rv1079 |

**TABLE S2: (continued)**

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML2396c | *cbs* | Probable cystathionine beta-synthase | 7 | Cyt. | 9.5 | Rv1077 |
| ML2430c | *proC* | Pyrroline-5-carboxylate reductase | 7 | Memb./Cw | 20.1 | Rv0500 |
| ML2441c | *gpm1* | Phosphoglycerate mutase 1 | 7 | Cyt. | 26.7 | Rv0489 |
| ML2573 | *gabD* | Probable succinate-semialdehyde dehydrogenase | 7 | Cyt. | 21.7 | Rv0234c |
| ML2613c | *ml2613* | Zinc metalloprotease | 7 | N.d. | 8.3 | Rv0198c |
| ML2624 | *pckA* | Iron regulated phosphoenolpyruvate carboxykinase | 7 | N.d. | 9.4 | Rv0211 |
| ML2703 | *trxC* | Thioredoxin | 7 | Cyt. | 41.3 | Rv3914 |
| ML2123 | *prrA* | Transcriptional regulatory protein | 9 | Nd | 17.2 | Rv0903c |
| ML0564 | *ml0564* | Conserved hypothetical protein | 10 | Nd | 9.7 | Rv1422 |
| ML0593 | *ml0593* | Conserved hypothetical protein | 10 | Memb. | 4.9 | Rv1461 |
| ML0594 | *ml0594* | Conserved hypothetical protein | 10 | Nd | 15.1 | Rv1462 |
| ML0703c | *ml0703* | Conserved hypothetical protein | 10 | Memb. | 18.7 | Rv3311 |
| ML0901 | *ml0901* | Conserved hypothetical protein | 10 | Cw | 14.5 | Rv2172c |
| ML1041c | *ml1041c* | Conserved hypothetical protein | 10 | Cw | 15.8 | Rv2680 |
| ML1045 | *ml1045* | Conserved hypothetical protein | 10 | N.d. | 10.8 | Rv2676c |
| ML1052c | *Ml1052c* | Conserved hypothetical protein | 10 | N.d. | 18.8 | Rv1194c |
| ML1149c | *ml1149c* | Conserved hypothetical protein | 10 | N.d. | 18.8 | Rv1314c |
| ML1391c | *ml1391* | Conserved hypothetical protein | 10 | N.d. | 14.7 | Rv1637c |
| ML1423c | *ml1423* | Conserved hypothetical protein | 10 | Memb. | 15.8 | Rv2037c |
| ML1540c | *ml1540* | Conserved hypothetical protein | 10 | N.d. | 18.3 | Rv1794 |
| ML1661c | *ml1661* | Conserved hypothetical protein | 10 | Cw | 22.4 | Rv2927c |
| ML2020 | *ml2020* | Conserved hypothetical protein | 10 | Cyt. | 20.1 | Rv1896c |
| ML2203 | *ml2203* | Conserved hypothetical protein | 10 | N.d. | 13.7 | Rv0811c |
| ML2336c | *ml2336* | Conserved hypothetical protein | 10 | Cw | 7.3 | Rv3722c |
| ML2627 | *ml2627* | Conserved hypothetical protein | 10 | Cw | 7.0 | Rv0216 |

N.d- Not determined
The confidence interval was of 100% to all identified proteins.
*The leproma identification (ID) and the functional category (FC) were obtained from Leproma ( http://genolist.pasteur.fr/Leproma/).
**The subcellular localization was obtained from data previously described in the literature (1;4 and 5). The abbreviations Cyt, Cw and Memb mean, respectively, cytosolic, cell wall and membrane fractions.

**TABLE S3: Cell surface-exposed proteins identified only in NaOH-treated *M. leprae***

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML2589 | *mce1A* | MCE family protein | 0 | N.d. | 8.4 | Rv0169 |
| ML2591 | *mce1C* | MCE family protein | 0 | N.d. | 5.2 | Rv0171 |
| ML0100 | *fadD32* | Probable fatty-acid-CoA synthetase | 1 | N.d. | 4.9 | Rv3801c |
| ML0120c | *echA1* | Possible enoyl-CoA hydratase | 1 | N.d. | 13.7 | Rv3774 |
| ML0135 | *pks1* | Probable polyketide synthase | 1 | Cw | 5.3 | Rv2946c/Rv2947c |
| ML1191 | *fas* | Probable fatty acid synthase | 1 | Memb./Cw | 4.9 | Rv2524c |
| ML1346 | *ml1346* | Possible long-chain acyl-CoA synthase | 1 | N.d. | 2.8 | Rv1683 |
| ML1807c | *fabG1* | Mycolic acid biosynthesis | 1 | N.d. | 9.5 | Rv1483 |
| ML2355c | *ppsC* | Involved in phenolpthiocerol and phthiocerol Dimycocerosate (DIM) biosynthesis | 1 | Memb./Cw | 2.2 | Rv2933 |
| ML2357c | *ppsA* | Phenolpthiocerol synthesis type-i polyketide synthase | 1 | N.d. | 2.5 | Rv2931 |
| ML2564c | *fadA2* | Probable acetyl-coA acyltransferase | 1 | N.d. | 2.2 | Rv0243 |
| ML0006 | *gyrA* | Probable DNA gyrase | 2 | N.d. | 2.2 | Rv0006 |
| ML0032 | *leuS* | Probable leucyl-tRNA synthetase LeuS | 2 | N.d. | 2.5 | Rv0041 |
| ML0245c | *rplY* | Probable 50S ribosomal protein L25 | 2 | N.d. | 5.6 | Rv1015c |
| ML0364 | *rplM* | Probable 50S ribosomal protein L13 | 2 | N.d. | 20.4 | Rv3443c |
| ML1022c | *sigA* | RNA polymerase sigma factor | 2 | N.d. | 4.2 | Rv2703 |
| ML1352 | *tyrS* | Probable Tyrosyl-tRNA synthase TyrS | 2 | N.d. | 6.6 | Rv1689 |
| ML1392 | *uvrA* | Probable excinuclease abc | 2 | N.d. | 2.6 | Rv1638 |
| ML1840c | *rplO* | Probable 50s ribosomal protein l15 | 2 | N.d. | 21.2 | Rv0723 |
| ML1842c | *rpsE* | Probable 30s ribosomal protein s5 | 2 | Cw | 20.3 | Rv0721 |
| ML1845c | *rpsH* | Probable 30s ribosomal protein s8 | 2 | Memb. | 25 | Rv0718 |
| ML1847c | *rplE* | Probable 50s ribosomal protein | 2 | Memb./Cw | 38 | Rv0716 |
| ML1857c | *rpsC* | Probable 30s ribosomal protein s3 | 2 | Memb. | 21 | Rv0707 |
| ML1864c | *rpsJ* | 30s ribosomal protein s10 | 2 | N.d. | 24.8 | Rv0700 |
| ML1879c | *rpsG* | 30s ribosomal protein | 2 | N.d. | 48.1 | Rv0683 |
| ML1895c | *rplL* | Probable 50s ribosomal protein | 2 | Cyt./Memb | 16.2 | Rv0652 |
| ML0093 | *glfT* | Bifunctional UDP-galactofuranosyl transferase | 3 | Memb. | 4 | Rv3808c |
| ML0178c | *mscL* | Possible large-condutance ion mechanosensitive | 3 | N.d. | 26.6 | Rv0985c |
| ML0201c | *ml0201c* | Conserved Transmemb. protein | 3 | N.d. | 3.8 | Rv3645 |
| ML0487 | *secD* | Protein export memb. protein | 3 | N.d. | 4.7 | Rv2587c |

## TABLE S3: (continued)

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML0640c | *ml0640c* | Probable conserved ATP binding protein | 3 | N.d. | 14 | Rv3197 |
| ML0872c | *ml0872c* | Conserved memb. protein | 3 | N.d. | 11.1 | Rv2203 |
| ML0914 | *murG* | Peptidoglycan synthesis | 3 | N.d. | 10.8 | Rv2153c |
| ML1096c | *ml1096c* | Possible memb. protein | 3 | N.d. | 13.4 | Rv1249c |
| ML1244 | *ml1244* | unknown | 3 | Nd | 6.1 | Rv2484c |
| ML1248 | *ml1248* | ATP-binding protein ABC transporter | 3 | Cw | 12.9 | Rv2477c |
| ML2228 | *ml2228* | Conserved Transmemb. protein | 3 | N.d. | 13.6 | Rv0779c |
| ML2306 | *ml2306* | Probable anion transporter ATPase | 3 | N.d. | 13.9 | Rv3680 |
| ML2347 | *ml2347* | putative memb. protein | 3 | N.d. | 14 | - |
| ML2395c | *pra* | unknown | 3 | N.d. | 10.8 | Rv1078 |
| ML2400c | *ml2400c* | Conserved Transmemb. protein | 3 | N.d. | 7.3 | Rv1072 |
| ML2454c | *hbhA* | Hemaglutinin | 3 | Cyt./Memb./Cw | 14.9 | Rv0475 |
| ML2535c | *ml2535c* | Memb. protein | 3 | N.d. | 1.8 | Rv0284 |
| ML2581 | *ml2581* | Probable conserved memb. protein | 3 | N.d. | 6.5 | Rv0227c |
| ML2671 | *ctpI* | Probable cation-transporter ATPaseI | 3 | N.d. | 5.2 | Rv0107c |
| ML1365 | *ml1365* | Probable integrase/recombinase | 5 | N.d. | 7.6 | Rv1701 |
| ML0065 | *ethA* | Monooxygenase | 7 | Cw | 6.9 | Rv3854c |
| ML0125 | *ml0125* | Glycosiltransferase | 7 | N.d. | 8.9 | Rv2962c |
| ML0248c | *prsA* | Probable ribose-phosphate pyrophosphokinase | 7 | N.d. | 10.1 | Rv1017c |
| ML0275c | *metZ* | Methionine biosynthesis | 7 | N.d. | 6.1 | Rv0391 |
| ML0458c | *ml0458c* | Possible oxidoreductase | 7 | Cyt. | 19.2 | - |
| ML0666c | *fprA* | Probable NADPH | 7 | N.d. | 5.5 | Rv3106 |
| ML0696c | *sdhB* | Probable succinate dehydrogenase | 7 | N.d. | 8.3 | Rv3319 |
| ML0874c | *asnB* | Asparagine synthetase | 7 | N.d. | 6.5 | Rv2201 |
| ML1078 | *htrA* | Serine protease | 7 | N.d. | 7.9 | Rv1223 |
| ML1142 | *atpH* | ATP synthetase | 7 | Memb. | 6.3 | Rv1307 |
| ML1340c | *ribD* | Possible bifunctional enzyme riboflavin biosynthesis protein | 7 | Cyt. | 11.2 | Rv2671 |
| ML1684c | *leuD* | Leucine biosinthesis | 7 | Cw | 13.6 | Rv2987c |
| ML2061 | *ndh* | Probable nadh dehydrogenase | 7 | N.d. | 4.9 | Rv1854c |
| ML2088c | *ml2088c* | Cytochrome P450c | 7 | Cyt./Memb | 13.5 | - |

## TABLE S3: (continued)

| Leproma(ID)* | Gene | Protein Description | FC* | Subcellular fraction** | Coverage (%) | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|---|---|
| ML2198 | cysA2 | Probable thiosulfate sulfurtransferase | 7 | N.d. | 12.6 | Rv0815c |
| ML2230c | purB | Purine Biosynthesis | 7 | N.d. | 4.9 | Rv0777 |
| **ML2276c** | ml2276c | Oxidoreductase | 7 | N.d. | 12.7 | Rv0561c |
| ML2322c | asd | Aspartate-semialdehyde dehydrogenase | 7 | Memb. | 7.7 | Rv3708c |
| ML2419c | hemB | Porphyrin and heme biosynthesis | 7 | Cw | 6.7 | Rv0512 |
| ML2420c | hemD | Probable uroporphyrin-III c-methyltransferase | 7 | N.d. | 12.3 | Rv0511 |
| ML2501 | ml2501 | Iron-sulfur-binding reductase | 7 | Cw | 4.5 | Rv0338c |
| ML2659c | pepA | Serine protease | 7 | Memb. | 5 | Rv0125 |
| ML0565 | whiA | Transciptional regulatory protein | 9 | Nd 9 | 8.9 | Rv1423 |
| ML1286 | ml1286 | Two-component system | 9 | Cw | 23.4 | Rv1626 |
| ML1753c | ml1753c | Transcriptional regulatory protein | 9 | N.d. | 2.5 | Rv1358 |
| ML2124 | prrB | Two component sensor histidine kinase | 9 | N.d. | 4.3 | Rv0902c |
| ML2302 | *ml2302* | Probable transcriptional regulatory protein | 9 | Cyt./Memb./Cw | 32.6 | Rv3676 |
| ML0798c | *ml0798c* | Conserved hypothetical protein | 10 | N.d. | 9.6 | Rv2787 |
| ML1809 | *ml1809* | Conserved hypothetical protein | 10 | N.d. | 7.2 | Rv1480 |
| ML2031 | *ml2031* | Conserved hypothetical protein | 10 | Cw | 15.9 | Rv1883c |
| **ML2309** | *ml2309* | Conserved hypothetical protein | 10 | N.d. | 10.9 | Rv3683 |
| ML2333 | *ml2333* | Conserved hypothetical protein | 10 | N.d. | 5.2 | Rv3719 |
| ML2427c | ml2427 | Conserved hypothetical protein | 10 | N.d. | 7.4 | Rv0502 |

N.d- Not determined
The confidence interval was of 100% to all identified proteins.
The bold proteins (ML2276c and Ml2309) were identified for the first in this work.
*The leproma identification (ID) and the functional category (FC) were obtained from Leproma ( http://genolist.pasteur.fr/Leproma/).
**The subcellular localization was obtained from data previously described in the literature (1; 4 and 5 ). The abbreviations Cyt, Cw and Memb mean, respectively, cytosolic, cell wall and membrane fractions.

## TABLE S4: False positive proteins identified in *M. leprae* cell surface

| Leproma(ID)* | Gene | Protein Description | FC* | *M.tb.* H37Rv (ortholog) |
|---|---|---|---|---|
| ML0726c | *accA3* | Probable bifunctional protein acetyl-/propionyl-coenzyme A carboxylase | 1 | Rv3285 |
| ML0731c | *accD5* | Probable propionyl-CoA carboxylase | 1 | Rv3280 |
| ML0540 | *mihF* | Putative integration host factor | 2 | Rv1388 |
| ML0853 | *rpsO* | 30S ribosomal protein | 2 | Rv2785c |
| ML0987 | *recA* | Recombinase protein | 2 | Rv2737c |
| ML1133 | *rpmE* | Probable 50s ribosomal protein | 2 | Rv1298 |
| ML1854c | rpsQ | Probable 30s ribosomal protein | 2 | Rv0710 |
| ML1863c | rplC | Probable 50s ribosomal protein | 2 | Rv0701 |
| ML1960c | *rpsM* | Probable 30s ribosomal protein | 2 | Rv3460c |
| ML0234 | *lsr2* | 15 kDa antigen | 3 | Rv3597c |
| ML0150c | *pgi* | Phosphoglucose isomerase | 7 | Rv0946c |
| ML0450c | *snzP* | Possible pyridoxine biosynthesis | 7 | Rv2606c |
| ML1712c | *fixA* | Probable electron transfer flavoprotein | 7 | Rv3029c |
| ML2440c | *senX3* | Putative two component sensor histidine kinase | 9 | Rv0490 |

The confidence interval was of 100% to all identified proteins.
*The leproma identification (ID) and the functional category (FC) were obtained from Leproma ( http://genolist.pasteur.fr/Leproma/).

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