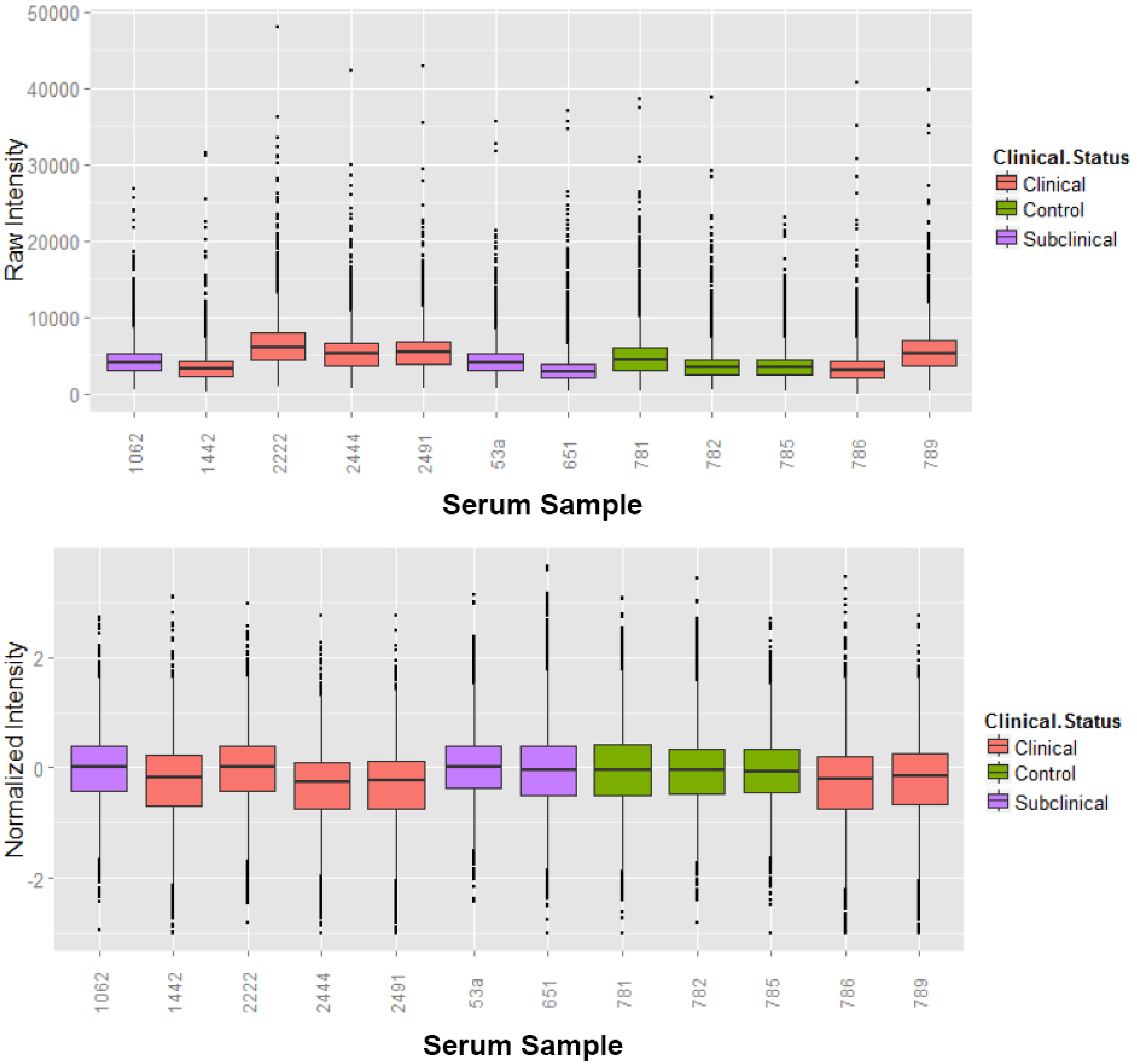

**Figure S1.** Box plots showing the overall distribution of antibody responses to Mtb proteins. Raw (A) and normalized (B) signal intensities for each health status are shown in box plots for all arrayed Mtb proteins. The black horizontal bar, box, whiskers, and dots indicate the median, range, 1.5 times the interquartile range, and outliers, respectively. Boxes are colored based on health status of the animal (Clinical – red; Subclinical – purple; Control – green).

# Table S1

Table S1. Percent identity of CDS for sequenced mycobacterial genomes using strain MAP4 as the reference.

| Mycobacterium avium subsp. paratuberculosis MAP4 | | | Mycobacterium tuberculosis H37Rv | | | | Mycobacterium bovis AF2122/97 | | | | Mycobacterium avium 104 | | | | Mycobacterium bovis BCG str. Pasteur 1173P2 | | | | Mycobacteriaum avium subsp. paratuberculosis K-10 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Locus Tag** | **Product** | **CDS length** | **Locus Tag** | **Product** | **% ID to MAP4** | **CDS Length** | **Locus Tag** | **Product** | **% ID to MAP4** | **CDS Length** | **Locus Tag** | **Product** | **% ID to MAP4** | **CDS Length** | **Locus Tag** | **Product** | **% ID to MAP4** | **CDS Length** | **Locus Tag** | **Product** | **CDS Length** | **% ID to MAP4** |
| MAP4_0001 | chromosomal replication initiator protein DnaA | 509 | Rv0001 | Chromosomal replication initiator pr | 88.06 | 507 | Mb0001 | chromosome replication initia | 87.67 | 507 | MAV_0001 | chromosomal replication initiation | 99.6 | 498 | BCG_0001 | chromosomal replication initia | 87.87 | 507 | MAP0001 | chromosomal replication initiation prot | 509 | 100 |
| MAP4_0002 | DNA polymerase III beta subunit | 399 | Rv0002 | DNA polymerase III (beta chain) Dna | 85.82 | 402 | Mb0002 | DNA polymerase III subunit b | 85.57 | 402 | MAV_0002 | DNA polymerase III subunit beta | 99.48 | 382 | BCG_0002 | DNA polymerase III subunit bet | 85.57 | 402 | MAP0002 | DNA polymerase III subunit beta | 399 | 99.75 |
| MAP4_0003 | DNA replication and repair protein RecF | 385 | Rv0003 | DNA replication and repair protein R | 76.62 | 385 | Mb0003 | recombination protein F | 76.36 | 385 | MAV_0003 | recombination protein F | 98.18 | 385 | BCG_0003 | recombination protein F | 76.36 | 385 | MAP0003 | recombination protein F | 385 | 100 |
| MAP4_0004 | hypothetical protein | 181 | Rv0004 | hypothetical protein | 81.93 | 187 | Mb0004 | hypothetical protein | 81.93 | 187 | MAV_0004 | hypothetical protein | 99.45 | 181 | BCG_0004 | hypothetical protein | 81.93 | 187 | MAP0004 | hypothetical protein | 166 | 99.4 |
| MAP4_0005 | DNA gyrase subunit B | 677 | Rv0005 | DNA gyrase (subunit B) GyrB (DNA t | 90.99 | 675 | Mb0005 | DNA gyrase subunit B | 90.69 | 714 | MAV_0005 | DNA gyrase subunit B | 100 | 677 | BCG_0005 | DNA gyrase subunit B | 90.69 | 714 | MAP0005 | DNA gyrase subunit B | 677 | 100 |
| MAP4_0006 | DNA gyrase subunit A | 839 | Rv0006 | DNA gyrase (subunit A) GyrA (DNA t | 94.12 | 838 | Mb0006 | DNA gyrase subunit A | 94.24 | 838 | MAV_0006 | DNA gyrase subunit A | 99.76 | 839 | BCG_0006 | DNA gyrase subunit A | 94.36 | 838 | MAP0006 | DNA gyrase subunit A | 839 | 100 |
| MAP4_0007 | putative conserved membrane protein | 283 | Rv0007 | Possible conserved membrane prote | 63.69 | 304 | Mb0007 | hypothetical protein | 63.38 | 304 | MAV_0007 | hypothetical protein | 97.57 | 287 | BCG_0007 | hypothetical protein | 63.69 | 304 | MAP0007 | hypothetical protein | 283 | 100 |
| MAP4_0008 | Transposase | 395 | Rv0755A | Putative transposase (fragment) | 90.57 | 61 | Mb0778c | transposase | 90.57 | 61 | MAV_0752 | transposase | 28.75 | 345 | BCG_0807c | transposase | 90.57 | 61 | MAP0428 | hypothetical protein | 395 | 100 |
| MAP4_0009 | Transposase | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 100 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0104 | hypothetical protein | 411 | 100 |
| MAP4_0010 | Transcriptional regulator, AraC family | 252 | Rv1317c | Probable bifunctional regulatory pro | 37.1 | 496 | Mb1350c | methylated-DNA--protein-cys | 37.1 | 416 | MAV_0221 | AraC family transcriptional regulato | 32.76 | 268 | BCG_1378c | ada regulatory protein alkA | 37.1 | 496 | MAP3758c | hypothetical protein | 252 | 100 |
| MAP4_0011 | hypothetical protein | 368 | Rv2307c | hypothetical protein | 40 | 281 | Mb2330c | hypothetical protein | 40 | 281 | MAV_2243 | alpha/beta hydrolase | 30.93 | 519 | BCG_2324c | hypothetical protein | 40 | 281 | MAP3757c | hypothetical protein | 368 | 100 |
| MAP4_0012 | putative oxidoreductase | 286 | Rv0044c | Possible oxidoreductase | 43.51 | 264 | Mb0045c | oxidoreductase | 43.51 | 264 | MAV_0061 | MmcI protein | 44.27 | 259 | BCG_0075c | oxidoreductase | 43.51 | 264 | MAP3756c | hypothetical protein | 286 | 100 |
| MAP4_0015 | Transposase | 74 | Rv1937 | Possible oxygenase | 55 | 839 | Mb1972 | oxygenase | 55 | 839 | MAV_3829 | thiamine monophosphate kinase | 47.83 | 315 | BCG_1976 | oxygenase | 55 | 839 | MAP3754 | hypothetical protein | 74 | 100 |
| MAP4_0016 | hypothetical protein | 450 | Rv2314c | hypothetical protein | 38.89 | 457 | Mb2341c | hypothetical protein | 38.89 | 457 | MAV_4881 | hypothetical protein | 45.68 | 450 | BCG_2335c | hypothetical protein | 38.89 | 457 | MAP3753 | hypothetical protein | 450 | 100 |
| MAP4_0017 | fatty-acid-CoA ligase FdD28 | 578 | Rv2941 | Fatty-acid-AMP ligase FadD28 (fatty- | 64.87 | 580 | Mb2966 | acyl-CoA synthetase | 64.59 | 580 | MAV_1328 | acyl-CoA synthetase | 61.25 | 579 | BCG_2963 | acyl-CoA synthetase | 64.87 | 580 | MAP3752 | acyl-CoA synthetase | 578 | 100 |
| MAP4_0018 | transmembrane transport protein, MmpL4_5 | 979 | Rv0450c | Probable conserved transmembrane | 65.69 | 967 | Mb0458c | transmembrane transport pro | 65.58 | 967 | MAV_3863 | MmpL4 protein | 65.4 | 972 | BCG_0489c | transmembrane transport prot | 65.69 | 967 | MAP3751 | hypothetical protein | 979 | 100 |
| MAP4_0019 | membrane protein, MmpS family | 154 | Rv0403c | Probable conserved membrane prot | 50.72 | 142 | Mb1582 | hypothetical protein | 55.17 | 148 | MAV_3864 | MmpS4 protein | 48.97 | 148 | BCG_1608 | membrane protein mmpS6 | 55.17 | 148 | MAP3750 | hypothetical protein | 154 | 100 |
| MAP4_0020 | dehydrogenase | 286 | Rv2750 | Probable dehydrogenase | 42.7 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 42.7 | 272 | MAV_1881 | carveol dehydrogenase | 60.35 | 285 | BCG_2766 | 3-ketoacyl-ACP reductase | 42.7 | 272 | MAP3749 | hypothetical protein | 286 | 100 |
| MAP4_0021 | transposase, IS1110 | 402 | Rv0797 | Putative transposase for insertion se | 29.53 | 364 | Mb0820 | IS1547 transposase | 29.25 | 364 | MAV_0496 | transposase IS116/IS110/IS902 | 31.65 | 404 | BCG_0849 | transposase for insertion seque | 29.25 | 364 | MAP3748c | IS1110 transposase | 402 | 100 |
| MAP4_0022 | putative cobalamin synthesis protein | 406 | Rv0106 | hypothetical protein | 52.32 | 398 | Mb0109 | hypothetical protein | 52.32 | 398 | MAV_4874 | CobW/P47K domain-containing pro | 53.99 | 381 | BCG_0139 | hypothetical protein | 52.32 | 398 | MAP3747c | hypothetical protein | 406 | 100 |
| MAP4_0023 | hypothetical protein | 104 | Rv0190 | hypothetical protein | 79.35 | 96 | Mb0196 | hypothetical protein | 79.35 | 96 | MAV_4988 | hypothetical protein | 77.66 | 96 | BCG_0227 | hypothetical protein | 79.35 | 96 | MAP3746 | hypothetical protein | 104 | 100 |
| MAP4_0024 | hypothetical protein | 250 | Rv2928 | Probable thioesterase TesA | 28.83 | 261 | Mb2953 | thioesterase | 28.83 | 261 | MAV_2010 | phenyloxazoline synthase mbtb | 30.7 | 220 | BCG_2950 | thioesterase tesA | 28.83 | 261 | MAP3745 | hypothetical protein | 250 | 100 |
| MAP4_0025 | hypothetical protein | 344 | Rv0617 | Possible toxin VapC29 Contains PIN | 45.83 | 133 | Mb0634 | hypothetical protein | 45.83 | 133 | MAV_1787 | sulfite reductase [ferredoxin] 2 | 24.32 | 569 | BCG_0664 | hypothetical protein | 45.83 | 133 | MAP3744 | hypothetical protein | 344 | 100 |
| MAP4_0026 | hypothetical protein | 348 | Rv2449c | hypothetical protein | 30.28 | 419 | Mb2476c | hypothetical protein | 30.28 | 419 | MAV_1153 | retinol dehydrogenase | 31.25 | 289 | BCG_2469c | hypothetical protein | 30.28 | 419 | MAP3743 | hypothetical protein | 348 | 100 |
| MAP4_0029 | putative non-ribosomal peptide synthase | 3068 | Rv2383c | Phenyloxazoline synthase MbtB (phe | 37.53 | 1414 | Mb2404c | phenyloxazoline synthase | 37.53 | 1414 | MAV_2009 | MbtB protein | 36.6 | 1164 | BCG_2397c | phenyloxazoline synthase mbt | 37.53 | 1414 | MAP3740 | hypothetical protein | 3068 | 100 |
| MAP4_0030 | putative transporter, major facilitator superfamily prot | 516 | Rv3728 | Probable conserved two-domain me | 36.67 | 1065 | Mb3755 | hypothetical protein | 36.67 | 1065 | MAV_1387 | drug transporter | 28.42 | 626 | BCG_3788 | hypothetical protein | 36.67 | 1065 | MAP3739c | hypothetical protein | 516 | 100 |
| MAP4_0031 | hypothetical protein | 244 | Rv3919c | Probable glucose-inhibited division | 34.62 | 224 | Mb3950c | 16S rRNA methyltransferase | 34.62 | 224 | MAV_2728 | hypothetical protein | 39.02 | 255 | BCG_0025c | 16S rRNA methyltransferase Gi | 34.62 | 224 | MAP3738c | hypothetical protein | 244 | 100 |
| MAP4_0032 | PPE family protein | 504 | Rv0453 | PPE family protein PPE11 | 43.16 | 518 | Mb0461 | PPE family protein | 43.16 | 518 | MAV_4867 | PPE family protein | 49.01 | 493 | BCG_0492 | PPE family protein | 43.16 | 518 | MAP3737 | hypothetical protein | 504 | 100 |
| MAP4_0033 | hypothetical protein | 319 | Rv1348 | Iron-regulated transporter IrtA | 40 | 859 | Mb1383 | drugs-transport transmembra | 40 | 859 | MAV_1566 | ABC transporter ATP-binding prote | 38.89 | 862 | BCG_1410 | drugs-transport transmembran | 40 | 859 | MAP3736c | hypothetical protein | 319 | 100 |
| MAP4_0034 | ABC transporter ATP-binding protein | 429 | Rv1348 | Iron-regulated transporter IrtA | 41.59 | 859 | Mb1383 | drugs-transport transmembra | 41.59 | 859 | MAV_1566 | ABC transporter ATP-binding prote | 40.51 | 862 | BCG_1410 | drugs-transport transmembran | 41.59 | 859 | MAP3735c | hypothetical protein | 429 | 100 |
| MAP4_0035 | putative ABC transporter ATPase and permease compo | 593 | Rv1349 | Iron-regulated transporter IrtB | 33.96 | 579 | Mb1384 | drugs-transport transmembra | 33.96 | 579 | MAV_1567 | ABC transporter ATP-binding prote | 33.73 | 578 | BCG_1411 | drugs-transport transmembran | 33.96 | 579 | MAP3734c | hypothetical protein | 593 | 100 |
| MAP4_0036 | hypothetical protein | 208 | Rv3031 | hypothetical protein | 42.86 | 526 | Mb3057 | hypothetical protein | 42.86 | 526 | | | | | BCG_3054 | hypothetical protein | 42.86 | 526 | MAP3733c | hypothetical protein | 208 | 100 |
| MAP4_0037 | ABC-type cobalt transport system, permease compone | 237 | Rv3305c | Possible N-acyl-L-amino acid amidoh | 34.29 | 389 | Mb3333c | N-acyl-L-amino acid amidohy | 34.29 | 389 | MAV_4091 | transferase | 40.91 | 321 | BCG_3370c | N-acyl-L-amino acid amidohydr | 34.29 | 389 | MAP3732c | hypothetical protein | 237 | 100 |
| MAP4_0038 | putative ABC transporter, ATP-binding protein | 500 | Rv3102c | Putative cell division ATP-binding pr | 33.33 | 229 | Mb3129c | cell division ATP-binding prot | 33.33 | 229 | MAV_4003 | cell division ATP-binding protein Ft | 32.89 | 230 | BCG_3127c | cell division ATP-binding protei | 33.33 | 229 | MAP3731c | hypothetical protein | 500 | 100 |
| MAP4_0039 | methyltransferase | 210 | Rv1377c | Putative transferase | 36.63 | 212 | Mb1412c | transferase | 36.63 | 212 | MAV_2216 | CheR methyltransferase SAM bindi | 35.97 | 216 | BCG_1438c | transferase | 36.63 | 212 | MAP3730 | hypothetical protein | 210 | 100 |
| MAP4_0040 | putative taurine dioxygenase | 258 | Rv3406 | Probable dioxygenase | 33.33 | 295 | Mb3440 | dioxygenase | 33.33 | 295 | MAV_4353 | alpha-ketoglutarate-dependent tau | 32.58 | 297 | BCG_3476 | dioxygenase | 33.33 | 295 | MAP3729 | hypothetical protein | 258 | 100 |
| MAP4_0041 | putative periplasmic binding protein | 345 | Rv0676c | Probable conserved transmembrane | 30 | 964 | Mb0695c | transmembrane transport pro | 30 | 964 | MAV_0022 | protein phosphatase 2C | 28.57 | 499 | BCG_0725c | transmembrane transport prot | 30 | 964 | MAP3728 | hypothetical protein | 345 | 100 |
| MAP4_0042 | putative ABC transporter, ATP-binding protein | 271 | Rv0933 | Phosphate-transport ATP-binding pr | 34.02 | 276 | Mb3067c | ABC transporter ATP-binding | 31.47 | 287 | MAV_3906 | molybdenum ABC transporter ATPa | 33.18 | 280 | BCG_3065c | ABC transporter ATP-binding p | 31.47 | 287 | MAP3727 | hypothetical protein | 271 | 100 |
| MAP4_0043 | putative transporter, FecCD transport family protein | 342 | Rv0565c | Probable monooxygenase | 41.86 | 486 | Mb0580c | monooxygenase | 41.86 | 486 | MAV_3243 | linear gramicidin synthetase subun | 28 | 2552 | BCG_0610c | monooxygenase | 41.86 | 486 | MAP3726 | hypothetical protein | 342 | 100 |
| MAP4_0044 | PPE family protein | 518 | Rv0256c | PPE family protein PPE2 | 60.67 | 556 | Mb0262c | PPE family protein | 60.67 | 556 | MAV_4349 | PPE family protein | 46.99 | 529 | BCG_0294c | PPE family protein | 60.67 | 556 | MAP3725 | hypothetical protein | 518 | 100 |
| MAP4_0045 | hypothetical protein | 302 | Rv0276 | hypothetical protein | 74.18 | 306 | Mb0282 | hypothetical protein | 74.18 | 306 | MAV_4880 | hypothetical protein | 84.71 | 314 | BCG_0314 | hypothetical protein | 74.18 | 306 | MAP3724 | hypothetical protein | 302 | 100 |
| MAP4_0046 | Transcriptional regulator, TetR family | 220 | Rv0275c | Possible transcriptional regulatory p | 77.67 | 241 | Mb0281c | TetR family transcriptional re | 78.16 | 241 | MAV_4882 | FadD27 protein | 86.82 | 220 | BCG_0313c | TetR family transcriptional regu | 78.16 | 241 | MAP3723c | FadD27 | 217 | 100 |
| MAP4_0047 | hypothetical protein | 451 | Rv2484c | Possible triacylglycerol synthase (dia | 25.8 | 491 | Mb2509c | hypothetical protein | 25.8 | 491 | MAV_4881 | hypothetical protein | 77.46 | 450 | BCG_2502c | hypothetical protein | 25.8 | 491 | MAP3753 | hypothetical protein | 450 | 43.79 |
| MAP4_0048 | polyketide synthase associated protein | 491 | Rv1182 | Probable conserved polyketide synt | 45.79 | 472 | Mb1214 | polyketide synthase | 45.79 | 472 | MAV_4883 | condensation domain-containing p | 84.93 | 491 | BCG_1244 | polyketide synthase associated | 45.79 | 472 | MAP3721 | hypothetical protein | 491 | 100 |
| MAP4_0049 | hypothetical protein | 182 | Rv1822 | Probable CDP-diacylglycerol--glycero | 26.5 | 209 | Mb1853 | CDP-diacylglycerol--glycerol-3 | 26.5 | 209 | MAV_4884 | hypothetical protein | 86.81 | 182 | BCG_1857 | CDP-diacylglycerol--glycerol-3- | 26.5 | 209 | MAP3720 | hypothetical protein | 182 | 100 |
| MAP4_0050 | putative glyoxalasebleomycin resistance protein/dioxy | 207 | Rv0274 | hypothetical protein | 90.16 | 193 | Mb0280 | hypothetical protein | 90.16 | 193 | MAV_4885 | glyoxalase/bleomycin resistance pr | 96.37 | 193 | BCG_0312 | hypothetical protein | 90.16 | 193 | MAP3719 | hypothetical protein | 207 | 100 |
| MAP4_0051 | Transcriptional regulator, TetR family | 216 | Rv0273c | Possible transcriptional regulatory p | 78.5 | 206 | Mb0279c | transcriptional regulator | 78.5 | 206 | MAV_4886 | TetR family transcriptional regulato | 88.26 | 218 | BCG_0311c | transcriptional regulatory prot | 78.5 | 206 | MAP3718c | hypothetical protein | 223 | 99.54 |
| MAP4_0052 | hypothetical protein | 376 | Rv0272c | hypothetical protein | 86.72 | 377 | Mb0278c | hypothetical protein | 86.45 | 377 | MAV_4023 | hypothetical protein | 38.75 | 391 | BCG_0310c | hypothetical protein | 86.72 | 377 | MAP3717c | hypothetical protein | 376 | 100 |
| MAP4_0053 | acyl-CoA dehydrogenase, short-chain specific | 733 | Rv0271c | Probable acyl-CoA dehydrogenase F | 84.26 | 731 | Mb0277c | acyl-CoA dehydrogenase | 84.26 | 731 | MAV_4888 | acyl-CoA dehydrogenase | 94.48 | 598 | BCG_0309c | acyl-CoA dehydrogenase fadE6 | 84.26 | 731 | MAP3716c | FadE6 | 733 | 100 |
| MAP4_0054 | hypothetical protein | 121 | Rv1536 | Isoleucyl-tRNA synthetase IleS | 42.86 | 1041 | Mb1563 | isoleucyl-tRNA synthetase | 42.86 | 1041 | MAV_1064 | hypothetical protein | 30.19 | 316 | BCG_1588 | isoleucyl-tRNA synthetase | 42.86 | 1041 | MAP0887c | hypothetical protein | 307 | 30.19 |
| MAP4_0055 | fatty-acid-CoA ligase FadD2 | 561 | Rv0270 | Probable fatty-acid-CoA ligase FadD | 84.29 | 560 | Mb0276 | acyl-CoA synthetase | 84.29 | 560 | MAV_4891 | acyl-CoA synthetase | 99.29 | 561 | BCG_0308 | acyl-CoA synthetase | 84.11 | 560 | MAP3714 | acyl-CoA synthetase | 561 | 100 |
| MAP4_0056 | hypothetical protein | 426 | Rv0269c | hypothetical protein | 78.5 | 397 | Mb0275c | hypothetical protein | 78.5 | 397 | MAV_4893 | hypothetical protein | 98.59 | 426 | BCG_0307c | hypothetical protein | 78.5 | 397 | MAP3713c | hypothetical protein | 426 | 100 |
| MAP4_0057 | membrane nitrite extrusion protein | 463 | Rv0267 | Probable integral membrane nitrite | 83.37 | 463 | Mb0273 | integral membrane nitrite ext | 83.37 | 463 | MAV_4892 | nitrite transporter | 99.78 | 463 | BCG_0305 | integral membrane nitrite extr | 83.37 | 463 | MAP3712 | NarU | 463 | 100 |
| MAP4_0058 | Transcriptional regulator, TetR family | 200 | Rv0691c | Probable transcriptional regulatory | 25.4 | 198 | Mb0710c | transcriptional regulator | 25.4 | 198 | MAV_4894 | TetR family transcriptional regulato | 100 | 194 | BCG_0740c | transcriptional regulatory prot | 25.4 | 198 | MAP3711c | hypothetical protein | 200 | 100 |
| MAP4_0059 | periplasmic iron-transport lipoprotein | 335 | Rv0265c | Probable periplasmic iron-transport | 74.33 | 330 | Mb0271c | periplasmic IRON-transport li | 74.33 | 330 | MAV_4895 | periplasmic binding protein | 99.68 | 317 | BCG_0303c | periplasmic iron-transport lipo | 74.03 | 330 | MAP3710c | hypothetical protein | 335 | 100 |
| MAP4_0060 | putative allophanate hydrolase 2 subunit 1 | 224 | Rv0264c | hypothetical protein | 68.12 | 210 | Mb0270c | hypothetical protein | 68.12 | 210 | MAV_4896 | allophanate hydrolase subunit 1 | 99.1 | 222 | BCG_0302c | hypothetical protein | 68.12 | 210 | MAP3709c | hypothetical protein | 224 | 100 |
| MAP4_0061 | putative allophanate hydrolase 2 subunit 2 | 303 | Rv0263c | hypothetical protein | 83 | 300 | Mb0269c | hypothetical protein | 83 | 300 | MAV_4897 | hypothetical protein | 100 | 303 | BCG_0301c | hypothetical protein | 83 | 300 | MAP3708c | hypothetical protein | 303 | 100 |
| MAP4_0063 | membrane nitrite extrusion protein NarK3 | 463 | Rv0261c | Probable integral membrane nitrite | 63.42 | 469 | Mb0267c | integral membrane nitrite ext | 63.42 | 469 | MAV_4899 | transporter, major facilitator family | 99.35 | 463 | BCG_0299c | integral membrane nitrite extr | 63.42 | 469 | MAP3707c | NarK3_2 | 463 | 99.78 |
| MAP4_0064 | transcriptional regulator | 387 | Rv0260c | Possible transcriptional regulatory p | 78.46 | 381 | Mb0266c | bifunctional uroporphyrinoge | 78.46 | 381 | MAV_4900 | bifunctional uroporphyrinogen-III s | 99.74 | 387 | BCG_0298c | bifunctional uroporphyrinogen | 78.46 | 381 | MAP3706c | bifunctional uroporphyrinogen-III synth | 383 | 99.74 |
| MAP4_0065 | hypothetical protein | 257 | Rv0259c | hypothetical protein | 68.12 | 247 | Mb0265c | hypothetical protein | 68.56 | 247 | MAV_4901 | sirohydrochlorin cobaltochelatase, | 99.61 | 257 | BCG_0297c | hypothetical protein | 68.56 | 247 | MAP3705c | hypothetical protein | 257 | 100 |
| MAP4_0066 | hypothetical protein | 150 | Rv0258c | hypothetical protein | 84 | 151 | Mb0264c | hypothetical protein | 84 | 151 | MAV_4902 | hypothetical protein | 98.53 | 136 | BCG_0296c | hypothetical protein | 84 | 151 | MAP3704c | hypothetical protein | 150 | 100 |
| MAP4_0067 | nitrite reductase small subunit NirD | 99 | Rv0253 | Probable nitrite reductase [NAD(P)H | 75.9 | 118 | Mb0259 | nitrite reductase [NAD(P)H] s | 75.9 | 118 | MAV_4903 | nitrite reductase [NAD(P)H], small s | 97.78 | 122 | BCG_0291 | nitrite reductase [NAD(P)H] sm | 75.9 | 118 | MAP3703 | NirD | 99 | 100 |
| MAP4_0068 | nitrite reductase large subunit NirB | 855 | Rv0252 | Probable nitrite reductase [NAD(P)H | 88.17 | 853 | Mb0258 | nitrite reductase [NAD(P)H] la | 88.17 | 853 | MAV_4904 | nitrite reductase [NAD(P)H], large s | 99.76 | 833 | BCG_0290 | nitrite reductase NAD(P)H] larg | 88.17 | 853 | MAP3702 | hypothetical protein | 855 | 99.88 |
| MAP4_0069 | heat shock protein hsp | 146 | Rv0251c | Heat shock protein Hsp (heat-stress- | 71.07 | 159 | Mb0257c | heat shock protein hsp (heat- | 71.07 | 159 | MAV_4906 | Hsp20/alpha crystallin family prote | 100 | 146 | BCG_0289c | heat shock protein hsp | 71.07 | 159 | MAP3701c | Hsp | 146 | 100 |
| MAP4_0070 | hypothetical protein | 104 | Rv0250c | hypothetical protein | 77.17 | 97 | Mb0256c | hypothetical protein | 77.17 | 97 | MAV_4907 | hypothetical protein | 100 | 104 | BCG_0288c | hypothetical protein | 77.17 | 97 | MAP3700c | hypothetical protein | 104 | 100 |
| MAP4_0071 | succinate dehydrogenase membrane anchor subunit | 275 | Rv0249c | Probable succinate dehydrogenase [ | 70.5 | 273 | Mb0255c | succinate dehydrogenase | 70.5 | 273 | MAV_4908 | integral membrane protein | 99.64 | 275 | BCG_0287c | succinate dehydrogenase mem | 70.5 | 273 | MAP3699c | hypothetical protein | 275 | 100 |
| MAP4_0072 | succinate dehydrogenase iron-sulfur subunit | 647 | Rv0248c | Probable succinate dehydrogenase [ | 85.56 | 646 | Mb0254c | succinate dehydrogenase flav | 85.56 | 646 | MAV_4909 | succinate dehydrogenase flavoprot | 95.98 | 646 | BCG_0286c | succinate dehydrogenase flavo | 85.56 | 646 | MAP3698c | succinate dehydrogenase flavoprotein s | 647 | 100 |
| MAP4_0073 | succinate dehydrogenase iron-sulfur subunit | 248 | Rv0247c | Probable succinate dehydrogenase [ | 90.32 | 248 | Mb0253c | fumarate reductase iron-sulfu | 90.32 | 248 | MAV_4910 | fumarate reductase iron-sulfur sub | 97.98 | 248 | BCG_0285c | fumarate reductase iron-sulfur | 90.32 | 248 | MAP3697c | fumarate reductase iron-sulfur subunit | 248 | 100 |
| MAP4_0074 | hypothetical protein | 54 | Rv0861c | DNA helicase Ercc3 | 45.45 | 542 | Mb0884c | DNA helicase | 45.45 | 542 | MAV_4911 | hypothetical protein | 98.15 | 54 | BCG_0913c | DNA helicase | 45.45 | 542 | MAP4065 | hypothetical protein | 453 | 33.33 |
| MAP4_0075 | oxidoreductase | 162 | Rv0245 | Possible oxidoreductase | 82.61 | 162 | Mb0251 | oxidoreductase | 82.61 | 162 | MAV_4912 | NADH-FMN oxidoreductase | 99.38 | 162 | BCG_0283 | oxidoreductase | 82.61 | 162 | MAP3696 | hypothetical protein | 162 | 100 |
| MAP4_0076 | putative oxidoreductase | 345 | Rv3391 | Possible multi-functional enzyme wi | 35.29 | 650 | Mb3423 | short chain dehydrogenase | 35.29 | 650 | MAV_4913 | oxidoreductase, 2OG-Fe(II) oxygena | 97.1 | 345 | BCG_3460 | short chain dehydrogenase | 35.29 | 650 | MAP3695 | hypothetical protein | 357 | 99.71 |
| MAP4_0077 | acyl-CoA dehydrogenase | 611 | Rv0244c | Probable acyl-CoA dehydrogenase F | 90.83 | 611 | Mb0250c | acyl-CoA dehydrogenase | 90.67 | 611 | MAV_4914 | acyl-CoA dehydrogenase | 100 | 611 | BCG_0282c | acyl-CoA dehydrogenase fadE5 | 90.51 | 611 | MAP3694c | FadE5 | 611 | 100 |
| MAP4_0078 | acetyl-CoA acetyltransferase | 448 | Rv0243 | Probable acetyl-CoA acyltransferase | 88.15 | 440 | Mb0249 | acetyl-CoA acetyltransferase | 88.15 | 440 | MAV_4915 | acetyl-CoA acetyltransferase | 99.53 | 427 | BCG_0281 | acetyl-CoA acetyltransferase | 88.15 | 440 | MAP3693 | acetyl-CoA acetyltransferase | 448 | 100 |
| MAP4_0079 | 3-oxoacyl-ACP reductase | 454 | Rv0242c | Probable 3-oxoacyl-[acyl-carrier pro | 89.87 | 454 | Mb0248c | 3-ketoacyl-ACP reductase | 89.87 | 454 | MAV_4916 | 3-ketoacyl-(acyl-carrier-protein) re | 99.78 | 454 | BCG_0280c | 3-ketoacyl-ACP reductase | 89.87 | 454 | MAP3692c | 3-ketoacyl-ACP reductase | 454 | 100 |
| MAP4_0080 | hypothetical protein | 280 | Rv0241c | Probable 3-hydroxyacyl-thioester de | 84.29 | 280 | Mb0247c | hypothetical protein | 84.29 | 280 | MAV_4917 | MaoC like domain-containing prote | 99.64 | 281 | BCG_0279c | hypothetical protein | 84.29 | 280 | MAP3691c | hypothetical protein | 280 | 100 |
| MAP4_0081 | putative chloride transporter, chloride channel family p | 417 | Rv0143c | Probable conserved transmembrane | 32.17 | 492 | Mb0148c | transmembrane protein | 32.17 | 492 | MAV_4918 | chloride transporter, chloride chan | 99.28 | 417 | BCG_0179c | hypothetical protein | 32.17 | 492 | MAP3690 | hypothetical protein | 420 | 100 |
| MAP4_0082 | transcriptional regulator, tetR-family | 215 | Rv0238 | Possible transcriptional regulatory p | 83.42 | 204 | Mb0244 | TetR family transcriptional re | 83.42 | 204 | MAV_4919 | TetR family transcriptional regulato | 100 | 215 | BCG_0276 | TetR family transcriptional regu | 83.42 | 204 | MAP3689 | hypothetical protein | 215 | 100 |
| MAP4_0083 | lipoprotein LpqI | 388 | Rv0237 | Probable conserved lipoprotein LpqI | 72.97 | 388 | Mb0243 | lipoprotein LpqI | 72.7 | 388 | MAV_4920 | glycosyl hydrolase 3 | 98.45 | 388 | BCG_0275 | lipoprotein lpqI | 72.7 | 388 | MAP3688 | hypothetical protein | 388 | 100 |
| MAP4_0084 | hypothetical protein | 90 | Rv3347c | PPE family protein PPE55 | 44.12 | 3157 | Mb0994 | metal cation transporter P-ty | 35.56 | 770 | MAV_3211 | malto-oligosyltrehalose synthase | 47.83 | 766 | BCG_1023 | metal cation transporter P-type | 35.56 | 770 | MAP3687c | hypothetical protein | 90 | 100 |
| MAP4_0085 | small secreted protein | 57 | Rv0236A | Small secreted protein | 96.49 | 57 | Mb0242c | hypothetical protein | 96.49 | 57 | MAV_4922 | secreted protein | 97.56 | 41 | BCG_0274c | hypothetical protein | 96.49 | 57 | MAP0105c | hypothetical protein | 889 | 50 |
| MAP4_0086 | hypothetical protein | 1393 | Rv0236c | Possible arabinofuranosyltransferas | 78.49 | 1400 | Mb0241c | transmembrane protein | 78.42 | 1400 | MAV_4923 | hypothetical protein | 99.35 | 1393 | BCG_0273c | hypothetical protein | 78.42 | 1400 | MAP3686c | hypothetical protein | 1393 | 100 |
| MAP4_0087 | hypothetical protein | 485 | Rv0235c | Probable conserved transmembrane | 79.96 | 482 | Mb0240c | transmembrane protein | 79.96 | 482 | MAV_4924 | integral membrane protein | 98.97 | 485 | BCG_0272c | hypothetical protein | 79.96 | 482 | MAP3685c | hypothetical protein | 485 | 100 |
| MAP4_0088 | putative glucose-methanol-choline (gmc) oxido reducta | 599 | Rv1279 | Probable dehydrogenase FAD flavop | 32.59 | 528 | Mb1310 | dehydrogenase FAD flavoprot | 32.59 | 528 | MAV_4925 | glucose-methanol-choline | 99.17 | 598 | BCG_1338 | dehydrogenase FAD flavoprote | 32.59 | 528 | MAP3684 | hypothetical protein | 618 | 99.83 |
| MAP4_0089 | catalase | 484 | Rv0670 | Probable endonuclease IV End (endo | 31.71 | 252 | Mb0689 | endonuclease IV | 31.71 | 252 | MAV_4926 | catalase KatA | 98.76 | 484 | BCG_0719 | endonuclease IV | 31.71 | 252 | MAP3683 | hypothetical protein | 484 | 100 |
| MAP4_0090 | catalase | 485 | Rv0670 | Probable endonuclease IV End (endo | 34.15 | 252 | Mb0689 | endonuclease IV | 34.15 | 252 | MAV_4927 | catalase KatA | 99.18 | 485 | BCG_0719 | endonuclease IV | 34.15 | 252 | MAP3682 | hypothetical protein | 485 | 100 |
| MAP4_0091 | hypothetical protein | 145 | Rv0592 | Mce-family protein Mce2D | 35.9 | 508 | Mb0607 | hypothetical protein | 35.9 | 478 | MAV_4928 | hypothetical protein | 97.39 | 115 | BCG_1150 | cellulase celA2b | 47.37 | 151 | MAP3681 | hypothetical protein | 145 | 100 |
| MAP4_0092 | formate dehydrogenase | 384 | Rv0728c | Possible D-3-phosphoglycerate dehy | 29.91 | 326 | Mb0749c | D-3-phosphoglycerate dehyd | 29.91 | 326 | MAV_4930 | formate dehydrogenase | 99.21 | 380 | BCG_0778c | D-3-phosphoglycerate dehydro | 29.91 | 326 | MAP3680c | formate dehydrogenase | 389 | 99.74 |
| MAP4_0093 | transmembrane alanine and valine and leucine rich pro | 336 | Rv2571c | Probable transmembrane alanine ar | 45.7 | 355 | Mb2601c | transmembrane alanine and v | 45.7 | 355 | MAV_4931 | hypothetical protein | 97.02 | 336 | BCG_2594c | transmembrane alanine and va | 45.4 | 355 | MAP3679 | hypothetical protein | 336 | 100 |
| MAP4_0094 | hypothetical protein | 125 | Rv0546c | hypothetical protein | 33.33 | 128 | Mb0560c | hypothetical protein | 33.33 | 128 | MAV_4932 | glyoxalase | 98.36 | 122 | BCG_0590c | hypothetical protein | 33.33 | 128 | MAP3678 | hypothetical protein | 125 | 100 |
| MAP4_0095 | hypothetical protein | 458 | Rv2242 | hypothetical protein | 37.61 | 414 | Mb2266 | hypothetical protein | 37.61 | 414 | MAV_4933 | hypothetical protein | 99.75 | 404 | BCG_2259 | hypothetical protein | 37.61 | 414 | MAP3677 | hypothetical protein | 458 | 100 |
| MAP4_0096 | transcriptional regulator, LysR family protein | 309 | Rv0117 | Oxidative stress response regulatory | 52.81 | 314 | Mb0121 | oxidative stress response reg | 52.81 | 314 | MAV_4934 | LysR family transcriptional regulato | 99.68 | 309 | BCG_0151 | oxidative stress response regul | 52.81 | 314 | MAP3676 | OxyS_2 | 309 | 100 |
| MAP4_0099 | succinate-semialdehyde dehydrogenase | 472 | Rv0234c | Succinate-semialdehyde dehydroger | 85.34 | 511 | Mb0239c | succinate-semialdehyde dehy | 85.34 | 511 | MAV_4936 | succinic semialdehyde dehydrogen | 99.79 | 472 | BCG_0271c | succinate-semialdehyde dehyd | 85.34 | 511 | MAP3673c | succinic semialdehyde dehydrogenase | 472 | 100 |
| MAP4_0100 | ribonucleoside-diphosphate reductase beta chain NrdB | 311 | Rv0233 | Ribonucleoside-diphosphate reducta | 82.69 | 314 | Mb0238 | ribonucleotide-diphosphate r | 82.69 | 314 | MAV_4937 | ribonucleotide-diphosphate reduct | 99.68 | 311 | BCG_0270 | ribonucleotide-diphosphate re | 82.69 | 314 | MAP3672 | ribonucleotide-diphosphate reductase s | 311 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0101 | Transcriptional regulator, TetR family | 227 | Rv0232 | Probable transcriptional regulatory | 86.09 | 229 | Mb0237 | TetR/ACRR family transcriptic | 86.09 | 229 | MAV_4938 | TetR family transcriptional regulatc | 99.56 | 227 | BCG_0269 | TetR family transcriptional regu | 86.09 | 229 | MAP3671 | hypothetical protein | 227 | 100 |
| MAP4_0102 | transposase | 329 | Rv2812 | Probable transposase | 32.65 | 469 | Mb2836 | transposase | 32.29 | 265 | MAV_0752 | transposase | 82.98 | 345 | BCG_2830 | transposase | 32.65 | 469 | MAP3078c | hypothetical protein | 329 | 100 |
| MAP4_0103 | Acyl-CoA dehydrogenase | 569 | Rv0231 | Probable acyl-CoA dehydrogenase F | 84.36 | 568 | Mb0236 | acyl-CoA dehydrogenase | 84.36 | 568 | MAV_4939 | acyl-CoA dehydrogenase | 99.12 | 569 | BCG_0268 | acyl-CoA dehydrogenase fadE4 | 84.36 | 568 | MAP3669 | FadE4 | 569 | 100 |
| MAP4_0104 | phosphotriesterase | 326 | Rv0230c | Probable phosphotriesterase Php (p | 92.31 | 326 | Mb0235c | phosphotriesterase | 92 | 326 | MAV_4940 | phosphotriesterase-like protein | 99.67 | 306 | BCG_0267c | phosphotriesterase PHP | 92 | 326 | MAP3668c | hypothetical protein | 326 | 100 |
| MAP4_0105 | membrane acyltransferase | 408 | Rv0228 | Probable integral membrane acyltra | 79.8 | 407 | Mb0233 | integral membrane acyltransf | 79.8 | 407 | MAV_4941 | acyltransferase | 98.98 | 393 | BCG_0265 | integral membrane acyltransfe | 79.8 | 407 | MAP3667 | hypothetical protein | 408 | 100 |
| MAP4_0106 | putative conserved membrane protein | 413 | Rv0227c | Probable conserved membrane prot | 81.75 | 421 | Mb0232c | hypothetical protein | 81.25 | 421 | MAV_4942 | hypothetical protein | 99.76 | 418 | BCG_0264c | hypothetical protein | 81.5 | 421 | MAP3666c | hypothetical protein | 413 | 99.76 |
| MAP4_0107 | conserved transmembrane protein | 565 | Rv0226c | Probable conserved transmembrane | 74.52 | 576 | Mb0231c | transmembrane protein | 74.52 | 576 | MAV_4944 | hypothetical protein | 98.41 | 565 | BCG_0263c | hypothetical protein | 74.52 | 576 | MAP3665c | hypothetical protein | 565 | 100 |
| MAP4_0108 | putative glycosyltransferase | 388 | Rv0225 | Possible conserved protein | 84.38 | 384 | Mb0230 | hypothetical protein | 84.38 | 384 | MAV_4943 | glycosyltransferase | 99.21 | 382 | BCG_0262 | hypothetical protein | 84.38 | 384 | MAP3664 | hypothetical protein | 388 | 100 |
| MAP4_0109 | methyltransferasemethylase | 255 | Rv0224c | Possible methyltransferase (methyla | 82.68 | 254 | Mb0229c | methyltransferase | 82.28 | 254 | MAV_4945 | SAM-dependent methyltransferase | 97.23 | 253 | BCG_0261c | methyltransferase | 82.28 | 254 | MAP3663c | hypothetical protein | 255 | 100 |
| MAP4_0110 | aldehyde dehydrogenase | 493 | Rv0223c | Probable aldehyde dehydrogenase | 83.5 | 487 | Mb0228c | aldehyde dehydrogenase | 78.36 | 385 | MAV_4946 | aldehyde dehydrogenase | 99.59 | 493 | BCG_0259c | aldehyde dehydrogenase | 76.73 | 269 | MAP3662c | hypothetical protein | 493 | 99.59 |
| MAP4_0111 | hypothetical protein | 43 | Rv1564c | Probable maltooligosyltrehalose syn | 33.33 | 721 | Mb1591c | malto-oligosyltrehalose synth | 33.33 | 721 | MAV_4947 | hypothetical protein | 100 | 43 | BCG_1617c | maltooligosyltrehalose synthas | 33.33 | 721 | MAP1900c | phospho-N-acetylmuramoyl-pentapept | 359 | 53.85 |
| MAP4_0112 | Transcriptional regulator, TetR family | 195 | Rv0196 | Possible transcriptional regulatory p | 38.46 | 194 | Mb0202 | transcriptional regulator | 38.46 | 194 | MAV_4948 | TetR family transcriptional regulatc | 100 | 213 | BCG_0233 | transcriptional regulatory prote | 38.46 | 194 | MAP3661c | hypothetical protein | 261 | 100 |
| MAP4_0113 | hypothetical protein | 87 | Rv1248c | Multifunctional alpha-ketoglutarate | 27.42 | 1231 | Mb1280c | alpha-ketoglutarate decarbox | 27.42 | 1231 | MAV_4949 | hypothetical protein | 98.85 | 98 | BCG_1308c | alpha-ketoglutarate decarboxy | 27.42 | 1214 | MAP3660 | hypothetical protein | 87 | 100 |
| MAP4_0115 | AMP-dependent synthetase and ligase | 509 | Rv0270 | Probable fatty-acid-CoA ligase FadD | 31.46 | 560 | Mb0276 | acyl-CoA synthetase | 31.46 | 560 | MAV_4950 | AMP-dependent synthetase and lig | 99.61 | 509 | BCG_0308 | acyl-CoA synthetase | 31.46 | 560 | MAP3659 | hypothetical protein | 509 | 100 |
| MAP4_0116 | enoyl-CoA hydratase | 264 | Rv0222 | Probable enoyl-CoA hydratase EchA | 84.92 | 262 | Mb3545 | enoyl-CoA hydratase | 42.97 | 263 | MAV_4951 | enoyl-CoA hydratase | 99.24 | 264 | BCG_3579 | enoyl-CoA hydratase | 42.97 | 263 | MAP3658 | enoyl-CoA hydratase | 264 | 100 |
| MAP4_0117 | putative acyltransferase | 469 | Rv0221 | Possible triacylglycerol synthase (dia | 80.38 | 469 | Mb0227 | hypothetical protein | 76.07 | 257 | MAV_4952 | acyltransferase, ws/dgat/mgat sub | 99.79 | 469 | BCG_0258 | hypothetical protein | 76.07 | 257 | MAP3657 | hypothetical protein | 469 | 100 |
| MAP4_0118 | esterase LipC | 398 | Rv0220 | Probable esterase LipC | 74.17 | 403 | Mb0226 | esterase | 74.17 | 403 | MAV_4953 | alpha/beta hydrolase | 100 | 398 | BCG_0257 | esterase lipC | 74.17 | 413 | MAP3656 | hypothetical protein | 415 | 100 |
| MAP4_0119 | esterase LipW | 294 | Rv0217c | Possible esterase LipW | 71.48 | 302 | Mb0223c | esterase | 71.48 | 302 | MAV_4954 | alpha/beta hydrolase | 99.29 | 307 | BCG_0254c | esterase lipW | 71.48 | 302 | MAP3655c | hypothetical protein | 299 | 99.65 |
| MAP4_0120 | amidohydrolase family protein | 437 | Rv2052c | hypothetical protein | 41.05 | 534 | Mb2078c | hypothetical protein | 41.05 | 534 | MAV_4955 | amidohydrolase | 99.31 | 437 | BCG_2071c | hypothetical protein | 41.05 | 534 | MAP3654 | hypothetical protein | 420 | 99.76 |
| MAP4_0121 | hypothetical protein | 396 | Rv3272 | hypothetical protein | 29.36 | 394 | Mb3300 | hypothetical protein | 29.36 | 394 | MAV_4956 | hypothetical protein | 97.47 | 396 | BCG_3301 | hypothetical protein | 29.36 | 394 | MAP3653 | hypothetical protein | 416 | 100 |
| MAP4_0122 | hypothetical protein | 340 | Rv0216 | Double hotdog hydratase | 80.77 | 337 | Mb0222 | hypothetical protein | 80.77 | 337 | MAV_4957 | p40 protein | 98.82 | 340 | BCG_0253 | hypothetical protein | 80.77 | 337 | MAP3652 | hypothetical protein | 340 | 100 |
| MAP4_0123 | acyl-CoA dehydrogenase | 405 | Rv0215c | Probable acyl-CoA dehydrogenase F | 86.69 | 357 | Mb0221c | acyl-CoA dehydrogenase | 87.01 | 388 | MAV_4958 | acyl-CoA dehydrogenase | 98.95 | 382 | BCG_0252c | acyl-CoA dehydrogenase fadE3 | 86.75 | 388 | MAP3651c | FadE3_2 | 405 | 100 |
| MAP4_0124 | putative enoyl-CoA hydratase isomerase | 320 | Rv1070c | Probable enoyl-CoA hydratase EchA | 35.33 | 257 | Mb1099c | enoyl-CoA hydratase | 35.33 | 257 | MAV_4960 | enoyl-CoA hydratase/isomerase | 97.81 | 320 | BCG_1128c | enoyl-CoA hydratase | 35.33 | 257 | MAP3650 | hypothetical protein | 320 | 100 |
| MAP4_0125 | fatty-acid-CoA ligase | 505 | Rv0214 | Probable fatty-acid-CoA ligase FadD | 80.79 | 537 | Mb0220 | long-chain-fatty-acid--CoA lig | 80.59 | 537 | MAV_4961 | long-chain-fatty-acid--CoA ligase | 99.21 | 505 | BCG_0251 | long-chain-fatty-acid--CoA ligas | 80.59 | 537 | MAP3649 | long-chain-fatty-acid--CoA ligase | 505 | 100 |
| MAP4_0128 | iron-regulated phosphoenol pyruvate carboxykinase Pc | 609 | Rv0211 | Probable iron-regulated phosphoen | 89.42 | 606 | Mb0217 | phosphoenolpyruvate carbox | 89.42 | 606 | MAV_4963 | phosphoenolpyruvate carboxykinas | 99.67 | 609 | BCG_0248 | phosphoenolpyruvate carboxyl | 89.42 | 606 | MAP3646 | phosphoenolpyruvate carboxykinase | 609 | 100 |
| MAP4_0129 | hypothetical protein | 511 | Rv0210 | Hypothetical protein | 62.96 | 492 | Mb0216 | hypothetical protein | 62.53 | 492 | MAV_4964 | hypothetical protein | 99.41 | 511 | BCG_0247 | hypothetical protein | 62.53 | 492 | MAP3645 | hypothetical protein | 511 | 100 |
| MAP4_0130 | hypothetical protein | 364 | Rv0209 | Hypothetical protein | 59.84 | 361 | Mb0215 | hypothetical protein | 60.11 | 361 | MAV_4965 | hypothetical protein | 97.83 | 368 | BCG_0246 | hypothetical protein | 60.11 | 361 | MAP3644 | hypothetical protein | 364 | 100 |
| MAP4_0131 | methyltransferase | 259 | Rv0208c | Hypothetical methlytransferase (me | 66.41 | 263 | Mb0214c | tRNA (guanine-N(7)-)-methylt | 66.41 | 263 | MAV_4966 | tRNA (guanine-N(7)-)-methyltransf | 98.84 | 259 | BCG_0245c | tRNA (guanine-N(7)-)-methyltr | 66.41 | 263 | MAP3643c | tRNA (guanine-N(7)-)-methyltransferase | 259 | 100 |
| MAP4_0132 | hypothetical protein | 237 | Rv0207c | hypothetical protein | 81.4 | 242 | Mb0213c | hypothetical protein | 81.4 | 242 | MAV_4967 | hypothetical protein | 99.16 | 237 | BCG_0244c | hypothetical protein | 81.4 | 242 | MAP3642c | hypothetical protein | 237 | 100 |
| MAP4_0133 | transmembrane transport protein | 957 | Rv0206c | Possible conserved transmembrane | 69.84 | 944 | Mb0212c | transmembrane transport pr | 69.63 | 944 | MAV_4968 | MmpL3 protein | 99.37 | 949 | BCG_0243c | transmembrane transport prot | 69.63 | 944 | MAP3641c | hypothetical protein | 957 | 100 |
| MAP4_0134 | hypothetical protein | 382 | Rv0205 | Probable conserved transmembrane | 79.56 | 367 | Mb0211 | transmembrane protein | 79.56 | 367 | MAV_4969 | hypothetical protein | 99.74 | 382 | BCG_0242 | hypothetical protein | 79.56 | 367 | MAP3640 | hypothetical protein | 382 | 100 |
| MAP4_0135 | hypothetical protein | 393 | Rv0204c | Probable conserved transmembrane | 80.45 | 412 | Mb0210c | transmembrane protein | 80.6 | 427 | MAV_4970 | hypothetical protein | 99.49 | 393 | BCG_0241c | hypothetical protein | 80.6 | 427 | MAP3639c | hypothetical protein | 393 | 100 |
| MAP4_0136 | hypothetical protein | 181 | Rv0203 | Possible exported protein | 67.16 | 136 | Mb0209 | hypothetical protein | 67.16 | 136 | MAV_4971 | hypothetical protein | 100 | 181 | BCG_0240 | hypothetical protein | 66.42 | 136 | MAP3638 | hypothetical protein | 181 | 100 |
| MAP4_0137 | transmembrane transport protein | 1007 | Rv0202c | Probable conserved transmembrane | 75.86 | 966 | Mb0208c | transmembrane transport pr | 75.86 | 966 | MAV_4973 | MmpL11 protein | 99.6 | 1007 | BCG_0239c | transmembrane transport prot | 75.86 | 966 | MAP3637c | hypothetical protein | 1007 | 100 |
| MAP4_0138 | oxidoreductase | 866 | Rv0197 | Possible oxidoreductase | 85.27 | 762 | Mb0203 | oxidoreductase | 85.41 | 748 | MAV_4983 | molybdopterin oxidoreductase Fe4 | 98.74 | 745 | BCG_0234 | oxidoreductase | 85.41 | 748 | MAP3636 | hypothetical protein | 866 | 99.88 |
| MAP4_0139 | Transcriptional regulator, TetR family | 201 | Rv0196 | Possible transcriptional regulatory p | 76.72 | 194 | Mb0202 | transcriptional regulator | 76.72 | 194 | MAV_4985 | TetR family transcriptional regulatc | 99 | 201 | BCG_0233 | transcriptional regulatory prote | 76.72 | 194 | MAP3635 | hypothetical protein | 201 | 100 |
| MAP4_0140 | hypothetical protein | 345 | Rv0192 | hypothetical protein | 71.31 | 366 | Mb0198 | hypothetical protein | 72 | 352 | MAV_4986 | ErfK/YbiS/YcfS/YnhG family protein | 100 | 339 | BCG_0229 | hypothetical protein | 71.6 | 352 | MAP3634 | hypothetical protein | 345 | 100 |
| MAP4_0141 | hypothetical protein | 414 | Rv0191 | Probable conserved integral membr | 76.46 | 413 | Mb0197 | hypothetical protein | 76.46 | 413 | MAV_4987 | sugar transporter family protein | 100 | 411 | BCG_0228 | integral membrane protein | 76.46 | 413 | MAP3633 | hypothetical protein | 414 | 100 |
| MAP4_0142 | hypothetical protein | 96 | Rv0190 | hypothetical protein | 89.58 | 96 | Mb0196 | hypothetical protein | 89.58 | 96 | MAV_4988 | hypothetical protein | 100 | 96 | BCG_0227 | hypothetical protein | 89.58 | 96 | MAP3632 | hypothetical protein | 96 | 100 |
| MAP4_0143 | dihydroxy-acid dehydratase | 575 | Rv0189c | Probable dihydroxy-acid dehydratas | 90.96 | 575 | Mb0195c | dihydroxy-acid dehydratase | 90.96 | 575 | MAV_4989 | dihydroxy-acid dehydratase | 99.83 | 575 | BCG_0226c | dihydroxy-acid dehydratase | 90.96 | 575 | MAP3631c | dihydroxy-acid dehydratase | 575 | 100 |
| MAP4_0144 | hypothetical protein | 144 | Rv0188 | Probable conserved transmembrane | 74.83 | 143 | Mb0194 | transmembrane protein | 74.83 | 143 | MAV_2241 | alpha/beta hydrolase | 26.95 | 520 | BCG_0225 | hypothetical protein | 74.83 | 143 | MAP3630 | hypothetical protein | 144 | 100 |
| MAP4_0145 | oxidoreductase | 327 | Rv3553 | Possible oxidoreductase | 32.04 | 355 | Mb3583 | oxidoreductase | 32.04 | 355 | MAV_4991 | oxidoreductase, 2-nitropropane dic | 97.86 | 327 | BCG_3617 | oxidoreductase | 32.04 | 355 | MAP3628c | hypothetical protein | 238 | 99.58 |
| MAP4_0146 | O-methyltransferase | 217 | Rv0187 | Probable O-methyltransferase | 73.85 | 220 | Mb0193 | O-methyltransferase | 73.85 | 220 | MAV_4992 | O-methyltransferase | 99.08 | 217 | BCG_0224 | o-methyltransferase | 73.39 | 220 | MAP3627 | hypothetical protein | 217 | 100 |
| MAP4_0147 | hypothetical protein | 51 | Rv0186A | Metallothionein, MymT | 79.59 | 53 | Mb1238 | long-chain-acyl-CoA syntheta | 28.57 | 597 | MAV_4993 | hypothetical protein | 100 | 51 | BCG_1266 | long-chain-acyl-CoA synthetase | 28.57 | 597 | MAP3626c | hypothetical protein | 51 | 100 |
| MAP4_0148 | beta-glucosidase | 691 | Rv0186 | Probable beta-glucosidase BglS (gen | 76.27 | 691 | Mb0192 | beta-glucosidase BGLS | 76.12 | 691 | MAV_4994 | glycosyl hydrolase 3 | 98.99 | 705 | BCG_0223 | beta-glucosidase bglS | 76.12 | 691 | MAP3625 | BglS | 691 | 100 |
| MAP4_0149 | hypothetical protein | 170 | Rv0185 | hypothetical protein | 80.84 | 169 | Mb0191 | hypothetical protein | 80.84 | 169 | MAV_4995 | hypothetical protein | 99.41 | 170 | BCG_0222 | hypothetical protein | 80.84 | 169 | MAP3624 | hypothetical protein | 170 | 100 |
| MAP4_0150 | hypothetical protein | 249 | Rv0184 | hypothetical protein | 88.26 | 249 | Mb0190 | hypothetical protein | 88.26 | 249 | MAV_4996 | hypothetical protein | 99.6 | 249 | BCG_0221 | hypothetical protein | 88.26 | 249 | MAP3623 | hypothetical protein | 249 | 100 |
| MAP4_0151 | lysophospholipase | 277 | Rv0183 | Possible lysophospholipase | 82.61 | 279 | Mb0189 | lysophospholipase | 82.61 | 279 | MAV_4997 | lysophospholipase | 99.64 | 277 | BCG_0220 | lysophospholipase | 82.61 | 279 | MAP3622 | hypothetical protein | 277 | 100 |
| MAP4_0152 | alternative RNA polymerase sigma factor SigG | 366 | Rv0182c | Probable alternative RNA polymeras | 80 | 370 | Mb0188c | RNA polymerase factor sigma | 80 | 370 | MAV_4998 | RNA polymerase factor sigma-70 | 98.78 | 327 | BCG_0219c | RNA polymerase factor sigma- | 80 | 370 | MAP3621c | RNA polymerase factor sigma-70 | 366 | 99.73 |
| MAP4_0153 | hypothetical protein | 467 | Rv0542c | Possible O-succinylbenzoic acid--Co | 26.21 | 362 | Mb0556c | O-succinylbenzoic acid--CoA l | 26.21 | 362 | MAV_5000 | hypothetical protein | 98.72 | 467 | BCG_0586c | O-succinylbenzoic acid--CoA lig | 26.21 | 362 | MAP3620c | hypothetical protein | 467 | 100 |
| MAP4_0154 | hypothetical protein | 377 | Rv0926c | hypothetical protein | 44.13 | 358 | Mb0949c | hypothetical protein | 44.13 | 358 | MAV_4999 | dihydrodipicolinate reductase N-te | 98.14 | 377 | BCG_0978c | hypothetical protein | 44.13 | 358 | MAP3619 | hypothetical protein | 377 | 100 |
| MAP4_0155 | putative transcriptional regulator | 296 | Rv1719 | Probable transcriptional regulatory | 30.77 | 259 | Mb1748 | transcriptional regulator | 30.77 | 259 | MAV_5001 | hypothetical protein | 98.65 | 296 | BCG_1758 | transcriptional regulatory prote | 30.77 | 259 | MAP3618c | hypothetical protein | 296 | 100 |
| MAP4_0156 | hypothetical protein | 241 | Rv0181c | hypothetical protein | 72.92 | 244 | Mb0187c | hypothetical protein | 72.92 | 244 | MAV_5002 | YhhW protein | 97.51 | 241 | BCG_0218c | hypothetical protein | 72.92 | 244 | MAP3617c | hypothetical protein | 241 | 100 |
| MAP4_0157 | hypothetical protein | 474 | Rv0180c | Probable conserved transmembrane | 74.12 | 452 | Mb0186c | transmembrane protein | 74.12 | 452 | MAV_5003 | ABC transporter | 98.31 | 474 | BCG_0217c | hypothetical protein | 74.12 | 452 | MAP3616c | hypothetical protein | 474 | 100 |
| MAP4_0158 | lipoprotein | 366 | Rv0179c | Possible lipoprotein LprO | 82.19 | 369 | Mb0185c | lipoprotein LPRO | 81.92 | 369 | MAV_5005 | LprO protein | 99.72 | 360 | BCG_0216c | lipoprotein lprO | 81.92 | 369 | MAP3615c | hypothetical protein | 366 | 100 |
| MAP4_0159 | hypothetical protein | 221 | Rv3365c | hypothetical protein | 28.79 | 876 | Mb3400c | hypothetical protein | 28.79 | 876 | MAV_5004 | hypothetical protein | 98.64 | 221 | BCG_3437c | hypothetical protein | 28.79 | 876 | MAP3614 | hypothetical protein | 216 | 99.54 |
| MAP4_0160 | mce associated membrane protein | 252 | Rv0178 | Probable conserved Mce associated | 63.39 | 244 | Mb0184 | mce associated membrane pr | 63.39 | 244 | MAV_5006 | hypothetical protein | 97.22 | 251 | BCG_0215 | MCE associated membrane pro | 63.39 | 244 | MAP3613 | hypothetical protein | 252 | 100 |
| MAP4_0161 | MCE associated protein | 184 | Rv0177 | Probable conserved Mce associated | 61.96 | 184 | Mb0183 | MCE associated protein | 61.96 | 184 | MAV_5007 | hypothetical protein | 100 | 184 | BCG_0214 | mce associated protein | 61.96 | 184 | MAP3612 | hypothetical protein | 184 | 100 |
| MAP4_0162 | mce associated transmembrane protein | 323 | Rv0176 | Probable conserved Mce associated | 58.64 | 322 | Mb0182 | mce associated transmembra | 59.26 | 322 | MAV_5008 | RDD family protein | 97.83 | 323 | BCG_0213 | mce associated transmembran | 59.26 | 322 | MAP3611 | hypothetical protein | 323 | 100 |
| MAP4_0163 | mce associated membrane protein | 213 | Rv0175 | Probable conserved Mce associated | 62.38 | 213 | Mb0181 | mce associated membrane pr | 62.38 | 213 | MAV_5009 | hypothetical protein | 97.66 | 233 | BCG_0212 | mce associated membrane pro | 62.38 | 213 | MAP3610 | hypothetical protein | 213 | 100 |
| MAP4_0164 | mce family protein | 516 | Rv0174 | Mce-family protein Mce1F | 77.28 | 515 | Mb0180 | MCE-family protein MCE1F | 77.48 | 515 | MAV_4546 | mce-family protein mce2f | 71.34 | 508 | BCG_0211 | MCE-family protein mce1F | 77.48 | 515 | MAP3609 | hypothetical protein | 516 | 100 |
| MAP4_0165 | MCE-family lipoprotein LprK | 386 | Rv0173 | Possible Mce-family lipoprotein Lpr | 77.72 | 390 | Mb0179 | MCE-family lipoprotein LprK | 77.72 | 390 | MAV_5011 | virulence factor Mce | 100 | 596 | BCG_0210 | mce family lipoprotein LprK | 77.72 | 390 | MAP3608 | hypothetical protein | 386 | 100 |
| MAP4_0166 | mce family protein | 537 | Rv0172 | Mce-family protein Mce1D | 81.1 | 530 | Mb0178 | MCE-family protein MCE1D | 81.1 | 530 | MAV_5012 | mce-family protein mce1d | 99.63 | 537 | BCG_0209 | MCE-family protein mce1D | 81.1 | 530 | MAP3607 | hypothetical protein | 537 | 99.81 |
| MAP4_0167 | mce family protein | 518 | Rv0171 | Mce-family protein Mce1C | 80.04 | 515 | Mb0177 | MCE-family protein MCE1C | 80.26 | 515 | MAV_5013 | mce-family protein mce1c | 99.79 | 521 | BCG_0208 | MCE-family protein mce1C | 80.26 | 515 | MAP3606 | hypothetical protein | 518 | 100 |
| MAP4_0168 | mce family protein | 346 | Rv0170 | Mce-family protein Mce1B | 78.03 | 346 | Mb0176 | MCE-family protein MCE1B | 77.75 | 346 | MAV_5014 | virulence factor Mce | 100 | 346 | BCG_0207 | MCE-family protein mce1B | 77.75 | 346 | MAP3605 | hypothetical protein | 346 | 100 |
| MAP4_0169 | MCE-family protein | 434 | Rv0169 | Mce-family protein Mce1A | 69.58 | 454 | Mb0175 | MCE-family protein MCE1A | 69.58 | 454 | MAV_5015 | virulence factor Mce | 94.93 | 434 | BCG_0206 | MCE-family protein mce1A | 69.58 | 454 | MAP3604 | Mce1_2 | 434 | 100 |
| MAP4_0170 | hypothetical protein | 289 | Rv0168 | Conserved integral membrane prote | 87.54 | 289 | Mb0174 | hypothetical protein | 87.54 | 289 | MAV_5016 | hypothetical protein | 100 | 289 | BCG_0205 | integral membrane protein Yrb | 87.54 | 289 | MAP3603 | hypothetical protein | 251 | 100 |
| MAP4_0171 | hypothetical protein | 271 | Rv0167 | Conserved integral membrane prote | 89.3 | 265 | Mb0173 | hypothetical protein | 89.3 | 265 | MAV_5017 | hypothetical protein | 99.61 | 258 | BCG_0204 | integral membrane protein Yrb | 89.3 | 265 | MAP3602 | hypothetical protein | 271 | 100 |
| MAP4_0174 | transcriptional regulator, GntR family | 234 | Rv0165c | Probable transcriptional regulatory | 86.55 | 223 | Mb0170c | GntR family transcriptional re | 84.68 | 271 | MAV_5020 | GntR family transcriptional regulatc | 99.13 | 229 | BCG_0201c | GntR family transcriptional reg | 84.68 | 271 | MAP3599c | hypothetical protein | 271 | 99.57 |
| MAP4_0175 | hypothetical protein | 153 | Rv0164 | Conserved protein TB18.5 | 80.92 | 161 | Mb0169 | hypothetical protein | 80.92 | 161 | MAV_5019 | cyclase/dehydrase | 100 | 146 | BCG_0200 | hypothetical protein | 80.92 | 161 | MAP3598 | hypothetical protein | 153 | 100 |
| MAP4_0176 | hypothetical protein | 161 | Rv0163 | hypothetical protein | 80.27 | 151 | Mb0168 | hypothetical protein | 80.27 | 151 | MAV_5021 | thioesterase | 98.65 | 148 | BCG_0199 | hypothetical protein | 80.27 | 151 | MAP3597 | hypothetical protein | 161 | 100 |
| MAP4_0177 | zinc-type alcohol dehydrogenase E subunit AdhE | 370 | Rv0162c | Probable zinc-type alcohol dehydrog | 80.98 | 383 | Mb0167c | zinc-type alcohol dehydrogen | 80.98 | 383 | MAV_5022 | zinc-binding dehydrogenase | 98.9 | 363 | BCG_0198c | zinc-type alcohol dehydrogena | 80.98 | 383 | MAP3596c | AdhE | 363 | 99.72 |
| MAP4_0178 | putative lipaseesterase | 305 | Rv0217c | Possible esterase LipW | 46.22 | 302 | Mb0223c | esterase | 46.22 | 302 | MAV_5118 | alpha/beta hydrolase | 99.67 | 308 | BCG_0254c | esterase lipW | 46.22 | 302 | MAP3595 | hypothetical protein | 305 | 100 |
| MAP4_0179 | putative monooxygenase | 499 | Rv3049c | Probable monooxygenase | 36.91 | 524 | Mb3075c | monooxygenase | 36.91 | 524 | MAV_5119 | lipolytic enzyme | 99.2 | 504 | BCG_3073c | monooxygenase | 36.91 | 524 | MAP3594 | hypothetical protein | 499 | 100 |
| MAP4_0180 | short chain dehydrogenase | 248 | Rv2002 | Possible 20-beta-hydroxysteroid deh | 38.3 | 260 | Mb2025 | 20-beta-hydroxysteroid dehy | 38.3 | 260 | MAV_5120 | oxidoreductase | 97.98 | 248 | BCG_2019 | 20-beta-hydroxysteroid dehydr | 38.3 | 260 | MAP3593 | hypothetical protein | 248 | 100 |
| MAP4_0181 | putative HpcHHpaI aldolasecitrate lyase family protein | 250 | Rv1308 | Probable ATP synthase alpha chain | 30.68 | 549 | Mb1340 | ATP synthase F0F1 subunit al | 30.68 | 549 | MAV_5121 | HpcH/HpaI aldolase/citrate lyase | 98.8 | 250 | BCG_1368 | F0F1 ATP synthase subunit alp | 30.68 | 549 | MAP3592 | hypothetical protein | 193 | 99.48 |
| MAP4_0182 | dehydrogenase | 322 | Rv1895 | Possible dehydrogenase | 29.27 | 384 | Mb1929 | dehydrogenase | 26.6 | 234 | MAV_5122 | zinc-binding dehydrogenase | 98.45 | 321 | BCG_1934 | dehydrogenase | 26.6 | 234 | MAP3591 | hypothetical protein | 322 | 100 |
| MAP4_0183 | cytochrome P450 superfamily protein | 403 | Rv1256c | Probable cytochrome P450 130 Cyp | 32.57 | 405 | Mb0789c | cytochrome P450 123 | 31.54 | 402 | MAV_5123 | cytochrome P450 | 99.5 | 403 | BCG_0818c | cytochrome P450 123 cyp123 | 30.66 | 541 | MAP3590 | hypothetical protein | 403 | 100 |
| MAP4_0184 | hypothetical protein | 234 | Rv0152c | PE family protein PE2 | 30.43 | 525 | Mb0157c | PE family protein | 30.43 | 525 | MAV_5124 | hypothetical protein | 99.57 | 234 | BCG_0188c | PE family protein | 30.43 | 525 | MAP3589 | hypothetical protein | 234 | 100 |
| MAP4_0185 | hypothetical protein | 187 | Rv2524c | Probable fatty acid synthase Fas (fat | 34.07 | 3069 | Mb2553c | fatty acid synthase | 34.07 | 3069 | MAV_5125 | hypothetical protein | 98.93 | 187 | BCG_2545c | fatty acid synthase fas | 34.07 | 3069 | MAP3588 | hypothetical protein | 149 | 99.33 |
| MAP4_0186 | hypothetical protein | 392 | Rv3272 | hypothetical protein | 30.98 | 394 | Mb3300 | hypothetical protein | 30.98 | 394 | MAV_5126 | caib/baif family protein | 99.23 | 392 | BCG_3301 | hypothetical protein | 31.23 | 394 | MAP3587 | hypothetical protein | 392 | 99.74 |
| MAP4_0187 | hypothetical protein | 228 | Rv1056 | hypothetical protein | 37.14 | 254 | Mb1085 | hypothetical protein | 37.14 | 254 | MAV_5128 | hypothetical protein | 100 | 228 | BCG_1114 | hypothetical protein | 37.14 | 254 | MAP3586c | hypothetical protein | 236 | 100 |
| MAP4_0188 | putative acyl-CoA dehydrogenase | 391 | Rv3504 | Probable acyl-CoA dehydrogenase F | 29.23 | 400 | Mb3534 | acyl-CoA dehydrogenase | 29.23 | 400 | MAV_5127 | acyl-CoA dehydrogenase middle do | 98.47 | 391 | BCG_3568 | acyl-CoA dehydrogenase fadE2 | 29.23 | 400 | MAP3585 | hypothetical protein | 391 | 100 |
| MAP4_0189 | putative luciferase family protein | 306 | Rv3079c | hypothetical protein | 38.46 | 275 | Mb3106c | hypothetical protein | 38.46 | 275 | MAV_5129 | hypothetical protein | 99.35 | 306 | BCG_3104c | hypothetical protein | 38.46 | 275 | MAP3584 | hypothetical protein | 298 | 100 |
| MAP4_0190 | hypothetical protein | 301 | Rv2605c | Probable acyl-CoA thioesterase II Te | 27.45 | 281 | Mb2637c | acyl-CoA thioesterase | 27.45 | 281 | MAV_5130 | hypothetical protein | 98.99 | 297 | BCG_2630c | acyl-CoA thioesterase II tesB2 | 27.45 | 281 | MAP3583 | hypothetical protein | 301 | 100 |
| MAP4_0191 | hypothetical protein | 157 | Rv1173 | Probable F420 biosynthesis protein | 35.71 | 856 | Mb1206 | FO synthase | 35.71 | 856 | MAV_5131 | hypothetical protein | 99.36 | 157 | BCG_1236 | FO synthase | 35.71 | 856 | MAP3582c | hypothetical protein | 157 | 100 |
| MAP4_0192 | putative gluconolactonase | 290 | Rv0931c | Transmembrane serine/threonine-p | 25.97 | 664 | Mb0954c | serine/threonine protein kina | 25.97 | 369 | MAV_5132 | senescence marker protein-30 (SM | 98.9 | 272 | BCG_0983c | Ser/Thr protein kinase | 25.97 | 369 | MAP3581c | hypothetical protein | 290 | 100 |
| MAP4_0193 | hypothetical protein | 272 | Rv0226c | Probable conserved transmembrane | 35.42 | 576 | Mb0231c | transmembrane protein | 35.42 | 576 | MAV_5133 | hypothetical protein | 99.26 | 272 | BCG_0263c | hypothetical protein | 35.42 | 576 | MAP3580c | hypothetical protein | 274 | 100 |
| MAP4_0194 | Transcriptional regulator, TetR family | 183 | Rv2160A | hypothetical protein | 33.33 | 211 | Mb2184c | hypothetical protein | 33.33 | 206 | MAV_5134 | TetR family transcriptional regulatc | 100 | 183 | BCG_2177c | hypothetical protein | 33.33 | 206 | MAP3579c | hypothetical protein | 183 | 100 |
| MAP4_0195 | oxidoreductase | 446 | Rv0161 | Possible oxidoreductase | 81.29 | 449 | Mb0166 | oxidoreductase | 81.29 | 449 | MAV_5135 | FAD linked oxidase | 99.1 | 446 | BCG_0197 | oxidoreductase | 81.29 | 449 | MAP3578 | hypothetical protein | 446 | 100 |
| MAP4_0196 | 20-beta-hydroxysteroid dehydrogenase | 246 | Rv2002 | Possible 20-beta-hydroxysteroid deh | 63.27 | 260 | Mb2025 | 20-beta-hydroxysteroid dehy | 63.27 | 260 | MAV_5136 | 3-alpha-(or 20-beta)-hydroxysteroi | 100 | 246 | BCG_2019 | 20-beta-hydroxysteroid dehydr | 63.27 | 260 | MAP3577 | FabG3_2 | 246 | 100 |
| MAP4_0197 | hypothetical protein | 366 | Rv0926c | hypothetical protein | 63.33 | 358 | Mb0949c | hypothetical protein | 63.33 | 358 | MAV_5137 | homoserine dehydrogenase | 99.18 | 366 | BCG_0978c | hypothetical protein | 63.33 | 358 | MAP3576 | hypothetical protein | 366 | 100 |
| MAP4_0198 | Transcriptional regulator, TetR family | 211 | Rv0158 | Probable transcriptional regulatory | 89.52 | 214 | Mb0163 | TetR family transcriptional re | 89.52 | 214 | MAV_5138 | TetR family transcriptional regulatc | 100 | 211 | BCG_0194 | TetR family transcriptional regu | 89.52 | 214 | MAP3575 | hypothetical protein | 211 | 100 |
| MAP4_0199 | hypothetical protein | 41 | Rv0157A | hypothetical protein | 87.8 | 42 | Mb0017c | cell division protein RodA | 33.33 | 469 | MAV_5139 | hypothetical protein | 100 | 41 | BCG_0047c | cell division protein rodA | 33.33 | 469 | MAP0020c | RodA | 469 | 37.14 |
| MAP4_0200 | NAD(P) transhydrogenase subunit beta | 474 | Rv0157 | Probable NAD(P) transhydrogenase | 91.77 | 475 | Mb0162 | NAD(P) transhydrogenase sub | 91.77 | 475 | MAV_5140 | NAD(P) transhydrogenase beta sub | 99.58 | 474 | BCG_0193 | NAD(p) transhydrogenase (sub | 91.77 | 475 | MAP3574 | hypothetical protein | 474 | 100 |
| MAP4_0201 | NAD(P) transhydrogenase alpha subunit | 105 | Rv0156 | Probable NAD(P) transhydrogenase | 84.55 | 110 | Mb0161 | NAD(P) transhydrogenase sub | 83.64 | 110 | MAV_5141 | PntAB protein | 100 | 105 | BCG_0192 | NAD(p) transhydrogenase (sub | 83.64 | 110 | MAP3573 | PntAB | 105 | 100 |
| MAP4_0202 | NAD(P) transhydrogenase alpha subunit | 365 | Rv0155 | Probable NAD(P) transhydrogenase | 88.95 | 366 | Mb0160 | NAD(P) transhydrogenase sub | 88.95 | 366 | MAV_5142 | alanine dehydrogenase/pyridine nu | 100 | 365 | BCG_0191 | NAD(p) transhydrogenase (sub | 88.95 | 366 | MAP3572 | PntAA | 365 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0203 | hypothetical protein | 137 | Rv2692 | TRK system potassium uptake prote | 45 | 220 | Mb2711 | TRK system potassium uptake | 45 | 220 | MAV_5143 | response regulator receiver domai | 97.08 | 153 | BCG_2705 | TRK system potassium uptake | 45 | 220 | MAP3571 | hypothetical protein | 137 | 100 |
| MAP4_0204 | acyl-CoA dehydrogenase | 410 | Rv0154c | Probable acyl-CoA dehydrogenase F | 85.61 | 403 | Mb0159c | acyl-CoA dehydrogenase | 85.61 | 403 | MAV_5144 | acyl-CoA dehydrogenase | 99.51 | 410 | BCG_0190c | acyl-CoA dehydrogenase fadE2 | 85.61 | 403 | MAP3570c | FadE2 | 410 | 100 |
| MAP4_0207 | short-chain type dehydrogenase reductase | 287 | Rv0148 | Probable short-chain type dehydrog | 87.76 | 286 | Mb0153 | short-chain type dehydrogena | 87.76 | 286 | MAV_5146 | peroxisomal multifunctional enzym | 98.94 | 284 | BCG_0184 | short-chain type dehydrogenas | 87.76 | 286 | MAP3567 | hypothetical protein | 287 | 100 |
| MAP4_0208 | aldehyde dehydrogenase NAD-dependent | 488 | Rv0147 | Probable aldehyde dehydrogenase ( | 78.46 | 506 | Mb0152 | aldehyde dehydrogenase | 78.46 | 506 | MAV_5147 | fatty aldehyde dehydrogenase | 100 | 473 | BCG_0183 | aldehyde dehydrogenase | 78.46 | 506 | MAP3566 | hypothetical protein | 488 | 100 |
| MAP4_0209 | putative cell envelope-associated transcriptional atten | 516 | Rv3484 | Possible conserved protein CpsA | 39.81 | 512 | Mb3514 | hypothetical protein | 39.81 | 512 | MAV_5148 | cell envelope-related function tran | 99.03 | 516 | BCG_3548 | protein cpsA | 39.81 | 512 | MAP3565 | hypothetical protein | 516 | 100 |
| MAP4_0210 | hypothetical protein | 313 | Rv0146 | Possible S-adenosylmethionine-depe | 74.76 | 310 | Mb0151 | hypothetical protein | 74.76 | 310 | MAV_5149 | methyltransferase, putative, family | 100 | 313 | BCG_0182 | hypothetical protein | 74.76 | 310 | MAP3564 | hypothetical protein | 313 | 100 |
| MAP4_0211 | hypothetical protein | 313 | Rv0145 | Possible S-adenosylmethionine-depe | 75.16 | 317 | Mb0150 | hypothetical protein | 75.16 | 317 | MAV_5150 | methyltransferase, putative, family | 98.72 | 313 | BCG_0181 | hypothetical protein | 75.16 | 317 | MAP3563 | hypothetical protein | 313 | 100 |
| MAP4_0212 | Transcriptional regulator, TetR family | 211 | Rv0144 | Probable transcriptional regulatory | 65.52 | 280 | Mb0149 | TetR family transcriptional re | 65.52 | 280 | MAV_5151 | TetR family transcriptional regulato | 99.05 | 211 | BCG_0180 | TetR family transcriptional regu | 65.52 | 280 | MAP3562 | hypothetical protein | 213 | 100 |
| MAP4_0213 | conserved hypothetical protein, pirin family | 328 | Rv0181c | hypothetical protein | 36.67 | 244 | Mb0187c | hypothetical protein | 36.67 | 244 | MAV_5152 | chromosome condensation protein | 98.78 | 328 | BCG_0218c | hypothetical protein | 36.67 | 244 | MAP3561 | hypothetical protein | 328 | 100 |
| MAP4_0214 | putative DNA-binding ferritin-like protein | 182 | Rv2903c | Probable signal peptidase I LepB (SP | 21.43 | 294 | Mb2927c | signal peptidase I LepB | 21.43 | 294 | MAV_5153 | starvation-induced DNA protecting | 100 | 182 | BCG_2924c | signal peptidase I lepB | 21.43 | 294 | MAP3560 | hypothetical protein | 182 | 100 |
| MAP4_0215 | hypothetical protein | 304 | Rv0142 | hypothetical protein | 81.88 | 308 | Mb0147 | hypothetical protein | 81.88 | 308 | MAV_5154 | hypothetical protein | 99.67 | 304 | BCG_0178 | hypothetical protein | 81.88 | 308 | MAP3559 | hypothetical protein | 321 | 99.67 |
| MAP4_0216 | hypothetical protein | 133 | Rv0141c | hypothetical protein | 66.14 | 136 | Mb0146c | hypothetical protein | 66.14 | 136 | MAV_5155 | hypothetical protein | 100 | 133 | BCG_0177c | hypothetical protein | 66.14 | 136 | MAP3558c | hypothetical protein | 132 | 100 |
| MAP4_0217 | hypothetical protein | 126 | Rv0140 | hypothetical protein | 77.24 | 126 | Mb0145 | hypothetical protein | 77.24 | 126 | MAV_5156 | hypothetical protein | 98.41 | 126 | BCG_0176 | hypothetical protein | 77.24 | 126 | MAP3557 | hypothetical protein | 126 | 100 |
| MAP4_0218 | oxidoreductase | 339 | Rv0139 | Possible oxidoreductase | 81.21 | 340 | Mb0144 | oxidoreductase | 80.91 | 340 | MAV_5157 | 3-beta hydroxysteroid dehydrogen | 99.41 | 339 | BCG_0175 | oxidoreductase | 81.21 | 340 | MAP3556 | hypothetical protein | 339 | 100 |
| MAP4_0219 | hypothetical protein | 168 | Rv0138 | hypothetical protein | 75.9 | 167 | Mb0143 | hypothetical protein | 75.3 | 167 | MAV_5158 | hypothetical protein | 99.4 | 168 | BCG_0174 | hypothetical protein | 75.9 | 167 | MAP3555 | hypothetical protein | 168 | 100 |
| MAP4_0220 | peptide methionine sulfoxide reductase MsrA | 171 | Rv0137c | Probable peptide methionine sulfox | 85.96 | 182 | Mb0142c | methionine sulfoxide reducta | 85.96 | 182 | MAV_5159 | methionine sulfoxide reductase A | 100 | 171 | BCG_0173c | methionine sulfoxide reductase | 85.96 | 182 | MAP3554c | methionine sulfoxide reductase A | 171 | 100 |
| MAP4_0221 | Cytochrome P450 | 439 | Rv0136 | Probable cytochrome P450 138 Cyp1 | 76.39 | 441 | Mb0141 | cytochrome P450 138 | 76.39 | 441 | MAV_5160 | cytochrome P450 monooxygenase | 98.59 | 438 | BCG_0172 | cytochrome p450 138 cyp138 | 76.39 | 441 | MAP3553 | hypothetical protein | 439 | 100 |
| MAP4_0222 | Transcriptional regulator, TetR family | 201 | Rv0135c | Possible transcriptional regulatory p | 76 | 201 | Mb0140c | transcriptional regulator | 76 | 201 | MAV_5161 | TetR family transcriptional regulato | 100 | 201 | BCG_0171c | transcriptional regulatory prot | 76 | 201 | MAP3552c | hypothetical protein | 201 | 100 |
| MAP4_0223 | hypothetical protein | 70 | Rv1345 | Probable fatty acyl-AMP ligase MbtM | 32.73 | 521 | Mb1380 | long-chain-fatty-acid--CoA lig | 32.73 | 521 | MAV_5162 | molybdenum-binding protein | 100 | 70 | BCG_1407 | long-chain-fatty-acid--ACP ligas | 32.73 | 521 | MAP3551c | hypothetical protein | 70 | 100 |
| MAP4_0224 | epoxide hydrolase | 296 | Rv0134 | Possible epoxide hydrolase EphF (ep | 79.05 | 300 | Mb1973 | epoxide hydrolase | 41.79 | 356 | MAV_5163 | alpha/beta hydrolase | 100 | 296 | BCG_1977 | epoxide hydrolase ephB | 41.79 | 356 | MAP3550 | EphF | 296 | 100 |
| MAP4_0225 | hypothetical protein | 409 | Rv3529c | hypothetical protein | 30.35 | 384 | Mb3559c | hypothetical protein | 30.35 | 384 | MAV_5164 | hypothetical protein | 98.78 | 409 | BCG_3593c | hypothetical protein | 30.35 | 384 | MAP3549 | hypothetical protein | 386 | 100 |
| MAP4_0226 | Transcriptional regulator, TetR family | 191 | Rv3167c | Probable transcriptional regulatory | 49.19 | 208 | Mb3192c | TetR family transcriptional re | 49.19 | 208 | MAV_5165 | TetR family transcriptional regulato | 98.94 | 189 | BCG_3191c | TetR family transcriptional regu | 49.19 | 208 | MAP3548c | hypothetical protein | 223 | 100 |
| MAP4_0227 | hypothetical protein | 370 | Rv3531c | Hypothetical protein | 27.45 | 375 | Mb3561c | hypothetical protein | 27.45 | 375 | MAV_5166 | hypothetical protein | 99.46 | 370 | BCG_3595c | hypothetical protein | 27.45 | 375 | MAP3547c | hypothetical protein | 370 | 100 |
| MAP4_0228 | fatty acid desaturase | 366 | Rv3229c | Possible linoleoyl-CoA desaturase (d | 47.91 | 427 | Mb3258c | linoleoyl-CoA desaturase | 47.91 | 427 | MAV_5167 | Fatty acid desaturase | 99.18 | 366 | BCG_3259c | linoleoyl-CoA desaturase | 47.91 | 427 | MAP3546 | DesA3_2 | 366 | 100 |
| MAP4_0229 | putative oxidoreductase | 364 | Rv3230c | Hypothetical oxidoreductase | 35.57 | 380 | Mb3259c | oxidoreductase | 35.29 | 380 | MAV_5168 | oxidoreductase FAD-binding subun | 98.63 | 364 | BCG_3260c | oxidoreductase | 35.29 | 380 | MAP3545 | hypothetical protein | 364 | 100 |
| MAP4_0230 | Transcriptional regulator, TetR family | 224 | Rv0767c | hypothetical protein | 35.48 | 213 | Mb0790c | hypothetical protein | 35.48 | 213 | MAV_5169 | TetR family transcriptional regulato | 99.07 | 215 | BCG_0819c | hypothetical protein | 35.48 | 213 | MAP3544c | hypothetical protein | 250 | 99.55 |
| MAP4_0231 | hypothetical protein | 117 | Rv0719 | 50S ribosomal protein L6 RplF | 25.27 | 179 | Mb0740 | 50S ribosomal protein L6 | 25.27 | 179 | MAV_5170 | hypothetical protein | 99.07 | 107 | BCG_0769 | 50S ribosomal protein L6 | 25.27 | 179 | MAP3543 | hypothetical protein | 117 | 100 |
| MAP4_0232 | acetyltransferase | 201 | Rv0133 | GCN5-related N-acetyltransferase | 75.62 | 201 | Mb0138 | acetyltransferase | 75.12 | 201 | MAV_5171 | acetyltransferase, gnat family prote | 99.5 | 201 | BCG_0167 | acetyltransferase | 72.5 | 160 | MAP3542 | hypothetical protein | 201 | 100 |
| MAP4_0233 | F420-dependent glucose-6-phosphate dehydrogenase | 363 | Rv0132c | Putative F420-dependent glucose-6- | 74.1 | 360 | Mb0137c | F420-dependent glucose-6-ph | 73.83 | 360 | MAV_5172 | F420-dependent glucose-6-phosph | 99.05 | 622 | BCG_0166c | F420-dependent glucose-6-pho | 74.1 | 360 | MAP3541c | hypothetical protein | 376 | 99.72 |
| MAP4_0234 | hypothetical protein | 233 | Rv1190 | hypothetical protein | 40.43 | 292 | Mb1222 | hypothetical protein | 40.43 | 292 | MAV_5172 | F420-dependent glucose-6-phosph | 99.57 | 622 | BCG_3601 | 3-ketosteroid-delta-1-dehydrog | 31.58 | 563 | MAP3540c | hypothetical protein | 233 | 100 |
| MAP4_0235 | acyl-CoA dehydrogenase FadE1 | 449 | Rv0131c | Probable acyl-CoA dehydrogenase F | 90.16 | 447 | Mb0136c | acyl-CoA dehydrogenase | 90.16 | 447 | MAV_5173 | acyl-CoA dehydrogenase | 99.54 | 431 | BCG_0165c | acyl-CoA dehydrogenase fadE1 | 90.16 | 447 | MAP3539c | FadE1_3 | 449 | 100 |
| MAP4_0236 | hypothetical protein | 151 | Rv0130 | Probable 3-hydroxyl-thioester dehy | 90.07 | 151 | Mb0135 | hypothetical protein | 90.07 | 151 | MAV_5174 | ZbpA protein | 100 | 151 | BCG_0164 | hypothetical protein | 90.07 | 151 | MAP3538 | hypothetical protein | 151 | 100 |
| MAP4_0237 | putative hydrolase, alphabeta hydrolase family protein | 278 | Rv0554 | Possible peroxidase BpoC (non-haem | 27.54 | 262 | Mb0569 | peroxidase BpoC | 27.54 | 262 | MAV_5175 | non-haem bromoperoxidase BPO-A | 99.64 | 278 | BCG_0599 | peroxidase bpoC | 27.54 | 262 | MAP3537c | BpoC_1 | 278 | 100 |
| MAP4_0238 | hypothetical protein | 57 | Rv2156c | Probable phospho-N-acetylmuramoy | 28.3 | 359 | Mb2180c | phospho-N-acetylmuramoyl-p | 28.3 | 359 | MAV_5176 | hypothetical protein | 100 | 57 | BCG_2173c | phospho-N-acetylmuramoyl-pe | 28.3 | 359 | MAP2540c | hypothetical protein | 403 | 45.16 |
| MAP4_0239 | hypothetical protein | 133 | Rv1640c | Lysyl-tRNA synthetase 2 LysX | 62.5 | 1172 | Mb1667c | lysyl-tRNA synthetase | 62.5 | 1172 | MAV_5177 | hypothetical protein | 98.5 | 133 | BCG_1679c | lysyl-tRNA synthetase | 62.5 | 1172 | MAP3536 | hypothetical protein | 133 | 100 |
| MAP4_0240 | hypothetical protein | 100 | Rv1766 | hypothetical protein | 66.28 | 89 | Mb1795A | hypothetical protein | 66.28 | 89 | MAV_5178 | hypothetical protein | 100 | 100 | BCG_0227 | hypothetical protein | 40.68 | 96 | MAP3535 | hypothetical protein | 100 | 100 |
| MAP4_0241 | hypothetical protein | 184 | Rv3203 | Possible lipase LipV | 33.33 | 224 | Mb3228 | lipase LipV | 33.33 | 224 | MAV_5179 | hypothetical protein | 98.86 | 175 | BCG_3229 | lipase lipV | 33.33 | 224 | MAP3534c | hypothetical protein | 184 | 100 |
| MAP4_0242 | Transcriptional regulator, MarR family | 153 | Rv1333 | Probable hydrolase | 25.97 | 344 | Mb1368 | hydrolase | 25.97 | 344 | MAV_5180 | MarR family transcriptional regulat | 98.54 | 137 | BCG_1395 | hydrolase | 25.97 | 344 | MAP1328c | hypothetical protein | 262 | 39.53 |
| MAP4_0243 | ABC transporter, ATP-binding component | 280 | Rv2936 | Daunorubicin-dim-transport ATP-bin | 42.04 | 331 | Mb2961 | daunorubicin-DIM-transport A | 42.04 | 331 | MAV_5181 | daunorubicin ABC transporter ATPa | 98.21 | 280 | BCG_2958 | daunorubicin-DIM-transport AT | 42.04 | 331 | MAP3533c | hypothetical protein | 387 | 100 |
| MAP4_0244 | putative ABC-2 type transporter, membrane protein | 315 | Rv2938 | Probable daunorubicin-dim-transpor | 24.39 | 276 | Mb2963 | daunorubicin-DIM-transport i | 24.39 | 276 | MAV_5182 | drug ABC transporter membrane p | 97.05 | 272 | BCG_2960 | daunorubicin-DIM-transport in | 24.39 | 276 | MAP3532c | hypothetical protein | 315 | 100 |
| MAP4_0245 | secreted fibronectin-binding protein C antigen85-C Fbp | 352 | Rv0129c | Secreted antigen 85-C FbpC (85C) (a | 85.28 | 340 | Mb0134c | secreted antigen 85-C FbpC | 85.28 | 340 | MAV_5183 | antigen 85-C | 99.72 | 355 | BCG_0163c | hypothetical protein | 85.28 | 340 | MAP3531c | FbpC2 | 352 | 100 |
| MAP4_0246 | hypothetical protein | 228 | Rv0128 | Probable conserved transmembrane | 72.69 | 259 | Mb0133 | transmembrane protein | 72.69 | 259 | MAV_5184 | hypothetical protein | 100 | 228 | BCG_0162 | hypothetical protein | 72.69 | 259 | MAP3530 | hypothetical protein | 228 | 100 |
| MAP4_0247 | hypothetical protein | 452 | Rv0127 | Maltokinase Mak | 78.37 | 455 | Mb0132 | hypothetical protein | 79.06 | 455 | MAV_5185 | trehalose synthase-fused maltokina | 99.34 | 452 | BCG_0161 | hypothetical protein | 79.06 | 455 | MAP3529 | hypothetical protein | 452 | 100 |
| MAP4_0248 | trehalose synthase | 590 | Rv0126 | Trehalose synthase TreS | 90.82 | 601 | Mb0131 | trehalose synthase TRES | 90.82 | 601 | MAV_5186 | trehalose synthase | 100 | 590 | BCG_0160 | trehalose synthase treS | 90.82 | 601 | MAP3528 | hypothetical protein | 590 | 100 |
| MAP4_0249 | serine protease PepA | 361 | Rv0125 | Probable serine protease PepA (seri | 70.17 | 355 | Mb0130 | serine protease PepA | 70.17 | 355 | MAV_5187 | trypsin | 99.72 | 371 | BCG_0159 | serine protease pepA | 70.17 | 355 | MAP3527 | PepA | 361 | 100 |
| MAP4_0250 | hypothetical protein | 145 | Rv0121c | hypothetical protein | 67.13 | 144 | Mb0126c | hypothetical protein | 67.13 | 144 | MAV_5188 | pyridoxamine 5'-phosphate oxidase | 100 | 145 | BCG_0155c | hypothetical protein | 67.13 | 144 | MAP3526c | hypothetical protein | 145 | 100 |
| MAP4_0251 | translation elongation factor G FusA2 | 720 | Rv0120c | Probable elongation factor G FusA2 | 87.62 | 714 | Mb0124c | elongation factor G | 88.7 | 597 | MAV_5189 | elongation factor G | 99.58 | 720 | BCG_0154c | elongation factor G | 87.62 | 714 | MAP3525c | elongation factor G | 720 | 100 |
| MAP4_0252 | fatty-acid-CoA ligase FadD7 | 529 | Rv0119 | Probable fatty-acid-CoA ligase FadD7 | 70.94 | 525 | Mb0123 | acyl-CoA synthetase | 70.94 | 525 | MAV_5190 | acyl-CoA synthetase | 99.05 | 552 | BCG_0153 | acyl-CoA synthetase | 70.94 | 525 | MAP3524 | acyl-CoA synthetase | 529 | 100 |
| MAP4_0253 | oxalyl-CoA decarboxylase OxcA | 580 | Rv0118c | Probable oxalyl-CoA decarboxylase ( | 79.79 | 582 | Mb0122c | oxalyl-CoA decarboxylase | 79.97 | 582 | MAV_2895 | hypothetical protein | 32.09 | 548 | BCG_0152c | oxalyl-CoA decarboxylase | 79.97 | 582 | MAP3523c | oxalyl-CoA decarboxylase | 594 | 100 |
| MAP4_0254 | oxidative stress response regulatory protein | 310 | Rv0117 | Oxidative stress response regulatory | 76.75 | 314 | Mb0121 | oxidative stress response regu | 76.75 | 314 | MAV_5191 | LysR family transcriptional regulato | 99.03 | 310 | BCG_0151 | oxidative stress response regul | 76.75 | 314 | MAP3522 | OxyS_1 | 312 | 99.68 |
| MAP4_0255 | putative isochorismatase family protein | 250 | Rv2043c | Pyrazinamidase/nicotinamidase Pnc | 23.53 | 186 | Mb2069c | pyrazinamidase | 23.53 | 186 | MAV_5193 | isochorismatase | 98 | 250 | BCG_2062c | pyrazinamidase/nicotinamidas | 23.53 | 186 | MAP3521 | hypothetical protein | 250 | 100 |
| MAP4_0256 | hypothetical protein | 252 | Rv0116c | Probable L,D-transpeptidase LdtA | 73.31 | 251 | Mb0120c | hypothetical protein | 73.31 | 251 | MAV_5194 | ErfK/YbiS/YcfS/YnhG family protein | 99.59 | 242 | BCG_0150c | hypothetical protein | 73.31 | 251 | MAP3520c | hypothetical protein | 252 | 100 |
| MAP4_0257 | hypothetical protein | 199 | Rv2796c | Probable conserved lipoprotein LppV | 31.71 | 187 | Mb2819c | lipoprotein LppV | 31.71 | 187 | MAV_5195 | hypothetical protein | 99.5 | 199 | BCG_2814c | lipoprotein lppV | 31.71 | 187 | MAP3519 | hypothetical protein | 205 | 99.5 |
| MAP4_0258 | putative oxidoreductase | 314 | Rv1454c | Probable quinone reductase Qor (NA | 30.03 | 328 | Mb1489c | quinone reductase | 30.03 | 328 | MAV_5196 | zinc-binding dehydrogenase | 99.36 | 314 | BCG_1515c | quinone reductase qor | 30.03 | 328 | MAP3518c | hypothetical protein | 341 | 100 |
| MAP4_0259 | putative cation-transport membrane protein | 589 | Rv0924c | Divalent cation-transport integral m | 26.35 | 428 | Mb0948c | manganese transport protein | 26.79 | 684 | MAV_5197 | manganese/iron transporter | 99.49 | 586 | BCG_0976c | manganese transport protein M | 26.12 | 428 | MAP3517 | hypothetical protein | 589 | 100 |
| MAP4_0260 | hypothetical protein | 71 | Rv2008c | hypothetical protein | 27.78 | 441 | Mb2031c | hypothetical protein | 27.78 | 441 | MAV_5198 | hypothetical protein | 100 | 52 | BCG_2025c | hypothetical protein | 27.78 | 441 | MAP3516 | hypothetical protein | 71 | 100 |
| MAP4_0261 | O-methyltransferase | 219 | Rv1703c | Probable catechol-O-methyltransfer | 36.96 | 196 | Mb1729c | catechol-o-methyltransferase | 36.96 | 196 | MAV_5200 | O-methyltransferase, family protei | 98.17 | 219 | BCG_1741c | catechol-o-methyltransferase | 37.68 | 196 | MAP3515c | hypothetical protein | 203 | 100 |
| MAP4_0262 | transmembrane acyltransferase | 689 | Rv0111 | Possible transmembrane acyltransfe | 82.82 | 685 | Mb0115 | transmembrane acyltransfera | 82.82 | 685 | MAV_5201 | acyltransferase | 98.95 | 664 | BCG_0144 | acyltransferase | 82.82 | 685 | MAP3514 | hypothetical protein | 689 | 100 |
| MAP4_0263 | aldehyde dehydrogenase | 478 | Rv0223c | Probable aldehyde dehydrogenase | 41.68 | 487 | Mb0791 | aldehyde dehydrogenase | 40.67 | 489 | MAV_5202 | aldehyde dehydrogenase | 99.37 | 478 | BCG_0820 | aldehyde dehydrogenase AldA | 40.67 | 489 | MAP3513 | hypothetical protein | 478 | 100 |
| MAP4_0264 | thiamine pyrophosphate-requiring enzyme s | 568 | Rv1820 | Probable acetolactate synthase IlvG | 27.37 | 547 | Mb1851 | hypothetical protein | 27.37 | 547 | MAV_5203 | thiamine pyrophosphate-binding p | 99.65 | 568 | BCG_1855 | hypothetical protein | 27.37 | 547 | MAP3512 | hypothetical protein | 568 | 100 |
| MAP4_0265 | putative CoA-transferase family protein | 389 | Rv3272 | hypothetical protein | 33.13 | 394 | Mb3300 | hypothetical protein | 30.28 | 394 | MAV_5204 | L-carnitine dehydratase/bile acid-i | 90.93 | 379 | BCG_3301 | hypothetical protein | 30.03 | 394 | MAP3511 | hypothetical protein | 389 | 100 |
| MAP4_0266 | putative short-chain dehydrogenase reductase | 316 | Rv0148 | Probable short-chain type dehydrog | 47.04 | 286 | Mb0153 | short-chain type dehydrogena | 47.04 | 286 | MAV_5205 | oxidoreductase, short chain dehydr | 99.01 | 302 | BCG_0184 | short-chain type dehydrogenas | 47.04 | 286 | MAP3510 | hypothetical protein | 316 | 100 |
| MAP4_0267 | monooxygenase | 615 | Rv1393c | Probable monoxygenase | 29.61 | 492 | Mb1428c | monoxygenase | 29.61 | 492 | MAV_5206 | cyclododecanone monooxygenase | 99.67 | 619 | BCG_1454c | monoxygenase | 29.61 | 492 | MAP3509 | hypothetical protein | 615 | 100 |
| MAP4_0268 | putative iron-sulfur protein, rieske (2Fe-2S) iron-sulfur | 466 | Rv3161c | Possible dioxygenase | 29.41 | 382 | Mb3186c | dioxygenase | 29.9 | 382 | MAV_5207 | Rieske (2Fe-2S) domain-containing | 100 | 466 | BCG_3185c | dioxygenase | 29.9 | 382 | MAP3508 | hypothetical protein | 467 | 100 |
| MAP4_0269 | oxidoreductase, short chaindehydrogenase/reductase | 282 | Rv0927c | Probable short-chain type dehydrog | 38.34 | 263 | Mb0950c | short chain dehydrogenase | 38.34 | 263 | MAV_5208 | oxidoreductase, short chain dehydr | 98.52 | 271 | BCG_0979c | short chain dehydrogenase | 38.34 | 263 | MAP3507 | hypothetical protein | 282 | 100 |
| MAP4_0270 | hypothetical protein | 560 | Rv0931c | Transmembrane serine/threonine-p | 29.06 | 664 | Mb0954c | serine/threonine protein kina | 29.06 | 369 | MAV_5210 | hypothetical protein | 98.86 | 525 | BCG_0983c | Ser/Thr protein kinase | 29.06 | 369 | MAP3506c | hypothetical protein | 560 | 100 |
| MAP4_0271 | Transcriptional regulator, GntR family | 249 | Rv0792c | Probable transcriptional regulatory | 27.39 | 269 | Mb0816c | GntR family transcriptional re | 27.39 | 269 | MAV_5211 | GntR family transcriptional regulato | 99.6 | 249 | BCG_0845c | GntR family transcriptional reg | 27.39 | 269 | MAP3505c | hypothetical protein | 249 | 100 |
| MAP4_0272 | putative AMP-binding enzyme | 538 | Rv3089 | Probable chain-fatty-acid-CoA ligase | 29.17 | 503 | Mb3116 | chain-fatty-acid-CoA ligase | 29.17 | 503 | MAV_5212 | AMP-binding enzyme, putative | 98.33 | 538 | BCG_3114 | chain-fatty-acid-CoA ligase fad | 29.17 | 503 | MAP3504c | hypothetical protein | 517 | 99.81 |
| MAP4_0273 | putative oxidoreductase, short chain dehydrogenase/re | 257 | Rv2857c | Probable short-chain type dehydrog | 32.52 | 258 | Mb2882c | short chain dehydrogenase | 32.52 | 258 | MAV_5213 | oxidoreductase, short chain dehydr | 99.22 | 257 | BCG_2879c | short chain dehydrogenase | 32.52 | 258 | MAP3503c | hypothetical protein | 260 | 100 |
| MAP4_0274 | zinc-type alcohol dehydrogenase NAD dependent | 386 | Rv0761c | Possible zinc-containing alcohol deh | 45.69 | 375 | Mb0784c | NAD dependent zinc-containi | 45.69 | 375 | MAV_5214 | alcohol dehydrogenase B | 98.42 | 380 | BCG_0813c | zinc-containing alcohol dehydr | 45.69 | 375 | MAP3502 | AdhD | 386 | 100 |
| MAP4_0275 | hypothetical protein | 164 | Rv1129c | Probable transcriptional regulator p | 38.71 | 486 | Mb1160c | transcriptional regulator | 38.71 | 486 | MAV_5215 | hypothetical protein | 99.39 | 164 | BCG_1190c | transcriptional regulator protei | 38.71 | 486 | MAP3501 | hypothetical protein | 164 | 100 |
| MAP4_0276 | hypothetical protein | 158 | Rv0310c | hypothetical protein | 32.05 | 163 | Mb0318c | hypothetical protein | 32.05 | 163 | MAV_5216 | hypothetical protein | 96.75 | 123 | BCG_0350c | hypothetical protein | 32.05 | 163 | MAP3500c | hypothetical protein | 158 | 100 |
| MAP4_0277 | hypothetical protein | 65 | Rv0108c | Hypothetical protein | 82.61 | 69 | Mb0112c | hypothetical protein | 82.61 | 69 | MAV_5217 | hypothetical protein | 98.46 | 76 | BCG_0141c | hypothetical protein | 82.61 | 69 | MAP3499c | hypothetical protein | 65 | 100 |
| MAP4_0278 | hypothetical protein | 103 | Rv2885c | Probable transposase | 30.23 | 460 | Mb2909c | transposase | 30.3 | 439 | MAV_5218 | hypothetical protein | 97.09 | 103 | BCG_2906c | transposase | 30.3 | 439 | MAP1176c | glucose-6-phosphate 1-dehydrogenase | 514 | 35.71 |
| MAP4_0279 | cation-transporting ATPase I | 1611 | Rv0107c | Probable cation-transporter ATPase | 83.71 | 1632 | Mb0111c | cation-transporter ATPase I | 83.26 | 1625 | MAV_5219 | ATPase P | 99.75 | 1592 | BCG_0140c | cation-transporter atpase I ctp | 83.26 | 1625 | MAP3498c | CtpI | 1611 | 100 |
| MAP4_0280 | long-chain fatty-acid-CoA ligase | 521 | Rv1427c | Possible long-chain-fatty-acid--CoA l | 41.12 | 535 | Mb1462c | acyl-CoA synthetase | 41.12 | 535 | MAV_5220 | acyl-CoA synthetase | 98.45 | 516 | BCG_1488c | acyl-CoA synthetase | 41.12 | 535 | MAP3497 | acyl-CoA synthetase | 521 | 100 |
| MAP4_0281 | fatty-acyl-CoA reductase | 312 | Rv1543 | Possible fatty acyl-CoA reductase | 43.38 | 341 | Mb1570 | fatty acyl-CoA reductase | 43.38 | 341 | MAV_5221 | NAD dependent epimerase/dehydr | 99.68 | 312 | BCG_1595 | fatty acyl-CoA reductase | 43.38 | 341 | MAP3496 | hypothetical protein | 312 | 100 |
| MAP4_0282 | cutinase Cut1 | 255 | Rv1758 | Probable cutinase Cut1 | 54.12 | 174 | Mb1788 | cutinase | 57.29 | 218 | MAV_2169 | serine esterase cutinase | 87.85 | 252 | BCG_1798 | cutinase cut1 | 57.29 | 218 | MAP3495c | hypothetical protein | 255 | 100 |
| MAP4_0283 | hypothetical protein | 468 | Rv0223c | Probable aldehyde dehydrogenase | 24.92 | 487 | Mb0228c | aldehyde dehydrogenase | 24.57 | 385 | MAV_5223 | hypothetical protein | 98.72 | 468 | BCG_0259c | aldehyde dehydrogenase | 26.07 | 269 | MAP3494 | hypothetical protein | 468 | 100 |
| MAP4_0284 | hypothetical protein | 362 | Rv2569c | hypothetical protein | 28.21 | 314 | Mb2599c | hypothetical protein | 28.21 | 314 | MAV_5224 | hypothetical protein | 98.62 | 396 | BCG_2592c | hypothetical protein | 28.21 | 314 | MAP3493 | hypothetical protein | 362 | 100 |
| MAP4_0285 | putative glycosyl hydrolase | 791 | Rv3401 | hypothetical protein | 86.01 | 786 | Mb3434 | hypothetical protein | 85.88 | 786 | MAV_4352 | glycoside hydrolase 65, central cata | 99.75 | 791 | BCG_3471 | hypothetical protein | 86.01 | 786 | MAP3492 | hypothetical protein | 791 | 100 |
| MAP4_0286 | hydrolase | 262 | Rv3400 | Probable hydrolase | 77.27 | 262 | Mb3433 | hydrolase | 77.27 | 262 | MAV_4350 | beta-phosphoglucomutase hydrola | 98.85 | 262 | BCG_3470 | hydrolase | 77.27 | 262 | MAP3491 | hypothetical protein | 262 | 100 |
| MAP4_0287 | PPE family protein | 531 | Rv0280 | PPE family protein PPE3 | 57.69 | 536 | Mb0288 | PPE family protein | 57.69 | 536 | MAV_4349 | PPE family protein | 98.31 | 529 | BCG_0320 | PPE family protein | 57.69 | 536 | MAP3490 | hypothetical protein | 531 | 100 |
| MAP4_0288 | GMP synthase | 525 | Rv3396c | Probable GMP synthase [glutamine- | 89.33 | 525 | Mb3429c | GMP synthase | 89.33 | 525 | MAV_4348 | GMP synthase | 99.61 | 509 | BCG_3466c | GMP synthase | 89.33 | 525 | MAP3489c | GMP synthase | 525 | 100 |
| MAP4_0289 | hypothetical protein | 229 | Rv3395c | hypothetical protein | 72.56 | 204 | Mb3427c | hypothetical protein | 71.63 | 204 | MAV_4346 | hypothetical protein | 99.13 | 229 | BCG_3464c | hypothetical protein | 71.63 | 204 | MAP3488c | hypothetical protein | 300 | 100 |
| MAP4_0290 | hypothetical protein | 527 | Rv3394c | hypothetical protein | 83.4 | 527 | Mb3426c | hypothetical protein | 83.4 | 527 | MAV_4344 | hypothetical protein | 99.61 | 513 | BCG_3463c | hypothetical protein | 83.4 | 527 | MAP3487c | hypothetical protein | 527 | 100 |
| MAP4_0291 | lactate 2-monooxygenase | 392 | Rv0694 | Possible L-lactate dehydrogenase (cy | 31.59 | 396 | Mb0713 | L-lactate dehydrogenase (cyto | 31.59 | 396 | MAV_4345 | lactate 2-monooxygenase | 98.72 | 392 | BCG_0743 | L-lactate dehydrogenase (cytoc | 31.59 | 396 | MAP3486 | hypothetical protein | 392 | 100 |
| MAP4_0292 | 3-oxoacyl-ACP synthase | 419 | Rv2246 | 3-oxoacyl-[acyl-carrier protein] synt | 85.68 | 438 | Mb2270 | 3-oxoacyl-ACP synthase | 85.68 | 438 | MAV_4343 | 3-oxoacyl-(acyl carrier protein) syn | 97.61 | 419 | BCG_2263 | 3-oxoacyl-ACP synthase | 85.68 | 438 | MAP3485 | 3-oxoacyl-ACP synthase II | 419 | 100 |
| MAP4_0293 | nucleoside hydrolase IunH | 343 | Rv3393 | Probable nucleoside hydrolase IunH | 60.95 | 308 | Mb3425 | nucleoside hydrolase IunH | 60.95 | 308 | MAV_4342 | inosine-uridine preferring nucleosi | 98.25 | 346 | BCG_3462 | nucleoside hydrolase iunH | 60.95 | 308 | MAP3484 | IunH | 343 | 100 |
| MAP4_0294 | hypothetical protein | 151 | Rv1256c | Probable cytochrome P450 130 Cyp1 | 50 | 405 | Mb0537 | glutamate-1-semialdehyde ar | 28.57 | 462 | MAV_2824 | hypothetical protein | 29.58 | 392 | BCG_0567 | glutamate-1-semialdehyde ami | 28.57 | 462 | MAP3483 | hypothetical protein | 151 | 100 |
| MAP4_0295 | acyl-CoA reductase AcrA1 | 675 | Rv3391 | Possible multi-functional enzyme wi | 79.11 | 650 | Mb3423 | short chain dehydrogenase | 79.11 | 650 | MAV_4340 | short chain dehydrogenase | 98.96 | 685 | BCG_3460 | short chain dehydrogenase | 79.11 | 650 | MAP3482 | short chain dehydrogenase | 675 | 100 |
| MAP4_0296 | lipoprotein LpqD | 237 | Rv3390 | Probable conserved lipoprotein Lpq | 66.81 | 236 | Mb3422 | lipoprotein LpqD | 66.81 | 236 | MAV_4339 | phosphoglycerate mutase | 98.23 | 226 | BCG_3459 | lipoprotein lpqD | 66.81 | 236 | MAP3481 | hypothetical protein | 237 | 100 |
| MAP4_0297 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_0298 | dehydrogenase | 288 | Rv3389c | Probable 3-hydroxyacyl-thioester de | 84.32 | 290 | Mb3421c | dehydrogenase | 83.97 | 290 | MAV_4337 | MaoC family protein | 100 | 288 | BCG_3458c | dehydrogenase | 84.32 | 290 | MAP3479c | hypothetical protein | 288 | 100 |
| MAP4_0299 | trehalose-6-phosphate phosphatase | 391 | Rv3372 | Trehalose 6-phosphate phosphatase | 72.31 | 391 | Mb3407 | trehalose 6-phosphate phosp | 72.31 | 391 | MAV_4338 | glycosyl hydrolase | 97.7 | 391 | BCG_3444 | trehalose 6-phosphate phosph | 72.31 | 391 | MAP3478 | OtsB2 | 391 | 100 |
| MAP4_0300 | putative acyltransferase, wsdgatmgat subfamily protei | 424 | Rv3371 | Possible triacylglycerol synthase (dia | 52.05 | 446 | Mb3406 | hypothetical protein | 51.41 | 446 | MAV_4336 | acyltransferase, ws/dgat/mgat sub | 96.96 | 441 | BCG_3443 | hypothetical protein | 51.41 | 446 | MAP3477 | hypothetical protein | 424 | 100 |
| MAP4_0301 | DNA polymerase III alpha subunit | 1093 | Rv3370c | Probable DNA polymerase III (alpha | 89.28 | 1079 | Mb3405c | error-prone DNA polymerase | 89.31 | 1091 | MAV_4335 | error-prone DNA polymerase | 98.9 | 1093 | BCG_3442c | error-prone DNA polymerase | 89.19 | 1079 | MAP3476c | error-prone DNA polymerase | 1093 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0302 | putative oxidoreductase | 215 | Rv3368c | Possible oxidoreductase | 80 | 214 | Mb3403c | oxidoreductase | 80 | 214 | MAV_4334 | nitroreductase | 99.07 | 215 | BCG_3440c | oxidoreductase | 80 | 214 | MAP3475c | hypothetical protein | 215 | 100 |
| MAP4_0303 | tRNArRNA methylase SpoU | 154 | Rv3366 | Probable tRNA/rRNA methylase Spo | 84.31 | 154 | Mb3401 | tRNA/rRNA methylase SpoU | 84.31 | 154 | MAV_4333 | RNA methyltransferase, TrmH fami | 99.35 | 154 | BCG_3438 | tRNA/rRNA methylase spoU | 84.31 | 154 | MAP3474 | hypothetical protein | 154 | 100 |
| MAP4_0304 | putative methyltransferase | 201 | Rv0089 | Possible methyltransferase/methyla | 39.02 | 197 | Mb0092 | methyltransferase/methylase | 39.02 | 197 | MAV_4332 | SAM-dependent methyltransferase | 99 | 201 | BCG_0122 | methyltransferase/methylase | 39.02 | 197 | MAP3473c | hypothetical protein | 201 | 100 |
| MAP4_0305 | hypothetical protein | 944 | Rv3365c | hypothetical protein | 67.61 | 876 | Mb3400c | hypothetical protein | 67.61 | 876 | MAV_4331 | hypothetical protein | 97.36 | 947 | BCG_3437c | hypothetical protein | 67.61 | 876 | MAP3472c | hypothetical protein | 944 | 100 |
| MAP4_0306 | hypothetical protein | 140 | Rv3364c | hypothetical protein | 90.4 | 130 | Mb3399c | hypothetical protein | 90.4 | 130 | MAV_4330 | roadblock/LC7 domain-contain pro | 99.29 | 140 | BCG_3436c | hypothetical protein | 89.6 | 130 | MAP3471c | hypothetical protein | 140 | 100 |
| MAP4_0307 | hypothetical protein | 124 | Rv3363c | hypothetical protein | 75.22 | 122 | Mb3398c | hypothetical protein | 75.22 | 122 | MAV_4329 | hypothetical protein | 99.19 | 124 | BCG_3435c | hypothetical protein | 75.22 | 122 | MAP3470c | hypothetical protein | 124 | 100 |
| MAP4_0308 | ATPGTP-binding protein | 195 | Rv3362c | Probable ATP/GTP-binding protein | 84.97 | 193 | Mb3397c | ATP/GTP-binding protein | 84.97 | 193 | MAV_4328 | ATP/GTP-binding protein | 100 | 195 | BCG_3434c | ATP/GTP-binding protein | 84.97 | 193 | MAP3469c | hypothetical protein | 195 | 100 |
| MAP4_0309 | hypothetical protein | 137 | Rv3361c | hypothetical protein | 55.49 | 183 | Mb3396c | hypothetical protein | 55.49 | 183 | MAV_4327 | hypothetical protein | 74.73 | 185 | BCG_3433c | hypothetical protein | 55.49 | 183 | MAP3468c | hypothetical protein | 137 | 100 |
| MAP4_0310 | transposase, IS4 family protein | 557 | Rv3386 | Possible transposase | 25.95 | 234 | Mb3418 | transposase | 25.95 | 234 | MAV_3010 | ABC transporter ATP-binding prote | 29.31 | 862 | BCG_3455 | transposase | 25.95 | 234 | MAP0338c | hypothetical protein | 557 | 100 |
| MAP4_0311 | conserved transmembrane ATP-binding protein ABC tr | 812 | Rv1747 | Probable conserved transmembrane | 62.18 | 865 | Mb1776 | ABC transporter ATP-binding | 62.18 | 865 | MAV_4326 | ABC transporter ATP-binding prote | 99.14 | 812 | BCG_1786 | transmembrane ABC transport | 62.18 | 865 | MAP3466 | hypothetical protein | 822 | 99.88 |
| MAP4_0312 | conserved transmembrane ATP-binding protein ABC tr | 873 | Rv1747 | Probable conserved transmembrane | 62.56 | 865 | Mb1776 | ABC transporter ATP-binding | 62.56 | 865 | MAV_4325 | ABC transporter ATP-binding prote | 99.65 | 846 | BCG_1786 | transmembrane ABC transport | 62.56 | 865 | MAP3465 | hypothetical protein | 873 | 100 |
| MAP4_0313 | oxidoreductase | 405 | Rv3359 | Possible oxidoreductase | 83.97 | 396 | Mb3394 | oxidoreductase | 83.97 | 396 | MAV_4324 | oxidoreductase, FAD/FMN-binding | 99.01 | 405 | BCG_3431 | oxidoreductase | 83.97 | 396 | MAP3464 | hypothetical protein | 405 | 100 |
| MAP4_0314 | bifunctional methylene tetra hydrofolate dehydrogena | 281 | Rv3356c | Probable bifunctional protein FolD: | 92.53 | 281 | Mb3391c | bifunctional 5,10-methylene- | 92.17 | 281 | MAV_4323 | bifunctional 5,10-methylene-tetrah | 99.29 | 281 | BCG_3428c | bifunctional 5,10-methylene-te | 92.17 | 281 | MAP3463c | bifunctional 5,10-methylene-tetrahydro | 281 | 100 |
| MAP4_0315 | hypothetical protein | 93 | Rv3355c | Probable integral membrane protein | 78.35 | 97 | Mb3390c | hypothetical protein | 78.35 | 97 | MAV_4322 | hypothetical protein | 98.92 | 93 | BCG_3427c | hypothetical protein | 78.35 | 97 | MAP3462c | hypothetical protein | 93 | 100 |
| MAP4_0316 | hypothetical protein | 167 | Rv3354 | hypothetical protein | 51.59 | 129 | Mb3389 | hypothetical protein | 51.59 | 129 | MAV_4321 | hypothetical protein | 100 | 167 | BCG_3426 | hypothetical protein | 51.59 | 129 | MAP3461 | hypothetical protein | 203 | 99.4 |
| MAP4_0317 | REP13E12 repeat protein | 462 | Rv1702c | hypothetical protein | 65.34 | 454 | Mb1728c | hypothetical protein | 65.34 | 454 | MAV_3043 | hypothetical protein | 92.81 | 447 | BCG_1740c | hypothetical protein | 65.34 | 454 | MAP3460c | hypothetical protein | 461 | 99.78 |
| MAP4_0318 | methyltransferasemethylase | 243 | Rv3342 | Possible methyltransferase (methyla | 85.19 | 243 | Mb3374 | methyltransferase | 85.19 | 243 | MAV_4317 | methyltransferase | 99.59 | 243 | BCG_3412 | methyltransferase | 85.19 | 243 | MAP3459 | hypothetical protein | 243 | 100 |
| MAP4_0319 | homoserine O-acetyltransferase | 392 | Rv3341 | Probable homoserine O-acetyltransf | 81.91 | 379 | Mb3373 | homoserine O-acetyltransfera | 81.91 | 379 | MAV_4316 | homoserine O-acetyltransferase | 99.74 | 392 | BCG_3411 | homoserine O-acetyltransferas | 81.91 | 379 | MAP3458 | homoserine O-acetyltransferase | 392 | 100 |
| MAP4_0320 | O-acetylhomoserine sulfhydrylase MetC | 456 | Rv3340 | Probable O-acetylhomoserine sulfhy | 89.04 | 449 | Mb3372 | O-acetylhomoserine aminoca | 89.04 | 449 | MAV_4315 | O-acetylhomoserine aminocarboxy | 99.78 | 456 | BCG_3410 | O-acetylhomoserine aminocar | 88.82 | 449 | MAP3457 | O-acetylhomoserine aminocarboxyprop | 456 | 100 |
| MAP4_0321 | hypothetical protein | 82 | Rv3573c | Probable acyl-CoA dehydrogenase F | 33.96 | 711 | Mb3604c | acyl-CoA dehydrogenase | 33.96 | 711 | MAV_4314 | hypothetical protein | 98.7 | 77 | BCG_3638c | acyl-CoA dehydrogenase fadE3 | 33.96 | 711 | MAP0492 | FadE34 | 707 | 32.08 |
| MAP4_0322 | isocitrate dehydrogenase Icd2 | 745 | Rv0066c | Probable isocitrate dehydrogenase [ | 84.68 | 745 | Mb0067c | isocitrate dehydrogenase | 84.54 | 745 | MAV_4313 | isocitrate dehydrogenase, NADP-de | 99.87 | 745 | BCG_0097c | isocitrate dehydrogenase | 84.54 | 745 | MAP3456c | Icd2 | 745 | 100 |
| MAP4_0323 | isocitrate dehydrogenase Icd1 | 412 | Rv3339c | Probable isocitrate dehydrogenase [ | 88.48 | 409 | Mb3371c | isocitrate dehydrogenase | 88.48 | 409 | MAV_4311 | isocitrate dehydrogenase | 99.27 | 412 | BCG_3409c | isocitrate dehydrogenase | 88.24 | 409 | MAP3455c | isocitrate dehydrogenase | 412 | 100 |
| MAP4_0324 | putative hydrolase, alphabeta fold family protein | 284 | Rv3338 | hypothetical protein | 75.36 | 214 | Mb3370 | hypothetical protein | 73.9 | 297 | MAV_4312 | alpha/beta hydrolase | 98.49 | 265 | BCG_3408 | hypothetical protein | 73.9 | 297 | MAP3454 | hypothetical protein | 284 | 100 |
| MAP4_0325 | tryptophanyl-tRNA synthetase | 343 | Rv3336c | Probable tryptophanyl-tRNA synthet | 86.43 | 336 | Mb3369c | tryptophanyl-tRNA synthetas | 86.43 | 336 | MAV_4310 | tryptophanyl-tRNA synthetase | 99.71 | 343 | BCG_3407c | tryptophanyl-tRNA synthetase | 86.43 | 336 | MAP3453c | tryptophanyl-tRNA synthetase | 343 | 100 |
| MAP4_0326 | putative conserved membrane protein | 342 | Rv3335c | Probable conserved integral membr | 67.86 | 289 | Mb3368c | hypothetical protein | 67.86 | 289 | MAV_2739 | hypothetical protein | 29.46 | 324 | BCG_3406c | integral membrane protein | 67.5 | 289 | MAP3452c | hypothetical protein | 342 | 100 |
| MAP4_0327 | small multidrug resistance protein | 104 | Rv3065 | Multidrugs-transport integral memb | 30.68 | 107 | Mb3092 | multidrugs-transport integral | 30.68 | 107 | MAV_4309 | multidrug resistance protein, SMR | 100 | 104 | BCG_3090 | multidrugs-transport integral | 30.68 | 107 | MAP3451 | SugE | 129 | 100 |
| MAP4_0329 | sugar-transport integral membrane protein SugI | 450 | Rv3331 | Probable sugar-transport integral m | 69.47 | 502 | Mb3364 | sugar-transport integral mem | 69.47 | 502 | MAV_4306 | transporter, major facilitator super | 99.11 | 450 | BCG_3401 | sugar-transport integral memb | 69.03 | 497 | MAP3449 | SugI | 450 | 100 |
| MAP4_0330 | penicillin-binding protein dacB1 | 394 | Rv3330 | Probable penicillin-binding protein D | 82.28 | 405 | Mb3363 | penicillin-binding protein Dac | 82.28 | 405 | MAV_4305 | D-alanyl-D-alanine carboxypeptidas | 99.24 | 419 | BCG_3400 | penicillin-binding protein dacB | 82.28 | 405 | MAP3448 | hypothetical protein | 394 | 100 |
| MAP4_0332 | aminotransferase | 437 | Rv3329 | Probable aminotransferase | 83.49 | 438 | Mb3362 | hypothetical protein | 83.72 | 438 | MAV_4304 | hypothetical protein | 99.31 | 443 | BCG_3399 | hypothetical protein | 83.72 | 438 | MAP3447 | hypothetical protein | 437 | 100 |
| MAP4_0333 | RNA polymerase sigma factor SigJ | 295 | Rv3328c | Probable alternative RNA polymeras | 79.79 | 312 | Mb3361c | RNA polymerase sigma factor | 80.14 | 312 | MAV_4301 | RNA polymerase sigma factor SigJ | 99.3 | 318 | BCG_3398c | RNA polymerase sigma factor S | 80.14 | 312 | MAP3446c | RNA polymerase sigma factor SigJ | 295 | 100 |
| MAP4_0334 | hypothetical protein | 252 | Rv3327 | Probable transposase fusion protein | 73.06 | 570 | Mb3360 | transposase | 73.06 | 570 | MAV_4302 | transposase | 98.53 | 204 | BCG_3397 | transposase fusion protein | 73.06 | 570 | MAP3445 | hypothetical protein | 252 | 100 |
| MAP4_0335 | succinate dehydrogenase iron-sulfur proteinsubunit Sd | 267 | Rv3319 | Probable succinate dehydrogenase ( | 90.64 | 263 | Mb3348 | succinate dehydrogenase iro | 90.64 | 263 | MAV_4300 | succinate dehydrogenase iron-sulfu | 99.63 | 267 | BCG_3385 | succinate dehydrogenase iron- | 90.64 | 263 | MAP3444 | succinate dehydrogenase iron-sulfur su | 267 | 100 |
| MAP4_0336 | succinate dehydrogenase flavoprotein subunit SdhA | 584 | Rv3318 | Probable succinate dehydrogenase ( | 93.73 | 590 | Mb3347 | succinate dehydrogenase flav | 93.73 | 590 | MAV_4299 | succinate dehydrogenase flavoprot | 100 | 584 | BCG_3384 | succinate dehydrogenase flavo | 93.73 | 590 | MAP3443 | succinate dehydrogenase flavoprotein s | 584 | 100 |
| MAP4_0337 | succinate dehydrogenase hydrophobic membrane anch | 156 | Rv3317 | Probable succinate dehydrogenase ( | 86.62 | 144 | Mb3346 | succinate dehydrogenase hyd | 87.32 | 144 | MAV_4298 | succinate dehydrogenase hydroph | 99.36 | 156 | BCG_3383 | succinate dehydrogenase (hyd | 87.32 | 144 | MAP3442 | SdhD | 156 | 100 |
| MAP4_0338 | succinate dehydrogenase cytochrome B-556 subunit Sc | 151 | Rv3316 | Probable succinate dehydrogenase ( | 84.82 | 112 | Mb3345 | succinate dehydrogenase cyt | 84.82 | 112 | MAV_4297 | succinate dehydrogenase, cytochro | 100 | 112 | BCG_3382 | succinate dehydrogenase (cyto | 84.82 | 112 | MAP3441 | hypothetical protein | 151 | 100 |
| MAP4_0339 | cytidine deaminase | 133 | Rv3315c | Probable cytidine deaminase Cdd (c | 78.03 | 133 | Mb3344c | cytidine deaminase | 78.03 | 133 | MAV_4296 | cytidine deaminase | 99.25 | 133 | BCG_3381c | cytidine deaminase | 78.03 | 133 | MAP3440c | cytidine deaminase | 133 | 100 |
| MAP4_0340 | thymidine phosphorylase | 427 | Rv3314c | Probable thymidine phosphorylase D | 82.94 | 427 | Mb3343c | thymidine phosphorylase | 82.7 | 427 | MAV_4295 | thymidine phosphorylase | 98.59 | 427 | BCG_3380c | thymidine phosphorylase | 82.7 | 427 | MAP3439c | thymidine phosphorylase | 427 | 100 |
| MAP4_0341 | adenosine deaminase | 366 | Rv3313c | Probable adenosine deaminase Add | 84.15 | 365 | Mb3342c | adenosine deaminase | 84.15 | 365 | MAV_4294 | adenosine deaminase | 100 | 366 | BCG_3379c | adenosine deaminase | 84.15 | 365 | MAP3438c | adenosine deaminase | 366 | 100 |
| MAP4_0342 | hypothetical protein | 280 | Rv3586 | hypothetical protein | 25.97 | 358 | Mb3617 | DNA integrity scanning protei | 25.97 | 358 | MAV_1459 | XRE family transcriptional regulator | 31.25 | 65 | BCG_3651 | DNA integrity scanning protein | 25.97 | 358 | MAP3437c | hypothetical protein | 280 | 100 |
| MAP4_0343 | hypothetical protein | 231 | Rv3401 | hypothetical protein | 30.88 | 786 | Mb3434 | hypothetical protein | 30.88 | 786 | MAV_0227 | hypothetical protein | 28.05 | 207 | BCG_3471 | hypothetical protein | 30.88 | 786 | MAP3436c | hypothetical protein | 231 | 100 |
| MAP4_0344 | hypothetical protein | 335 | Rv1481 | Probable membrane protein | 64.07 | 335 | Mb1517 | hypothetical protein | 64.07 | 335 | MAV_4290 | hypothetical protein | 98.81 | 335 | BCG_1543 | hypothetical protein | 64.07 | 335 | MAP3435c | hypothetical protein | 335 | 100 |
| MAP4_0345 | hypothetical protein | 327 | Rv1481 | Probable membrane protein | 57.44 | 335 | Mb1517 | hypothetical protein | 57.44 | 335 | MAV_3297 | hypothetical protein | 56.25 | 335 | BCG_1543 | hypothetical protein | 57.74 | 335 | MAP3434 | hypothetical protein | 330 | 99.69 |
| MAP4_0346 | hypothetical protein | 437 | Rv3311 | hypothetical protein | 74.31 | 420 | Mb3339 | hypothetical protein | 74.31 | 420 | MAV_4288 | hypothetical protein | 99.31 | 437 | BCG_3376 | hypothetical protein | 74.31 | 420 | MAP3433 | hypothetical protein | 437 | 100 |
| MAP4_0347 | putative acid phosphatase | 300 | Rv3310 | Acid phosphatase (acid phosphomo | 69.87 | 299 | Mb3338 | acid phosphatase | 70.2 | 299 | MAV_4287 | secreted acid phosphatase | 98.91 | 276 | BCG_3375 | acid phosphatase | 70.2 | 299 | MAP3432 | hypothetical protein | 300 | 100 |
| MAP4_0348 | uracil phosphoribosyltransferase Upp | 257 | Rv3309c | Probable uracil phosphoribosyltrans | 77.18 | 207 | Mb3337c | uracil phosphoribosyltransfer | 77.18 | 207 | MAV_4285 | uracil phosphoribosyltransferase | 99.22 | 303 | BCG_3374c | uracil phosphoribosyltransfera | 77.18 | 207 | MAP3431c | uracil phosphoribosyltransferase | 257 | 100 |
| MAP4_0349 | phosphomannomutase PmmB | 526 | Rv3308 | Probable phosphomannomutase Pm | 74.34 | 534 | Mb3336 | phosphomannomutase | 74.63 | 534 | MAV_4286 | phosphoglucomutase/phosphoma | 99.05 | 526 | BCG_3373 | phosphomannomutase pmmB | 74.63 | 534 | MAP3430 | PmmB | 526 | 100 |
| MAP4_0350 | purine nucleoside phosphorylase | 271 | Rv3307 | Probable purine nucleoside phosph | 82.09 | 268 | Mb3335 | purine nucleoside phosphory | 82.09 | 268 | MAV_4284 | purine nucleoside phosphorylase | 99.26 | 271 | BCG_3372 | purine nucleoside phosphoryla | 82.09 | 268 | MAP3429 | purine nucleoside phosphorylase | 271 | 100 |
| MAP4_0351 | cutinase precursor | 235 | Rv3451 | Probable cutinase precursor Cut3 | 43.93 | 262 | Mb3481 | cutinase | 43.93 | 262 | MAV_4283 | cutinase Cut3 | 99.46 | 184 | BCG_3517 | cutinase precursor cut3 | 43.93 | 261 | MAP3428c | hypothetical protein | 235 | 100 |
| MAP4_0352 | amidohydrolase | 400 | Rv3306c | Probable amidohydrolase AmiB1 (a | 81.91 | 394 | Mb3334c | amidase | 81.91 | 394 | MAV_4282 | amidohydrolase | 99.75 | 400 | BCG_3371c | amidase amiB1 | 81.91 | 394 | MAP3427c | AmiB | 400 | 100 |
| MAP4_0353 | N-acyl-L-amino acid amidohydrolase AmiA1 | 392 | Rv3305c | Possible N-acyl-L-amino acid amido | 87.86 | 389 | Mb3333c | N-acyl-L-amino acid amidohy | 87.86 | 389 | MAV_4281 | amidohydrolase | 99.74 | 392 | BCG_3370c | N-acyl-L-amino acid amidohyd | 87.86 | 389 | MAP3426c | AmiA | 392 | 100 |
| MAP4_0354 | hypothetical protein | 155 | Rv3304 | hypothetical protein | 94.84 | 159 | Mb3332 | hypothetical protein | 94.84 | 159 | MAV_4280 | L308_f3_97 | 100 | 155 | BCG_3369 | hypothetical protein | 94.84 | 159 | MAP3425 | hypothetical protein | 155 | 100 |
| MAP4_0355 | dihydrolipoamide dehydrogenase LpdA | 492 | Rv3303c | NAD(P)H quinone reductase LpdA | 88.96 | 493 | Mb3331c | flavoprotein disulfide reducta | 88.96 | 471 | MAV_4687 | dihydrolipoamide dehydrogenase | 28.14 | 465 | BCG_3368c | flavoprotein disulfide reductas | 88.96 | 471 | MAP3424c | flavoprotein disulfide reductase | 492 | 100 |
| MAP4_0356 | glycerol-3-phosphate dehydrogenase | 584 | Rv3302c | Probable glycerol-3-phosphate dehy | 89.23 | 585 | Mb3330c | glycerol-3-phosphate dehydr | 89.23 | 585 | MAV_4278 | glycerol-3-phosphate dehydrogena | 99.83 | 584 | BCG_3331c | glycerol-3-phosphate dehydrog | 89.23 | 585 | MAP3423c | GlpD2 | 584 | 100 |
| MAP4_0357 | putative RNA pseudouridine synthase | 290 | Rv3300c | hypothetical protein | 77.86 | 305 | Mb3328c | hypothetical protein | 77.86 | 305 | MAV_4277 | RNA pseudouridine synthase | 99.3 | 287 | BCG_3329c | hypothetical protein | 77.86 | 305 | MAP3422c | hypothetical protein | 290 | 100 |
| MAP4_0358 | hypothetical protein | 152 | Rv2913c | Possible D-amino acid aminohydrola | 28.81 | 611 | Mb2937c | D-amino acid aminohydrolase | 28.81 | 611 | MAV_4276 | diguanylate cyclase/phosphodieste | 99.34 | 198 | BCG_2934c | D-amino acid aminohydrolase | 28.81 | 611 | MAP2981c | hypothetical protein | 620 | 28.81 |
| MAP4_0359 | hypothetical protein | 95 | Rv0061c | Hypothetical protein | 31.03 | 112 | Mb2990c | methyltransferase | 53.33 | 188 | MAV_4275 | hypothetical protein | 100 | 95 | BCG_2987c | methyltransferase | 53.33 | 188 | MAP1242 | hypothetical protein | 4027 | 31.88 |
| MAP4_0360 | PPE family protein | 378 | Rv1705c | PPE family protein PPE22 | 37.24 | 385 | Mb1731c | PPE family protein | 37.24 | 385 | MAV_4274 | PPE family protein | 100 | 378 | BCG_1743c | PPE family protein | 36.91 | 385 | MAP3420c | hypothetical protein | 379 | 100 |
| MAP4_0361 | PPE family protein | 378 | Rv1801 | PPE family protein PPE29 | 47.13 | 423 | Mb1829 | PPE family protein | 47.13 | 423 | MAV_4273 | PPE family protein | 100 | 378 | BCG_1833 | PPE family protein | 47.13 | 423 | MAP3419c | hypothetical protein | 378 | 100 |
| MAP4_0362 | hypothetical protein | 70 | Rv0594 | Mce-family protein Mce2F | 36.96 | 516 | Mb0610 | MCE-family protein MCE2F | 36.96 | 516 | MAV_4272 | hypothetical protein | 100 | 70 | BCG_0640 | mce-family protein mce2F | 36.96 | 516 | MAP1476c | hypothetical protein | 234 | 36.23 |
| MAP4_0363 | hypothetical protein | 149 | Rv1271c | Conserved hypothetical secreted pr | 37.5 | 113 | Mb1302c | hypothetical protein | 37.5 | 113 | MAV_4271 | hypothetical protein | 99.15 | 117 | BCG_1330c | hypothetical protein | 37.5 | 113 | MAP3418 | hypothetical protein | 149 | 100 |
| MAP4_0364 | esterase lipoprotein LpqC | 305 | Rv3298c | Possible esterase lipoprotein LpqC | 70.49 | 304 | Mb3326c | esterase | 70.49 | 304 | MAV_4268 | LpqC protein | 99.67 | 305 | BCG_3327c | esterase lipoprotein lpqC | 70.49 | 304 | MAP3417c | hypothetical protein | 305 | 100 |
| MAP4_0365 | endonuclease VIII | 250 | Rv3297 | Probable endonuclease VIII Nei | 78.43 | 255 | Mb3325 | endonuclease VIII | 78.43 | 255 | MAV_1708 | endonuclease VIII and DNA n-glyco | 30.63 | 268 | BCG_3326 | endonuclease VIII nei | 78.43 | 255 | MAP3416 | hypothetical protein | 250 | 100 |
| MAP4_0366 | ATP-dependent helicase Lhr | 1546 | Rv3296 | Probable ATP-dependent helicase Lh | 82.41 | 1513 | Mb3324 | ATP-dependent helicase | 82.28 | 1513 | MAV_4267 | DEAD/DEAH box helicase | 99.03 | 1543 | BCG_3325 | ATP-dependent helicase lhr | 82.28 | 1513 | MAP3415 | hypothetical protein | 1546 | 100 |
| MAP4_0367 | Transcriptional regulator, TetR family | 219 | Rv3295 | Probable transcriptional regulatory | 79.19 | 221 | Mb3323 | TetR family transcriptional re | 79.19 | 221 | MAV_4266 | hypothetical protein | 99.09 | 219 | BCG_3324 | TetR family transcriptional regu | 79.19 | 221 | MAP3414 | hypothetical protein | 219 | 99.54 |
| MAP4_0368 | piperideine-6-carboxylic acid dehydrogenase Pcd | 509 | Rv3293 | Probable piperideine-6-carboxilic ac | 79.6 | 494 | Mb3321 | piperideine-6-carboxilic acid | 79.6 | 494 | MAV_4265 | aldehyde dehydrogenase (NAD) fa | 99.02 | 509 | BCG_3322 | piperideine-6-carboxilic acid de | 79.6 | 494 | MAP3413 | AldB | 509 | 100 |
| MAP4_0369 | hypothetical protein | 419 | Rv3292 | hypothetical protein | 76.37 | 415 | Mb3320 | hypothetical protein | 76.37 | 415 | MAV_4264 | hypothetical protein | 99.51 | 405 | BCG_3321 | hypothetical protein | 76.37 | 415 | MAP3412 | hypothetical protein | 419 | 100 |
| MAP4_0370 | transcriptional regulator, asnC-family | 150 | Rv3291c | Probable transcriptional regulatory | 84.67 | 150 | Mb3319c | AsnC family transcriptional re | 84 | 150 | MAV_4263 | leucine-responsive regulatory prot | 100 | 150 | BCG_3320c | AsnC family transcriptional reg | 84 | 150 | MAP3411c | hypothetical protein | 150 | 100 |
| MAP4_0371 | L-lysine-epsilon aminotransferase Lat | 446 | Rv3290c | Probable L-lysine-epsilon aminotran | 77.68 | 449 | Mb3318c | L-lysine aminotransferase | 77.68 | 449 | MAV_4262 | L-lysine aminotransferase | 99.1 | 446 | BCG_3319c | L-lysine aminotransferase | 77.68 | 449 | MAP3410c | L-lysine aminotransferase | 446 | 100 |
| MAP4_0372 | putative transmembrane protein | 127 | Rv3289c | Possible transmembrane protein | 66.67 | 125 | Mb3317c | transmembrane protein | 66.67 | 125 | MAV_4261 | hypothetical protein | 99.07 | 108 | BCG_3318c | hypothetical protein | 66.67 | 125 | MAP3409c | hypothetical protein | 127 | 100 |
| MAP4_0373 | hypothetical protein UsfY | 103 | Rv3288c | Putative protein UsfY | 78.79 | 137 | Mb3316c | hypothetical protein | 78.79 | 137 | MAV_4260 | UsfY protein | 100 | 103 | BCG_3317c | protein usfY | 78.79 | 137 | MAP3408c | hypothetical protein | 103 | 100 |
| MAP4_0374 | hypothetical protein | 49 | Rv1293 | Diaminopimelate decarboxylase Lys | 32.43 | 447 | Mb1325 | diaminopimelate decarboxyla | 32.43 | 447 | MAV_4259 | hypothetical protein | 100 | 49 | BCG_1353 | diaminopimelate decarboxylas | 32.43 | 447 | MAP1803 | hypothetical protein | 233 | 28.26 |
| MAP4_0375 | anti-sigma factor RsbW | 172 | Rv3287c | Anti-sigma factor RsbW (sigma nega | 84.83 | 145 | Mb3315c | anti-sigma factor rsbW (sigma | 84.83 | 145 | MAV_4258 | RsbW protein | 100 | 145 | BCG_3316c | anti-sigma factor rsbW | 84.83 | 145 | MAP3407c | hypothetical protein | 172 | 100 |
| MAP4_0376 | RNA polymerase sigma factor SigF | 262 | Rv3286c | Alternative RNA polymerase sigma f | 85.88 | 261 | Mb3314c | RNA polymerase sigma factor | 85.88 | 261 | MAV_4256 | RNA polymerase sigma factor SigF | 99.59 | 241 | BCG_3315c | RNA polymerase sigma factor S | 85.88 | 261 | MAP3406c | RNA polymerase sigma factor SigF | 262 | 100 |
| MAP4_0377 | hypothetical protein | 144 | Rv0516c | Possible anti-anti-sigma factor | 36.05 | 158 | Mb0529c | hypothetical protein | 36.05 | 158 | MAV_4257 | STAS domain-containing protein | 99.29 | 140 | BCG_0559c | hypothetical protein | 36.05 | 158 | MAP3405 | hypothetical protein | 144 | 100 |
| MAP4_0378 | bifunctional acetyl-propionyl-coenzyme Acarboxylase a | 598 | Rv3285 | Probable bifunctional protein acetyl | 90.18 | 600 | Mb3313 | CoA carboxylase subunit alph | 90.18 | 600 | MAV_4255 | acetyl-/propionyl-coenzyme A carb | 99.66 | 587 | BCG_3314 | bifunctional protein acetyl-/pr | 90.18 | 600 | MAP3404 | AccA3 | 607 | 99.83 |
| MAP4_0379 | putative Fe-S metabolism associated protein, SufE fami | 140 | Rv3284 | hypothetical protein | 86.86 | 143 | Mb3312 | hypothetical protein | 86.86 | 143 | MAV_4254 | Fe-S metabolism associated domai | 100 | 140 | BCG_3313 | hypothetical protein | 86.86 | 143 | MAP3403 | hypothetical protein | 140 | 100 |
| MAP4_0380 | thiosulfate sulfurtransferase SseA | 298 | Rv3283 | Probable thiosulfate sulfurtransfera | 87.46 | 297 | Mb3311 | thiosulfate sulfurtransferase | 87.12 | 297 | MAV_4253 | thiosulfate sulfurtransferase | 100 | 298 | BCG_3312 | thiosulfate sulfurtransferase ss | 87.46 | 297 | MAP3402 | hypothetical protein | 298 | 100 |
| MAP4_0381 | conserved hypothetical protein, Maf-likeprotein | 210 | Rv3282 | hypothetical protein | 65.73 | 222 | Mb3310 | Maf-like protein | 65.73 | 222 | MAV_4252 | Maf-like protein | 98.54 | 206 | BCG_3311 | Maf-like protein | 65.73 | 222 | MAP3401 | Maf-like protein | 210 | 100 |
| MAP4_0382 | hypothetical protein | 86 | Rv3281 | Probable bifunctional protein acetyl | 60.87 | 177 | Mb3309 | hypothetical protein | 60.87 | 156 | MAV_4251 | hypothetical protein | 98.84 | 86 | BCG_3310 | hypothetical protein | 60.87 | 156 | MAP3400 | hypothetical protein | 86 | 100 |
| MAP4_0383 | propionyl-CoA carboxylase beta chain 5 AccD5 | 546 | Rv3280 | Probable propionyl-CoA carboxylase | 91.07 | 548 | Mb3308 | propionyl-CoA carboxylase su | 90.89 | 548 | MAV_4250 | propionyl-CoA carboxylase beta ch | 100 | 546 | BCG_3309 | propionyl-CoA carboxylase bet | 90.89 | 548 | MAP3399 | AccD5 | 546 | 100 |
| MAP4_0384 | dehydrogenase | 512 | Rv3537 | Probable dehydrogenase | 35.74 | 563 | Mb3567 | 3-ketosteroid-delta-1-dehydr | 35.74 | 563 | MAV_4249 | 3-ketosteroid-delta-1-dehydrogena | 98.53 | 517 | BCG_3601 | 3-ketosteroid-delta-1-dehydro | 35.74 | 563 | MAP3398c | 3-ketosteroid-delta-1-dehydrogenase | 512 | 100 |
| MAP4_0385 | bifunctional biotin biosynthesis protein BirA | 264 | Rv3279c | Possible bifunctional protein BirA: b | 68.94 | 266 | Mb3307c | biotin--protein ligase | 68.56 | 266 | MAV_4248 | biotin-[acetyl-CoA-carboxylase] liga | 98.86 | 264 | BCG_3308c | bifunctional protein birA: bioti | 68.56 | 266 | MAP3397c | biotin--protein ligase | 281 | 99.62 |
| MAP4_0386 | hypothetical protein | 172 | Rv3278c | Probable conserved transmembrane | 83.72 | 172 | Mb3306c | transmembrane protein | 83.14 | 172 | MAV_4246 | hypothetical protein | 99.42 | 172 | BCG_3307c | hypothetical protein | 83.14 | 172 | MAP3396c | hypothetical protein | 172 | 100 |
| MAP4_0387 | hypothetical protein | 221 | Rv3277 | Probable conserved transmembrane | 87.44 | 272 | Mb3305 | transmembrane protein | 87.39 | 272 | MAV_4247 | hypothetical protein | 100 | 221 | BCG_3306 | hypothetical protein | 87.39 | 272 | MAP3395 | hypothetical protein | 221 | 100 |
| MAP4_0388 | phosphoribosylaminoimidazole carboxylase ATPase sub | 426 | Rv3276c | Probable phosphoribosylaminoimida | 77.38 | 429 | Mb3304c | phosphoribosylaminoimidazo | 77.38 | 429 | MAV_4245 | phosphoribosylaminoimidazole car | 99.5 | 397 | BCG_3305c | phosphoribosylaminoimidazole | 77.38 | 429 | MAP3394c | phosphoribosylaminoimidazole carboxy | 426 | 100 |
| MAP4_0389 | phosphoribosylaminoimidazole carboxylase catalytic su | 173 | Rv3275c | Probable phosphoribosylaminoimida | 85.03 | 174 | Mb3303c | phosphoribosylaminoimidazo | 85.63 | 174 | MAV_4244 | phosphoribosylaminoimidazole car | 99.42 | 173 | BCG_3304c | phosphoribosylaminoimidazole | 85.63 | 174 | MAP3393c | phosphoribosylaminoimidazole carboxy | 173 | 100 |
| MAP4_0390 | acyl-CoA dehydrogenase | 389 | Rv3274c | Probable acyl-CoA dehydrogenase F | 88.95 | 389 | Mb3302c | acyl-CoA dehydrogenase | 88.95 | 389 | MAV_4243 | acyl-CoA dehydrogenase | 100 | 389 | BCG_3303c | acyl-CoA dehydrogenase fadE2 | 88.95 | 389 | MAP3392c | FadE25_4 | 389 | 100 |
| MAP4_0392 | two-component sensor histidine kinase | 531 | Rv0902c | Two component sensor histidine kin | 27.06 | 446 | Mb0926c | two component sensor histid | 27.06 | 446 | MAV_4241 | two-component sensor protein | 98.32 | 535 | BCG_0954c | two component sensor histidin | 27.06 | 446 | MAP3390c | hypothetical protein | 531 | 100 |
| MAP4_0393 | two-component system response regulator | 146 | Rv1033c | Two component transcriptional regu | 28.46 | 257 | Mb1062c | two component transcription | 28.46 | 257 | MAV_4240 | two-component system response r | 100 | 146 | BCG_1091c | two component transcriptional | 28.46 | 257 | MAP3389c | hypothetical protein | 146 | 100 |
| MAP4_0394 | periplasmic phosphate-binding lipoprotein PstS2 | 366 | Rv0932c | Periplasmic phosphate-binding lipop | 77.84 | 370 | Mb0956c | periplasmic phosphate-bindi | 78.11 | 370 | MAV_4239 | phosphate ABC transporter phosph | 99.73 | 366 | BCG_0985c | periplasmic phosphate-binding | 78.11 | 370 | MAP3388c | hypothetical protein | 378 | 99.73 |
| MAP4_0395 | transmembrane serinethreonine-protein kinase DPknD | 656 | Rv0931c | Transmembrane serine/threonine-p | 68.15 | 664 | Mb0954c | serine/threonine protein kina | 65.16 | 369 | MAV_4238 | serine/threonine protein kinase | 99.24 | 656 | BCG_0983c | Ser/Thr protein kinase | 65.16 | 369 | MAP3387c | hypothetical protein | 656 | 100 |
| MAP4_0396 | putative CoA-transferase family III protein | 406 | Rv3272 | hypothetical protein | 73.8 | 394 | Mb3300 | hypothetical protein | 73.55 | 394 | MAV_4237 | YfdE protein | 99.75 | 406 | BCG_3301 | hypothetical protein | 73.3 | 394 | MAP3386 | hypothetical protein | 406 | 100 |
| MAP4_0397 | putative methyltransferase | 304 | Rv3787c | hypothetical protein | 61.24 | 308 | Mb3816c | hypothetical protein | 61.24 | 308 | MAV_4236 | methyltransferase, putative, family | 99.67 | 304 | BCG_3849c | hypothetical protein | 61.24 | 308 | MAP3385 | hypothetical protein | 304 | 100 |
| MAP4_0398 | metal cation-transporting P-type ATPase CtpC | 726 | Rv3270 | Probable metal cation-transporting | 89.93 | 718 | Mb3298 | metal cation-transporting P-t | 89.93 | 718 | MAV_4235 | cadmium-translocating P-type ATP | 99.58 | 712 | BCG_3299 | metal cation-transporting P-ty | 89.93 | 718 | MAP3384 | CtpC | 726 | 100 |
| MAP4_0399 | hypothetical protein | 93 | Rv3269 | hypothetical protein | 75.27 | 93 | Mb3297 | hypothetical protein | 75.27 | 93 | MAV_4234 | hypothetical protein | 98.92 | 93 | BCG_3298 | hypothetical protein | 75.27 | 93 | MAP3383 | hypothetical protein | 93 | 100 |
| MAP4_0400 | hypothetical protein | 223 | Rv3268 | hypothetical protein | 81.22 | 229 | Mb3296 | hypothetical protein | 81.22 | 229 | MAV_4233 | hypothetical protein | 98.65 | 237 | BCG_3297 | hypothetical protein | 81.22 | 229 | MAP3382 | hypothetical protein | 223 | 100 |
| MAP4_0401 | hypothetical protein | 490 | Rv3267 | Conserved protein (CPSA-related pr | 81.96 | 498 | Mb3295 | hypothetical protein | 81.96 | 498 | MAV_4232 | cell envelope-related function tran | 99.79 | 482 | BCG_3296 | hypothetical protein | 81.96 | 498 | MAP3381 | hypothetical protein | 490 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0402 | dTDP-6-deoxy-L-lyxo-4-hexulose reductase RmlD | 307 | Rv3266c | dTDP-6-deoxy-L-lyxo-4-hexulose red | 72.55 | 304 | Mb3294c | dTDP-rhamnose modification | 72.88 | 304 | MAV_4231 | dTDP-4-dehydrorhamnose reducta | 98.68 | 302 | BCG_3295c | dTDP-rhamnose modification | 72.88 | 304 | MAP3380c | RmlD | 307 | 100 |
| MAP4_0403 | dTDP-Rha:a-D-GlcNAc-diphosphoryl polyprenol,a-3-L-r | 288 | Rv3265c | dTDP-RHA:a-D-GlcNAc-diphosphoryl | 82.06 | 301 | Mb3293c | dTDP-rha:a-D-glcnac-diphosp | 83.16 | 297 | MAV_4230 | dTDP-RhA:a-D-GlcNAc-diphosphory | 99.65 | 291 | BCG_3294c | dTDP-RHA:A-D-GlcNAc-diphos | 83.16 | 297 | MAP3379c | WbbL | 288 | 100 |
| MAP4_0404 | D-alpha-D-mannose-1-phosphateguanylyl transferase | 358 | Rv3264c | D-alpha-D-mannose-1-phosphate gu | 87.47 | 359 | Mb3292c | mannose-1-phosphate guany | 87.47 | 359 | MAV_4228 | nucleotidyl transferase | 99.72 | 358 | BCG_3293c | mannose-1-phosphate guanylt | 87.47 | 359 | MAP3378c | RmlA2 | 358 | 100 |
| MAP4_0405 | putative hydrolase, nudix family protein, putative | 179 | Rv3672c | hypothetical protein | 36.05 | 273 | Mb3696c | hypothetical protein | 36.05 | 273 | MAV_4227 | hydrolase, nudix family protein, pu | 98.89 | 180 | BCG_3730c | hypothetical protein | 36.05 | 273 | MAP3377 | hypothetical protein | 177 | 99.44 |
| MAP4_0406 | DNA methylase | 526 | Rv3263 | Probable DNA methylase (modificat | 76.37 | 553 | Mb3291 | DNA methylase | 76.37 | 553 | MAV_4226 | BpmI methyltransferase | 99.05 | 526 | BCG_3292 | DNA methylase | 76.37 | 553 | MAP3376 | hypothetical protein | 526 | 100 |
| MAP4_0407 | F420 biosynthesis protein FbiB | 449 | Rv3262 | Probable F420 biosynthesis protein | 84.68 | 448 | Mb3290 | F420-0--gamma-glutamyl liga | 84.68 | 448 | MAV_4225 | F420-0--gamma-glutamyl ligase | 99.33 | 449 | BCG_3291 | F420-0--gamma-glutamyl ligas | 84.68 | 448 | MAP3375 | F420-0--gamma-glutamyl ligase | 449 | 100 |
| MAP4_0408 | F420 biosynthesis protein FbiA | 337 | Rv3261 | Probable F420 biosynthesis protein | 80.3 | 331 | Mb3289 | 2-phospho-L-lactate transfera | 80.3 | 331 | MAV_4224 | LPPG:FO 2-phospho-L-lactate trans | 100 | 337 | BCG_3290 | LPPG:FO 2-phospho-L-lactate t | 80.3 | 331 | MAP3374 | LPPG:FO 2-phospho-L-lactate transfera | 343 | 99.7 |
| MAP4_0409 | hypothetical protein | 88 | | | | | | | | | MAV_2924 | PPE family protein | 62.5 | 405 | | | | | MAP3373 | hypothetical protein | 88 | 100 |
| MAP4_0410 | transcriptional regulator whib-like WhiB2 | 121 | Rv3260c | Probable transcriptional regulatory | 87.78 | 89 | Mb3288c | transcriptional regulator Whi | 87.78 | 89 | MAV_4223 | transcription factor WhiB | 100 | 112 | BCG_3289c | transcriptional regulatory prot | 87.78 | 89 | MAP3372c | WhiB2 | 121 | 100 |
| MAP4_0411 | hypothetical protein | 140 | Rv3259 | hypothetical protein | 91.37 | 139 | Mb3287 | hypothetical protein | 91.37 | 139 | MAV_4222 | hypothetical protein | 100 | 197 | BCG_3288 | hypothetical protein | 91.37 | 139 | MAP3371 | hypothetical protein | 140 | 100 |
| MAP4_0412 | hypothetical protein | 165 | Rv3258c | hypothetical protein | 75.9 | 163 | Mb3286c | hypothetical protein | 75.9 | 163 | MAV_4221 | hypothetical protein | 99.24 | 132 | BCG_3287c | hypothetical protein | 75.9 | 163 | MAP3370c | hypothetical protein | 165 | 100 |
| MAP4_0413 | phosphomannomutase PmmA | 471 | Rv3257c | Probable phosphomannomutase Pm | 85.19 | 465 | Mb3285c | phosphomannomutase | 85.4 | 465 | MAV_4384 | phosphoglucosamine mutase | 31.08 | 444 | BCG_3286c | phosphomannomutase | 85.4 | 465 | MAP3369c | phosphomannomutase/phosphoglucom | 471 | 100 |
| MAP4_0414 | hypothetical protein | 366 | Rv3256c | hypothetical protein | 72.36 | 346 | Mb3284c | hypothetical protein | 72.36 | 346 | MAV_4219 | hypothetical protein | 99.73 | 366 | BCG_3285c | hypothetical protein | 72.36 | 346 | MAP3368c | hypothetical protein | 366 | 100 |
| MAP4_0415 | mannose-6-phosphate isomerase ManA | 408 | Rv3255c | Probable mannose-6-phosphate iso | 83.82 | 408 | Mb3283c | mannose-6-phosphate isome | 83.82 | 408 | MAV_4217 | mannose-6-phosphate isomerase, | 100 | 408 | BCG_3284c | mannose-6-phosphate isomera | 83.82 | 408 | MAP3367c | hypothetical protein | 408 | 100 |
| MAP4_0416 | hypothetical protein | 469 | Rv3254 | hypothetical protein | 71.4 | 462 | Mb3282 | hypothetical protein | 71.4 | 462 | MAV_4218 | hypothetical protein | 99.36 | 469 | BCG_3283 | hypothetical protein | 71.4 | 462 | MAP3366 | hypothetical protein | 469 | 100 |
| MAP4_0417 | cationic amino acid transport membrane protein | 505 | Rv3253c | Possible cationic amino acid transpo | 84.87 | 495 | Mb3281c | cationic amino acid transport | 84.87 | 495 | MAV_4216 | cationic amino acid transporter | 100 | 505 | BCG_3282c | cationic amino acid transport i | 84.87 | 495 | MAP3365c | hypothetical protein | 505 | 100 |
| MAP4_0418 | transmembrane alkane 1-monooxygenase AlkB | 415 | Rv3252c | Probable transmembrane alkane 1- | 85.19 | 416 | Mb3280c | transmembrane alkane 1-mo | 85.19 | 416 | MAV_4215 | alkane-1-monooxygenase | 99.28 | 415 | BCG_3281c | transmembrane alkane 1-mon | 85.19 | 416 | MAP3364c | hypothetical protein | 447 | 100 |
| MAP4_0419 | rubredoxin RubA | 57 | Rv3251c | Probable rubredoxin RubA | 74.55 | 55 | Mb3279c | rubredoxin RUBA | 74.55 | 55 | MAV_4214 | rubredoxin | 98.25 | 57 | BCG_3280c | rubredoxin rubA | 74.55 | 55 | MAP0172 | hypothetical protein | 1527 | 43.24 |
| MAP4_0420 | rubredoxin RubB | 60 | Rv3250c | Probable rubredoxin RubB | 88.14 | 60 | Mb3278c | rubredoxin RubB | 88.14 | 60 | MAV_4213 | rubredoxin | 98.33 | 60 | BCG_3279c | rubredoxin rubB | 88.14 | 60 | MAP0970 | hypothetical protein | 697 | 47.06 |
| MAP4_0421 | Transcriptional regulator, TetR family | 210 | Rv3249c | Possible transcriptional regulatory p | 86.21 | 211 | Mb3277c | TetR family transcriptional re | 86.21 | 211 | MAV_4212 | transcriptional regulator | 99.5 | 201 | BCG_3278c | TetR family transcriptional regu | 86.21 | 211 | MAP2519 | hypothetical protein | 197 | 41.79 |
| MAP4_0422 | adenosylhomocysteinase SahH | 496 | Rv3248c | Probable adenosylhomocysteinase | 84.79 | 495 | Mb3276c | S-adenosyl-L-homocysteine h | 84.58 | 495 | MAV_4211 | S-adenosyl-L-homocysteine hydrol | 99.8 | 496 | BCG_3277c | S-adenosyl-L-homocysteine hy | 84.79 | 495 | MAP3362c | S-adenosyl-L-homocysteine hydrolase | 496 | 100 |
| MAP4_0423 | thymidylate kinase Tmk | 210 | Rv3247c | Thymidylate kinase Tmk (dTMP kina | 77.88 | 214 | Mb3275c | thymidylate kinase | 77.88 | 214 | MAV_4210 | thymidylate kinase | 100 | 210 | BCG_3276c | thymidylate kinase | 77.88 | 214 | MAP3361c | thymidylate kinase | 210 | 100 |
| MAP4_0424 | two component system transcriptional regulator MtrA | 228 | Rv3246c | Two component sensory transducti | 99.56 | 228 | Mb3274c | two component sensory tran | 99.56 | 228 | MAV_4209 | DNA-binding response regulator M | 100 | 228 | BCG_3275c | two component sensory trans | 99.56 | 228 | MAP3360c | hypothetical protein | 228 | 100 |
| MAP4_0425 | two component system sensor histidine kinase MtrB | 564 | Rv3245c | Two component sensory transducti | 87.8 | 567 | Mb3273c | two component sensory tran | 87.98 | 567 | MAV_4208 | sensor histidine kinase | 100 | 543 | BCG_3274c | two component sensory trans | 87.98 | 567 | MAP3359c | hypothetical protein | 564 | 100 |
| MAP4_0426 | lipoprotein LpqB | 585 | Rv3244c | Probable conserved lipoprotein Lpq | 86.08 | 583 | Mb3272c | lipoprotein LpqB | 86.08 | 583 | MAV_0232 | oxidoreductase, FAD-binding | 24 | 466 | BCG_3273c | lipoprotein LpqB | 86.08 | 583 | MAP3358c | lipoprotein LpqB | 585 | 100 |
| MAP4_0427 | transposase, IS4 family protein | 557 | Rv3386 | Possible transposase | 25.95 | 234 | Mb3418 | transposase | 25.95 | 234 | MAV_3010 | ABC transporter ATP-binding prote | 29.31 | 862 | BCG_3455 | transposase | 25.95 | 234 | MAP0338c | hypothetical protein | 557 | 100 |
| MAP4_0428 | hypothetical protein | 213 | Rv3242c | hypothetical protein | 69.61 | 213 | Mb3270c | hypothetical protein | 69.61 | 213 | MAV_4206 | hypothetical protein | 97.01 | 213 | BCG_3271c | hypothetical protein | 69.12 | 213 | MAP3356c | hypothetical protein | 213 | 100 |
| MAP4_0429 | conserved hypothetical protein, ribosomal S30AE famil | 231 | Rv3241c | hypothetical protein | 74.67 | 214 | Mb3269c | hypothetical protein | 74.67 | 214 | MAV_4204 | S30AE family protein | 98.67 | 226 | BCG_3270c | hypothetical protein | 74.67 | 214 | MAP3355c | hypothetical protein | 231 | 100 |
| MAP4_0430 | preprotein translocase SecA | 940 | Rv3240c | Probable preprotein translocase Sec | 89.67 | 949 | Mb3268c | preprotein translocase subun | 89.67 | 949 | MAV_2894 | preprotein translocase subunit Sec | 39.54 | 777 | BCG_3269c | preprotein translocase subunit | 89.67 | 949 | MAP3354c | preprotein translocase subunit SecA | 940 | 100 |
| MAP4_0431 | hypothetical protein | 248 | Rv0998 | hypothetical protein | 34.38 | 333 | Mb1025 | hypothetical protein | 34.38 | 333 | MAV_1457 | hypothetical protein | 30.88 | 413 | BCG_1055 | hypothetical protein | 34.38 | 333 | MAP3353c | hypothetical protein | 260 | 100 |
| MAP4_0432 | transcriptional regulator, LuxR family protein | 523 | Rv3133c | Two component transcriptional regu | 39.66 | 217 | Mb3157c | two component transcription | 39.66 | 217 | MAV_4201 | LuxR family transcriptional regulat | 99.43 | 523 | BCG_3156c | two component transcriptional | 39.66 | 217 | MAP3352c | hypothetical protein | 523 | 100 |
| MAP4_0433 | hypothetical protein | 254 | Rv3238c | Probable conserved integral membr | 70.25 | 244 | Mb3266c | hypothetical protein | 70.25 | 244 | MAV_4200 | hypothetical protein | 99.61 | 266 | BCG_3267c | integral membrane protein | 70.25 | 244 | MAP3351c | hypothetical protein | 254 | 100 |
| MAP4_0434 | hypothetical protein | 160 | Rv3237c | hypothetical protein | 81.25 | 160 | Mb3265c | hypothetical protein | 81.25 | 160 | MAV_4199 | TrkA domain-containing protein | 100 | 160 | BCG_3266c | hypothetical protein | 81.25 | 160 | MAP3350c | hypothetical protein | 160 | 100 |
| MAP4_0435 | conserved membrane transport protein | 382 | Rv3236c | Probable conserved integral membr | 81.28 | 385 | Mb3264c | integral membrane transport | 81.28 | 385 | MAV_4198 | transporter, monovalent cation:pr | 99.48 | 382 | BCG_3265c | integral membrane transport p | 81.28 | 385 | MAP3349c | hypothetical protein | 382 | 100 |
| MAP4_0436 | putative alanine, arginine and proline rich protein | 186 | Rv3235 | Hypothetical alanine arginine prolin | 56.15 | 213 | Mb3263 | hypothetical protein | 56.15 | 213 | MAV_4197 | hypothetical protein | 97.85 | 186 | BCG_3264 | hypothetical protein | 56.15 | 213 | MAP3348 | hypothetical protein | 186 | 100 |
| MAP4_0437 | acyl-CoA acyltransferase, Wax ester synthase-like prot | 473 | Rv3234c | Putative triacylglycerol synthase (dia | 83.83 | 271 | Mb3262c | hypothetical protein | 84.53 | 469 | MAV_4196 | acyltransferase, ws/dgat/mgat sub | 100 | 473 | BCG_3263c | hypothetical protein | 84.53 | 469 | MAP3347c | hypothetical protein | 473 | 100 |
| MAP4_0438 | transcriptional regulator PvdS | 292 | Rv3232c | Polyphosphate kinase Ppk2 (polyph | 82.94 | 295 | Mb3261c | transcriptional regulator Pvd | 82.94 | 295 | MAV_4195 | polyphosphate kinase 2 | 98.95 | 285 | BCG_3262c | transcriptional regulatory prot | 82.94 | 295 | MAP3346c | PvdS | 292 | 100 |
| MAP4_0439 | hypothetical protein | 170 | Rv3231c | hypothetical protein | 80.59 | 169 | Mb3260c | hypothetical protein | 80.59 | 169 | MAV_4194 | hypothetical protein | 100 | 170 | BCG_3261c | hypothetical protein | 80.59 | 169 | MAP3345c | hypothetical protein | 170 | 100 |
| MAP4_0440 | oxidoreductase, flavodoxin reductase family protein | 384 | Rv3230c | Hypothetical oxidoreductase | 83.42 | 380 | Mb3259c | oxidoreductase | 83.16 | 380 | MAV_4193 | 2Fe-2S iron-sulfur cluster binding d | 100 | 384 | BCG_3260c | oxidoreductase | 83.16 | 380 | MAP3344c | hypothetical protein | 384 | 100 |
| MAP4_0441 | linoleoyl-CoA desaturase | 427 | Rv3229c | Possible linoleoyl-CoA desaturase (d | 85.25 | 427 | Mb3258c | linoleoyl-CoA desaturase | 85.25 | 427 | MAV_4192 | Fatty acid desaturase | 100 | 427 | BCG_3259c | linoleoyl-CoA desaturase | 85.25 | 427 | MAP3343c | DesA3_1 | 427 | 100 |
| MAP4_0442 | hypothetical protein | 274 | Rv3564 | Probable acyl-CoA dehydrogenase F | 28.36 | 318 | Mb3594 | acyl-CoA dehydrogenase | 28.36 | 318 | MAV_4191 | hypothetical protein | 99.27 | 274 | BCG_3628 | acyl-CoA dehydrogenase fadE3 | 28.36 | 318 | MAP3342 | hypothetical protein | 274 | 100 |
| MAP4_0444 | Transcriptional regulator, TetR family | 208 | Rv1255c | Probable transcriptional regulatory | 31.31 | 202 | Mb0482c | TetR family transcriptional re | 34.12 | 234 | MAV_4189 | TetR family transcriptional regulat | 99.04 | 208 | BCG_0513c | TetR family transcriptional regu | 27.49 | 234 | MAP3340 | hypothetical protein | 221 | 100 |
| MAP4_0445 | hypothetical protein | 380 | Rv3882c | ESX conserved component EccE1 ES | 24.7 | 462 | Mb3912c | hypothetical protein | 24.7 | 462 | MAV_4188 | hypothetical protein | 98.16 | 380 | BCG_3937c | hypothetical protein | 24.7 | 462 | MAP3339c | hypothetical protein | 380 | 100 |
| MAP4_0446 | hypothetical protein | 174 | Rv0803 | Phosphoribosylformylglycinamidine | 34.92 | 754 | Mb0826 | phosphoribosylformylglycina | 34.92 | 754 | MAV_4187 | hypothetical protein | 97.7 | 174 | BCG_0855 | phosphoribosylformylglycinam | 34.92 | 754 | MAP3338 | hypothetical protein | 174 | 100 |
| MAP4_0447 | acetyl-CoA acetyltransferase | 391 | Rv3556c | Probable acetyl-CoA acetyltransfera | 47.74 | 386 | Mb3586c | acetyl-CoA acetyltransferase | 47.74 | 386 | MAV_4185 | FadA6_4 | 99.23 | 391 | BCG_3620c | acetyl-CoA acetyltransferase | 47.74 | 386 | MAP3337 | FadA6_4 | 391 | 100 |
| MAP4_0448 | Transcriptional regulator, HxlR family | 158 | Rv3095 | Hypothetical transcriptional regulat | 34.71 | 158 | Mb3122 | transcriptional regulator | 34.71 | 158 | MAV_4183 | transcriptional regulator | 98.73 | 158 | BCG_3120 | transcriptional regulator | 34.71 | 158 | MAP3336c | hypothetical protein | 156 | 99.36 |
| MAP4_0449 | hypothetical protein | 331 | Rv3228 | hypothetical protein | 89.1 | 330 | Mb3257 | hypothetical protein | 89.1 | 330 | MAV_4184 | GTPase EngC | 99.09 | 331 | BCG_3351 | hypothetical protein | 89.1 | 330 | MAP3335 | hypothetical protein | 331 | 100 |
| MAP4_0450 | 3-phosphoshikimate 1-carboxyvinyltransferase | 435 | Rv3227 | 3-phosphoshikimate 1-carboxyvinyl | 83.45 | 450 | Mb3256 | 3-phosphoshikimate 1-carbo | 83.69 | 450 | MAV_4182 | 3-phosphoshikimate 1-carboxyviny | 98.16 | 435 | BCG_3257 | 3-phosphoshikimate 1-carboxy | 83.45 | 450 | MAP3334 | 3-phosphoshikimate 1-carboxyvinyltran | 435 | 100 |
| MAP4_0451 | hypothetical protein | 254 | Rv3226c | hypothetical protein | 72.83 | 252 | Mb3255c | hypothetical protein | 72.83 | 252 | MAV_4181 | hypothetical protein | 98.82 | 254 | BCG_3256c | hypothetical protein | 72.83 | 252 | MAP3333c | hypothetical protein | 254 | 100 |
| MAP4_0452 | REP13E12 repeat protein | 462 | Rv1128c | hypothetical protein | 65.43 | 451 | Mb1159c | hypothetical protein | 65.65 | 451 | MAV_3043 | hypothetical protein | 95.32 | 447 | BCG_1189c | hypothetical protein | 65.65 | 451 | MAP3332 | hypothetical protein | 462 | 100 |
| MAP4_0453 | hypothetical protein | 82 | Rv0990c | Hypothetical protein | 37.04 | 218 | Mb1017c | hypothetical protein | 37.04 | 218 | MAV_4179 | hypothetical protein | 98.78 | 82 | BCG_1045c | hypothetical protein | 37.04 | 218 | MAP3788 | hypothetical protein | 240 | 39.13 |
| MAP4_0454 | Transcriptional regulator, TetR family | 207 | Rv3066 | Probable transcriptional regulatory | 31.03 | 202 | Mb3093 | DeoR family transcriptional r | 31.03 | 202 | MAV_4178 | hypothetical protein | 98.9 | 182 | BCG_3091 | DeoR family transcriptional reg | 31.03 | 202 | MAP3331 | hypothetical protein | 207 | 100 |
| MAP4_0455 | putative dehydrogenasereductase | 256 | Rv0769 | Probable dehydrogenase/reductase | 38.71 | 248 | Mb0792 | short chain dehydrogenase | 38.31 | 248 | MAV_4177 | short chain type dehydrogenase/re | 99.22 | 256 | BCG_0821 | short chain dehydrogenase | 38.31 | 248 | MAP3330 | hypothetical protein | 267 | 100 |
| MAP4_0456 | putative hydrolase | 425 | Rv3762c | Possible hydrolase | 28.19 | 626 | Mb3788c | hydrolase | 28.19 | 626 | MAV_4176 | metallo-beta-lactamase | 97.18 | 421 | BCG_3821c | hydrolase | 28.19 | 626 | MAP3329c | hypothetical protein | 395 | 100 |
| MAP4_0457 | putative short-chain type dehydrogenase/reductase | 249 | Rv3549c | Probable short-chain type dehydrog | 34.94 | 259 | Mb3579c | short chain dehydrogenase | 34.94 | 259 | MAV_4175 | oxidoreductase, short chain dehyd | 97.19 | 249 | BCG_3613c | short chain dehydrogenase | 34.94 | 259 | MAP3328c | hypothetical protein | 249 | 100 |
| MAP4_0458 | hypothetical protein | 394 | Rv3529c | hypothetical protein | 28.39 | 384 | Mb3559c | hypothetical protein | 28.39 | 384 | MAV_4174 | hypothetical protein | 99.75 | 394 | BCG_3593c | hypothetical protein | 28.39 | 384 | MAP3327c | hypothetical protein | 394 | 100 |
| MAP4_0459 | putative dehydrogenase | 336 | Rv1895 | Possible dehydrogenase | 30.06 | 384 | Mb3753 | dehydrogenase | 32.89 | 397 | MAV_4173 | zinc-binding dehydrogenase | 97.89 | 332 | BCG_3786 | dehydrogenase | 32.89 | 397 | MAP3326c | hypothetical protein | 315 | 99.68 |
| MAP4_0460 | putative iron-regulated short-chain dehydrogenase/re | 282 | Rv3224 | Possible iron-regulated short-chain | 88.17 | 282 | Mb3251 | short chain dehydrogenase | 88.17 | 282 | MAV_4172 | short chain dehydrogenase | 98.94 | 282 | BCG_3252 | short chain dehydrogenase | 88.17 | 282 | MAP3325 | short chain dehydrogenase | 282 | 100 |
| MAP4_0461 | RNA polymerase sigma factor SigH | 268 | Rv3223c | Alternative RNA polymerase sigma- | 93.94 | 216 | Mb3250c | RNA polymerase sigma factor | 93.94 | 216 | MAV_4171 | RNA polymerase sigma factor RpoE | 99.63 | 268 | BCG_3251c | RNA polymerase sigma factor | 93.94 | 216 | MAP3324c | RNA polymerase sigma factor RpoE | 268 | 100 |
| MAP4_0462 | putative anti-sigma factor | 104 | Rv3221A | Anti-sigma factor RshA | 75.49 | 101 | Mb3248c | anti-sigma factor | 75.49 | 101 | MAV_4774 | hypothetical protein | 43.33 | 146 | BCG_3249c | anti-sigma factor | 75.49 | 101 | MAP3323c | hypothetical protein | 104 | 100 |
| MAP4_0463 | biotinylated protein | 73 | Rv3221c | Biotinylated protein TB7.3 | 91.55 | 71 | Mb3247c | acetyl-CoA carboxylase biotin | 91.55 | 71 | MAV_4169 | acetyl-CoA carboxylase biotin carb | 100 | 73 | BCG_3248c | acetyl-CoA carboxylase biotin | 91.55 | 71 | MAP3322c | acetyl-CoA carboxylase biotin carboxyl | 73 | 100 |
| MAP4_0464 | two component sensor kinase | 499 | Rv3220c | Probable two component sensor kin | 84.23 | 501 | Mb3246c | two component sensor kinas | 84.03 | 501 | MAV_4168 | sensor histidine kinase | 99.8 | 499 | BCG_3247c | two component sensor kinase | 84.03 | 501 | MAP3321c | hypothetical protein | 499 | 100 |
| MAP4_0465 | transcriptional regulator WhiB | 84 | Rv3219 | Transcriptional regulatory protein W | 97.62 | 84 | Mb3245 | transcriptional regulator Whi | 97.62 | 84 | MAV_4167 | transcription factor WhiB | 100 | 84 | BCG_3246 | transcriptional regulatory prot | 97.62 | 84 | MAP3320 | WhiB1 | 84 | 100 |
| MAP4_0466 | diacylglycerol kinase catalytic subunit | 321 | Rv3218 | hypothetical protein | 81.62 | 321 | Mb3244 | hypothetical protein | 81.62 | 321 | MAV_4166 | diacylglycerol kinase catalytic subu | 100 | 321 | BCG_3245 | hypothetical protein | 81.62 | 321 | MAP3319 | hypothetical protein | 321 | 100 |
| MAP4_0467 | putative conserved membrane protein | 143 | Rv3217c | Probable conserved integral membr | 72.66 | 143 | Mb3243c | hypothetical protein | 72.66 | 143 | MAV_4164 | hypothetical protein | 100 | 143 | BCG_3244c | integral membrane protein | 72.66 | 143 | MAP3318c | hypothetical protein | 163 | 99.3 |
| MAP4_0468 | acetyltransferase | 160 | Rv0510 | Probable porphobilinogen deamina | 28.3 | 309 | Mb3242 | acetyltransferase | 76.64 | 110 | MAV_4165 | acetyltransferase | 97.5 | 160 | BCG_3243 | acetyltransferase | 76.64 | 110 | MAP3317 | hypothetical protein | 160 | 100 |
| MAP4_0469 | isochorismate synthase | 364 | Rv3215 | Probable isochorismate synthase En | 76.31 | 372 | Mb3241 | isochorismate synthase | 76.31 | 372 | MAV_4163 | isochorismate synthase DhbC | 98.63 | 364 | BCG_3242 | isochorismate synthase entC | 76.31 | 372 | MAP3316 | isochorismate synthase | 364 | 100 |
| MAP4_0470 | phosphoglycerate mutase Gpm2 | 194 | Rv3214 | Possible phosphoglycerate mutase | 75.26 | 203 | Mb3240 | acid phosphatase | 75.26 | 203 | MAV_4162 | acid phosphatase | 100 | 194 | BCG_3241 | acid phosphatase | 75.26 | 203 | MAP3315 | acid phosphatase | 217 | 100 |
| MAP4_0471 | chromosome partitioning protein | 266 | Rv3213c | Possible SOJ/para-related protein | 90.23 | 266 | Mb3239c | SOJ/PARA-like protein | 90.6 | 266 | MAV_4161 | cobyrinic acid a,c-diamide synthase | 99.62 | 266 | BCG_3240c | soj/parA-related protein | 90.6 | 266 | MAP3314c | hypothetical protein | 266 | 100 |
| MAP4_0472 | onserved alanine and valine rich protein | 408 | Rv3212 | Conserved alanine valine rich protei | 75.67 | 407 | Mb3238 | hypothetical protein | 75.67 | 407 | MAV_4160 | hypothetical protein | 99.48 | 396 | BCG_3239 | hypothetical protein | 75.43 | 407 | MAP3313 | hypothetical protein | 408 | 100 |
| MAP4_0473 | ATP-dependent RNA helicase RhlE | 505 | Rv3211 | Probable ATP-dependent RNA helica | 75.44 | 527 | Mb3237 | ATP-dependent RNA helicase | 75.25 | 527 | MAV_1401 | ATP-dependent rna helicase, dead/ | 43.23 | 566 | BCG_3238 | ATP-dependent RNA helicase r | 75.44 | 527 | MAP3312 | RhlE | 505 | 100 |
| MAP4_0474 | hypothetical protein | 239 | Rv3210c | hypothetical protein | 88.39 | 231 | Mb3236c | hypothetical protein | 88.39 | 231 | MAV_4158 | hypothetical protein | 99 | 201 | BCG_3237c | hypothetical protein | 88.39 | 231 | MAP3311c | hypothetical protein | 239 | 100 |
| MAP4_0475 | putative conserved proline and threonine rich protein | 245 | Rv3209 | Conserved hypothetical threonine a | 61.66 | 186 | Mb3235 | hypothetical protein | 61.66 | 186 | MAV_4157 | hypothetical protein | 100 | 245 | BCG_3236 | hypothetical protein | 61.66 | 186 | MAP3310 | hypothetical protein | 191 | 99.48 |
| MAP4_0476 | hypothetical protein | 87 | Rv3208A | Conserved protein TB9.4 | 74.12 | 90 | Mb3234c | hypothetical protein | 74.12 | 90 | MAV_4156 | hypothetical protein | 100 | 87 | BCG_3235c | hypothetical protein | 74.12 | 90 | MAP3309c | hypothetical protein | 87 | 100 |
| MAP4_0477 | Transcriptional regulator, TetR family | 228 | Rv3208 | Probable transcriptional regulatory | 86.4 | 228 | Mb3233 | TetR family transcriptional re | 86.4 | 228 | MAV_4155 | TetR family transcriptional regulat | 99.56 | 228 | BCG_3234 | TetR family transcriptional regu | 86.4 | 228 | MAP3308 | hypothetical protein | 228 | 100 |
| MAP4_0478 | hypothetical protein | 366 | Rv3207c | hypothetical protein | 81.88 | 285 | Mb3232c | hypothetical protein | 81.53 | 285 | MAV_4154 | hypothetical protein | 99.18 | 379 | BCG_3233c | hypothetical protein | 81.53 | 285 | MAP3307c | hypothetical protein | 366 | 99.73 |
| MAP4_0479 | molybdenum cofactor biosynthesis protein MoeB1 | 398 | Rv3206c | Probable molybdenum cofactor bios | 79.9 | 392 | Mb3231c | molybdopterin biosynthesis-l | 79.65 | 391 | MAV_4153 | molybdopterin biosynthesis-like pr | 99.25 | 398 | BCG_3232c | molybdopterin biosynthesis-lik | 79.9 | 392 | MAP3306c | molybdopterin biosynthesis-like protei | 398 | 100 |
| MAP4_0480 | hypothetical protein | 284 | Rv3205c | hypothetical protein | 86.97 | 292 | Mb3230c | hypothetical protein | 86.97 | 292 | MAV_4151 | hypothetical protein | 99.65 | 284 | BCG_3231c | hypothetical protein | 86.97 | 292 | MAP3305c | hypothetical protein | 284 | 100 |
| MAP4_0481 | DNA-methyltransferase | 100 | Rv3204 | Possible DNA-methyltransferase (m | 80.61 | 101 | Mb3229 | DNA-methyltransferase | 81.63 | 101 | MAV_4152 | 6-O-methylguanine DNA methyltra | 98 | 100 | BCG_3230 | DNA-methyltransferase | 81.63 | 101 | MAP3304 | hypothetical protein | 100 | 100 |
| MAP4_0482 | lipase LipV | 261 | Rv3203 | Possible lipase LipV | 66.52 | 224 | Mb3228 | lipase LipV | 66.52 | 224 | MAV_4150 | alpha/beta hydrolase | 98.47 | 261 | BCG_3229 | lipase lipV | 66.52 | 224 | MAP3303 | hypothetical protein | 261 | 100 |
| MAP4_0483 | hypothetical protein | 78 | Rv2554c | hypothetical protein | 42.86 | 170 | Mb2584c | Holliday junction resolvase-li | 42.86 | 170 | MAV_4149 | hypothetical protein | 100 | 66 | BCG_3228 | hypothetical protein | 58.73 | 72 | MAP3302 | hypothetical protein | 78 | 100 |
| MAP4_0484 | ATP-dependent DNA helicase | 1040 | Rv3202c | Possible ATP-dependent DNA helica | 76.06 | 1055 | Mb3227c | ATP-dependent DNA helicase | 76.06 | 1055 | MAV_4148 | helicase, UvrD/Rep family protein | 98.85 | 1042 | BCG_3227c | ATP-dependent DNA helicase | 76.06 | 1055 | MAP3301c | hypothetical protein | 1044 | 100 |
| MAP4_0485 | ATP-dependent DNA helicase | 1096 | Rv3201c | Probable ATP-dependent DNA helica | 77.77 | 1101 | Mb3226c | ATP-dependent DNA helicase | 77.77 | 1101 | MAV_4147 | superfamily protein I DNA and RNA | 99.09 | 1096 | BCG_3226c | ATP-dependent DNA helicase | 77.77 | 1101 | MAP3300c | hypothetical protein | 1096 | 99.91 |
| MAP4_0486 | NADH pyrophosphatase NudC | 666 | Rv3199c | Probable NADH pyrophosphatase N | 84.31 | 313 | Mb3224c | NADH pyrophosphatase | 84.64 | 313 | MAV_4146 | ion channel membrane protein | 100 | 356 | BCG_3224c | NADH pyrophosphatase | 84.64 | 313 | MAP3299c | hypothetical protein | 666 | 100 |
| MAP4_0487 | glutaredoxin protein | 84 | Rv3198A | Possible glutaredoxin protein | 72.84 | 84 | Mb3223 | glutaredoxin protein | 72.84 | 84 | MAV_4144 | hypothetical protein | 97.62 | 84 | BCG_3223 | glutaredoxin protein | 72.84 | 84 | MAP3298 | hypothetical protein | 84 | 100 |
| MAP4_0488 | ATP-dependent DNA helicase II UvrD2 | 703 | Rv3198c | Probable ATP-dependent DNA helica | 84.78 | 700 | Mb3222c | DNA helicase II | 84.78 | 700 | MAV_4143 | ATP-dependent DNA helicase | 99.15 | 743 | BCG_3222c | DNA helicase II | 84.78 | 700 | MAP3297c | hypothetical protein | 703 | 100 |
| MAP4_0489 | transcriptional regulator whib-like WhiB7 | 90 | Rv3197A | Probable transcriptional regulatory | 68.89 | 92 | Mb3221c | transcriptional regulator Whi | 68.89 | 92 | MAV_4142 | transcription factor WhiB | 98.89 | 90 | BCG_3221c | transcriptional regulatory prot | 68.89 | 92 | MAP3296c | hypothetical protein | 90 | 100 |
| MAP4_0490 | ABC transporter ATP-binding protein | 447 | Rv3197 | Probable conserved ATP-binding pr | 87.02 | 447 | Mb3220 | ABC transporter ATP-binding | 87.02 | 447 | MAV_4141 | ABC transporter | 99.55 | 442 | BCG_3220 | ABC transporter ATP-binding p | 87.02 | 447 | MAP3295 | hypothetical protein | 447 | 100 |
| MAP4_0491 | hypothetical protein | 289 | Rv3196 | hypothetical protein | 74.74 | 299 | Mb3218 | hypothetical protein | 74.74 | 299 | MAV_4140 | hypothetical protein | 98.27 | 289 | BCG_3218 | hypothetical protein | 74.74 | 299 | MAP3294 | hypothetical protein | 289 | 100 |
| MAP4_0492 | hypothetical protein | 459 | Rv3195 | hypothetical protein | 81.2 | 472 | Mb3217 | hypothetical protein | 81.2 | 472 | MAV_4139 | hypothetical protein | 99.78 | 454 | BCG_3217 | hypothetical protein | 81.2 | 472 | MAP3293 | hypothetical protein | 459 | 100 |
| MAP4_0493 | putative secreted protein | 340 | Rv3194c | Possible conserved secreted protein | 80 | 340 | Mb3216c | hypothetical protein | 80 | 340 | MAV_4138 | PDZ domain-containing protein | 99.71 | 340 | BCG_3216c | hypothetical protein | 80 | 340 | MAP3292c | hypothetical protein | 340 | 100 |
| MAP4_0494 | hypothetical protein | 993 | Rv3193c | Probable conserved transmembrane | 89.81 | 992 | Mb3215c | hypothetical protein | 89.91 | 992 | MAV_4137 | hypothetical protein | 99.7 | 993 | BCG_3215c | hypothetical protein | 89.81 | 992 | MAP3291c | hypothetical protein | 993 | 100 |
| MAP4_0495 | hypothetical protein | 198 | Rv1980c | Immunogenic protein Mpt64 (antige | 49.3 | 228 | Mb2002c | hypothetical protein | 49.3 | 228 | MAV_4130 | immunogenic protein MPT64 | 100 | 258 | BCG_3060c | hypothetical protein | 42.86 | 227 | MAP3290c | Mpt64 | 198 | 100 |
| MAP4_0496 | MCE-family protein | 441 | Rv0169 | Mce-family protein Mce1A | 68.81 | 454 | Mb0175 | MCE-family protein MCE1A | 68.81 | 454 | MAV_4125 | virulence factor Mce | 93.98 | 438 | BCG_0206 | MCE-family protein mce1A | 68.81 | 454 | MAP3289c | Mce1_1 | 441 | 100 |
| MAP4_0497 | conserved alanine, valine and leucine rich membrane p | 305 | Rv2729c | Probable conserved integral membr | 51.11 | 301 | Mb2748c | hypothetical protein | 51.85 | 301 | MAV_4124 | dehydrogenase | 99.67 | 636 | BCG_2742c | integral membrane alanine an | 51.85 | 301 | MAP3288 | hypothetical protein | 305 | 100 |
| MAP4_0498 | putative oxidoreductase | 293 | Rv0068 | Probable oxidoreductase | 45.69 | 303 | Mb0069 | short chain dehydrogenase | 46.01 | 303 | MAV_4124 | dehydrogenase | 99.66 | 636 | BCG_0099 | short chain dehydrogenase | 46.01 | 303 | MAP3287 | hypothetical protein | 293 | 100 |
| MAP4_0499 | putative transposase | 367 | Rv0797 | Putative transposase for insertion se | 71.79 | 364 | Mb0820 | IS1547 transposase | 72.08 | 364 | MAV_1059 | transposase | 86 | 350 | BCG_0849 | transposase for insertion seque | 72.08 | 364 | MAP1952c | IS1547_1 transposase | 367 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0500 | hypothetical protein | 354 | Rv2870c | Probable 1-deoxy-D-xylulose 5-phos | 25.75 | 413 | Mb2895c | 1-deoxy-D-xylulose 5-phosph | 25.75 | 413 | MAV_4123 | hypothetical protein | 99.71 | 343 | BCG_2892c | 1-deoxy-D-xylulose 5-phosphat | 25.75 | 413 | MAP3285c | hypothetical protein | 354 | 100 |
| MAP4_0501 | AMP-binding reductase | 1083 | Rv2950c | Fatty-acid-AMP ligase FadD29 (fatty | 34.42 | 619 | Mb2974c | acyl-CoA synthetase | 34.42 | 582 | MAV_4122 | AMP-binding enzyme | 99.72 | 1083 | BCG_2971c | acyl-CoA synthetase | 34.42 | 619 | MAP3284c | FadD29 | 1115 | 100 |
| MAP4_0502 | hypothetical protein | 302 | Rv2777c | hypothetical protein | 74.75 | 356 | Mb2799c | hypothetical protein | 74.75 | 356 | MAV_4121 | FF domain-containing protein | 100 | 302 | BCG_2794c | hypothetical protein | 74.75 | 356 | MAP3283c | hypothetical protein | 302 | 100 |
| MAP4_0503 | putative hydrolase, alphabeta fold family protein | 309 | Rv2214c | Possible short-chain dehydrogenase | 36.13 | 592 | Mb2237c | short chain dehydrogenase | 36.13 | 592 | MAV_4120 | alpha/beta hydrolase | 97.73 | 309 | BCG_2230c | short chain dehydrogenase | 36.13 | 592 | MAP3282c | hypothetical protein | 309 | 100 |
| MAP4_0504 | oxidoreductase | 360 | Rv2776c | Probable oxidoreductase | 78.96 | 309 | Mb2798c | oxidoreductase | 78.96 | 309 | MAV_4119 | oxidoreductase | 99.17 | 360 | BCG_2793c | oxidoreductase | 78.96 | 309 | MAP3281c | hypothetical protein | 362 | 100 |
| MAP4_0505 | putative transporter, sodium hydrogen exchanger fami | 392 | Rv2262c | hypothetical protein | 37.65 | 360 | Mb2285c | hypothetical protein | 37.65 | 502 | MAV_4118 | transporter, monovalent cation:pro | 98.47 | 392 | BCG_2279c | hypothetical protein | 37.65 | 502 | MAP3280c | hypothetical protein | 392 | 100 |
| MAP4_0506 | hypothetical protein | 351 | Rv2756c | Possible type I restriction/modificati | 31.03 | 540 | Mb2777c | type I restriction/modificatior | 31.03 | 540 | MAV_4117 | hypothetical protein | 98.01 | 351 | BCG_2772c | type I restriction/modification | 31.03 | 540 | MAP3279 | hypothetical protein | 351 | 100 |
| MAP4_0507 | hypothetical protein | 427 | Rv2946c | Probable polyketide synthase Pks1 | 28.21 | 1616 | Mb2971c | polyketide synthase | 28.21 | 2112 | MAV_4116 | hypothetical protein | 97.66 | 427 | BCG_2968c | polyketide synthase pks1 | 28.21 | 2112 | MAP3278c | hypothetical protein | 427 | 100 |
| MAP4_0508 | hypothetical protein | 96 | Rv0084 | Possible formate hydrogenlyase Hyc | 51.85 | 316 | Mb0087 | formate hydrogenlyase HYCD | 51.85 | 316 | MAV_4115 | hypothetical protein | 100 | 96 | BCG_0117 | formate hydrogenlyase hycD (F | 51.85 | 316 | MAP3277c | hypothetical protein | 104 | 100 |
| MAP4_0509 | hypothetical protein | 444 | Rv2963 | Probable integral membrane proteir | 27.96 | 406 | Mb2987 | hypothetical protein | 27.96 | 406 | MAV_4113 | hypothetical protein | 97.95 | 440 | BCG_2984 | integral membrane protein | 27.96 | 406 | MAP3276c | hypothetical protein | 444 | 100 |
| MAP4_0510 | putative nitratenitrite response transcriptional regulato | 221 | Rv0844c | Possible nitrate/nitrite response trar | 43.15 | 216 | Mb0867c | nitrate/nitrite response trans | 43.15 | 216 | MAV_4114 | response regulator receiver domair | 99.1 | 221 | BCG_0896c | nitrate/nitrite response transcr | 43.15 | 216 | MAP3275 | NarL_2 | 221 | 100 |
| MAP4_0511 | hypothetical protein | 386 | Rv0758 | Possible two component system res | 31.67 | 485 | Mb0781 | two component system respo | 31.67 | 485 | MAV_4112 | hypothetical protein | 98.7 | 386 | BCG_0810 | two component system respon | 31.67 | 485 | MAP3274 | hypothetical protein | 386 | 100 |
| MAP4_0512 | hypothetical protein | 324 | Rv3131 | hypothetical protein | 66.87 | 332 | Mb3155 | hypothetical protein | 66.87 | 332 | MAV_4111 | hypothetical protein | 98.77 | 324 | BCG_3154 | hypothetical protein | 66.87 | 332 | MAP3273c | hypothetical protein | 324 | 100 |
| MAP4_0513 | hypothetical protein | 138 | Rv3129 | hypothetical protein | 58.24 | 110 | Mb3153 | hypothetical protein | 58.24 | 110 | MAV_4110 | pyridoxamine 5'-phosphate oxidase | 96.38 | 138 | BCG_3152 | hypothetical protein | 58.24 | 110 | MAP3272 | hypothetical protein | 138 | 100 |
| MAP4_0514 | two-component transcriptional system regulatory prot | 222 | Rv3133c | Two component transcriptional regu | 85.12 | 217 | Mb3157c | two component transcription | 85.12 | 217 | MAV_4109 | DevR family transcriptional regulato | 99.55 | 222 | BCG_3156c | two component transcriptional | 85.12 | 217 | MAP3271c | hypothetical protein | 222 | 100 |
| MAP4_0515 | putative two component system sensor histidine kinase | 551 | Rv3132c | Two component sensor histidine kin | 44.06 | 578 | Mb3156c | two component sensor histid | 44.06 | 578 | MAV_4108 | GAF family protein | 99.46 | 551 | BCG_3155c | two component sensor histidin | 44.06 | 578 | MAP3270c | hypothetical protein | 551 | 100 |
| MAP4_0516 | hypothetical protein | 242 | Rv0837c | Hypothetical protein | 34.62 | 342 | Mb0860c | hypothetical protein | 34.62 | 342 | MAV_4107 | ANTAR domain-containing protein | 98.68 | 227 | BCG_0889c | hypothetical protein | 34.62 | 342 | MAP3269 | hypothetical protein | 242 | 100 |
| MAP4_0517 | heat shock protein, 18kD | 147 | Rv2031c | Heat shock protein HspX (alpha-crys | 32.63 | 144 | Mb2057c | heat shock protein hspX | 32.63 | 144 | MAV_4106 | Hsp20/alpha crystallin family prote | 97.96 | 147 | BCG_2050c | heat shock protein hspX | 32.63 | 144 | MAP3268 | Hsp18_3 | 147 | 100 |
| MAP4_0518 | merR-family heat shock protein transcriptional repress | 120 | Rv0353 | Probable heat shock protein transcri | 53.62 | 126 | Mb0361 | HEAT shock protein transcript | 53.62 | 126 | MAV_4105 | MerR family transcriptional regulat | 100 | 120 | BCG_0392 | heat shock protein transcriptio | 53.62 | 126 | MAP3267c | hypothetical protein | 120 | 100 |
| MAP4_0519 | hypothetical protein | 178 | Rv3196A | hypothetical protein | 44 | 66 | Mb3219c | hypothetical protein | 44 | 66 | MAV_4104 | hypothetical protein | 99.44 | 178 | BCG_3219c | hypothetical protein | 44 | 66 | MAP3266c | hypothetical protein | 198 | 100 |
| MAP4_0520 | hypothetical protein | 434 | Rv1854c | Probable NADH dehydrogenase Ndh | 30.3 | 463 | Mb1885c | NADH dehydrogenase | 30.3 | 463 | MAV_4103 | dehydrogenase | 99.07 | 430 | BCG_1890c | NADH dehydrogenase ndh | 30.05 | 463 | MAP3265 | hypothetical protein | 434 | 100 |
| MAP4_0521 | conserved hypothetical ANTAR domain-containing prot | 235 | Rv2006 | Probable trehalose-6-phosphate pho | 36.11 | 1327 | Mb2029 | trehalose-6-phosphate phosp | 36.11 | 1327 | MAV_4102 | ANTAR domain-containing protein | 99.57 | 235 | BCG_2023 | trehalose-6-phosphate phosph | 36.11 | 1327 | MAP3264c | hypothetical protein | 245 | 100 |
| MAP4_0522 | dehydrogenase | 393 | Rv1895 | Possible dehydrogenase | 35.28 | 384 | Mb1929 | dehydrogenase | 36.8 | 234 | MAV_4101 | S-(hydroxymethyl)glutathione dehy | 99.75 | 393 | BCG_1934 | dehydrogenase | 36.8 | 234 | MAP3263c | hypothetical protein | 393 | 100 |
| MAP4_0523 | malto-oligosyltrehalose synthase | 716 | Rv1564c | Probable maltooligosyltrehalose syn | 66.39 | 721 | Mb1591c | malto-oligosyltrehalose synth | 66.39 | 721 | MAV_4100 | glycogen debranching enzyme GlgX | 99.72 | 716 | BCG_1617c | maltooligosyltrehalose synthas | 66.39 | 721 | MAP3262c | GlgX_2 | 716 | 100 |
| MAP4_0524 | oxidoreductase | 259 | Rv0765c | Probable oxidoreductase | 31.31 | 275 | Mb0788c | short chain dehydrogenase | 31.31 | 275 | MAV_4099 | NAD dependent epimerase/dehydr | 99.22 | 255 | BCG_0817c | short chain dehydrogenase | 31.31 | 275 | MAP3261c | hypothetical protein | 271 | 100 |
| MAP4_0525 | putative aldoketo reductase | 324 | Rv2298 | hypothetical protein | 82.04 | 323 | Mb2320 | hypothetical protein | 82.04 | 323 | MAV_4098 | aldo/keto reductase | 99.69 | 324 | BCG_2314 | hypothetical protein | 82.04 | 323 | MAP3260 | hypothetical protein | 324 | 100 |
| MAP4_0526 | putative protein kinase | 333 | Rv2088 | Transmembrane serine/threonine-p | 38.14 | 589 | Mb2115 | Ser/Thr protein kinase | 38.14 | 589 | MAV_4097 | PknJ protein | 99.4 | 333 | BCG_2108 | transmembrane serine/threoni | 38.14 | 589 | MAP3259 | hypothetical protein | 333 | 100 |
| MAP4_0527 | hypothetical protein | 374 | Rv0376c | hypothetical protein | 28.57 | 380 | Mb0383c | hypothetical protein | 28.57 | 380 | MAV_4096 | hypothetical protein | 98.28 | 348 | BCG_0414c | hypothetical protein | 28.57 | 380 | MAP3258 | hypothetical protein | 374 | 100 |
| MAP4_0528 | hypothetical protein | 186 | Rv2148c | hypothetical protein | 31.25 | 258 | Mb2172c | hypothetical protein | 31.25 | 258 | MAV_4095 | hemerythrin HHE cation binding do | 100 | 186 | BCG_2165c | hypothetical protein | 31.25 | 258 | MAP3257c | hypothetical protein | 210 | 100 |
| MAP4_0529 | putative uracil-DNA glycosylase | 221 | Rv1259 | Probable uracil DNA glycosylase, Ud | 29.25 | 299 | Mb1289 | hypothetical protein | 29.25 | 299 | MAV_4094 | uracil DNA glycosylase | 99.55 | 221 | BCG_1317 | hypothetical protein | 29.25 | 299 | MAP3256c | hypothetical protein | 221 | 100 |
| MAP4_0530 | putative thiamine pyrophosphate enzyme | 597 | Rv3003c | Acetolactate synthase (large subunit | 28.47 | 618 | Mb3028c | acetolactate synthase 1 cataly | 28.47 | 618 | MAV_4093 | thiamine pyrophosphate protein | 98.99 | 597 | BCG_3025c | acetolactate synthase 1 catalyt | 28.47 | 618 | MAP3255 | thiamine pyrophosphate protein | 597 | 100 |
| MAP4_0531 | putative UDP-glucose 6-dehydrogenase | 434 | Rv0322 | Probable UDP-glucose 6-dehydroger | 38.29 | 443 | Mb0330 | UDP-glucose 6-dehydrogenas | 38.29 | 443 | MAV_4092 | UDP-glucose 6-dehydrogenase | 99.54 | 434 | BCG_0362 | udp-glucose 6-dehydrogenase | 38.29 | 443 | MAP3254 | hypothetical protein | 578 | 100 |
| MAP4_0532 | putative glycosyltransferase | 321 | Rv2677c | Probable protoporphyrinogen oxida | 28.76 | 452 | Mb2696c | protoporphyrinogen oxidase | 28.76 | 452 | MAV_4091 | transferase | 98.44 | 321 | BCG_2690c | protoporphyrinogen oxidase | 28.76 | 452 | MAP3252 | hypothetical protein | 989 | 30.77 |
| MAP4_0533 | short-chain type dehydrogenase reductase | 231 | Rv0851c | Probable short-chain type dehydrog | 33.7 | 275 | Mb0874c | short chain dehydrogenase | 33.7 | 275 | MAV_4090 | oxidoreductase, short chain dehydr | 100 | 231 | BCG_0903c | short chain dehydrogenase | 33.7 | 275 | MAP3253 | hypothetical protein | 231 | 100 |
| MAP4_0534 | hypothetical protein | 989 | Rv0338c | Probable iron-sulfur-binding reducta | 36.36 | 882 | Mb0345c | iron-sulfur-binding reductase | 36.36 | 882 | MAV_4087 | transferase | 99.35 | 339 | BCG_0377c | iron-sulfur-binding reductase | 36.36 | 882 | MAP3252 | hypothetical protein | 989 | 100 |
| MAP4_0535 | putative transferase | 496 | Rv0114 | Possible D-alpha,beta-D-heptose-1,7 | 38.68 | 190 | Mb0118 | dehydratase | 38.68 | 190 | MAV_4086 | transferase | 97.98 | 496 | BCG_0147 | dehydratase | 38.68 | 190 | MAP3250 | hypothetical protein | 333 | 100 |
| MAP4_0536 | carbamoyltransferase | 546 | Rv0193c | Hypothetical protein | 36.92 | 615 | Mb0199c | hypothetical protein | 36.92 | 615 | MAV_4085 | transferase | 99.27 | 546 | BCG_0230c | hypothetical protein | 36.92 | 615 | MAP3249 | hypothetical protein | 546 | 100 |
| MAP4_0537 | putative NAD-dependent epimerase dehydratase | 358 | Rv3784 | Possible dTDP-glucose 4,6-dehydrat | 29.81 | 326 | Mb3813 | dTDP-glucose 4,6-dehydratas | 29.81 | 326 | MAV_4084 | UDP-glucuronic acid decarboxylase | 97.77 | 361 | BCG_3846 | dTDP-glucose 4,6-dehydratase | 29.81 | 326 | MAP3248 | hypothetical protein | 358 | 100 |
| MAP4_0540 | putative glycosyltransferase | 406 | Rv0486 | Glycosyltransferase MshA | 35.82 | 480 | Mb0496 | mannosyltransferase | 35.82 | 480 | MAV_4082 | transferase | 99.01 | 406 | BCG_0527 | mannosyltransferase | 35.82 | 480 | MAP3246 | hypothetical protein | 413 | 100 |
| MAP4_0541 | hypothetical protein | 322 | Rv2188c | Mannosyltransferase PimB | 32.61 | 385 | Mb2211c | hypothetical protein | 32.61 | 385 | MAV_4081 | transferase | 98.05 | 308 | BCG_2204c | hypothetical protein | 32.61 | 385 | MAP3245 | hypothetical protein | 322 | 100 |
| MAP4_0542 | putative DNA topoisomerase | 351 | Rv2744c | Conserved 35 kDa alanine rich prote | 34.18 | 270 | Mb2765c | hypothetical protein | 34.18 | 270 | MAV_3466 | extracellular solute-binding protein | 78.57 | 557 | BCG_2760c | hypothetical protein | 34.18 | 270 | MAP3244 | hypothetical protein | 399 | 100 |
| MAP4_0544 | hypothetical protein | 278 | Rv2047c | hypothetical protein | 31.07 | 854 | Mb2073c | hypothetical protein | 31.07 | 854 | MAV_4078 | hypothetical protein | 96.15 | 285 | BCG_2066c | hypothetical protein | 31.07 | 854 | MAP3242 | hypothetical protein | 346 | 99.64 |
| MAP4_0545 | hypothetical protein | 78 | Rv1379 | Probable pyrimidine operon regulato | 36 | 193 | Mb1414 | bifunctional pyrimidine regula | 36 | 193 | MAV_4077 | hypothetical protein | 98.72 | 78 | BCG_1440 | bifunctional pyrimidine regulat | 36 | 193 | MAP2391 | hypothetical protein | 111 | 57.69 |
| MAP4_0546 | hypothetical protein | 103 | Rv0543c | hypothetical protein | 38.2 | 100 | Mb0557c | hypothetical protein | 38.2 | 100 | MAV_4075 | hypothetical protein | 98.06 | 103 | BCG_0587c | hypothetical protein | 38.2 | 100 | MAP1764 | hypothetical protein | 95 | 39.08 |
| MAP4_0547 | putative endonuclease exonuclease phosphatase | 254 | Rv3130c | Triacylglycerol synthase (diacylglyce | 30.12 | 463 | Mb3154c | hypothetical protein | 30.12 | 463 | MAV_4076 | endonuclease/exonuclease/phosph | 98.81 | 252 | BCG_3153c | hypothetical protein | 30.12 | 463 | MAP3240 | hypothetical protein | 260 | 100 |
| MAP4_0548 | conserved hypothetical protein, glcNAc-PIde-N-acetyla | 255 | Rv0323c | hypothetical protein | 31.09 | 223 | Mb0331c | hypothetical protein | 31.09 | 223 | MAV_4074 | GlcNAc-PI de-N-acetylase | 97.65 | 255 | BCG_0363c | hypothetical protein | 31.09 | 223 | MAP3239 | hypothetical protein | 252 | 99.6 |
| MAP4_0549 | hypothetical protein | 319 | Rv3061c | Probable acyl-CoA dehydrogenase F | 39.53 | 721 | Mb3087c | acyl-CoA dehydrogenase | 39.53 | 600 | MAV_4073 | dehydrogenase | 99.68 | 317 | BCG_3086c | acyl-CoA dehydrogenase fadE2 | 39.53 | 721 | MAP3238 | hypothetical protein | 319 | 100 |
| MAP4_0550 | hypothetical protein | 191 | Rv0078A | Hypothetical protein | 39.53 | 197 | Mb0081c | hypothetical protein | 39.53 | 197 | MAV_4071 | hypothetical protein | 99.48 | 191 | BCG_0110c | hypothetical protein | 39.53 | 197 | MAP3237c | hypothetical protein | 191 | 100 |
| MAP4_0551 | hypothetical protein | 85 | Rv1297 | Probable transcription termination f | 36.11 | 602 | Mb1329 | transcription termination fact | 36.11 | 602 | MAV_4070 | hypothetical protein | 100 | 85 | BCG_1357 | transcription termination facto | 36.11 | 602 | MAP2464c | transcription termination factor Rho | 620 | 27.14 |
| MAP4_0552 | catalase | 706 | Rv3496c | Mce-family protein Mce4D | 31.25 | 451 | Mb3526c | MCE-family protein MCE4D | 31.25 | 451 | MAV_4069 | catalase HPII | 99.43 | 721 | BCG_3560c | Mce-family protein mce4D | 31.25 | 451 | MAP3236 | CatB | 706 | 100 |
| MAP4_0553 | putative protein-glutamate methylesterase | 339 | Rv1783 | ESX conserved component EccC5 ES | 30 | 1391 | Mb1812 | hypothetical protein | 30 | 1391 | MAV_4066 | protein-glutamate methylesterase | 37.02 | 305 | BCG_1816 | hypothetical protein | 30 | 1391 | MAP3235c | hypothetical protein | 339 | 100 |
| MAP4_0554 | hypothetical protein | 252 | Rv0941c | hypothetical protein | 44.94 | 257 | Mb0966c | hypothetical protein | 44.94 | 257 | MAV_4067 | stas domain-containing protein | 99.6 | 252 | BCG_0995c | hypothetical protein | 44.94 | 257 | MAP3234c | hypothetical protein | 252 | 100 |
| MAP4_0555 | putative methyltransferase | 616 | Rv1126c | hypothetical protein | 31.43 | 201 | Mb1157c | hypothetical protein | 31.43 | 201 | MAV_4065 | CheR methyltransferase SAM bindi | 99.84 | 616 | BCG_1187c | hypothetical protein | 31.43 | 201 | MAP3233c | hypothetical protein | 616 | 100 |
| MAP4_0556 | putative CheB methylesterase | 309 | Rv2800 | Possible hydrolase | 33.85 | 549 | Mb2823 | hydrolase | 33.85 | 549 | MAV_4066 | protein-glutamate methylesterase | 98.69 | 305 | BCG_2818 | hydrolase | 33.85 | 549 | MAP3232 | hypothetical protein | 309 | 100 |
| MAP4_0557 | putative glycosyl transferase | 390 | Rv3032 | Alpha (1->4) glucosyltransferase | 26.91 | 414 | Mb3058 | transferase | 26.91 | 414 | MAV_4064 | glycosyl transferase, group 1 family | 99.23 | 390 | BCG_3055 | transferase | 26.67 | 414 | MAP3231c | hypothetical protein | 392 | 99.74 |
| MAP4_0558 | transcriptional regulator, AraC family | 358 | Rv3833 | Transcriptional regulatory protein (p | 23.71 | 263 | Mb3863 | AraC family transcriptional re | 23.71 | 263 | MAV_4063 | AraC family transcriptional regulato | 98.88 | 358 | BCG_3896 | AraC family transcriptional reg | 23.71 | 263 | MAP3230c | hypothetical protein | 358 | 100 |
| MAP4_0559 | non-heme haloperoxidase | 316 | Rv3171c | Possible non-heme haloperoxidase H | 72.24 | 299 | Mb3196c | non-Heme haloperoxidase Hp | 71.91 | 299 | MAV_4061 | alpha/beta hydrolase | 99.05 | 316 | BCG_3195c | non-heme haloperoxidase hpx | 71.91 | 299 | MAP3229c | Hpx | 316 | 100 |
| MAP4_0560 | flavin-containing monoamine oxidase | 448 | Rv3170 | Probable flavin-containing monoami | 80.36 | 448 | Mb3195 | flavin-containing monoamine | 80.36 | 448 | MAV_4062 | flavin-containing monoamine oxida | 99.78 | 448 | BCG_3194 | flavin-containing monoamine c | 80.36 | 448 | MAP3228 | hypothetical protein | 448 | 100 |
| MAP4_0561 | putative membrane transporter | 439 | Rv1200 | Probable conserved integral membr | 39.62 | 425 | Mb1232 | integral membrane transport | 39.62 | 425 | MAV_4059 | monoxygenase | 99.77 | 896 | BCG_1260 | integral membrane transport p | 39.62 | 425 | MAP3227c | hypothetical protein | 470 | 99.77 |
| MAP4_0562 | monooxygenase | 457 | Rv1855c | Possible oxidoreductase | 24.19 | 307 | Mb1886c | oxidoreductase | 24.19 | 307 | MAV_4059 | monoxygenase | 99.12 | 896 | BCG_1891c | oxidoreductase | 24.19 | 307 | MAP3226c | hypothetical protein | 457 | 100 |
| MAP4_0563 | hypothetical protein | 371 | Rv3169 | hypothetical protein | 87.87 | 374 | Mb3194 | hypothetical protein | 87.87 | 374 | MAV_4060 | hypothetical protein | 99.19 | 371 | BCG_3193 | hypothetical protein | 87.87 | 374 | MAP3225 | hypothetical protein | 371 | 100 |
| MAP4_0564 | putative phosphotransferase | 377 | Rv3168 | Putative aminoglycoside phosphotra | 85.15 | 378 | Mb3193 | hypothetical protein | 84.88 | 378 | MAV_4058 | phosphotransferase enzyme family | 99.2 | 377 | BCG_3192 | hypothetical protein | 85.15 | 378 | MAP3224 | hypothetical protein | 381 | 99.73 |
| MAP4_0565 | Transcriptional regulator, TetR family | 200 | Rv3167c | Probable transcriptional regulatory p | 88 | 208 | Mb3192c | TetR family transcriptional re | 88 | 208 | MAV_4057 | TetR family transcriptional regulato | 99 | 200 | BCG_3191c | TetR family transcriptional regu | 88 | 208 | MAP3223c | hypothetical protein | 214 | 100 |
| MAP4_0566 | oxidoreductase, short chain dehydrogenase family prot | 301 | Rv1928c | Probable short-chain type dehydrog | 28.69 | 255 | Mb1963c | short chain dehydrogenase | 28.69 | 255 | MAV_4056 | oxidoreductase, short chain dehydr | 93.99 | 461 | BCG_1967c | short chain dehydrogenase | 28.69 | 255 | MAP3222c | hypothetical protein | 268 | 99.63 |
| MAP4_0567 | hypothetical protein | 508 | Rv1148c | hypothetical protein | 39.83 | 482 | Mb1179c | hypothetical protein | 39.83 | 482 | MAV_4055 | hypothetical protein | 97.61 | 460 | BCG_1984 | hypothetical protein | 39.83 | 454 | MAP3221 | hypothetical protein | 508 | 99.8 |
| MAP4_0568 | hypothetical protein | 317 | Rv3166c | hypothetical protein | 60.88 | 319 | Mb3191c | hypothetical protein | 60.88 | 319 | MAV_4054 | hypothetical protein | 97.17 | 320 | BCG_3190c | hypothetical protein | 60.88 | 319 | MAP3220c | hypothetical protein | 317 | 100 |
| MAP4_0569 | hypothetical protein | 160 | Rv3165c | hypothetical protein | 75.62 | 160 | Mb3190c | hypothetical protein | 75.62 | 160 | MAV_4053 | hypothetical protein | 98.72 | 156 | BCG_3189c | hypothetical protein | 75.62 | 160 | MAP3219c | hypothetical protein | 160 | 100 |
| MAP4_0570 | methanol dehydrogenase transcriptional regulatory pro | 325 | Rv3164c | Probable methanol dehydrogenase t | 93.35 | 320 | Mb3189c | methanol dehydrogenase tra | 93.04 | 320 | MAV_4052 | ATPase | 99.67 | 304 | BCG_3188c | methanol dehydrogenase trans | 93.35 | 320 | MAP3218c | MoxR3 | 325 | 100 |
| MAP4_0571 | conserved secreted protein | 383 | Rv3163c | Possible conserved secreted protein | 80 | 423 | Mb3188c | hypothetical protein | 79.68 | 423 | MAV_4050 | hypothetical protein | 98.39 | 371 | BCG_3187c | hypothetical protein | 80 | 423 | MAP3217c | hypothetical protein | 383 | 100 |
| MAP4_0572 | O-methyltransferase | 276 | Rv1153c | Probable O-methyltransferase Omt | 31.69 | 282 | Mb1184c | O-methyltransferase | 31.15 | 282 | MAV_4048 | Omt protein | 99.28 | 276 | BCG_1214c | O-methyltransferase omt | 31.15 | 282 | MAP3216 | Omt | 276 | 100 |
| MAP4_0573 | TetR family transcriptional regulator | 230 | Rv1219c | Probable transcriptional regulatory p | 39.52 | 212 | Mb1251c | transcriptional regulator | 39.52 | 212 | MAV_4046 | TetR family transcriptional regulato | 99.13 | 230 | BCG_1279c | transcriptional regulatory prote | 39.52 | 212 | MAP3215c | hypothetical protein | 230 | 100 |
| MAP4_0574 | NADH dehydrogenase I chain N | 527 | Rv3158 | Probable NADH dehydrogenase I (ch | 82.49 | 531 | Mb3182 | NADH dehydrogenase subuni | 82.49 | 531 | MAV_4047 | NADH dehydrogenase subunit N | 99.62 | 527 | BCG_3181 | NADH dehydrogenase subunit | 82.49 | 531 | MAP3214 | NADH dehydrogenase subunit N | 527 | 100 |
| MAP4_0575 | NADH dehydrogenase I chain M | 522 | Rv3157 | Probable NADH dehydrogenase I (ch | 82.58 | 553 | Mb3181 | NADH dehydrogenase subuni | 82.21 | 553 | MAV_4045 | NADH dehydrogenase subunit M | 99.62 | 522 | BCG_3180 | NADH dehydrogenase subunit | 82.4 | 553 | MAP3213 | NADH dehydrogenase subunit M | 522 | 100 |
| MAP4_0576 | NADH dehydrogenase I chain L | 628 | Rv3156 | Probable NADH dehydrogenase I (ch | 86.39 | 633 | Mb3180 | NADH dehydrogenase subuni | 86.39 | 633 | MAV_4044 | NADH dehydrogenase subunit L | 99.2 | 640 | BCG_3179 | NADH dehydrogenase subunit | 86.39 | 633 | MAP3212 | NADH dehydrogenase subunit L | 628 | 99.84 |
| MAP4_0577 | NADH dehydrogenase I chain K | 99 | Rv3155 | Probable NADH dehydrogenase I (ch | 94.95 | 99 | Mb3179 | NADH dehydrogenase subuni | 94.95 | 99 | MAV_4043 | NADH dehydrogenase subunit K | 100 | 99 | BCG_3178 | NADH dehydrogenase subunit | 94.95 | 99 | MAP3211 | NADH dehydrogenase subunit K | 99 | 100 |
| MAP4_0578 | NADH dehydrogenase I chain J | 274 | Rv3154 | Probable NADH dehydrogenase I (ch | 84.05 | 262 | Mb3178 | NADH dehydrogenase subuni | 84.05 | 262 | MAV_4042 | NADH dehydrogenase subunit J | 99.64 | 274 | BCG_3177 | NADH dehydrogenase subunit | 84.05 | 262 | MAP3210 | NADH dehydrogenase subunit J | 274 | 100 |
| MAP4_0579 | NADH dehydrogenase I chain I | 181 | Rv3153 | Probable NADH dehydrogenase I (ch | 87.43 | 211 | Mb3177 | NADH dehydrogenase subuni | 88.46 | 211 | MAV_4041 | NADH dehydrogenase subunit I | 100 | 181 | BCG_3176 | NADH dehydrogenase subunit | 88.46 | 211 | MAP3209 | NADH dehydrogenase subunit I | 181 | 100 |
| MAP4_0580 | NADH dehydrogenase I chain H | 424 | Rv3152 | Probable NADH dehydrogenase I (ch | 80.95 | 410 | Mb3176 | NADH dehydrogenase subuni | 80.95 | 410 | MAV_4040 | NADH dehydrogenase subunit H | 100 | 418 | BCG_3175 | NADH dehydrogenase subunit | 80.95 | 410 | MAP3208 | NADH dehydrogenase subunit H | 409 | 99.76 |
| MAP4_0581 | NADH dehydrogenase I chain G | 793 | Rv3151 | Probable NADH dehydrogenase I (ch | 83.12 | 806 | Mb3175 | NADH dehydrogenase subuni | 83.38 | 806 | MAV_4039 | NADH dehydrogenase subunit G | 99.62 | 793 | BCG_3174 | NADH dehydrogenase subunit | 83.38 | 806 | MAP3207 | NADH dehydrogenase subunit G | 778 | 99.87 |
| MAP4_0582 | NADH dehydrogenase I chain F | 453 | Rv3150 | Probable NADH dehydrogenase I (ch | 90.5 | 445 | Mb3174 | NADH dehydrogenase I subur | 90.5 | 445 | MAV_4038 | NADH-quinone oxidoreductase, F s | 99.78 | 453 | BCG_3173 | NADH dehydrogenase I subunit | 90.5 | 445 | MAP3206 | hypothetical protein | 453 | 100 |
| MAP4_0583 | NADH dehydrogenase I chain E | 252 | Rv3149 | Probable NADH dehydrogenase I (ch | 84.08 | 252 | Mb3173 | NADH dehydrogenase subuni | 84.08 | 252 | MAV_4037 | NADH dehydrogenase subunit E | 98.41 | 252 | BCG_3172 | NADH dehydrogenase subunit | 84.08 | 252 | MAP3205 | NADH dehydrogenase subunit E | 252 | 100 |
| MAP4_0584 | NADH dehydrogenase I chain D | 441 | Rv3148 | Probable NADH dehydrogenase I (ch | 90.43 | 440 | Mb3172 | NADH dehydrogenase subuni | 90.43 | 440 | MAV_4036 | NADH dehydrogenase subunit D | 100 | 441 | BCG_3171 | NADH dehydrogenase subunit | 90.43 | 440 | MAP3204 | NADH dehydrogenase subunit D | 441 | 100 |
| MAP4_0585 | NADH dehydrogenase I chain C | 235 | Rv3147 | Probable NADH dehydrogenase I (ch | 79.24 | 236 | Mb3171 | NADH dehydrogenase subuni | 79.24 | 236 | MAV_4035 | NADH dehydrogenase subunit C | 99.15 | 235 | BCG_3170 | NADH dehydrogenase subunit | 79.24 | 236 | MAP3203 | NADH dehydrogenase subunit C | 235 | 100 |
| MAP4_0586 | NADH dehydrogenase I chain B | 184 | Rv3146 | Probable NADH dehydrogenase I (ch | 97.28 | 184 | Mb3170 | NADH dehydrogenase subuni | 97.28 | 184 | MAV_4034 | NADH dehydrogenase subunit B | 100 | 184 | BCG_3169 | NADH dehydrogenase subunit | 97.28 | 184 | MAP3202 | NADH dehydrogenase subunit B | 184 | 100 |
| MAP4_0587 | NADH dehydrogenase I chain A | 125 | Rv3145 | Probable NADH dehydrogenase I (ch | 82.03 | 128 | Mb3169 | NADH dehydrogenase subuni | 82.03 | 128 | MAV_4033 | NADH dehydrogenase subunit A | 99.2 | 154 | BCG_3168 | NADH dehydrogenase subunit | 82.03 | 128 | MAP3201 | NADH dehydrogenase subunit A | 125 | 100 |
| MAP4_0588 | response regulator | 137 | Rv3143 | Probable response regulator | 83.85 | 133 | Mb3167 | response regulator | 83.85 | 133 | MAV_4032 | two-component system response r | 99.27 | 137 | BCG_3166 | response regulator | 83.85 | 133 | MAP3200 | hypothetical protein | 137 | 100 |
| MAP4_0589 | hypothetical protein | 175 | Rv3506 | Fatty-acid-CoA synthetase FadD17 (f | 34.48 | 502 | Mb3536 | acyl-CoA synthetase | 34.48 | 502 | MAV_4031 | YceI like family protein | 98.29 | 175 | BCG_3570 | acyl-CoA synthetase | 34.48 | 502 | MAP3199 | hypothetical protein | 178 | 99.43 |
| MAP4_0590 | hypothetical protein | 128 | Rv0034 | hypothetical protein | 26.67 | 131 | Mb0035 | hypothetical protein | 26.67 | 131 | MAV_5155 | hypothetical protein | 33.33 | 133 | BCG_0065 | hypothetical protein | 26.67 | 131 | MAP3198 | hypothetical protein | 128 | 100 |
| MAP4_0591 | hypothetical protein | 112 | Rv0767c | hypothetical protein | 39.22 | 213 | Mb0790c | hypothetical protein | 39.22 | 213 | MAV_4029 | hypothetical protein | 98.21 | 112 | BCG_0819c | hypothetical protein | 39.22 | 213 | MAP0709 | hypothetical protein | 269 | 37.5 |
| MAP4_0592 | putative aminoglycoside phosphotransferase | 332 | Rv3168 | Putative aminoglycoside phosphotra | 26.07 | 378 | Mb3193 | hypothetical protein | 26.07 | 378 | MAV_4028 | aminoglycoside phosphotransferas | 98.19 | 332 | BCG_3192 | hypothetical protein | 26.07 | 378 | MAP3197 | hypothetical protein | 265 | 100 |
| MAP4_0593 | acyl-CoA dehydrogenase | 412 | Rv0972c | Acyl-CoA dehydrogenase FadE12 | 29.79 | 388 | Mb0159c | acyl-CoA dehydrogenase | 34.27 | 403 | MAV_4027 | acyl-CoA dehydrogenase | 99.27 | 412 | BCG_0190c | acyl-CoA dehydrogenase fadE2 | 34.27 | 403 | MAP3196 | FadE12_3 | 412 | 100 |
| MAP4_0594 | Transcriptional regulator, TetR family | 203 | Rv0273c | Possible transcriptional regulatory p | 31.03 | 206 | Mb0279c | transcriptional regulator | 31.03 | 206 | MAV_4026 | TetR family transcriptional regulato | 99.51 | 203 | BCG_0311c | transcriptional regulatory prote | 31.03 | 206 | MAP3195 | hypothetical protein | 209 | 100 |
| MAP4_0595 | putative pyruvate carboxyltransferase | 301 | Rv3534c | Probable 4-hydroxy-2-oxovalerate a | 30.17 | 346 | Mb3564c | 4-hydroxy-2-ketovalerate ald | 30.17 | 346 | MAV_4025 | pyruvate carboxyltransferase | 98.99 | 297 | BCG_3598c | 4-hydroxy-2-ketovalerate aldol | 30.17 | 346 | MAP3194 | hypothetical protein | 301 | 100 |
| MAP4_0596 | putative CoA-transferase | 404 | Rv1866 | hypothetical protein | 33.74 | 778 | Mb1897 | hypothetical protein | 33.74 | 778 | MAV_4024 | caib/baif family protein | 99.5 | 404 | BCG_1902 | hypothetical protein | 33.74 | 778 | MAP3193 | hypothetical protein | 404 | 100 |
| MAP4_0597 | putative hydrolase | 391 | Rv0272c | hypothetical protein | 41.24 | 377 | Mb0278c | hypothetical protein | 41.24 | 377 | MAV_4023 | hypothetical protein | 99.74 | 391 | BCG_0310c | hypothetical protein | 41.24 | 377 | MAP3192 | hypothetical protein | 391 | 100 |
| MAP4_0598 | putative homogentisate 1,2-dioxygenase | 364 | Rv1662 | Probable polyketide synthase Pks8 | 23.73 | 1602 | Mb1690 | polyketide synthase | 23.73 | 1602 | MAV_4022 | homogentisate 1,2-dioxygenase | 98.9 | 364 | BCG_1701 | polyketide synthase | 23.73 | 1601 | MAP3191 | hypothetical protein | 381 | 100 |
| MAP4_0599 | NADPH quinone oxidoreductase FadB4 | 323 | Rv3141 | Probable NADPH quinone oxidoredu | 84.47 | 323 | Mb3165 | NADPH quinone oxidoreducta | 84.47 | 323 | MAV_4021 | zinc-binding dehydrogenase | 99.38 | 323 | BCG_3164 | NADPH quinone oxidoreductas | 84.47 | 323 | MAP3190 | FadB4 | 323 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0600 | acyl-CoA dehydrogenase | 401 | Rv3140 | Probable acyl-CoA dehydrogenase F | 88.28 | 401 | Mb3164 | acyl-CoA dehydrogenase | 88.28 | 401 | MAV_4019 | acyl-CoA dehydrogenase | 99.5 | 401 | BCG_3163 | acyl-CoA dehydrogenase fadE2 | 88.28 | 401 | MAP3189 | FadE23 | 401 | 100 |
| MAP4_0601 | putative acyl-CoA dehydrogenase | 463 | Rv3139 | Probable acyl-CoA dehydrogenase F | 87.64 | 468 | Mb3163 | acyl-CoA dehydrogenase | 87.64 | 468 | MAV_4018 | acyl-CoA dehydrogenase | 99.57 | 463 | BCG_3162 | acyl-CoA dehydrogenase fadE2 | 87.64 | 468 | MAP3188 | FadE24 | 463 | 100 |
| MAP4_0602 | monophosphatase | 259 | Rv3137 | Probable monophosphatase | 78.6 | 260 | Mb3161 | monophosphatase | 78.99 | 260 | MAV_4017 | inositol monophosphatase | 99.23 | 259 | BCG_3160 | monophosphatase | 78.99 | 260 | MAP3187 | hypothetical protein | 259 | 100 |
| MAP4_0603 | hypothetical protein | 114 | Rv3136A | hypothetical protein | 75.47 | 110 | Mb2218 | Rieske iron-sulfur protein Qcr | 47.62 | 429 | MAV_4016 | hypothetical protein | 100 | 117 | BCG_2211 | Rieske iron-sulfur protein QcrA | 47.62 | 429 | MAP3186c | hypothetical protein | 114 | 100 |
| MAP4_0604 | PPE family protein | 362 | Rv3136 | PPE family protein PPE51 | 52.21 | 380 | Mb3160 | PPE family protein | 52.21 | 380 | MAV_4015 | PPE family protein | 98.9 | 362 | BCG_3159 | PPE family protein | 52.21 | 380 | MAP3185 | hypothetical protein | 362 | 100 |
| MAP4_0605 | PPE family protein | 391 | Rv3136 | PPE family protein PPE51 | 49.63 | 380 | Mb3160 | PPE family protein | 49.63 | 380 | MAV_4014 | PPE family protein | 99.49 | 391 | BCG_3159 | PPE family protein | 49.63 | 380 | MAP3184 | hypothetical protein | 391 | 100 |
| MAP4_0606 | hypothetical protein | 265 | Rv1488 | Possible exported conserved protein | 35.03 | 381 | Mb1524 | hypothetical protein | 35.03 | 381 | MAV_4013 | SPFH domain-containing protein/ba | 99.25 | 265 | BCG_1550 | hypothetical protein | 35.03 | 381 | MAP3183 | hypothetical protein | 265 | 100 |
| MAP4_0607 | hypothetical protein | 208 | Rv3401 | hypothetical protein | 32.58 | 786 | Mb3434 | hypothetical protein | 32.58 | 786 | MAV_4012 | hypothetical protein | 99.04 | 208 | BCG_3471 | hypothetical protein | 32.58 | 786 | MAP3182 | hypothetical protein | 208 | 100 |
| MAP4_0610 | hypothetical protein | 252 | Rv3134c | Universal stress protein family prote | 53.65 | 268 | Mb3158c | hypothetical protein | 53.65 | 268 | MAV_4010 | hypothetical protein | 100 | 252 | BCG_3157c | hypothetical protein | 53.65 | 268 | MAP3179c | hypothetical protein | 252 | 100 |
| MAP4_0611 | hypothetical protein | 154 | Rv1001 | Probable arginine deiminase ArcA (a | 39.58 | 402 | Mb1028 | arginine deiminase | 39.58 | 402 | MAV_4008 | hypothetical protein | 98.7 | 154 | BCG_1058 | arginine deiminase | 39.58 | 402 | MAP3178c | hypothetical protein | 154 | 100 |
| MAP4_0612 | putative pyridoxamine 5'-phosphate oxidase | 151 | Rv3129 | hypothetical protein | 70.3 | 110 | Mb3153 | hypothetical protein | 70.3 | 110 | MAV_4009 | hypothetical protein | 99.3 | 143 | BCG_3152 | hypothetical protein | 70.3 | 110 | MAP3177 | hypothetical protein | 151 | 100 |
| MAP4_0613 | NADPH:adrenodoxin oxidoreductase | 455 | Rv3106 | NADPH:adrenodoxin oxidoreductase | 79.61 | 456 | Mb3133 | NADPH:adrenodoxin oxidored | 79.82 | 456 | MAV_4007 | NADPH-ferredoxin reductase fpra | 99.34 | 455 | BCG_3131 | NADPH:adrenodoxin oxidoredu | 79.82 | 456 | MAP3176 | FprA | 455 | 100 |
| MAP4_0614 | peptide chain release factor 2 | 370 | Rv3105c | Probable peptide chain release facto | 90.84 | 378 | Mb3132c | peptide chain release factor 2 | 90.84 | 378 | MAV_4006 | peptide chain release factor 2 | 99.73 | 370 | BCG_3130c | peptide chain release factor 2 | 90.84 | 378 | MAP3175c | peptide chain release factor 2 | 373 | 99.73 |
| MAP4_0615 | hypothetical protein | 331 | Rv3104c | Possible conserved transmembrane | 72.05 | 308 | Mb3131c | transmembrane protein | 72.05 | 308 | MAV_4005 | transporter, small conductance me | 99.66 | 292 | BCG_3129c | hypothetical protein | 72.05 | 308 | MAP3174c | hypothetical protein | 331 | 100 |
| MAP4_0616 | putative proline rich protein | 166 | Rv3103c | Hypothetical proline-rich protein | 63.01 | 145 | Mb3130c | hypothetical protein | 63.01 | 145 | MAV_4004 | hypothetical protein | 99.4 | 166 | BCG_3128c | hypothetical protein | 63.01 | 145 | MAP3173c | hypothetical protein | 166 | 100 |
| MAP4_0617 | cell division ATP-binding protein FtsE | 229 | Rv3102c | Putative cell division ATP-binding pr | 93.01 | 229 | Mb3129c | cell division ATP-binding prot | 93.01 | 229 | MAV_4003 | cell division ATP-binding protein Fts | 100 | 230 | BCG_3127c | cell division ATP-binding protei | 93.01 | 229 | MAP3172c | hypothetical protein | 229 | 100 |
| MAP4_0618 | cell division protein FtsX | 297 | Rv3101c | Putative cell division protein FtsX (se | 80.47 | 297 | Mb3128c | cell division protein FtsX | 80.13 | 297 | MAV_4002 | efflux ABC transporter permease | 99.66 | 297 | BCG_3126c | cell division protein ftsX | 80.13 | 297 | MAP3171c | hypothetical protein | 297 | 100 |
| MAP4_0619 | SsrA-binding protein | 169 | Rv3100c | Probable SSRA-binding protein Smp | 84.31 | 160 | Mb3127c | SsrA-binding protein | 84.31 | 160 | MAV_4001 | SsrA-binding protein | 98.11 | 53 | BCG_3125c | SsrA-binding protein | 84.31 | 160 | MAP3170c | SsrA-binding protein | 169 | 100 |
| MAP4_0620 | hypothetical protein | 261 | Rv0676c | Probable conserved transmembrane | 24 | 964 | Mb0695c | transmembrane transport pro | 24 | 964 | MAV_4000 | hypothetical protein | 100 | 248 | BCG_0725c | transmembrane transport prot | 24 | 964 | MAP3169c | hypothetical protein | 261 | 100 |
| MAP4_0621 | hypothetical protein | 283 | Rv3099c | hypothetical protein | 72.44 | 283 | Mb3126c | hypothetical protein | 72.44 | 283 | MAV_0050 | hypothetical protein | 27.67 | 257 | BCG_3124c | hypothetical protein | 72.44 | 283 | MAP3168c | hypothetical protein | 283 | 100 |
| MAP4_0622 | hypothetical protein | 158 | Rv2728c | Conserved alanine rich protein | 26.67 | 231 | Mb2747c | hypothetical protein | 26.67 | 231 | MAV_3997 | hypothetical protein | 97.87 | 102 | BCG_2741c | hypothetical protein | 26.67 | 231 | MAP3167c | hypothetical protein | 158 | 100 |
| MAP4_0623 | hypothetical protein | 241 | Rv1283c | Probable oligopeptide-transport inte | 50 | 325 | Mb1314c | oligopeptide-transport integr | 50 | 325 | MAV_3995 | hypothetical protein | 96.68 | 241 | BCG_1342c | oligopeptide-transport integral | 50 | 325 | MAP3166c | hypothetical protein | 241 | 100 |
| MAP4_0624 | putative glycosyltransferase family protein | 388 | Rv1524 | Probable glycosyltransferase | 53.12 | 414 | Mb1551 | glycosyltransferase | 53.12 | 414 | MAV_3994 | glycosyltransferase GtfB | 96.91 | 356 | BCG_1576 | glycosyltransferase | 53.12 | 414 | MAP3165 | hypothetical protein | 388 | 100 |
| MAP4_0625 | hypothetical protein | 167 | Rv0481c | Hypothetical protein | 38.76 | 174 | Mb0491c | hypothetical protein | 38.76 | 174 | MAV_3993 | hypothetical protein | 99.4 | 168 | BCG_0522c | hypothetical protein | 38.76 | 174 | MAP3164 | hypothetical protein | 167 | 100 |
| MAP4_0626 | hypothetical protein | 232 | Rv2719c | Possible conserved membrane prote | 44.44 | 165 | Mb2738c | hypothetical protein | 44.44 | 165 | MAV_4517 | cyclopropane-fatty-acyl-phospholip | 33.33 | 298 | BCG_2732c | hypothetical protein | 44.44 | 165 | MAP3163 | hypothetical protein | 232 | 100 |
| MAP4_0629 | phytanoyl-CoA dioxygenase (PhyH) family protein | 287 | Rv3633 | hypothetical protein | 36.87 | 291 | Mb3657 | hypothetical protein | 36.87 | 291 | MAV_3990 | phytanoyl-CoA dioxygenase (PhyH) | 98.61 | 287 | BCG_3691 | hypothetical protein | 36.87 | 291 | MAP3160 | hypothetical protein | 277 | 99.64 |
| MAP4_0630 | hypothetical protein | 486 | Rv1002c | hypothetical protein | 28.79 | 503 | Mb1029c | hypothetical protein | 28.79 | 503 | MAV_3989 | phospholipase D family protein | 99.38 | 486 | BCG_1059c | hypothetical protein | 28.79 | 503 | MAP3159 | hypothetical protein | 486 | 100 |
| MAP4_0631 | hypothetical protein | 110 | Rv1810 | hypothetical protein | 50.96 | 118 | Mb1840 | hypothetical protein | 50.96 | 118 | MAV_3988 | hypothetical protein | 100 | 131 | BCG_1844 | hypothetical protein | 50.96 | 118 | MAP3158c | hypothetical protein | 131 | 100 |
| MAP4_0632 | hypothetical protein | 334 | Rv1645c | hypothetical protein | 24.09 | 351 | Mb1672c | hypothetical protein | 24.09 | 351 | MAV_3987 | hypothetical protein | 99.4 | 334 | BCG_1684c | hypothetical protein | 24.09 | 351 | MAP3157 | hypothetical protein | 334 | 100 |
| MAP4_0633 | Transcriptional regulator, TetR family | 198 | Rv0825c | hypothetical protein | 33.33 | 213 | Mb0848c | hypothetical protein | 33.33 | 213 | MAV_3986 | TetR family transcriptional regulato | 99.49 | 198 | BCG_0878c | hypothetical protein | 33.33 | 213 | MAP3156c | hypothetical protein | 198 | 100 |
| MAP4_0634 | hypothetical protein | 90 | Rv0194 | Probable transmembrane multidrug | 33.33 | 1194 | Mb0200 | drugs-transport transmembra | 33.33 | 1194 | MAV_3985 | hypothetical protein | 97.78 | 90 | BCG_0231 | drugs-transport transmembran | 33.33 | 1194 | MAP3155c | hypothetical protein | 90 | 100 |
| MAP4_0635 | hypothetical protein | 135 | Rv1364c | Possible sigma factor regulatory pro | 32.04 | 653 | Mb1399c | hypothetical protein | 32.04 | 653 | MAV_3984 | hypothetical protein | 99.26 | 135 | BCG_1426c | hypothetical protein | 32.04 | 653 | MAP0903 | bifunctional phosphoribosylaminoimida | 533 | 30.19 |
| MAP4_0636 | hypothetical protein | 491 | Rv1646 | PE family protein PE17 | 39.58 | 310 | Mb1673 | PE family protein | 39.58 | 310 | MAV_3983 | hypothetical protein | 98.78 | 491 | BCG_1685 | PE family protein | 39.58 | 310 | MAP3154 | hypothetical protein | 491 | 100 |
| MAP4_0637 | hypothetical protein | 187 | Rv1794 | hypothetical protein | 30.16 | 300 | Mb1822 | hypothetical protein | 30.16 | 300 | MAV_3982 | hemerythrin HHE cation binding do | 98.93 | 187 | BCG_1826 | hypothetical protein | 30.16 | 300 | MAP3153 | hypothetical protein | 187 | 100 |
| MAP4_0638 | putative HpcHHpaI aldolasecitrate lyase | 306 | Rv3075c | hypothetical protein | 83.99 | 307 | Mb3102c | hypothetical protein | 83.99 | 307 | MAV_3981 | HpcH/HpaI aldolase/citrate lyase, p | 99.67 | 306 | BCG_3100c | hypothetical protein | 83.99 | 307 | MAP3152c | hypothetical protein | 306 | 100 |
| MAP4_0639 | conserved 13E12 repeat family protein | 428 | Rv3074 | hypothetical protein | 80.42 | 424 | Mb3101 | hypothetical protein | 80.42 | 424 | MAV_3980 | hypothetical protein | 99.05 | 419 | BCG_3099 | hypothetical protein | 80.42 | 424 | MAP3151 | hypothetical protein | 428 | 100 |
| MAP4_0640 | hypothetical protein | 118 | Rv3073c | hypothetical protein | 69.37 | 118 | Mb3100c | hypothetical protein | 69.37 | 118 | MAV_3979 | hypothetical protein | 97.27 | 110 | BCG_3098c | hypothetical protein | 69.37 | 118 | MAP3150c | hypothetical protein | 118 | 100 |
| MAP4_0641 | hypothetical protein | 208 | Rv1347c | Lysine N-acetyltransferase MbtK | 56.91 | 210 | Mb1382c | hypothetical protein | 56.91 | 210 | MAV_3978 | hypothetical protein | 98.56 | 208 | BCG_1409c | hypothetical protein | 56.91 | 210 | MAP3149c | hypothetical protein | 208 | 100 |
| MAP4_0642 | hypothetical protein | 122 | Rv3070 | Probable conserved integral membr | 75.63 | 126 | Mb3097 | camphor resistance protein C | 75.63 | 126 | MAV_3977 | camphor resistance protein CrcB | 97.54 | 122 | BCG_3095 | camphor resistance protein Cr | 75.63 | 126 | MAP3148 | camphor resistance protein CrcB | 122 | 100 |
| MAP4_0643 | hypothetical protein | 132 | Rv3069 | Probable conserved transmembrane | 84.43 | 132 | Mb3096 | camphor resistance protein C | 84.43 | 132 | MAV_3976 | camphor resistance protein CrcB | 99.24 | 132 | BCG_3094 | camphor resistance protein Cr | 84.43 | 132 | MAP3147 | camphor resistance protein CrcB | 132 | 100 |
| MAP4_0644 | phosphoglucomutase | 547 | Rv3068c | Probable phosphoglucomutase Pgm | 86.11 | 547 | Mb3095c | phosphoglucomutase | 86.11 | 547 | MAV_4286 | phosphoglucomutase/phosphomar | 26.97 | 526 | BCG_3093c | phosphoglucomutase | 86.11 | 547 | MAP3146c | phosphoglucomutase | 547 | 100 |
| MAP4_0645 | putative transporter, major facilitator super family prot | 412 | Rv3728 | Probable conserved two-domain me | 26.06 | 1065 | Mb3755 | hypothetical protein | 26.06 | 1065 | MAV_3974 | permease of the major facilitator su | 98.69 | 393 | BCG_3788 | hypothetical protein | 26.06 | 1065 | MAP3145c | hypothetical protein | 412 | 100 |
| MAP4_0646 | hypothetical protein | 68 | Rv2803 | hypothetical protein | 38.71 | 155 | Mb0020c | hypothetical protein | 40.54 | 521 | MAV_3972 | hypothetical protein | 97.67 | 43 | BCG_2821 | hypothetical protein | 38.71 | 155 | MAP1853 | hypothetical protein | 359 | 30.67 |
| MAP4_0647 | hypothetical protein | 127 | | | | | | | | | MAV_3971 | death-on-curing protein | 99.21 | 127 | | | | | MAP3144c | hypothetical protein | 127 | 100 |
| MAP4_0648 | hypothetical protein | 71 | Rv0266c | Probable 5-oxoprolinase OplA (5-oxo | 34.04 | 1209 | Mb0170c | GntR family transcriptional re | 72.22 | 271 | MAV_3970 | hypothetical protein | 97.87 | 47 | BCG_0201c | GntR family transcriptional reg | 72.22 | 271 | MAP3293 | hypothetical protein | 459 | 34.04 |
| MAP4_0649 | hypothetical protein | 64 | Rv2522c | hypothetical protein | 39.39 | 470 | Mb2551c | hypothetical protein | 39.39 | 470 | MAV_3968 | long chain fatty acid-CoA synthetas | 96.88 | 64 | BCG_2543c | hypothetical protein | 39.39 | 470 | MAP1165 | phosphoglycerate kinase | 415 | 36.17 |
| MAP4_0652 | putative dioxygenasesdiooxygenase, rieske(2Fe-2S) do | 422 | Rv3161c | Possible dioxygenase | 31.4 | 382 | Mb3186c | dioxygenase | 31.88 | 382 | MAV_3967 | Rieske (2Fe-2S) domain-containing | 99.53 | 422 | BCG_3185c | dioxygenase | 31.88 | 382 | MAP3141c | hypothetical protein | 422 | 100 |
| MAP4_0653 | hypothetical protein | 111 | | | | | | | | | MAV_3966 | hypothetical protein | 99.1 | 111 | | | | | MAP0719c | hypothetical protein | 109 | 64.42 |
| MAP4_0654 | putative amidohydrolase family protein | 415 | Rv0074 | hypothetical protein | 30.17 | 411 | Mb0076 | hypothetical protein | 30.17 | 411 | MAV_0903 | Xaa-Pro dipeptidase | 58.37 | 409 | BCG_0105 | hypothetical protein | 30.17 | 411 | MAP3140c | hypothetical protein | 415 | 100 |
| MAP4_0655 | Transcriptional regulator, MarR family | 150 | Rv2887 | Probable transcriptional regulatory | 36.28 | 139 | Mb2911 | transcriptional regulator | 36.28 | 139 | MAV_3964 | MarR family transcriptional regulat | 98.67 | 150 | BCG_2908 | transcriptional regulatory prot | 36.28 | 139 | MAP3139c | hypothetical protein | 150 | 100 |
| MAP4_0656 | putative iron-sulfur protein | 273 | Rv3571 | Reductase component of 3-ketoster | 35.83 | 358 | Mb3602 | hemoglobine-like protein | 35.83 | 358 | MAV_3963 | 2Fe-2S iron-sulfur cluster binding d | 98.17 | 273 | BCG_3636 | hemoglobine-related protein h | 35.83 | 358 | MAP3138c | hypothetical protein | 273 | 100 |
| MAP4_0657 | putative short chain dehydrogenase reductase | 246 | Rv1483 | 3-oxoacyl-[acyl-carrier protein] redu | 35.34 | 247 | Mb1519 | 3-oxoacyl-ACP reductase | 35.34 | 247 | MAV_3962 | NAD-dependent epimerase/dehydr | 98.37 | 252 | BCG_1545 | 3-oxoacyl-ACP reductase | 35.34 | 247 | MAP3137c | hypothetical protein | 246 | 100 |
| MAP4_0658 | putative dioxygenase, rieske (2Fe-2S) iron-sulfur domai | 420 | Rv3161c | Possible dioxygenase | 32.56 | 382 | Mb3186c | dioxygenase | 33.02 | 382 | MAV_3961 | Rieske (2Fe-2S) domain-containing | 99.52 | 420 | BCG_3185c | dioxygenase | 33.02 | 382 | MAP3136c | hypothetical protein | 420 | 100 |
| MAP4_0659 | hypothetical protein | 112 | Rv1139c | hypothetical protein | 40 | 166 | Mb1171c | hypothetical protein | 40 | 166 | MAV_3960 | hypothetical protein | 98.21 | 112 | BCG_1201c | hypothetical protein | 40 | 166 | MAP0719c | hypothetical protein | 109 | 45.87 |
| MAP4_0660 | putative dioxygenase | 281 | Rv3406 | Probable dioxygenase | 33.33 | 295 | Mb3440 | dioxygenase | 33.33 | 295 | MAV_3959 | taurine catabolism dioxygenase Tau | 98.58 | 281 | BCG_3476 | dioxygenase | 33.33 | 295 | MAP3135c | hypothetical protein | 281 | 100 |
| MAP4_0661 | hypothetical protein | 184 | Rv1531 | hypothetical protein | 25 | 188 | Mb1558 | hypothetical protein | 25 | 188 | MAV_3958 | hypothetical protein | 99.45 | 185 | BCG_1583 | hypothetical protein | 25 | 188 | MAP3134c | hypothetical protein | 184 | 100 |
| MAP4_0662 | enolase | 427 | Rv1023 | Probable enolase Eno | 38.81 | 429 | Mb1051 | phosphopyruvate hydratase | 38.81 | 429 | MAV_3957 | enolase | 98.83 | 426 | BCG_1080 | phosphopyruvate hydratase | 38.81 | 429 | MAP3133c | hypothetical protein | 427 | 99.77 |
| MAP4_0663 | transmembrane ATP-binding protein ABC transporter | 960 | Rv2326c | Possible transmembrane ATP-bindin | 70.18 | 697 | Mb2353c | transmembrane ATP-binding | 70.18 | 697 | MAV_3955 | ABC transporter | 99.12 | 493 | BCG_2347c | transmembrane ABC transport | 70.18 | 697 | MAP3132 | hypothetical protein | 960 | 100 |
| MAP4_0664 | membrane protein, MmpL family | 942 | Rv0450c | Probable conserved transmembrane | 47.74 | 967 | Mb0458c | transmembrane transport pro | 47.63 | 967 | MAV_1755 | MmpL4 protein | 46.96 | 968 | BCG_0489c | transmembrane transport prot | 47.74 | 967 | MAP3131 | hypothetical protein | 942 | 100 |
| MAP4_0665 | membrane protein, MmpS family | 147 | Rv0677c | Possible conserved membrane prote | 33.81 | 142 | Mb0696c | hypothetical protein | 33.81 | 142 | MAV_3953 | MmpS2 protein | 98.55 | 138 | BCG_0726c | membrane protein mmpS5 | 33.81 | 142 | MAP3130 | hypothetical protein | 147 | 100 |
| MAP4_0666 | hypothetical protein | 141 | Rv3331 | Probable sugar-transport integral m | 41.51 | 502 | Mb3364 | sugar-transport integral mem | 39.62 | 502 | MAV_3952 | hypothetical protein | 99.29 | 141 | BCG_3401 | sugar-transport integral memb | 39.62 | 497 | MAP3129 | hypothetical protein | 141 | 100 |
| MAP4_0667 | hypothetical protein | 61 | Rv3176c | Probable epoxide hydrolase MesT (e | 50 | 318 | Mb3202c | epoxide hydrolase | 50 | 208 | MAV_3951 | hypothetical protein | 100 | 61 | BCG_3410 | O-acetylhomoserine aminocarb | 37.5 | 449 | MAP3457 | O-acetylhomoserine aminocarboxyprop | 456 | 41.38 |
| MAP4_0668 | hypothetical protein | 473 | Rv3157 | Probable NADH dehydrogenase I (ch | 25.69 | 553 | Mb3181 | NADH dehydrogenase subuni | 25 | 553 | MAV_3950 | hypothetical protein | 95.58 | 459 | BCG_3180 | NADH dehydrogenase subunit | 25 | 553 | MAP3128 | hypothetical protein | 473 | 100 |
| MAP4_0669 | multidrugs transport membrane protein Mmr | 107 | Rv3065 | Multidrugs-transport integral memb | 83.18 | 107 | Mb3092 | multidrugs-transport integral | 83.18 | 107 | MAV_3949 | transporter, small multidrug resista | 99.07 | 114 | BCG_3090 | multidrugs-transport integral n | 83.18 | 107 | MAP3127 | EmrE | 134 | 99.07 |
| MAP4_0670 | putative hydrolase | 305 | Rv0169 | Mce-family protein Mce1A | 33.33 | 454 | Mb1764c | hypothetical protein | 44.12 | 165 | MAV_3948 | hypothetical protein | 99.67 | 305 | BCG_1774c | hypothetical protein | 44.12 | 165 | MAP3126c | hypothetical protein | 269 | 99.63 |
| MAP4_0671 | putative dehydrogenasereductase | 268 | Rv3224 | Possible iron-regulated short-chain c | 29.69 | 282 | Mb3251 | short chain dehydrogenase | 29.69 | 282 | MAV_3947 | NAD dependent epimerase/dehydr | 98.13 | 268 | BCG_3252 | short chain dehydrogenase | 29.69 | 282 | MAP3125c | hypothetical protein | 268 | 100 |
| MAP4_0672 | putative phosphotransferase enzyme family protein | 324 | Rv3761c | Possible acyl-CoA dehydrogenase Fa | 29.5 | 351 | Mb3787c | acyl-CoA dehydrogenase | 29.5 | 351 | MAV_3946 | phosphotransferase enzyme family | 96.91 | 324 | BCG_3820c | acyl-CoA dehydrogenase fadE3 | 29.5 | 351 | MAP3124c | hypothetical protein | 281 | 99.64 |
| MAP4_0673 | hypothetical protein | 81 | Rv2107 | PE family protein PE22 | 30.14 | 98 | Mb2131 | hypothetical protein | 30.14 | 98 | MAV_3945 | hypothetical protein | 100 | 81 | BCG_2124 | PE family protein | 30.14 | 98 | MAP3067c | hypothetical protein | 244 | 47.06 |
| MAP4_0674 | hypothetical protein | 220 | Rv2752c | hypothetical protein | 31.91 | 558 | Mb2773c | hypothetical protein | 31.91 | 558 | MAV_3943 | hypothetical protein | 99.55 | 227 | BCG_2768c | hypothetical protein | 31.91 | 558 | MAP3123c | hypothetical protein | 220 | 100 |
| MAP4_0675 | acyl-CoA dehydrogenase | 431 | Rv0131c | Probable acyl-CoA dehydrogenase F | 58.31 | 447 | Mb0136c | acyl-CoA dehydrogenase | 58.31 | 447 | MAV_3944 | acyl-CoA dehydrogenase | 100 | 431 | BCG_0165c | acyl-CoA dehydrogenase fadE1 | 58.31 | 447 | MAP3122 | FadE1_2 | 431 | 100 |
| MAP4_0676 | enoyl-CoA hydratase | 260 | Rv1472 | Possible enoyl-CoA hydratase EchA1 | 41.74 | 285 | Mb1507 | enoyl-CoA hydratase | 41.74 | 285 | MAV_3942 | enoyl-CoA hydratase/isomerase | 98.46 | 260 | BCG_1533 | enoyl-CoA hydratase | 41.74 | 285 | MAP3121 | hypothetical protein | 284 | 99.62 |
| MAP4_0677 | putative dehydrogenase | 318 | Rv0407 | F420-dependent glucose-6-phospha | 32.93 | 336 | Mb0415 | F420-dependent glucose-6-ph | 32.93 | 336 | MAV_0425 | dehydrogenase | 39.57 | 336 | BCG_0446 | glucose-6-phosphate dehydrog | 32.93 | 336 | MAP3120c | hypothetical protein | 318 | 100 |
| MAP4_0678 | molecular chaperone | 505 | Rv0350 | Probable chaperone protein DnaK (h | 30.43 | 625 | Mb0358 | molecular chaperone DnaK | 30.43 | 625 | MAV_3939 | DnaK family protein | 99.21 | 505 | BCG_0389 | molecular chaperone DnaK | 30.43 | 625 | MAP3119 | hypothetical protein | 505 | 100 |
| MAP4_0679 | carbon starvation protein A CstA | 747 | Rv3063 | Probable carbon starvation protein A | 74.46 | 758 | Mb3090 | carbon starvation protein A C | 74.32 | 758 | MAV_3938 | carbon starvation protein A | 98.15 | 758 | BCG_3088 | carbon starvation protein A cst | 74.32 | 758 | MAP3118 | hypothetical protein | 747 | 100 |
| MAP4_0680 | ATP-dependent DNA ligase | 519 | Rv3062 | Probable ATP-dependent DNA ligase | 78.98 | 507 | Mb3089 | ATP-dependent DNA ligase | 78.98 | 507 | MAV_3937 | ATP-dependent DNA ligase | 97.53 | 526 | BCG_3087 | ATP-dependent DNA ligase | 78.98 | 507 | MAP3117 | ATP-dependent DNA ligase | 519 | 100 |
| MAP4_0681 | short-chain type dehydrogenase reductase | 252 | Rv1144 | Probable short-chain type dehydrog | 47.24 | 250 | Mb1176 | short-chain type dehydrogena | 47.24 | 250 | MAV_3936 | 3-hydroxyacyl-CoA dehydrogenase | 100 | 252 | BCG_1206 | short-chain type dehydrogenas | 47.24 | 250 | MAP3116c | hypothetical protein | 252 | 100 |
| MAP4_0684 | hypothetical protein | 121 | Rv3542c | hypothetical protein | 45.61 | 311 | Mb3572c | hypothetical protein | 45.61 | 311 | MAV_3934 | hypothetical protein | 94.59 | 111 | BCG_3606c | hypothetical protein | 45.61 | 311 | MAP3114 | hypothetical protein | 121 | 100 |
| MAP4_0685 | hypothetical protein | 400 | Rv3540c | Probable lipid transfer protein or ke | 34.4 | 386 | Mb3570c | lipid-transfer protein | 34.4 | 386 | MAV_1865 | DitF protein | 46.68 | 403 | BCG_3604c | lipid-transfer protein | 34.4 | 386 | MAP3113c | hypothetical protein | 400 | 100 |
| MAP4_0686 | Transcriptional regulator, GntR family | 485 | Rv3060c | Probable transcriptional regulatory | 72.82 | 490 | Mb3086c | GntR family transcriptional re | 72.82 | 490 | MAV_3932 | GntR family transcriptional regulato | 100 | 485 | BCG_3085c | GntR family transcriptional reg | 72.82 | 490 | MAP3112c | hypothetical protein | 485 | 100 |
| MAP4_0687 | putative regulator of sigma factor | 322 | Rv1206 | Probable fatty-acid-CoA ligase FadD | 44.83 | 597 | Mb1238 | long-chain-acyl-CoA syntheta | 44.83 | 597 | MAV_3931 | regulator of Sig8 | 99.38 | 330 | BCG_1266 | long-chain-acyl-CoA synthetase | 44.83 | 597 | MAP3111c | hypothetical protein | 322 | 100 |
| MAP4_0688 | hypothetical protein | 174 | Rv3710 | 2-isopropylmalate synthase LeuA (al | 19.28 | 644 | Mb3737 | 2-isopropylmalate synthase | 37.04 | 661 | MAV_3928 | hypothetical protein | 97.13 | 174 | BCG_3770 | 2-isopropylmalate synthase | 37.04 | 834 | MAP3110c | hypothetical protein | 174 | 100 |
| MAP4_0689 | Cytochrome P450 | 492 | Rv3059 | Probable cytochrome P450 136 Cyp1 | 73.47 | 492 | Mb3085 | cytochrome P450 136 | 73.67 | 492 | MAV_3927 | cytochrome p450 | 99.39 | 492 | BCG_3084 | cytochrome P450 136 cyp136 | 73.67 | 492 | MAP3109 | hypothetical protein | 492 | 100 |
| MAP4_0690 | Transcriptional regulator, TetR family | 217 | Rv3058c | Possible transcriptional regulatory p | 69.34 | 216 | Mb3084c | TetR family transcriptional re | 69.34 | 216 | MAV_3926 | TetR family transcriptional regulato | 98.58 | 211 | BCG_3083c | TetR family transcriptional regu | 69.34 | 216 | MAP3108c | hypothetical protein | 217 | 100 |
| MAP4_0691 | short-chain type alcoholdehydrogenase/reductase | 310 | Rv3057c | Probable short chain alcohol dehydr | 84.32 | 287 | Mb3083c | short chain dehydrogenase | 84.32 | 287 | MAV_3924 | short chain dehydrogenase | 99.35 | 310 | BCG_3082c | short chain dehydrogenase | 84.32 | 287 | MAP3107c | short chain dehydrogenase | 310 | 100 |
| MAP4_0692 | DNA-damage-inducible protein P DinP | 347 | Rv3056 | Possible DNA-damage-inducible pro | 77.97 | 346 | Mb3082 | DNA polymerase IV | 77.97 | 346 | MAV_3925 | DNA polymerase IV | 99.12 | 342 | BCG_3081 | DNA polymerase IV | 77.97 | 346 | MAP3106 | DNA polymerase IV | 347 | 100 |
| MAP4_0693 | Transcriptional regulator, TetR family | 204 | Rv3055 | Possible transcriptional regulatory p | 79.31 | 204 | Mb3081 | TetR family transcriptional re | 79.31 | 204 | MAV_3923 | TetR family transcriptional regulato | 98.53 | 204 | BCG_3080 | TetR family transcriptional regu | 79.31 | 204 | MAP3105 | hypothetical protein | 204 | 100 |
| MAP4_0694 | putative NADPH-dependent FMN reductase family prot | 198 | Rv3054c | hypothetical protein | 78.02 | 184 | Mb3080c | hypothetical protein | 78.02 | 184 | MAV_3922 | secreted protein | 98.86 | 176 | BCG_3079c | hypothetical protein | 78.02 | 184 | MAP3104c | hypothetical protein | 198 | 100 |
| MAP4_0695 | hypothetical protein | 88 | Rv1541c | Possible lipoprotein LprI | 31.71 | 197 | Mb1568c | lipoprotein LprI | 31.71 | 197 | MAV_1170 | sensor protein KdpD | 26.92 | 854 | BCG_3078c | hypothetical protein | 43.59 | 122 | MAP3103c | hypothetical protein | 88 | 100 |
| MAP4_0696 | glutaredoxin-like electron transport protein NrdH | 79 | Rv3053c | Probable glutaredoxin electron trans | 88.61 | 79 | Mb3079c | glutaredoxin electron transpo | 88.61 | 79 | MAV_3921 | glutaredoxin | 100 | 79 | BCG_3077c | glutaredoxin electron transpor | 88.61 | 79 | MAP3102c | NrdH | 79 | 100 |
| MAP4_0697 | ribonucleotide reductase stimulatory protein | 150 | Rv3052c | Probable NrdI protein | 86.67 | 150 | Mb3078c | ribonucleotide reductase stim | 86.67 | 150 | MAV_3920 | ribonucleotide reductase stimulato | 100 | 150 | BCG_3076c | ribonucleotide reductase stimu | 86.67 | 150 | MAP3101c | ribonucleotide reductase stimulatory pr | 150 | 100 |
| MAP4_0698 | ribonucleoside-diphosphate reductase alphachain NrdE | 726 | Rv3051c | Ribonucleoside-diphosphate reducta | 96.83 | 693 | Mb3077c | ribonucleotide-diphosphate r | 96.83 | 693 | MAV_3919 | ribonucleotide-diphosphate reduct | 99.72 | 705 | BCG_3075c | ribonucleotide-diphosphate re | 96.83 | 693 | MAP3100c | ribonucleotide-diphosphate reductase s | 726 | 100 |
| MAP4_0699 | Transcriptional regulator, TetR family | 246 | Rv3050c | Probable transcriptional regulatory | 81.63 | 246 | Mb3076c | AsnC family transcriptional re | 81.63 | 246 | MAV_3917 | TetR family transcriptional regulato | 100 | 249 | BCG_3074c | AsnC family transcriptional reg | 81.63 | 246 | MAP3099c | hypothetical protein | 246 | 100 |
| MAP4_0700 | monooxygenase | 512 | Rv3049c | Probable monooxygenase | 83.6 | 524 | Mb3075c | monooxygenase | 83.6 | 524 | MAV_3915 | flavin-containing monooxygenase F | 99.61 | 512 | BCG_3073c | monooxygenase | 83.6 | 524 | MAP3098c | hypothetical protein | 512 | 100 |
| MAP4_0701 | Transcriptional regulator, TetR family | 181 | Rv1219c | Probable transcriptional regulatory | 41.51 | 212 | Mb1251c | transcriptional regulator | 41.51 | 212 | MAV_3916 | TetR family transcriptional regulato | 98.34 | 181 | BCG_1279c | transcriptional regulatory prote | 41.51 | 212 | MAP3097 | hypothetical protein | 181 | 100 |
| MAP4_0702 | hypothetical protein | 148 | Rv1883c | hypothetical protein | 31.25 | 153 | Mb1915c | hypothetical protein | 30.77 | 158 | MAV_3914 | hypothetical protein | 100 | 148 | BCG_1920c | hypothetical protein | 30.77 | 158 | MAP3096 | hypothetical protein | 170 | 100 |
| MAP4_0703 | ribonucleoside-diphosphate reductase beta chain NrdF | 324 | Rv3048c | Ribonucleoside-diphosphate reducta | 93.52 | 324 | Mb3074c | ribonucleotide-diphosphate r | 93.52 | 324 | MAV_3913 | ribonucleotide-diphosphate reduct | 99.69 | 324 | BCG_3072c | ribonucleotide-diphosphate re | 93.52 | 324 | MAP3095c | ribonucleotide-diphosphate reductase s | 324 | 100 |
| MAP4_0704 | hypothetical protein | 137 | Rv3046c | hypothetical protein | 69.6 | 124 | Mb3072c | hypothetical protein | 69.6 | 124 | MAV_3912 | hypothetical protein | 99.27 | 137 | BCG_3070c | hypothetical protein | 69.6 | 124 | MAP3094c | hypothetical protein | 137 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0705 | NADP-dependent alcohol dehydrogenase AdhC | 346 | Rv3045 | Probable NADP-dependent alcohol d | 83.82 | 346 | Mb3071 | NADP-dependent alcohol deh | 83.82 | 346 | MAV_3911 | NADP-dependent alcohol dehydrog | 99.71 | 346 | BCG_3069 | NADP-dependent alcohol dehy | 83.82 | 346 | MAP3093 | AdhC | 346 | 100 |
| MAP4_0706 | Fe(III)-dicitrate-binding periplasmic lipoprotein FecB | 364 | Rv3044 | Probable FEIII-dicitrate-binding peri | 74.19 | 359 | Mb3070 | FEIII-dicitrate-binding peripla | 74.19 | 359 | MAV_3910 | periplasmic binding protein | 98.89 | 360 | BCG_3068 | FeIII-dicitrate-binding periplasr | 74.19 | 359 | MAP3092 | hypothetical protein | 364 | 100 |
| MAP4_0707 | cytochrome C oxidase polypeptide I CtaD | 581 | Rv3043c | Probable cytochrome C oxidase poly | 92.91 | 573 | Mb3069c | cytochrome C oxidase polype | 92.91 | 573 | MAV_3908 | cytochrome C oxidase, subunit I | 100 | 543 | BCG_3067c | cytochrome C oxidase polypep | 92.91 | 573 | MAP3091c | CtaD | 581 | 100 |
| MAP4_0708 | phosphoserine phosphatase SerB2 | 411 | Rv3042c | Probable phosphoserine phosphata | 84.07 | 409 | Mb3068c | phosphoserine phosphatase | 84.07 | 409 | MAV_3907 | phosphoserine phosphatase SerB | 99.51 | 411 | BCG_3066c | phosphoserine phosphatase se | 84.07 | 409 | MAP3090c | SerB2 | 411 | 99.76 |
| MAP4_0709 | ABC transporter ATP-binding protein | 280 | Rv3041c | Probable conserved ATP-binding pro | 89.45 | 287 | Mb3067c | ABC transporter ATP-binding | 89.45 | 287 | MAV_3906 | molybdenum ABC transporter ATPa | 99.64 | 280 | BCG_3065c | ABC transporter ATP-binding p | 89.45 | 287 | MAP3089c | hypothetical protein | 280 | 100 |
| MAP4_0710 | hypothetical protein | 276 | Rv3040c | hypothetical protein | 79.78 | 288 | Mb3066c | hypothetical protein | 79.78 | 288 | MAV_3905 | hydrolase, nudix family protein, pu | 99.28 | 276 | BCG_3064c | hypothetical protein | 79.78 | 288 | MAP3088c | hypothetical protein | 276 | 100 |
| MAP4_0711 | enoyl-CoA hydratase | 257 | Rv3039c | Probable enoyl-CoA hydratase EchA | 84.77 | 254 | Mb3065c | enoyl-CoA hydratase | 84.77 | 254 | MAV_3904 | enoyl-CoA hydratase | 99.61 | 257 | BCG_3063c | enoyl-CoA hydratase | 84.77 | 254 | MAP3087c | enoyl-CoA hydratase | 257 | 100 |
| MAP4_0712 | putative methyltransferase | 323 | Rv3038c | hypothetical protein | 84.1 | 327 | Mb3064c | hypothetical protein | 84.1 | 327 | MAV_3903 | methyltransferase, UbiE/COQ5 fam | 100 | 323 | BCG_3062c | hypothetical protein | 84.1 | 327 | MAP3086c | hypothetical protein | 323 | 100 |
| MAP4_0713 | hypothetical protein | 365 | Rv3037c | hypothetical protein | 76.88 | 358 | Mb3063c | hypothetical protein | 76.88 | 358 | MAV_3902 | SAM-dependent methyltransferase | 96.71 | 391 | BCG_3061c | hypothetical protein | 76.88 | 358 | MAP3085c | hypothetical protein | 365 | 100 |
| MAP4_0714 | conserved secreted protein | 227 | Rv3036c | Probable conserved secreted protei | 71.81 | 227 | Mb3062c | hypothetical protein | 71.37 | 227 | MAV_3901 | immunogenic protein MPB64/MPT | 99.12 | 227 | BCG_3060c | hypothetical protein | 71.81 | 227 | MAP3084c | hypothetical protein | 227 | 100 |
| MAP4_0715 | hypothetical protein | 125 | Rv3454 | Probable conserved integral membr | 29.41 | 422 | Mb3483 | transmembrane protein | 29.41 | 561 | MAV_3900 | hypothetical protein | 98.25 | 57 | BCG_3519 | hypothetical protein | 29.41 | 561 | MAP2843c | hypothetical protein | 328 | 40 |
| MAP4_0716 | hypothetical protein | 423 | Rv3035 | hypothetical protein | 79.89 | 360 | Mb3061 | hypothetical protein | 79.89 | 360 | MAV_3899 | hypothetical protein | 99.53 | 423 | BCG_3059 | hypothetical protein | 79.89 | 360 | MAP3083 | hypothetical protein | 372 | 99.73 |
| MAP4_0717 | putative transferase | 254 | Rv3034c | Possible transferase | 91.67 | 300 | Mb3060c | transferase | 91.67 | 300 | MAV_3898 | hexapeptide transferase | 100 | 245 | BCG_3058c | transferase | 91.67 | 300 | MAP3082c | hypothetical protein | 254 | 100 |
| MAP4_0718 | deoxyribodipyrimidine photolyase | 442 | Rv3292 | hypothetical protein | 31.43 | 415 | Mb3320 | hypothetical protein | 31.43 | 415 | MAV_3897 | Phr protein | 97.96 | 442 | BCG_3321 | hypothetical protein | 31.43 | 415 | MAP3081 | Phr | 442 | 100 |
| MAP4_0719 | putative tryptophan-rich sensory protein | 109 | Rv1881c | Possible conserved lipoprotein LppE | 37.14 | 140 | Mb1913c | lipoprotein LppE | 37.14 | 140 | MAV_3896 | peripheral-type benzodiazepine re | 76.85 | 90 | BCG_1918c | lipoprotein lppE | 37.14 | 140 | MAP2115c | hypothetical protein | 342 | 30.77 |
| MAP4_0720 | transmembrane transport protein, MMPL family | 687 | Rv1522c | Probable conserved transmembrane | 35.09 | 1146 | Mb1549c | transmembrane transport pr | 35.09 | 1107 | MAV_3895 | MmpL family protein | 98.84 | 687 | BCG_1574c | transmembrane transport prot | 35.09 | 1107 | MAP3080 | hypothetical protein | 687 | 100 |
| MAP4_0721 | putative isopentenyl pyrophosphate isomerase | 344 | Rv0694 | Possible L-lactate dehydrogenase (c | 35.71 | 396 | Mb0713 | L-lactate dehydrogenase (cyt | 35.71 | 396 | MAV_3894 | isopentenyl pyrophosphate isomer | 98.26 | 344 | BCG_0743 | L-lactate dehydrogenase (cyto | 35.71 | 396 | MAP3079c | isopentenyl pyrophosphate isomerase | 344 | 100 |
| MAP4_0722 | transposase | 329 | Rv2812 | Probable transposase | 32.65 | 469 | Mb2836 | transposase | 32.29 | 265 | MAV_0752 | transposase | 82.98 | 345 | BCG_2830 | transposase | 32.65 | 469 | MAP3078c | hypothetical protein | 329 | 100 |
| MAP4_0723 | Transcriptional regulator, MarR family | 188 | Rv0880 | Possible transcriptional regulatory p | 26.14 | 143 | Mb0904 | MarR family transcriptional re | 26.14 | 143 | MAV_3893 | MarR family transcriptional regulat | 97.87 | 188 | BCG_0932 | MarR family transcriptional reg | 26.14 | 143 | MAP3077 | hypothetical protein | 188 | 100 |
| MAP4_0724 | rieske (2Fe-2S) domain-containing protein | 336 | Rv3526 | Oxygenase component of 3-ketoster | 34.62 | 386 | Mb3556 | oxidoreductase | 34.62 | 386 | MAV_3891 | methylesterase | 98.51 | 336 | BCG_3590 | oxidoreductase | 34.62 | 386 | MAP3076 | hypothetical protein | 336 | 100 |
| MAP4_0725 | amine oxidase | 509 | Rv2677c | Probable protoporphyrinogen oxida | 33.33 | 452 | Mb2696c | protoporphyrinogen oxidase | 33.33 | 452 | MAV_3890 | dehydrogenase | 99.21 | 509 | BCG_2690c | protoporphyrinogen oxidase | 33.33 | 452 | MAP3075 | hypothetical protein | 509 | 100 |
| MAP4_0726 | putative methyltransferase, CrtT protein | 241 | Rv0558 | Probable ubiquinone/menaquinone | 28.63 | 234 | Mb0573 | ubiquinone/menaquinone bi | 28.63 | 234 | MAV_3889 | methyltransferase, UbiE/COQ5 fam | 100 | 241 | BCG_0603 | ubiquinone/menaquinone bios | 28.63 | 234 | MAP3074 | CrtT | 241 | 100 |
| MAP4_0727 | hypothetical protein | 103 | Rv0853c | Probable pyruvate or indole-3-pyru | 34.85 | 560 | Mb0876c | pyruvate or indole-3-pyruvate | 34.85 | 560 | MAV_3888 | lycopene cyclase | 98.06 | 103 | BCG_0905c | pyruvate or indole-3-pyruvate | 34.85 | 560 | MAP3073 | hypothetical protein | 103 | 100 |
| MAP4_0728 | hypothetical protein | 107 | Rv0960 | Possible toxin VapC9 | 32.79 | 127 | Mb0985 | hypothetical protein | 32.79 | 127 | MAV_3887 | hypothetical protein | 98.13 | 122 | BCG_1014 | hypothetical protein | 32.79 | 127 | MAP3072 | hypothetical protein | 107 | 100 |
| MAP4_0729 | phytoene synthase | 316 | Rv3397c | Probable phytoene synthase PhyA | 30.88 | 302 | Mb3430c | phytoene synthase | 30.88 | 302 | MAV_3886 | phytoene synthase | 99.05 | 316 | BCG_3467c | phytoene synthase phyA | 30.88 | 302 | MAP3071 | hypothetical protein | 243 | 99.59 |
| MAP4_0730 | putative phytoene dehydrogenase | 506 | Rv3829c | Probable dehydrogenase | 24.13 | 536 | Mb3859c | dehydrogenase | 24.34 | 536 | MAV_3885 | phytoene dehydrogenase | 99.6 | 508 | BCG_3892c | dehydrogenase | 24.34 | 536 | MAP3070 | hypothetical protein | 506 | 100 |
| MAP4_0731 | geranylgeranyl pyrophosphate synthetase | 382 | Rv2173 | Probable geranylgeranyl pyrophosp | 37.42 | 352 | Mb2195 | geranylgeranyl pyrophosphat | 37.42 | 352 | MAV_3884 | polyprenyl synthetase | 98.69 | 392 | BCG_2188 | geranylgeranyl pyrophosphate | 37.42 | 352 | MAP3069 | IdsA2_2 | 382 | 100 |
| MAP4_0732 | hypothetical protein | 163 | Rv0516c | Possible anti-anti-sigma factor | 29.13 | 158 | Mb0529c | hypothetical protein | 29.13 | 158 | MAV_3883 | stas domain-containing protein | 99.3 | 143 | BCG_0559c | hypothetical protein | 29.13 | 158 | MAP3068 | hypothetical protein | 163 | 100 |
| MAP4_0733 | hypothetical protein | 244 | Rv1815 | hypothetical protein | 42.11 | 221 | Mb1845 | hypothetical protein | 42.11 | 221 | MAV_3882 | hypothetical protein | 98.36 | 244 | BCG_1849 | hypothetical protein | 42.11 | 221 | MAP3067c | hypothetical protein | 244 | 100 |
| MAP4_0734 | hypothetical protein | 239 | Rv3164c | Probable methanol dehydrogenase | 28.57 | 320 | Mb3189c | methanol dehydrogenase tra | 28.57 | 320 | MAV_3881 | hypothetical protein | 97.76 | 223 | BCG_3188c | methanol dehydrogenase trans | 28.57 | 320 | MAP3066c | hypothetical protein | 253 | 99.58 |
| MAP4_0735 | putative nucleoside-diphosphate sugar epimerase | 451 | Rv2216 | hypothetical protein | 45.67 | 301 | Mb2239 | hypothetical protein | 45.67 | 301 | MAV_3880 | nucleoside-diphosphate sugar epim | 97.29 | 443 | BCG_2232 | hypothetical protein | 45.67 | 301 | MAP3065 | hypothetical protein | 433 | 99.76 |
| MAP4_0736 | transferase | 418 | Rv3032 | Alpha (1->4) glucosyltransferase | 87.08 | 414 | Mb3058 | transferase | 87.08 | 414 | MAV_3879 | glycosyl transferase, group 1 family | 99.28 | 418 | BCG_3055 | transferase | 87.08 | 414 | MAP3064 | hypothetical protein | 418 | 100 |
| MAP4_0737 | hypothetical protein | 534 | Rv3031 | hypothetical protein | 86.33 | 526 | Mb3057 | hypothetical protein | 86.33 | 526 | MAV_3878 | glycosyl hydrolase, family protein 5 | 99.25 | 534 | BCG_3054 | hypothetical protein | 86.33 | 526 | MAP3063 | hypothetical protein | 534 | 100 |
| MAP4_0738 | hypothetical protein | 274 | Rv3030 | hypothetical protein | 76.26 | 274 | Mb3056 | hypothetical protein | 76.26 | 274 | MAV_3877 | hypothetical protein | 98.18 | 274 | BCG_3053 | hypothetical protein | 76.26 | 274 | MAP3062 | hypothetical protein | 274 | 100 |
| MAP4_0739 | Electron transfer flavoprotein, beta subunit | 263 | Rv3029c | Probable electron transfer flavoprot | 92.11 | 266 | Mb3055c | electron transfer flavoprotein | 92.11 | 266 | MAV_3876 | electron transfer protein, beta sub | 100 | 263 | BCG_3052c | electron transfer flavoprotein ( | 92.11 | 266 | MAP3061c | hypothetical protein | 263 | 100 |
| MAP4_0740 | Electron transfer flavoprotein, alpha subunit | 318 | Rv3028c | Probable electron transfer flavoprot | 91.19 | 318 | Mb3054c | electron transfer flavoprotein | 90.88 | 318 | MAV_3875 | electron transfer flavoprotein, alph | 99.36 | 311 | BCG_3051c | electron transfer flavoprotein ( | 90.88 | 318 | MAP3060c | hypothetical protein | 318 | 100 |
| MAP4_0741 | putative acetyltransferase | 281 | Rv3027c | GCN5-related N-acetyltransferase | 80.29 | 281 | Mb3053c | hypothetical protein | 80.33 | 246 | MAV_3874 | hypothetical protein | 99.29 | 281 | BCG_3050c | hypothetical protein | 80.33 | 246 | MAP3059c | hypothetical protein | 281 | 100 |
| MAP4_0742 | cysteine desulfurase IscS | 392 | Rv3025c | Cysteine desulfurase IscS (NIFS prot | 85.9 | 393 | Mb3051c | cysteine desulfurase | 85.9 | 393 | MAV_3872 | cysteine desulfurase | 99.49 | 392 | BCG_3048c | cysteine desulfurase iscS | 85.9 | 393 | MAP3058c | hypothetical protein | 392 | 100 |
| MAP4_0743 | tRNA(5-methylaminomethyl-2-thiouridylate)- methylt | 358 | Rv3024c | Probable tRNA (5-methylaminometh | 85.15 | 367 | Mb3050c | tRNA-specific 2-thiouridylase | 85.15 | 367 | MAV_3871 | tRNA-specific 2-thiouridylase Mnm | 98.86 | 352 | BCG_3047c | tRNA-specific 2-thiouridylase M | 85.15 | 367 | MAP3057c | tRNA-specific 2-thiouridylase MnmA | 358 | 100 |
| MAP4_0744 | lipoprotein LpqA | 214 | Rv3016 | Probable lipoprotein LpqA | 65.02 | 209 | Mb3041 | lipoprotein LpqA | 65.02 | 209 | MAV_3288 | LpqQ protein | 27.27 | 99 | BCG_3038 | lipoprotein lpqA | 65.02 | 209 | MAP3056 | hypothetical protein | 214 | 100 |
| MAP4_0745 | putative cobalamin-independent methionine synthase | 342 | Rv3015c | hypothetical protein | 77.84 | 337 | Mb3040c | hypothetical protein | 77.84 | 337 | MAV_3869 | methionine synthase, vitamin-B12 | 100 | 342 | BCG_3037c | hypothetical protein | 77.84 | 337 | MAP3055c | hypothetical protein | 342 | 100 |
| MAP4_0746 | NAD-dependent DNA ligase LigA | 693 | Rv3014c | DNA ligase [NAD dependent] LigA (p | 81.37 | 691 | Mb3039c | NAD-dependent DNA ligase L | 81.37 | 691 | MAV_3868 | NAD-dependent DNA ligase LigA | 99.71 | 693 | BCG_3036c | NAD-dependent DNA ligase Lig | 81.37 | 691 | MAP2226c | hypothetical protein | 286 | 34.88 |
| MAP4_0747 | cystathionine gamma-synthase | 370 | Rv1079 | Cystathionine gamma-synthase Met | 39.7 | 388 | Mb1108 | cystathionine gamma-syntha | 39.7 | 388 | MAV_3867 | cystathionine gamma-lyase | 98.92 | 370 | BCG_1137 | cystathionine gamma-synthase | 39.7 | 388 | MAP3053c | cystathionine gamma-lyase | 370 | 100 |
| MAP4_0748 | Transcriptional regulator, TetR family | 200 | Rv1556 | Possible regulatory protein | 77.78 | 202 | Mb1581 | regulatory protein | 77.78 | 202 | MAV_3866 | TetR family transcriptional regulato | 100 | 196 | BCG_1607 | regulatory protein | 77.78 | 202 | MAP3052c | hypothetical protein | 200 | 100 |
| MAP4_0749 | putative pyridoxamine 5'-phosphate oxidase family pro | 172 | Rv2991 | hypothetical protein | 22.78 | 163 | Mb3015 | hypothetical protein | 24.05 | 163 | MAV_3865 | pyridoxamine 5'-phosphate oxidase | 99.42 | 172 | BCG_3012 | hypothetical protein | 24.05 | 163 | MAP3051 | hypothetical protein | 172 | 100 |
| MAP4_0751 | putative transmembrane transport protein MmpL2 | 972 | Rv0450c | Probable conserved transmembrane | 59.33 | 967 | Mb1583 | transmembrane transport pr | 75.03 | 967 | MAV_3863 | MmpL4 protein | 100 | 972 | BCG_1609 | transmembrane transport prot | 75.03 | 967 | MAP3049c | hypothetical protein | 972 | 100 |
| MAP4_0752 | hypothetical protein | 144 | Rv3101c | Putative cell division protein FtsX (s | 25 | 297 | Mb3128c | cell division protein FtsX | 25 | 297 | MAV_3862 | hypothetical protein | 100 | 144 | BCG_3126c | cell division protein ftsX | 25 | 297 | MAP3048c | hypothetical protein | 144 | 100 |
| MAP4_0753 | hypothetical protein | 221 | Rv3013 | hypothetical protein | 87.96 | 218 | Mb3038 | hypothetical protein | 87.96 | 218 | MAV_3861 | ACT domain-containing protein | 100 | 221 | BCG_3035 | hypothetical protein | 87.96 | 218 | MAP3047 | hypothetical protein | 221 | 100 |
| MAP4_0754 | aspartylglutamyl-tRNA amidotransferase subunitC | 98 | Rv3012c | Probable glutamyl-tRNA(GLN) amid | 84.69 | 99 | Mb3037c | aspartyl/glutamyl-tRNA amid | 84.69 | 99 | MAV_3860 | aspartyl/glutamyl-tRNA amidotrans | 100 | 98 | BCG_3034c | aspartyl/glutamyl-tRNA amido | 84.69 | 99 | MAP3046c | aspartyl/glutamyl-tRNA amidotransfera | 98 | 100 |
| MAP4_0755 | aspartylglutamyl-tRNA amidotransferase subunitA | 493 | Rv3011c | Probable glutamyl-tRNA(GLN) amid | 90.89 | 494 | Mb3036c | aspartyl/glutamyl-tRNA amid | 91.09 | 494 | MAV_3859 | aspartyl/glutamyl-tRNA amidotrans | 99.39 | 493 | BCG_3033c | aspartyl/glutamyl-tRNA amido | 91.09 | 494 | MAP3045c | aspartyl/glutamyl-tRNA amidotransfera | 493 | 100 |
| MAP4_0756 | 6-phosphofructokinase | 343 | Rv3010c | Probable 6-phosphofructokinase Pf | 93.29 | 343 | Mb3035c | 6-phosphofructokinase | 93.29 | 343 | MAV_3858 | 6-phosphofructokinase | 100 | 343 | BCG_3032c | 6-phosphofructokinase | 93.29 | 343 | MAP3044c | 6-phosphofructokinase | 343 | 100 |
| MAP4_0757 | hypothetical protein | 388 | Rv0530 | hypothetical protein | 38.67 | 405 | Mb0543 | hypothetical protein | 38.67 | 405 | MAV_3857 | hypothetical protein | 98.13 | 375 | BCG_0573 | hypothetical protein | 38.67 | 405 | MAP3043c | hypothetical protein | 388 | 100 |
| MAP4_0758 | glutamyl-tRNA(gln) amidotransferase subunit BGatB | 503 | Rv3009c | Probable glutamyl-tRNA(GLN) amid | 91.53 | 509 | Mb3034c | aspartyl/glutamyl-tRNA amid | 91.53 | 509 | MAV_3856 | aspartyl/glutamyl-tRNA amidotrans | 100 | 503 | BCG_3031c | aspartyl/glutamyl-tRNA amido | 91.53 | 509 | MAP3042c | aspartyl/glutamyl-tRNA amidotransfera | 503 | 100 |
| MAP4_0759 | lipoprotein LppZ | 400 | Rv3006 | Probable conserved lipoprotein Lpp | 91.6 | 373 | Mb3031 | lipoprotein LppZ | 91.33 | 373 | MAV_3855 | LppZ protein | 99.72 | 356 | BCG_3028 | lipoprotein lppZ | 91.33 | 373 | MAP3041 | hypothetical protein | 400 | 100 |
| MAP4_0760 | hypothetical protein | 286 | Rv3005c | hypothetical protein | 70.28 | 279 | Mb3030c | hypothetical protein | 70.28 | 279 | MAV_3854 | DoxX subfamily protein, putative | 99.3 | 285 | BCG_3027c | hypothetical protein | 70.28 | 279 | MAP3040c | hypothetical protein | 286 | 100 |
| MAP4_0761 | Low molecular weight protein antigen 6 | 119 | Rv3004 | Low molecular weight protein antig | 79.46 | 112 | Mb3029 | low molecular weight protein | 79.46 | 112 | MAV_3853 | low molecular weight protein antig | 98.26 | 115 | BCG_3026 | low molecular weight protein a | 79.46 | 112 | MAP1142 | hypothetical protein | 154 | 34.78 |
| MAP4_0762 | acetolactate synthase large subunit | 622 | Rv3003c | Acetolactate synthase (large subuni | 87.82 | 618 | Mb3028c | acetolactate synthase 1 catal | 87.82 | 618 | MAV_4935 | acetolactate synthase | 30.84 | 548 | BCG_3025c | acetolactate synthase 1 catalyt | 87.82 | 618 | MAP3038c | acetolactate synthase 1 catalytic subun | 622 | 100 |
| MAP4_0763 | acetolactate synthase small subunit | 168 | Rv3002c | Probable acetolactate synthase (sm | 89.88 | 168 | Mb3027c | acetolactate synthase 3 regul | 89.88 | 168 | MAV_3851 | acetolactate synthase 3 regulatory | 100 | 168 | BCG_3024c | acetolactate synthase 3 regula | 89.29 | 168 | MAP3037c | acetolactate synthase 3 regulatory sub | 168 | 100 |
| MAP4_0764 | ketol-acid reductoisomerase | 343 | Rv3001c | Probable KETOL-acid reductoisomer | 88.29 | 333 | Mb3026c | ketol-acid reductoisomerase | 88.29 | 333 | MAV_3850 | ketol-acid reductoisomerase | 100 | 333 | BCG_3023c | ketol-acid reductoisomerase | 88.29 | 333 | MAP3036c | ketol-acid reductoisomerase | 343 | 100 |
| MAP4_0765 | putative NAD(P)H:quinone oxidoreductase | 199 | Rv0107c | Probable cation-transporter ATPase | 39.58 | 1632 | Mb0111c | cation-transporter ATPase I | 39.58 | 1625 | MAV_3849 | NAD(P)H:quinone oxidoreductase, | 100 | 199 | BCG_0140c | cation-transporter atpase I ctp | 39.58 | 1625 | MAP3035 | hypothetical protein | 199 | 100 |
| MAP4_0766 | phytoene dehydrogenase | 475 | Rv2997 | Possible alanine rich dehydrogenase | 80.98 | 480 | Mb3021 | dehydrogenase | 80.77 | 480 | MAV_3848 | P49 protein | 98.95 | 475 | BCG_3018 | alanine rich dehydrogenase | 80.77 | 480 | MAP3034 | hypothetical protein | 475 | 100 |
| MAP4_0767 | D-3-phosphoglycerate dehydrogenase | 528 | Rv2996c | Probable D-3-phosphoglycerate deh | 88.64 | 528 | Mb3020c | D-3-phosphoglycerate dehyd | 88.64 | 528 | MAV_3847 | D-3-phosphoglycerate dehydrogen | 99.62 | 528 | BCG_3017c | D-3-phosphoglycerate dehydro | 88.64 | 528 | MAP3033c | D-3-phosphoglycerate dehydrogenase | 528 | 100 |
| MAP4_0768 | 3-isopropylmalate dehydrogenase | 336 | Rv2995c | Probable 3-isopropylmalate dehydr | 88.1 | 336 | Mb3019c | 3-isopropylmalate dehydroge | 87.8 | 336 | MAV_3845 | 3-isopropylmalate dehydrogenase | 99.7 | 336 | BCG_3016c | 3-isopropylmalate dehydrogen | 87.8 | 336 | MAP3032c | 3-isopropylmalate dehydrogenase | 336 | 100 |
| MAP4_0769 | hypothetical protein | 434 | Rv2994 | Probable conserved integral membr | 74.88 | 445 | Mb3018 | hypothetical protein | 74.88 | 445 | MAV_3846 | sugar transporter family protein | 99.54 | 463 | BCG_3015 | integral membrane protein | 74.88 | 445 | MAP3031 | hypothetical protein | 434 | 100 |
| MAP4_0770 | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase | 268 | Rv2993c | Possible 2-hydroxyhepta-2,4-diene- | 90.04 | 239 | Mb3017c | 2-hydroxyhepta-2,4-diene-1, | 90.04 | 239 | MAV_3844 | 5-carboxymethyl-2-hydroxymucon | 100 | 268 | BCG_3014c | 2-hydroxyhepta-2,4-diene-1,7- | 90.04 | 239 | MAP3030c | hypothetical protein | 242 | 100 |
| MAP4_0771 | glutamyl-tRNA synthetase | 492 | Rv2992c | Glutamyl-tRNA synthetase GltS (glut | 87.12 | 490 | Mb3016c | glutamyl-tRNA synthetase | 87.12 | 490 | MAV_0326 | endoglucanase A | 23.48 | 305 | BCG_3013c | glutamyl-tRNA synthetase | 86.91 | 490 | MAP3029c | glutamyl-tRNA synthetase | 492 | 100 |
| MAP4_0772 | hypothetical protein | 170 | Rv2991 | hypothetical protein | 84.66 | 163 | Mb3015 | hypothetical protein | 84.05 | 163 | MAV_3840 | pyridoxamine 5'-phosphate oxidas | 100 | 170 | BCG_3012 | hypothetical protein | 84.05 | 163 | MAP3028 | hypothetical protein | 170 | 100 |
| MAP4_0773 | Transcriptional regulator, IclR family | 233 | Rv2989 | Probable transcriptional regulatory | 85.84 | 233 | Mb3013 | transcriptional regulator | 85.84 | 233 | MAV_3839 | IclR family transcriptional regulato | 99.55 | 220 | BCG_3010 | transcriptional regulatory prot | 85.84 | 233 | MAP3027 | hypothetical protein | 233 | 100 |
| MAP4_0774 | 3-isopropylmalate dehydratase large subunit | 476 | Rv2988c | Probable 3-isopropylmalate dehydr | 91.26 | 473 | Mb3012c | isopropylmalate isomerase la | 91.04 | 473 | MAV_3838 | isopropylmalate isomerase large s | 99.58 | 476 | BCG_3009c | isopropylmalate isomerase lar | 91.04 | 473 | MAP3026c | isopropylmalate isomerase large subun | 476 | 100 |
| MAP4_0775 | 3-isopropylmalate dehydratase small subunit | 198 | Rv2987c | Probable 3-isopropylmalate dehydr | 90.31 | 198 | Mb3011c | isopropylmalate isomerase s | 90.31 | 198 | MAV_3837 | isopropylmalate isomerase small s | 99.49 | 198 | BCG_3008c | isopropylmalate isomerase sm | 90.31 | 198 | MAP3025c | isopropylmalate isomerase small subun | 200 | 100 |
| MAP4_0776 | DNA-binding protein | 212 | Rv2986c | DNA-binding protein HU homolog H | 97.17 | 214 | Mb3010c | DNA-binding protein HU | 97.17 | 214 | MAV_3836 | DNA-binding protein HU | 100 | 217 | BCG_3007c | DNA-binding protein HU hupB | 97.17 | 205 | MAP3024c | HupB | 212 | 100 |
| MAP4_0777 | putative hydrolase mutT1 | 315 | Rv2985 | Possible hydrolase MutT1 | 75.79 | 317 | Mb3009 | hydrolase MutT1 | 75.79 | 317 | MAV_3835 | hydrolase, NUDIX family protein | 99.68 | 315 | BCG_3006 | hydrolase mutT1 | 75.79 | 317 | MAP3023 | MutT1 | 315 | 100 |
| MAP4_0778 | polyphosphate kinase | 730 | Rv2984 | Polyphosphate kinase PPK (polypho | 86.16 | 742 | Mb3008 | polyphosphate kinase | 86.16 | 742 | MAV_3834 | polyphosphate kinase | 99.73 | 730 | BCG_3005 | polyphosphate kinase | 86.16 | 742 | MAP3022 | polyphosphate kinase | 730 | 100 |
| MAP4_0779 | conserved alanine rich protein | 220 | Rv2983 | Conserved hypothetical alanine rich | 81.46 | 214 | Mb3007 | hypothetical protein | 81.46 | 214 | MAV_4435 | methyltransferase, putative, family | 32.65 | 303 | BCG_3004 | hypothetical protein | 81.46 | 214 | MAP3021 | hypothetical protein | 220 | 100 |
| MAP4_0780 | glycerol-3-phosphate dehydrogenase GpdA2 | 333 | Rv2982c | Probable glycerol-3-phosphate deh | 84.08 | 334 | Mb3006c | NAD(P)H-dependent glycerol- | 84.38 | 334 | MAV_4577 | NAD(P)H-dependent glycerol-3-ph | 39.75 | 341 | BCG_3003c | NAD(P)H-dependent glycerol-3 | 84.38 | 334 | MAP3020c | NAD(P)H-dependent glycerol-3-phosph | 333 | 100 |
| MAP4_0781 | D-alanyl-alanine synthetase A | 369 | Rv2981c | Probable D-alanine--D-alanine ligase | 84.59 | 373 | Mb3005c | D-alanyl-alanine synthetase A | 84.93 | 370 | MAV_3830 | D-alanyl-alanine synthetase A | 99.73 | 369 | BCG_3002c | D-alanyl-alanine synthetase A | 84.87 | 373 | MAP3019c | D-alanyl-alanine synthetase A | 369 | 100 |
| MAP4_0782 | conserved secreted protein | 187 | Rv2980 | Possible conserved secreted protein | 64.13 | 181 | Mb3004 | hypothetical protein | 64.13 | 181 | MAV_3831 | hypothetical protein | 98.93 | 187 | BCG_3001 | hypothetical protein | 64.13 | 181 | MAP3018 | hypothetical protein | 187 | 99.47 |
| MAP4_0783 | thiamine-monophosphate kinase | 315 | Rv2977c | Probable thiamine-monophosphate | 78.59 | 333 | Mb3001c | thiamine monophosphate kin | 78.59 | 333 | MAV_3829 | thiamine monophosphate kinase | 98.73 | 315 | BCG_2998c | thiamine monophosphate kina | 78.59 | 333 | MAP3017c | thiamine monophosphate kinase | 341 | 99.68 |
| MAP4_0784 | uracil-DNA glycosylase | 227 | Rv2976c | Probable uracil-DNA glycosylase Un | 88.11 | 227 | Mb3000c | uracil-DNA glycosylase | 88.11 | 227 | MAV_3828 | uracil-DNA glycosylase | 99.56 | 227 | BCG_2997c | uracil-DNA glycosylase | 88.11 | 227 | MAP3016c | uracil-DNA glycosylase | 227 | 100 |
| MAP4_0785 | short-chain type dehydrogenase reductase | 276 | Rv1245c | Probable short-chain type dehydrog | 32.11 | 276 | Mb1277c | short-chain type dehydrogen | 32.11 | 276 | MAV_3827 | short chain dehydrogenase | 99.64 | 276 | BCG_1305c | short-chain type dehydrogena | 32.11 | 276 | MAP3015 | short chain dehydrogenase | 276 | 100 |
| MAP4_0786 | hypothetical protein | 414 | Rv3531c | Hypothetical protein | 26.56 | 375 | Mb3561c | hypothetical protein | 26.56 | 375 | MAV_2441 | hypothetical protein | 28.17 | 409 | BCG_3595c | hypothetical protein | 26.56 | 375 | MAP3014 | hypothetical protein | 477 | 100 |
| MAP4_0787 | hypothetical protein | 147 | Rv3472 | hypothetical protein | 26.67 | 168 | Mb3501 | hypothetical protein | 26.67 | 168 | MAV_3825 | hypothetical protein | 98.64 | 147 | BCG_3537 | hypothetical protein | 26.67 | 168 | MAP0717c | hypothetical protein | 148 | 25 |
| MAP4_0788 | dehydrogenase | 296 | Rv2263 | Possible oxidoreductase | 39.53 | 317 | Mb2286 | short chain dehydrogenase | 39.53 | 317 | MAV_3824 | dehydrogenase | 98.99 | 296 | BCG_2280 | short chain dehydrogenase | 39.53 | 317 | MAP3013c | hypothetical protein | 296 | 100 |
| MAP4_0789 | short-chain dehydrogenasereductase | 273 | Rv2750 | Probable dehydrogenase | 47.78 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 47.78 | 272 | MAV_3823 | carveol dehydrogenase | 98.17 | 273 | BCG_2766 | 3-ketoacyl-ACP reductase | 47.78 | 272 | MAP3012c | hypothetical protein | 273 | 100 |
| MAP4_0790 | 50S ribosomal protein L28 | 64 | Rv0105c | 50S ribosomal protein L28-1 RpmB1 | 67.65 | 94 | Mb0108c | 50S ribosomal protein L28 | 67.65 | 94 | MAV_3822 | 50S ribosomal protein L28 | 100 | 64 | BCG_0138c | 50S ribosomal protein L28 | 67.65 | 94 | MAP3976 | hypothetical protein | 446 | 34.21 |
| MAP4_0791 | hypothetical protein | 256 | Rv3896c | hypothetical protein | 45.76 | 302 | Mb3926c | hypothetical protein | 42.47 | 288 | MAV_5286 | transglycosylase | 41.27 | 288 | BCG_3953c | hypothetical protein | 42.47 | 288 | MAP3011c | hypothetical protein | 256 | 100 |
| MAP4_0792 | putative alanine rich protein, dihydroxyacetone kinase | 575 | Rv2974c | Conserved hypothetical alanine rich | 76.6 | 470 | Mb2999c | hypothetical protein | 75.44 | 553 | MAV_3819 | DAK2 domain-containing protein | 99.3 | 575 | BCG_2996c | hypothetical protein | 75.44 | 553 | MAP3010c | hypothetical protein | 575 | 100 |
| MAP4_0793 | ATP-dependent DNA helicase RecG | 738 | Rv2973c | Probable ATP-dependent DNA helica | 80.11 | 737 | Mb2998c | ATP-dependent DNA helicase | 80.11 | 737 | MAV_3818 | ATP-dependent DNA helicase RecG | 99.46 | 738 | BCG_2995c | ATP-dependent DNA helicase R | 79.97 | 737 | MAP3009c | ATP-dependent DNA helicase RecG | 738 | 100 |
| MAP4_0794 | hypothetical protein | 238 | Rv2972c | Possible conserved membrane or ex | 80.17 | 237 | Mb2997c | hypothetical protein | 80.17 | 237 | MAV_3817 | hypothetical protein | 99.16 | 238 | BCG_2994c | hypothetical protein | 80.17 | 237 | MAP3008c | hypothetical protein | 238 | 100 |
| MAP4_0795 | oxidoreductase | 281 | Rv2971 | Probable oxidoreductase | 78.72 | 282 | Mb2996 | oxidoreductase | 78.72 | 282 | MAV_3816 | 2,5-diketo-D-gluconic acid reducta | 99.62 | 262 | BCG_2993 | oxidoreductase | 78.72 | 282 | MAP3007 | hypothetical protein | 281 | 100 |
| MAP4_0796 | lipase-esterase LipN | 373 | Rv2970c | Probable lipase/esterase LipN | 74.07 | 376 | Mb2994c | lipase/esterase | 74.07 | 376 | MAV_3814 | alpha/beta hydrolase | 99.46 | 373 | BCG_2991c | lipase/esterase lipN | 74.07 | 376 | MAP3006c | hypothetical protein | 373 | 100 |
| MAP4_0797 | hypothetical protein | 255 | Rv2969c | Possible conserved membrane or se | 74.41 | 255 | Mb2993c | hypothetical protein | 74.41 | 255 | MAV_3813 | hypothetical protein | 100 | 255 | BCG_2990c | membrane or hypothetical pro | 74.41 | 255 | MAP3005c | hypothetical protein | 255 | 100 |
| MAP4_0798 | hypothetical protein | 211 | Rv2968c | Probable conserved integral membr | 69.16 | 210 | Mb2992c | hypothetical protein | 69.16 | 210 | MAV_3812 | integral membrane protein | 99.05 | 211 | BCG_2989c | integral membrane protein | 69.16 | 210 | MAP3004c | hypothetical protein | 211 | 100 |
| MAP4_0799 | methyltransferasemethylase | 184 | Rv2966c | Possible methyltransferase (methyl | 79.35 | 188 | Mb2990c | methyltransferase | 79.35 | 188 | MAV_3811 | methyltransferase | 98.37 | 184 | BCG_2987c | methyltransferase | 79.35 | 188 | MAP3003c | hypothetical protein | 184 | 100 |
| MAP4_0800 | phosphopantetheine adenylyltransferase KdtB | 160 | Rv2965c | Probable phosphopantetheine aden | 91.08 | 161 | Mb2989c | phosphopantetheine adenyly | 91.08 | 161 | MAV_3810 | phosphopantetheine adenylyltrans | 100 | 160 | BCG_2986c | phosphopantetheine adenylylt | 91.08 | 161 | MAP3002c | phosphopantetheine adenylyltransfera | 160 | 100 |
| MAP4_0801 | hypothetical protein | 414 | Rv2015c | hypothetical protein | 71.53 | 418 | Mb1794c | hypothetical protein | 71.53 | 418 | MAV_0036 | hypothetical protein | 97.77 | 414 | BCG_2032c | hypothetical protein | 71.53 | 418 | MAP3001 | hypothetical protein | 414 | 100 |
| MAP4_0802 | acetolactate synthase catalytic subunit | 569 | Rv1820 | Probable acetolactate synthase IlvG | 27.76 | 547 | Mb1851 | hypothetical protein | 27.76 | 547 | MAV_3788 | acetolactate synthase catalytic sub | 99.82 | 569 | BCG_1855 | hypothetical protein | 27.76 | 547 | MAP3000c | acetolactate synthase catalytic subunit | 569 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0803 | putative integral membrane protein | 387 | Rv2963 | Probable integral membrane protei | 81.17 | 406 | Mb2987 | hypothetical protein | 81.17 | 406 | MAV_3787 | hypothetical protein | 99.22 | 387 | BCG_2984 | integral membrane protein | 81.17 | 406 | MAP2999 | hypothetical protein | 387 | 100 |
| MAP4_0804 | hypothetical protein | 268 | Rv2182c | 1-acylglycerol-3-phosphate O-acyltra | 50 | 247 | Mb2204c | 1-acylglycerol-3-phosphate O | 50 | 247 | MAV_3786 | hypothetical protein | 97.01 | 326 | BCG_2197c | 1-acylglycerol-3-phosphate O-a | 50 | 247 | MAP2998c | hypothetical protein | 268 | 100 |
| MAP4_0805 | hypothetical protein | 245 | Rv2927c | hypothetical protein | 93.47 | 245 | Mb2952c | hypothetical protein | 93.47 | 245 | MAV_3785 | hypothetical protein | 99.59 | 245 | BCG_2949c | hypothetical protein | 93.47 | 245 | MAP2997c | hypothetical protein | 245 | 100 |
| MAP4_0806 | hypothetical protein | 209 | Rv2926c | hypothetical protein | 69.67 | 207 | Mb2951c | hypothetical protein | 69.67 | 207 | MAV_3784 | hypothetical protein | 99.44 | 177 | BCG_2948c | hypothetical protein | 69.67 | 207 | MAP2996c | hypothetical protein | 209 | 100 |
| MAP4_0807 | ribonuclease III Rnc | 237 | Rv2925c | Probable ribonuclease III Rnc (RNase | 89.12 | 240 | Mb2950c | ribonuclease III | 89.12 | 240 | MAV_3783 | ribonuclease III | 99.58 | 237 | BCG_2947c | ribonuclease III | 89.12 | 240 | MAP2995c | ribonuclease III | 237 | 100 |
| MAP4_0808 | formamidopyrimidine-DNA glycosylase | 283 | Rv2924c | Probable formamidopyrimidine-DNA | 83.68 | 289 | Mb2949c | formamidopyrimidine-DNA gl | 83.68 | 289 | MAV_3782 | formamidopyrimidine-DNA glycosy | 95.41 | 283 | BCG_2946c | formamidopyrimidine-DNA gly | 83.68 | 289 | MAP2994c | formamidopyrimidine-DNA glycosylase | 283 | 100 |
| MAP4_0809 | glcNAc-PI de-N-acetylase family protein | 258 | Rv1082 | Mycothiol conjugate amidase Mca ( | 30.2 | 288 | Mb1111 | mycothiol conjugate amidase | 30.2 | 288 | MAV_3781 | GlcNAc-PI de-N-acetylase | 100 | 258 | BCG_1140 | Mycothiol conjugate amidase M | 30.2 | 288 | MAP2993 | hypothetical protein | 258 | 100 |
| MAP4_0810 | hypothetical protein | 141 | Rv2923c | hypothetical protein | 78.03 | 137 | Mb2948c | hypothetical protein | 78.03 | 137 | MAV_3780 | hypothetical protein | 98.31 | 118 | BCG_2945c | hypothetical protein | 78.03 | 137 | MAP2992c | hypothetical protein | 141 | 100 |
| MAP4_0811 | acylphosphatase AcyP | 97 | Rv2922A | Probable acylphosphatase AcyP (acy | 75.26 | 93 | Mb2947c | acylphosphatase | 75.26 | 93 | MAV_3779 | acylphosphatase | 100 | 97 | BCG_2944c | acylphosphatase | 75.26 | 93 | MAP2991c | acylphosphatase | 97 | 100 |
| MAP4_0812 | chromosome partition protein Smc | 1196 | Rv2922c | Probable chromosome partition pro | 83.97 | 1205 | Mb2946c | chromosome partition protei | 83.8 | 1205 | MAV_3777 | chromosome segregation protein S | 99.41 | 1196 | BCG_2943c | chromosome partition protein | 83.8 | 1205 | MAP2990c | hypothetical protein | 1236 | 99.83 |
| MAP4_0813 | cell division protein FtsY | 444 | Rv2921c | Probable cell division protein FtsY (S | 83.78 | 422 | Mb2945c | cell division protein FtsY | 83.78 | 422 | MAV_3776 | signal recognition particle-docking | 94.82 | 428 | BCG_2942c | cell division protein ftsY | 83.78 | 422 | MAP2989c | hypothetical protein | 444 | 100 |
| MAP4_0814 | ammonium-transport membrane protein Amt | 479 | Rv2920c | Probable ammonium-transport inte | 85.65 | 477 | Mb2944c | ammonium transporter | 85.65 | 477 | MAV_3775 | ammonium transporter | 99.79 | 477 | BCG_2941c | ammonium-transport integral | 85.65 | 477 | MAP2988c | Amt_2 | 479 | 100 |
| MAP4_0815 | nitrogen regulatory protein P-II | 112 | Rv2919c | Probable nitrogen regulatory protei | 98.21 | 112 | Mb2943c | nitrogen regulatory protein P | 98.21 | 112 | MAV_3774 | nitrogen regulatory protein P-II | 100 | 112 | BCG_2940c | nitrogen regulatory protein P-I | 98.21 | 112 | MAP2987c | GlnB | 112 | 100 |
| MAP4_0816 | protein-pii uridylyltransferase GlnD | 814 | Rv2918c | Probable [protein-PII] uridylyltransfe | 75.65 | 808 | Mb2942c | PII uridylyl-transferase | 75.65 | 808 | MAV_3773 | PII uridylyl-transferase | 99.63 | 814 | BCG_2939c | PII uridylyl-transferase | 75.65 | 808 | MAP2986c | PII uridylyl-transferase | 814 | 100 |
| MAP4_0817 | hypothetical protein | 579 | Rv2917 | Conserved hypothetical alanine and | 83.13 | 626 | Mb2941 | hypothetical protein | 83.3 | 626 | MAV_3772 | DNA or RNA helicase of superfamily | 99.31 | 579 | BCG_2938 | hypothetical protein | 83.3 | 626 | MAP2985 | hypothetical protein | 590 | 99.83 |
| MAP4_0818 | putative hydrolase, alphabeta fold family protein | 263 | Rv0134 | Possible epoxide hydrolase EphF (ep | 28.11 | 300 | Mb3502c | peroxidase BpoA | 34.95 | 261 | MAV_3771 | alpha/beta hydrolase | 99.62 | 263 | BCG_3538c | peroxidase bpoA | 34.95 | 261 | MAP2984 | hypothetical protein | 263 | 100 |
| MAP4_0819 | signal recognition particle protein Ffh | 517 | Rv2916c | Probable signal recognition particle | 88.57 | 525 | Mb2940c | signal recognition particle pro | 88.57 | 525 | MAV_3770 | signal recognition particle protein | 99.42 | 517 | BCG_2937c | signal recognition particle prot | 88.57 | 525 | MAP2983c | hypothetical protein | 517 | 100 |
| MAP4_0820 | amidohydrolase family protein | 363 | Rv2915c | hypothetical protein | 79.11 | 370 | Mb2939c | hypothetical protein | 79.11 | 370 | MAV_3769 | amidohydrolase | 99.72 | 363 | BCG_2936c | hypothetical protein | 79.11 | 370 | MAP2982c | hypothetical protein | 363 | 100 |
| MAP4_0821 | D-amino acid aminohydrolase | 620 | Rv2913c | Possible D-amino acid aminohydrola | 84.51 | 611 | Mb2937c | D-amino acid aminohydrolase | 84.51 | 611 | MAV_3768 | N-acyl-D-glutamate amidohydrolas | 98 | 601 | BCG_2934c | D-amino acid aminohydrolase | 84.51 | 611 | MAP2981c | hypothetical protein | 620 | 100 |
| MAP4_0822 | Transcriptional regulator, TetR family | 197 | Rv2912c | Probable transcriptional regulatory | 78.46 | 195 | Mb2936c | TetR family transcriptional re | 78.46 | 195 | MAV_3767 | TetR family transcriptional regulato | 98.98 | 197 | BCG_2933c | TetR family transcriptional regu | 78.46 | 195 | MAP2980c | hypothetical protein | 197 | 99.49 |
| MAP4_0823 | D-alanyl-D-alanine carboxypeptidase | 289 | Rv2911 | Probable penicillin-binding protein D | 85.4 | 291 | Mb2935 | D-alanyl-D-alanine carboxype | 85.4 | 291 | MAV_3766 | D-alanyl-D-alanine carboxypeptidas | 100 | 298 | BCG_2932 | D-alanyl-D-alanine carboxypep | 85.4 | 291 | MAP2979 | DacB | 289 | 100 |
| MAP4_0824 | hypothetical protein | 139 | Rv2910c | hypothetical protein | 82.73 | 147 | Mb2934c | hypothetical protein | 82.73 | 147 | MAV_3765 | hypothetical protein | 100 | 139 | BCG_2931c | hypothetical protein | 82.73 | 147 | MAP2978c | hypothetical protein | 139 | 100 |
| MAP4_0825 | 30S ribosomal protein S16 | 171 | Rv2909c | 30S ribosomal protein S16 RpsP | 76.61 | 162 | Mb2933c | 30S ribosomal protein S16 | 76.61 | 162 | MAV_3764 | 30S ribosomal protein S16 | 100 | 170 | BCG_2930c | 30S ribosomal protein S16 | 76.61 | 162 | MAP2977c | 30S ribosomal protein S16 | 171 | 100 |
| MAP4_0826 | putative RNA-binding protein | 80 | Rv2908c | hypothetical protein | 96.25 | 80 | Mb2932c | hypothetical protein | 96.25 | 80 | MAV_3763 | hypothetical protein | 100 | 80 | BCG_2929c | hypothetical protein | 96.25 | 80 | MAP2976c | hypothetical protein | 80 | 100 |
| MAP4_0827 | 16S rRNA processing protein RimM | 175 | Rv2907c | Probable 16S rRNA processing prote | 72.63 | 176 | Mb2931c | 16S rRNA-processing protein | 72.63 | 176 | MAV_3762 | 16S rRNA-processing protein RimM | 99.43 | 175 | BCG_2928c | 16S rRNA-processing protein R | 72.63 | 176 | MAP2975c | 16S rRNA-processing protein RimM | 175 | 100 |
| MAP4_0828 | tRNA-methyltransferase | 239 | Rv2906c | Probable tRNA (guanine-N1)-methyl | 88.94 | 230 | Mb2930c | tRNA (guanine-N(1)-)-methylt | 88.94 | 230 | MAV_3760 | tRNA (guanine-N(1)-)-methyltransfe | 98.74 | 239 | BCG_2927c | tRNA (guanine-N(1)-)-methyltr | 88.94 | 230 | MAP2974c | tRNA (guanine-N(1)-)-methyltransferase | 239 | 100 |
| MAP4_0829 | alanine rich lipoprotein LppW | 322 | Rv2905 | Probable conserved alanine rich lipo | 70.13 | 314 | Mb2929 | hypothetical protein | 70.13 | 314 | MAV_3761 | LppW protein | 100 | 322 | BCG_2926 | alanine rich lipoprotein lppW | 70.13 | 314 | MAP2973 | hypothetical protein | 322 | 100 |
| MAP4_0830 | 50S ribosomal protein L19 | 113 | Rv2904c | 50S ribosomal protein L19 RplS | 92.92 | 113 | Mb2928c | 50S ribosomal protein L19 | 92.92 | 113 | MAV_3759 | 50S ribosomal protein L19 | 100 | 113 | BCG_2925c | 50S ribosomal protein L19 | 92.92 | 113 | MAP2972c | 50S ribosomal protein L19 | 162 | 100 |
| MAP4_0831 | signal peptidase I | 299 | Rv2903c | Probable signal peptidase I LepB (SP | 71.05 | 294 | Mb2927c | signal peptidase I LepB | 71.05 | 294 | MAV_3758 | signal peptidase I | 100 | 299 | BCG_2924c | signal peptidase I lepB | 71.05 | 294 | MAP2971c | hypothetical protein | 299 | 100 |
| MAP4_0832 | Ribonuclease HII | 239 | Rv2902c | Probable ribonuclease HII protein Rr | 84.12 | 264 | Mb2926c | ribonuclease HII | 83.69 | 264 | MAV_3757 | ribonuclease HII | 99.57 | 230 | BCG_2923c | ribonuclease HII | 84.12 | 264 | MAP2970c | ribonuclease HII | 239 | 100 |
| MAP4_0833 | hypothetical protein | 101 | Rv2901c | hypothetical protein | 97.03 | 101 | Mb2925c | hypothetical protein | 97.03 | 101 | MAV_3756 | hypothetical protein | 100 | 101 | BCG_2922c | hypothetical protein | 97.03 | 101 | MAP2969c | hypothetical protein | 101 | 100 |
| MAP4_0834 | hypothetical protein | 256 | Rv1626 | Probable two-component system tra | 28.33 | 205 | Mb1652 | two-component system trans | 28.33 | 205 | MAV_3755 | ANTAR domain-containing protein | 99.22 | 256 | BCG_1664 | two-component system transc | 28.33 | 205 | MAP2968 | hypothetical protein | 256 | 100 |
| MAP4_0835 | NAD dependent epimerasedehydratase | 329 | Rv0501 | Possible UDP-glucose 4-epimerase G | 25.76 | 376 | Mb0513 | UDP-glucose 4-epimerase | 25.76 | 376 | MAV_3754 | NAD dependent epimerase/dehydr | 99.69 | 327 | BCG_0544 | udp-glucose 4-epimerase galE2 | 25.76 | 376 | MAP2967c | hypothetical protein | 329 | 100 |
| MAP4_0836 | formate dehydrogenase accessory protein | 272 | Rv2899c | Possible FdhD protein homolog | 74.17 | 276 | Mb2923c | formate dehydrogenase acce | 74.17 | 276 | MAV_3753 | formate dehydrogenase accessory | 98.16 | 272 | BCG_2920c | formate dehydrogenase access | 74.17 | 276 | MAP2966c | formate dehydrogenase accessory prot | 272 | 100 |
| MAP4_0837 | hypothetical protein | 98 | Rv2898c | hypothetical protein | 83.67 | 128 | Mb2922c | hypothetical protein | 83.67 | 128 | MAV_3752 | hypothetical protein | 96.23 | 128 | BCG_2919c | hypothetical protein | 83.67 | 128 | MAP2965c | hypothetical protein | 98 | 100 |
| MAP4_0838 | phage integrase family protein | 372 | Rv1701 | Probable integrase/recombinase | 34.15 | 311 | Mb1727 | site-specific tyrosine recombi | 34.15 | 311 | MAV_3070 | site-specific tyrosine recombinase X | 35.12 | 313 | BCG_1739 | site-specific tyrosine recombin | 34.15 | 311 | MAP2964c | hypothetical protein | 372 | 100 |
| MAP4_0841 | magnesium chelatase family protein | 503 | Rv2897c | hypothetical protein | 87.67 | 503 | Mb2921c | hypothetical protein | 87.67 | 503 | MAV_3751 | Mg-chelatase subunits D/I family p | 99.6 | 503 | BCG_2918c | hypothetical protein | 87.67 | 503 | MAP2962c | hypothetical protein | 503 | 100 |
| MAP4_0842 | hypothetical protein | 91 | Rv0768 | Probable aldehyde dehydrogenase N | 36.67 | 489 | Mb0791 | aldehyde dehydrogenase | 36.67 | 489 | MAV_3750 | hypothetical protein | 100 | 91 | BCG_0820 | aldehyde dehydrogenase AldA | 36.67 | 489 | MAP2832 | hypothetical protein | 343 | 26.97 |
| MAP4_0843 | DNA recombination-mediator protein, Smf family | 388 | Rv2896c | hypothetical protein | 77.93 | 389 | Mb2920c | hypothetical protein | 77.66 | 389 | MAV_3749 | smf family protein | 99.23 | 388 | BCG_2917c | hypothetical protein | 77.66 | 389 | MAP2961c | hypothetical protein | 388 | 100 |
| MAP4_0844 | mycobactin utilization protein | 283 | Rv2895c | Possible mycobactin utilization prot | 81.79 | 283 | Mb2919c | mycobactin utilization protei | 81.79 | 283 | MAV_3748 | siderophore utilization protein | 100 | 283 | BCG_2916c | mycobactin utilization protein | 81.79 | 283 | MAP2960c | ViuB | 231 | 99.57 |
| MAP4_0845 | lactate 2-monooxygenase | 386 | Rv0694 | Possible L-lactate dehydrogenase (c | 35.39 | 396 | Mb0713 | L-lactate dehydrogenase (cyt | 35.39 | 396 | MAV_3747 | lactate 2-monooxygenase | 99.48 | 386 | BCG_0743 | L-lactate dehydrogenase (cyto | 35.39 | 396 | MAP2959c | hypothetical protein | 386 | 100 |
| MAP4_0846 | integrase XerC | 301 | Rv2894c | Probable integrase/recombinase Xe | 84.18 | 298 | Mb2918c | site-specific tyrosine recombi | 84.18 | 298 | MAV_3746 | site-specific tyrosine recombinase X | 99.67 | 301 | BCG_2915c | site-specific tyrosine recombin | 84.18 | 298 | MAP2958c | site-specific tyrosine recombinase XerC | 301 | 100 |
| MAP4_0847 | M23 peptidase domain-containing protein | 167 | Rv2891 | hypothetical protein | 72.22 | 249 | Mb2915 | hypothetical protein | 72.22 | 249 | MAV_3745 | M23 peptidase domain-containing | 97.01 | 167 | BCG_2912 | hypothetical protein | 72.22 | 249 | MAP2957 | hypothetical protein | 167 | 100 |
| MAP4_0848 | 30S ribosomal protein S2 | 276 | Rv2890c | 30S ribosomal protein S2 RpsB | 91.64 | 287 | Mb2914c | 30S ribosomal protein S2 | 91.64 | 287 | MAV_3744 | 30S ribosomal protein S2 | 100 | 276 | BCG_2911c | 30S ribosomal protein S2 | 91.64 | 287 | MAP2956c | 30S ribosomal protein S2 | 276 | 100 |
| MAP4_0849 | Translation elongation factor Ts | 275 | Rv2889c | Probable elongation factor Tsf (EF-ts | 89.09 | 271 | Mb2913c | elongation factor Ts | 88.73 | 271 | MAV_3743 | elongation factor Ts | 99.64 | 275 | BCG_2910c | elongation factor Ts | 88.73 | 271 | MAP2955c | elongation factor Ts | 275 | 100 |
| MAP4_0850 | putative amidase AmiC | 471 | Rv2888c | Probable amidase AmiC (aminohydr | 76.22 | 473 | Mb2912c | amidase | 76.22 | 473 | MAV_0676 | 6-aminohexanoate-cyclic-dimer hy | 35.22 | 492 | BCG_2909c | amidase | 76.22 | 473 | MAP2954c | amidase | 471 | 100 |
| MAP4_0851 | Transcriptional regulator, MarR family | 140 | Rv2887 | Probable transcriptional regulatory | 78.42 | 139 | Mb2911 | transcriptional regulator | 78.42 | 139 | MAV_3741 | MarR family transcriptional regulat | 99.29 | 175 | BCG_2908 | transcriptional regulatory prot | 78.42 | 139 | MAP2953 | hypothetical protein | 140 | 100 |
| MAP4_0852 | hypothetical protein | 137 | Rv0481c | Hypothetical protein | 25.97 | 174 | Mb0491c | hypothetical protein | 25.97 | 174 | MAV_3740 | ChaB family protein | 99.27 | 137 | BCG_0522c | hypothetical protein | 25.97 | 174 | MAP2952c | hypothetical protein | 137 | 100 |
| MAP4_0853 | putative dehydrogenasereductase | 279 | Rv0769 | Probable dehydrogenase/reductase | 37.25 | 248 | Mb0792 | short chain dehydrogenase | 37.25 | 248 | MAV_1242 | short chain dehydrogenase/reducta | 35.66 | 245 | BCG_0821 | short chain dehydrogenase | 37.25 | 248 | MAP2951 | hypothetical protein | 279 | 100 |
| MAP4_0854 | hypothetical protein | 58 | Rv2906c | Probable tRNA (guanine-N1)-methyl | 36.36 | 230 | Mb2930c | tRNA (guanine-N(1)-)-methylt | 36.36 | 230 | MAV_3738 | hypothetical protein | 100 | 58 | BCG_2927c | tRNA (guanine-N(1)-)-methyltr | 36.36 | 230 | MAP3616c | hypothetical protein | 474 | 29.55 |
| MAP4_0855 | hypothetical protein | 190 | Rv1926c | Immunogenic protein Mpt63 (antige | 43.41 | 159 | Mb1961c | hypothetical protein | 43.41 | 159 | MAV_3737 | hypothetical protein | 98.42 | 190 | BCG_1965c | immunogenic protein mpt63 | 43.41 | 159 | MAP2950c | hypothetical protein | 190 | 100 |
| MAP4_0856 | acyltransferase domain-containing protein | 312 | Rv1428c | hypothetical protein | 33.58 | 275 | Mb1463c | hypothetical protein | 33.58 | 275 | MAV_3736 | acyltransferase domain-containing | 99.36 | 322 | BCG_1489c | hypothetical protein | 33.58 | 275 | MAP2949c | hypothetical protein | 312 | 100 |
| MAP4_0857 | Transcriptional regulatory protein glnR | 233 | Rv2884 | Probable transcriptional regulatory | 65.18 | 252 | Mb2908 | transcriptional regulator | 65.18 | 252 | MAV_3735 | GlnR family transcriptional regulato | 99.57 | 231 | BCG_2905 | transcriptional regulatory prot | 65.18 | 252 | MAP2948 | hypothetical protein | 253 | 99.57 |
| MAP4_0858 | hypothetical protein | 79 | Rv2160A | hypothetical protein | 30.23 | 211 | Mb2184c | hypothetical protein | 30.23 | 206 | MAV_3734 | hypothetical protein | 100 | 79 | BCG_2177c | hypothetical protein | 30.23 | 206 | MAP2947 | hypothetical protein | 152 | 100 |
| MAP4_0859 | uridylate kinase | 265 | Rv2883c | Probable uridylate kinase PyrH (UK) | 88.89 | 261 | Mb2907c | uridylate kinase | 88.89 | 261 | MAV_3733 | uridylate kinase | 99.13 | 229 | BCG_2904c | uridylate kinase | 88.89 | 261 | MAP2946c | uridylate kinase | 265 | 100 |
| MAP4_0860 | ribosome recycling factor | 185 | Rv2882c | Ribosome recycling factor Frr (ribos | 95.14 | 185 | Mb2906c | ribosome recycling factor | 95.14 | 185 | MAV_3732 | ribosome recycling factor | 100 | 185 | BCG_2903c | ribosome recycling factor | 94.59 | 185 | MAP2945c | ribosome recycling factor | 185 | 100 |
| MAP4_0861 | membrane phosphatidate cytidylyl transferase CdsA | 311 | Rv2881c | Probable integral membrane phosph | 72.12 | 306 | Mb2905c | integral membrane phosphat | 72.12 | 306 | MAV_3731 | phosphatidate cytidylyltransferase | 100 | 311 | BCG_2902c | integral membrane phosphatid | 72.12 | 306 | MAP2944c | hypothetical protein | 311 | 100 |
| MAP4_0862 | ribosomal RNA large subunit methyltransferase N | 364 | Rv2879c | hypothetical protein | 89.36 | 189 | Mb2904c | ribosomal RNA large subunit | 88.46 | 364 | MAV_5167 | Fatty acid desaturase | 24.03 | 366 | BCG_2901c | ribosomal RNA large subunit m | 88.46 | 364 | MAP2943c | ribosomal RNA large subunit methyltra | 364 | 100 |
| MAP4_0863 | soluble secreted antigen MPT53 precursor | 172 | Rv2878c | Soluble secreted antigen Mpt53 pre | 72.51 | 173 | Mb2903c | soluble secreted antigen mpb | 72.51 | 173 | MAV_3729 | 15 kDa antigen | 98.09 | 157 | BCG_2900c | hypothetical protein | 72.51 | 173 | MAP2942c | Mpt53 | 172 | 100 |
| MAP4_0864 | integral conserved membrane protein | 409 | Rv2877c | Probable conserved integral membr | 71.43 | 287 | Mb2902c | hypothetical protein | 71.43 | 287 | MAV_3728 | cytochrome C biogenesis protein tr | 97.31 | 409 | BCG_2899c | integral membrane protein | 71.43 | 287 | MAP2941c | hypothetical protein | 409 | 100 |
| MAP4_0865 | 1-deoxy-D-xylulose 5-phosphate-reducto-isomerase | 407 | Rv2870c | Probable 1-deoxy-D-xylulose 5-phos | 84.24 | 413 | Mb2895c | 1-deoxy-D-xylulose 5-phosph | 84.24 | 413 | MAV_3727 | 1-deoxy-D-xylulose 5-phosphate re | 99.51 | 407 | BCG_2892c | 1-deoxy-D-xylulose 5-phosphat | 84.24 | 413 | MAP2940c | 1-deoxy-D-xylulose 5-phosphate reduct | 419 | 99.75 |
| MAP4_0866 | conserved membrane protein, peptidase family M50 | 407 | Rv2869c | Membrane bound metalloprotease | 82.56 | 404 | Mb2894c | transmembrane protein | 82.8 | 404 | MAV_3726 | peptidase M50 | 99.75 | 407 | BCG_2891c | hypothetical protein | 82.56 | 404 | MAP2939c | hypothetical protein | 407 | 100 |
| MAP4_0867 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | 388 | Rv2868c | Probable GcpE protein | 92.78 | 387 | Mb2893c | 4-hydroxy-3-methylbut-2-en- | 92.78 | 387 | MAV_3725 | 4-hydroxy-3-methylbut-2-en-1-yl di | 100 | 364 | BCG_2890c | 4-hydroxy-3-methylbut-2-en-1- | 92.78 | 387 | MAP2938c | 4-hydroxy-3-methylbut-2-en-1-yl dipho | 388 | 100 |
| MAP4_0868 | hypothetical protein | 284 | Rv2867c | GCN5-related N-acetyltransferase | 87.32 | 284 | Mb2892c | hypothetical protein | 87.32 | 284 | MAV_3724 | acetyltransferase | 98.89 | 270 | BCG_2889c | hypothetical protein | 87.32 | 284 | MAP2937c | hypothetical protein | 284 | 100 |
| MAP4_0869 | penicillin-binding protein | 620 | Rv2864c | Possible penicillin-binding lipoprotei | 84.3 | 603 | Mb2889c | penicillin-binding lipoprotein | 84.3 | 603 | MAV_3723 | hypothetical protein | 99.83 | 599 | BCG_2886c | penicillin-binding lipoprotein | 84.3 | 603 | MAP2936c | hypothetical protein | 620 | 100 |
| MAP4_0870 | hypothetical protein | 195 | Rv2862c | hypothetical protein | 85.86 | 194 | Mb2887c | hypothetical protein | 85.86 | 194 | MAV_1086 | hypothetical protein | 32.24 | 201 | BCG_2884c | hypothetical protein | 85.86 | 194 | MAP2935c | hypothetical protein | 195 | 100 |
| MAP4_0871 | methionine aminopeptidase | 285 | Rv2861c | Methionine aminopeptidase MapB ( | 91.87 | 285 | Mb2886c | methionine aminopeptidase | 91.87 | 285 | MAV_3721 | methionine aminopeptidase | 99.3 | 285 | BCG_2883c | methionine aminopeptidase | 91.87 | 285 | MAP2934c | methionine aminopeptidase | 285 | 100 |
| MAP4_0872 | cobyric acid synthase | 497 | Rv0255c | Probable cobyric acid synthase Cob( | 53.05 | 494 | Mb0261c | cobyric acid synthase | 53.05 | 494 | MAV_3720 | cobyric acid synthase | 98.79 | 497 | BCG_0293c | cobyric acid synthase | 53.05 | 494 | MAP2933c | cobyric acid synthase | 497 | 100 |
| MAP4_0873 | hypothetical protein | 183 | Rv3203 | Possible lipase LipV | 35.56 | 224 | Mb3228 | lipase LipV | 35.56 | 224 | MAV_3719 | hypothetical protein | 100 | 186 | BCG_3229 | lipase lipV | 35.56 | 224 | MAP2932c | hypothetical protein | 183 | 100 |
| MAP4_0874 | glutamine synthetase | 461 | Rv2860c | Probable glutamine synthetase GlnA | 78.96 | 457 | Mb2885c | glutamine synthetase | 78.96 | 457 | MAV_3718 | glutamine synthetase catalytic dom | 98.92 | 468 | BCG_2882c | glutamine synthetase | 78.96 | 457 | MAP2931c | GlnA4 | 461 | 100 |
| MAP4_0875 | amidotransferase | 254 | Rv2859c | Possible amidotransferase | 75.58 | 308 | Mb2884c | amidotransferase | 75.58 | 308 | MAV_3717 | class I glutamine amidotransferase, | 98.31 | 236 | BCG_2881c | amidotransferase | 75.58 | 308 | MAP2930c | hypothetical protein | 254 | 100 |
| MAP4_0876 | aldehyde dehydrogenase | 455 | Rv2858c | Probable aldehyde dehydrogenase A | 85.68 | 455 | Mb2883c | aldehyde dehydrogenase | 85.68 | 455 | MAV_2765 | P-cumic aldehyde dehydrogenase | 39.35 | 484 | BCG_2880c | aldehyde dehydrogenase aldC | 85.68 | 455 | MAP2929c | AldC | 455 | 100 |
| MAP4_0877 | short-chain type dehydrogenase reductase | 258 | Rv2857c | Probable short-chain type dehydrog | 87.21 | 258 | Mb2882c | short chain dehydrogenase | 87.21 | 258 | MAV_3714 | short chain dehydrogenase | 99.61 | 258 | BCG_2879c | short chain dehydrogenase | 87.21 | 258 | MAP2928c | short chain dehydrogenase | 258 | 100 |
| MAP4_0878 | PPE family protein | 312 | Rv1801 | PPE family protein PPE29 | 36.54 | 423 | Mb1829 | PPE family protein | 36.54 | 423 | MAV_3715 | PPE family protein | 97.73 | 309 | BCG_1833 | PPE family protein | 36.54 | 423 | MAP2927 | hypothetical protein | 312 | 100 |
| MAP4_0879 | hypothetical protein | 148 | Rv1592c | hypothetical protein | 36 | 446 | Mb1618c | hypothetical protein | 36 | 446 | MAV_3713 | hypothetical protein | 90 | 186 | BCG_1630c | hypothetical protein | 36 | 446 | MAP2926 | hypothetical protein | 148 | 100 |
| MAP4_0880 | type I phosphodiesterase nucleotide pyrophosphatase | 377 | Rv1426c | Probable esterase LipO | 42.31 | 420 | Mb1461c | esterase | 42.31 | 420 | MAV_3712 | type I phosphodiesterase / nucleot | 98.94 | 377 | BCG_1487c | esterase lipO | 42.31 | 420 | MAP2925 | hypothetical protein | 377 | 100 |
| MAP4_0881 | nickel-transport membrane protein | 381 | Rv2856 | Possible nickel-transport integral me | 75.13 | 372 | Mb2881 | nickel-transport integral mem | 75.13 | 372 | MAV_3711 | transition metal uptake transporte | 99.21 | 381 | BCG_2876 | nickel-transport integral memb | 75.13 | 372 | MAP2924 | NicT | 410 | 99.74 |
| MAP4_0882 | NADPH-dependent mycothiol reductase Mtr | 459 | Rv2855 | NADPH-dependent mycothiol reduc | 82.97 | 459 | Mb2880 | mycothione reductase | 82.97 | 459 | MAV_3710 | mycothione reductase | 99.35 | 459 | BCG_2875 | mycothione reductase | 82.97 | 459 | MAP2923 | mycothione reductase | 459 | 100 |
| MAP4_0883 | hypothetical protein | 344 | Rv2854 | hypothetical protein | 71.18 | 346 | Mb2879 | hypothetical protein | 71.18 | 346 | MAV_3709 | hypothetical protein | 99.11 | 336 | BCG_2874 | hypothetical protein | 71.18 | 346 | MAP2922 | hypothetical protein | 344 | 100 |
| MAP4_0884 | malate:quinone oxidoreductase | 501 | Rv2852c | Probable malate:quinone oxidoredu | 76.47 | 493 | Mb2877c | malate:quinone oxidoreducta | 76.47 | 493 | MAV_3708 | malate:quinone oxidoreductase | 99 | 501 | BCG_2872c | malate:quinone oxidoreducta | 76.47 | 493 | MAP2921c | malate:quinone oxidoreductase | 501 | 100 |
| MAP4_0885 | hypothetical protein | 156 | Rv2851c | GCN5-related N-acetyltransferase | 87.18 | 156 | Mb2876c | hypothetical protein | 87.18 | 156 | MAV_3707 | acetyltransferase, gnat family prote | 100 | 156 | BCG_2871c | hypothetical protein | 87.18 | 156 | MAP2920c | hypothetical protein | 156 | 100 |
| MAP4_0886 | magnesium chelatase | 613 | Rv2850c | Possible magnesium chelatase | 81.32 | 629 | Mb2875c | magnesium chelatase | 81 | 629 | MAV_3706 | chelatase | 99.35 | 613 | BCG_2870c | magnesium chelatase | 81 | 629 | MAP2919c | hypothetical protein | 613 | 100 |
| MAP4_0887 | cob(I)alamin adenosyltransferase CobO | 204 | Rv2849c | Probable cob(I)alamin adenosyltrans | 83.57 | 207 | Mb2874c | cob(I)yrinic acid a,c-diamide a | 83.09 | 207 | MAV_3705 | cob(I)yrinic acid a,c-diamide adeno | 99.02 | 204 | BCG_2869c | cob(I)yrinic acid a,c-diamide ad | 83.09 | 207 | MAP2918c | cob(I)yrinic acid a,c-diamide adenosyltr | 204 | 100 |
| MAP4_0888 | cobyrinic acid a,c-diamide synthase CobB | 470 | Rv2848c | Probable cobyrinic acid A,C-diamide | 79.63 | 457 | Mb2873c | cobyrinic acid a,c-diamide syr | 79.63 | 457 | MAV_3704 | cobyrinic acid a,c-diamide synthase | 97.66 | 470 | BCG_2868c | cobyrinic acid a,c-diamide synt | 79.63 | 457 | MAP2917c | cobyrinic acid a,c-diamide synthase | 470 | 99.79 |
| MAP4_0889 | multifunctional siroheme synthase CysG | 401 | Rv2847c | Possible multifunctional enzyme sirc | 88.64 | 405 | Mb2872c | multifunctional uroporphyrin | 88.64 | 405 | MAV_3703 | uroporphyrin-III C-methyltransfera | 100 | 401 | BCG_2867c | multifunctional enzyme sirohe | 88.64 | 405 | MAP2916c | CysG2 | 401 | 100 |
| MAP4_0890 | membrane efflux protein | 538 | Rv2846c | Possible integral membrane efflux p | 88.29 | 530 | Mb2871c | integral membrane efflux pro | 88.1 | 530 | MAV_3702 | transporter, major facilitator family | 100 | 538 | BCG_2866c | integral membrane efflux prote | 88.1 | 530 | MAP2915c | EfpA_2 | 538 | 100 |
| MAP4_0891 | putative enhanced intracellular survival protein | 412 | Rv2416c | Enhanced intracellular survival prote | 33.17 | 402 | Mb2439c | hypothetical protein | 32.92 | 408 | MAV_3701 | hypothetical protein | 99.51 | 412 | BCG_2432c | hypothetical protein | 33.17 | 408 | MAP2914c | hypothetical protein | 412 | 100 |
| MAP4_0892 | prolyl-tRNA synthetase | 582 | Rv2845c | Probable prolyl-tRNA synthetase Pro | 89.69 | 582 | Mb2870c | prolyl-tRNA synthetase | 89.35 | 582 | MAV_3700 | prolyl-tRNA synthetase | 99.83 | 582 | BCG_2865c | prolyl-tRNA synthetase | 89.35 | 582 | MAP2913c | prolyl-tRNA synthetase | 582 | 100 |
| MAP4_0893 | conserved alanine rich protein | 148 | Rv2844 | Conserved alanine rich protein | 76.03 | 162 | Mb2869 | hypothetical protein | 76.03 | 162 | MAV_3699 | hypothetical protein | 100 | 148 | BCG_2864 | hypothetical protein | 76.03 | 162 | MAP2912 | hypothetical protein | 148 | 100 |
| MAP4_0894 | conserved alanine rich membrane protein | 179 | Rv2843 | Probable conserved transmembrane | 67.21 | 181 | Mb2868 | hypothetical protein | 67.21 | 181 | MAV_3698 | hypothetical protein | 98.67 | 150 | BCG_2863 | transmembrane alanine rich pr | 67.21 | 181 | MAP2911 | hypothetical protein | 179 | 100 |
| MAP4_0895 | hypothetical protein | 178 | Rv2842c | hypothetical protein | 73.81 | 183 | Mb2867c | hypothetical protein | 73.81 | 183 | MAV_3696 | hypothetical protein | 99.44 | 178 | BCG_2862c | hypothetical protein | 73.81 | 183 | MAP2910c | hypothetical protein | 178 | 100 |
| MAP4_0896 | Transcription elongation factor NusA | 351 | Rv2841c | Probable N utilization substance pro | 92.02 | 347 | Mb2866c | transcription elongation facto | 92.02 | 347 | MAV_3695 | transcription elongation factor Nus | 99.72 | 351 | BCG_2861c | transcription elongation factor | 92.02 | 347 | MAP2909c | transcription elongation factor NusA | 351 | 100 |
| MAP4_0897 | hypothetical protein | 102 | Rv2840c | hypothetical protein | 78.26 | 99 | Mb2865c | hypothetical protein | 78.26 | 99 | MAV_3694 | hypothetical protein | 98.81 | 84 | BCG_2860c | hypothetical protein | 78.26 | 99 | MAP2908c | hypothetical protein | 102 | 100 |
| MAP4_0898 | translation initiation factor IF-2 | 925 | Rv2839c | Probable translation initiation factor | 62.16 | 900 | Mb2864c | translation initiation factor IF | 62.16 | 900 | MAV_3693 | translation initiation factor IF-2 | 98.28 | 914 | BCG_2859c | translation initiation factor IF-2 | 62.16 | 900 | MAP2907c | translation initiation factor IF-2 | 925 | 100 |
| MAP4_0899 | ribosome-binding factor A | 162 | Rv2838c | Probable ribosome-binding factor a | 78.23 | 183 | Mb2863c | ribosome-binding factor A | 78.23 | 183 | MAV_3692 | ribosome-binding factor A | 100 | 162 | BCG_2858c | ribosome-binding factor A | 78.23 | 183 | MAP2906c | ribosome-binding factor A | 162 | 100 |
| MAP4_0900 | hypothetical protein | 331 | Rv2837c | hypothetical protein | 76.85 | 336 | Mb2862c | hypothetical protein | 76.85 | 336 | MAV_3691 | DHH family protein | 99.37 | 317 | BCG_2857c | hypothetical protein | 76.85 | 336 | MAP2905c | hypothetical protein | 331 | 100 |
| MAP4_0901 | hypothetical protein | 188 | Rv2903c | Probable signal peptidase I LepB (SP | 29.51 | 294 | Mb2927c | signal peptidase I LepB | 29.51 | 294 | MAV_3690 | hypothetical protein | 98.4 | 188 | BCG_2924c | signal peptidase I lepB | 29.51 | 294 | MAP0282c | hypothetical protein | 263 | 43.01 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_0902 | enoyl-CoA hydratase | 249 | Rv2831 | Probable enoyl-CoA hydratase EchA | 88.35 | 249 | Mb2855 | enoyl-CoA hydratase | 87.95 | 249 | MAV_3689 | enoyl-CoA hydratase | 99.2 | 249 | BCG_2851 | enoyl-CoA hydratase | 88.35 | 249 | MAP2904 | enoyl-CoA hydratase | 249 | 100 |
| MAP4_0903 | hypothetical protein | 89 | Rv2828A | hypothetical protein | 83.15 | 89 | Mb0813c | hypothetical protein | 38.89 | 199 | MAV_3688 | hypothetical protein | 95.51 | 89 | BCG_2848c | hypothetical protein | 83.15 | 89 | MAP1566 | hypothetical protein | 357 | 24.71 |
| MAP4_0904 | hypothetical protein | 186 | Rv2828c | hypothetical protein | 81.67 | 181 | Mb2852c | hypothetical protein | 81.11 | 181 | MAV_3686 | hypothetical protein | 98.92 | 186 | BCG_2847c | hypothetical protein | 81.67 | 181 | MAP2903c | hypothetical protein | 186 | 100 |
| MAP4_0905 | hydrolase | 575 | Rv2800 | Possible hydrolase | 71.17 | 549 | Mb2823 | hydrolase | 71.17 | 549 | MAV_3687 | hydrolase CocE/NonD family protei | 99.3 | 575 | BCG_2818 | hydrolase | 71.17 | 549 | MAP2902 | hypothetical protein | 575 | 100 |
| MAP4_0906 | membrane protein | 196 | Rv2799 | Probable membrane protein | 73.1 | 209 | Mb2822 | hypothetical protein | 73.23 | 210 | MAV_3685 | hypothetical protein | 99.49 | 196 | BCG_2817 | hypothetical protein | 73.1 | 209 | MAP2901 | hypothetical protein | 217 | 99.49 |
| MAP4_0907 | hypothetical protein | 329 | Rv2795c | hypothetical protein | 88.75 | 324 | Mb2818c | hypothetical protein | 88.75 | 324 | MAV_3684 | metallophosphoesterase | 99.38 | 321 | BCG_2813c | hypothetical protein | 88.75 | 324 | MAP2900c | hypothetical protein | 329 | 100 |
| MAP4_0908 | putative phosphopantetheinyl transferase family prote | 225 | Rv2794c | Phosphopantetheinyl transferase Pp | 80.44 | 227 | Mb2817c | hypothetical protein | 80.89 | 227 | MAV_3683 | Sfp-type phosphopantetheinyl tran | 99.11 | 225 | BCG_2812c | hypothetical protein | 80.89 | 227 | MAP2899c | hypothetical protein | 225 | 100 |
| MAP4_0909 | tRNA pseudouridine synthase B | 293 | Rv2793c | Probable tRNA pseudouridine synth | 75.86 | 298 | Mb2816c | tRNA pseudouridine synthase | 75.86 | 298 | MAV_3682 | tRNA pseudouridine synthase B | 94.41 | 309 | BCG_2811c | tRNA pseudouridine synthase E | 75.86 | 298 | MAP2898c | tRNA pseudouridine synthase B | 293 | 100 |
| MAP4_0910 | lipid-transfer protein | 396 | Rv2790c | Probable lipid-transfer protein Ltp1 | 86.84 | 401 | Mb2813c | lipid-transfer protein | 86.84 | 401 | MAV_3681 | lipid-transfer protein | 99.24 | 396 | BCG_2808c | lipid-transfer protein | 86.84 | 401 | MAP2897c | lipid-transfer protein | 396 | 100 |
| MAP4_0911 | acyl-CoA dehydrogenase | 418 | Rv2789c | Probable acyl-CoA dehydrogenase F | 80.77 | 410 | Mb2812c | acyl-CoA dehydrogenase | 80.77 | 410 | MAV_3680 | acyl-CoA dehydrogenase | 98.8 | 418 | BCG_2807c | acyl-CoA dehydrogenase fadE2 | 80.77 | 410 | MAP2896c | FadE21 | 418 | 100 |
| MAP4_0914 | bifunctional FAD synthetase riboflavin biosynthesis pro | 324 | Rv2786c | Probable bifunctional FAD synthetas | 91.36 | 331 | Mb2809c | bifunctional riboflavin kinase/ | 91.36 | 331 | MAV_3678 | bifunctional riboflavin kinase/FMN | 99.67 | 307 | BCG_2804c | bifunctional riboflavin kinase/F | 91.36 | 331 | MAP2893c | bifunctional riboflavin kinase/FMN ader | 327 | 99.69 |
| MAP4_0915 | 30S ribosomal protein S15 | 89 | Rv2785c | 30S ribosomal protein S15 RpsO | 91.01 | 89 | Mb2808c | 30S ribosomal protein S15 | 91.01 | 89 | MAV_3677 | 30S ribosomal protein S15 | 100 | 89 | BCG_2803c | 30S ribosomal protein S15 | 91.01 | 89 | MAP2892c | 30S ribosomal protein S15 | 89 | 100 |
| MAP4_0916 | bifunctional polyribonucleotide nucleotidyl transferase | 757 | Rv2783c | Bifunctional protein polyribonucleot | 90.48 | 752 | Mb2806c | polynucleotide phosphorylase | 90.48 | 752 | MAV_3676 | polynucleotide phosphorylase/poly | 99.73 | 748 | BCG_2801c | polynucleotide phosphorylase | 90.48 | 752 | MAP2891c | polynucleotide phosphorylase/polyader | 757 | 100 |
| MAP4_0917 | zinc protease PepR | 440 | Rv2782c | Probable zinc protease PepR | 85.55 | 438 | Mb2805c | zinc protease PEPR | 85.55 | 438 | MAV_3675 | protease | 99.09 | 457 | BCG_2800c | zinc protease pepR | 85.55 | 438 | MAP2890c | PepR | 440 | 100 |
| MAP4_0918 | alanine rich oxidoreductase | 341 | Rv2781c | Possible alanine rich oxidoreductase | 78.04 | 344 | Mb2804c | oxidoreductase | 78.04 | 344 | MAV_3673 | dioxygenase | 95.89 | 330 | BCG_2799c | alanine rich oxidoreductase | 78.04 | 344 | MAP2889c | hypothetical protein | 341 | 100 |
| MAP4_0919 | 40 kda secreted L-alanine dehydrogenase Ald | 373 | Rv2780 | Secreted L-alanine dehydrogenase A | 83.24 | 371 | Mb2803 | L-alanine dehydrogenase | 83.19 | 239 | MAV_3674 | alanine dehydrogenase | 98.93 | 373 | BCG_2798 | L-alanine dehydrogenase | 83.19 | 239 | MAP2888 | hypothetical protein | 373 | 100 |
| MAP4_0920 | hypothetical protein | 153 | Rv2778c | hypothetical protein | 71.81 | 156 | Mb2800c | hypothetical protein | 71.81 | 156 | MAV_3672 | hypothetical protein | 98.69 | 153 | BCG_2795c | hypothetical protein | 71.81 | 156 | MAP2887c | hypothetical protein | 153 | 100 |
| MAP4_0921 | metal-dependent hydrolase family protein | 302 | Rv2777c | hypothetical protein | 74.75 | 356 | Mb2799c | hypothetical protein | 74.75 | 356 | MAV_3671 | FF domain-containing protein | 98.68 | 302 | BCG_2794c | hypothetical protein | 74.75 | 356 | MAP2886c | hypothetical protein | 302 | 100 |
| MAP4_0922 | short chain dehydrogenase | 594 | Rv2214c | Possible short-chain dehydrogenase | 36.83 | 592 | Mb2237c | short chain dehydrogenase | 36.83 | 592 | MAV_3670 | short chain dehydrogenase | 98.15 | 594 | BCG_2230c | short chain dehydrogenase | 36.83 | 592 | MAP2885c | short chain dehydrogenase | 594 | 100 |
| MAP4_0923 | oxidoreductase | 366 | Rv2776c | Probable oxidoreductase | 80.58 | 309 | Mb2798c | oxidoreductase | 80.58 | 309 | MAV_3669 | oxidoreductase | 98.63 | 366 | BCG_2793c | oxidoreductase | 80.58 | 309 | MAP2884c | hypothetical protein | 366 | 100 |
| MAP4_0924 | hypothetical protein | 216 | Rv0302 | Probable transcriptional regulatory p | 29.58 | 210 | Mb0310 | TetR/ACRR family transcriptio | 29.58 | 210 | MAV_3668 | hypothetical protein | 100 | 191 | BCG_0342 | TetR family transcriptional regu | 29.58 | 210 | MAP2883 | hypothetical protein | 216 | 100 |
| MAP4_0925 | putative oxidoreductase, rieske (2Fe-2S) domain-conta | 331 | Rv3526 | Oxygenase component of 3-ketoster | 24.92 | 386 | Mb3556 | oxidoreductase | 24.92 | 386 | MAV_3666 | Rieske (2Fe-2S) domain-containing | 99.7 | 331 | BCG_3590 | oxidoreductase | 24.92 | 386 | MAP2882c | hypothetical protein | 353 | 100 |
| MAP4_0926 | hypothetical protein | 360 | Rv0926c | hypothetical protein | 28.65 | 358 | Mb0949c | hypothetical protein | 28.65 | 358 | MAV_3665 | dihydrodipicolinate reductase N-te | 99.44 | 360 | BCG_0978c | hypothetical protein | 28.65 | 358 | MAP2881c | hypothetical protein | 360 | 100 |
| MAP4_0927 | REP13E12 repeat protein | 451 | Rv1128c | hypothetical protein | 49.77 | 451 | Mb1159c | hypothetical protein | 49.77 | 451 | MAV_3664 | hypothetical protein | 97.12 | 451 | BCG_1189c | hypothetical protein | 49.77 | 451 | MAP2880 | hypothetical protein | 451 | 100 |
| MAP4_0928 | hypothetical protein | 186 | Rv0519c | Possible conserved membrane prote | 23.08 | 300 | Mb0532c | hypothetical protein | 23.08 | 300 | MAV_3663 | hypothetical protein | 98.39 | 186 | BCG_0562c | hypothetical protein | 23.08 | 300 | MAP2879c | hypothetical protein | 186 | 100 |
| MAP4_0929 | dihydrodipicolinate reductase | 245 | Rv2773c | Dihydrodipicolinate reductase DapB | 90.57 | 245 | Mb2795c | dihydrodipicolinate reductase | 89.75 | 245 | MAV_3662 | dihydrodipicolinate reductase | 99.18 | 245 | BCG_2790c | dihydrodipicolinate reductase | 90.16 | 245 | MAP2878c | dihydrodipicolinate reductase | 245 | 100 |
| MAP4_0930 | hypothetical protein | 151 | Rv2772c | Probable conserved transmembrane | 74.5 | 157 | Mb2794c | transmembrane protein | 74.5 | 157 | MAV_3661 | TPR repeat-containing protein | 99.34 | 151 | BCG_2789c | hypothetical protein | 74.5 | 157 | MAP2877c | hypothetical protein | 151 | 100 |
| MAP4_0931 | hypothetical protein | 155 | Rv2771c | hypothetical protein | 83.78 | 150 | Mb2793c | hypothetical protein | 83.78 | 150 | MAV_3660 | multimeric flavodoxin WrbA | 100 | 155 | BCG_2788c | hypothetical protein | 83.78 | 150 | MAP2876c | hypothetical protein | 155 | 100 |
| MAP4_0932 | putative thioesterase-like superfamily protein | 277 | Rv0499 | hypothetical protein | 36.96 | 291 | Mb0510 | hypothetical protein | 36.96 | 291 | MAV_3659 | hypothetical protein | 98.19 | 277 | BCG_0541 | hypothetical protein | 36.96 | 291 | MAP2875 | hypothetical protein | 280 | 99.64 |
| MAP4_0933 | fatty-acid-CoA ligase | 510 | Rv3089 | Probable chain-fatty-acid-CoA ligase | 35.2 | 503 | Mb3116 | chain-fatty-acid-CoA ligase | 35.2 | 503 | MAV_3658 | acyl-CoA dehydrogenase | 99.02 | 510 | BCG_3114 | chain-fatty-acid-CoA ligase fad | 35.2 | 503 | MAP2874c | FadD13 | 510 | 100 |
| MAP4_0934 | putative carbamoyl-phosphate synthasecarboxyl transf | 1075 | Rv2501c | Probable acetyl-/propionyl-coenzym | 43.15 | 654 | Mb2529c | acetyl-/propionyl-coenzyme A | 43.15 | 654 | MAV_3657 | carbamoyl-phosphate synthase/car | 98.88 | 1075 | BCG_2521c | acetyl-/propionyl-coenzyme A | 43.15 | 654 | MAP2873c | hypothetical protein | 1075 | 100 |
| MAP4_0935 | hypothetical protein | 108 | Rv3878 | ESX-1 secretion-associated protein E | 32.08 | 280 | Mb3908 | hypothetical protein | 32.08 | 280 | MAV_3656 | hypothetical protein | 100 | 108 | BCG_3588 | hypothetical protein | 34.21 | 343 | | | | |
| MAP4_0936 | short-chain type dehydrogenase reductase | 259 | Rv2766c | Probable short-chain type dehydrog | 87.55 | 260 | Mb2788c | 3-ketoacyl-ACP reductase | 87.55 | 260 | MAV_3655 | 3-ketoacyl-(acyl-carrier-protein) re | 99.61 | 259 | BCG_2783c | 3-ketoacyl-ACP reductase | 87.55 | 260 | MAP2872c | 3-ketoacyl-ACP reductase | 259 | 100 |
| MAP4_0937 | putative glycosyl transferase family protein | 405 | Rv1524 | Probable glycosyltransferase | 27.01 | 414 | Mb1551 | glycosyltransferase | 27.01 | 414 | MAV_3653 | glycosyltransferase GtfE | 95.7 | 409 | BCG_1576 | glycosyltransferase | 27.01 | 414 | MAP2871c | hypothetical protein | 405 | 100 |
| MAP4_0938 | alanine rich hydrolase | 246 | Rv2765 | Probable alanine rich hydrolase | 73.36 | 245 | Mb2787 | hypothetical protein | 73.36 | 245 | MAV_3654 | hydrolase | 99.59 | 246 | BCG_2782 | alanine rich hydrolase | 72.95 | 245 | MAP2870 | hypothetical protein | 246 | 100 |
| MAP4_0939 | thymidylate synthase | 266 | Rv2764c | Probable thymidylate synthase ThyA | 91.6 | 263 | Mb2786c | thymidylate synthase | 91.6 | 263 | MAV_3652 | thymidylate synthase | 99.62 | 266 | BCG_2781c | thymidylate synthase | 91.6 | 263 | MAP2869c | thymidylate synthase | 266 | 100 |
| MAP4_0940 | dihydrofolate reductase | 181 | Rv2763c | Dihydrofolate reductase DfrA (DHFR | 70.19 | 159 | Mb2785c | dihydrofolate reductase | 70.19 | 159 | MAV_3651 | dihydrofolate reductase | 98.3 | 176 | BCG_2780c | dihydrofolate reductase dfrA | 70.19 | 159 | MAP2868c | DfrA | 181 | 100 |
| MAP4_0941 | hypothetical protein | 244 | Rv1682 | Probable coiled-coil structural prote | 40.08 | 305 | Mb1709 | coiled-coil structural protein | 40.08 | 305 | MAV_3650 | hypothetical protein | 99.59 | 244 | BCG_1720 | coiled-coil structural protein | 40.08 | 305 | MAP2867c | hypothetical protein | 246 | 99.59 |
| MAP4_0942 | hypothetical protein | 412 | Rv2762c | hypothetical protein | 59.52 | 139 | Mb2783c | hypothetical protein | 59.52 | 90 | MAV_3649 | type I restriction-modification enzy | 100 | 335 | BCG_2778c | hypothetical protein | 59.52 | 90 | MAP2866c | hypothetical protein | 412 | 100 |
| MAP4_0943 | thymidylate synthase ThyX | 250 | Rv2754c | Probable thymidylate synthase ThyX | 91.2 | 250 | Mb2775c | FAD-dependent thymidylate s | 91.2 | 250 | MAV_3645 | FAD-dependent thymidylate syntha | 100 | 250 | BCG_2770c | FAD-dependent thymidylate sy | 91.2 | 250 | MAP2865c | FAD-dependent thymidylate synthase | 250 | 100 |
| MAP4_0944 | dihydrodipicolinate synthase | 300 | Rv2753c | Probable dihydrodipicolinate syntha | 88.67 | 300 | Mb2774c | dihydrodipicolinate synthase | 88.67 | 300 | MAV_3644 | dihydrodipicolinate synthase | 99.67 | 300 | BCG_2769c | dihydrodipicolinate synthase | 88.67 | 300 | MAP2864c | dihydrodipicolinate synthase | 300 | 100 |
| MAP4_0945 | putative hydrolase of themetallo-beta-lactamase super | 558 | Rv2752c | hypothetical protein | 89.07 | 558 | Mb2773c | hypothetical protein | 89.07 | 558 | MAV_3643 | hydrolase of the metallo-beta-lacta | 99.82 | 558 | BCG_2768c | hypothetical protein | 89.07 | 558 | MAP2863c | hypothetical protein | 558 | 100 |
| MAP4_0946 | putative methyltransferase family protein | 290 | Rv2751 | hypothetical protein | 83.45 | 296 | Mb2772 | hypothetical protein | 83.45 | 296 | MAV_3642 | methyltransferase, putative, family | 99.64 | 277 | BCG_2767 | hypothetical protein | 83.45 | 296 | MAP2862 | hypothetical protein | 290 | 100 |
| MAP4_0947 | dehydrogenase | 276 | Rv2750 | Probable dehydrogenase | 76.95 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 76.95 | 272 | MAV_3641 | 3-ketoacyl-(acyl-carrier-protein) re | 99.28 | 276 | BCG_2766 | 3-ketoacyl-ACP reductase | 76.95 | 272 | MAP2861 | 3-ketoacyl-ACP reductase | 276 | 100 |
| MAP4_0948 | antibiotic biosynthesis monooxygenase domain-contai | 104 | Rv2749 | hypothetical protein | 82.52 | 104 | Mb2770 | hypothetical protein | 82.52 | 104 | MAV_3640 | antibiotic biosynthesis monooxyge | 99.04 | 104 | BCG_2765 | hypothetical protein | 82.52 | 104 | MAP2860 | hypothetical protein | 104 | 100 |
| MAP4_0949 | cell division transmembrane protein FtsK | 895 | Rv2748c | Possible cell division transmembran | 77.8 | 883 | Mb2769c | DNA translocase FtsK | 77.8 | 883 | MAV_3639 | FtsK/SpoIIIE family protein | 99.74 | 775 | BCG_2764c | cell division transmembrane pr | 77.8 | 883 | MAP2859c | hypothetical protein | 895 | 100 |
| MAP4_0950 | transferase | 174 | Rv2747 | Probable L-glutamate alpha-N-acety | 89.66 | 174 | Mb2768 | N-acetylglutamate synthase | 89.66 | 174 | MAV_3638 | N-acetylglutamate synthase | 100 | 174 | BCG_2763 | N-acetylglutamate synthase | 89.66 | 174 | MAP2858 | N-acetylglutamate synthase | 174 | 100 |
| MAP4_0951 | phosphatidylglycerophosphate synthase PgsA3 | 199 | Rv2746c | Probable PGP synthase PgsA3 (CDP- | 74.87 | 209 | Mb2767c | CDP-diacylglycerol--glycerol-3 | 74.87 | 209 | MAV_3637 | CDP-diacylglycerol--glycerol-3-phos | 100 | 190 | BCG_2762c | pgp synthase pgsA3 | 74.87 | 209 | MAP2857c | hypothetical protein | 199 | 100 |
| MAP4_0952 | transcriptional regulatory protein | 108 | Rv2745c | Transcriptional regulatory protein Cl | 75 | 112 | Mb2766c | transcriptional regulator | 75 | 112 | MAV_3636 | DNA-binding protein | 100 | 108 | BCG_2761c | transcriptional regulatory prote | 75 | 112 | MAP2856c | hypothetical protein | 108 | 100 |
| MAP4_0953 | conserved alanine rich protein | 275 | Rv2744c | Conserved 35 kDa alanine rich prote | 87.32 | 270 | Mb2765c | hypothetical protein | 86.96 | 270 | MAV_3635 | 35kd antigen | 99.27 | 275 | BCG_2760c | hypothetical protein | 87.32 | 270 | MAP2855c | hypothetical protein | 275 | 100 |
| MAP4_0954 | conserved alanine rich membrane protein | 269 | Rv2743c | Possible conserved transmembrane | 74.53 | 270 | Mb2764c | hypothetical protein | 74.53 | 270 | MAV_3634 | hypothetical protein | 98.51 | 269 | BCG_2759c | membrane alanine rich protein | 74.53 | 270 | MAP2854c | hypothetical protein | 269 | 100 |
| MAP4_0955 | conserved arginine rich protein | 141 | Rv2742c | Conserved hypothetical arginine rich | 71.56 | 277 | Mb2763c | hypothetical protein | 71.56 | 195 | MAV_3632 | hypothetical protein | 97.64 | 170 | BCG_2758c | hypothetical protein | 71.56 | 195 | MAP2853c | hypothetical protein | 141 | 100 |
| MAP4_0956 | hypothetical protein | 143 | Rv2740 | Epoxide hydrolase | 65.1 | 149 | Mb2760 | hypothetical protein | 65.1 | 149 | MAV_3633 | hypothetical protein | 99.3 | 143 | BCG_2754 | epoxide hydrolase | 65.1 | 149 | MAP2852 | hypothetical protein | 143 | 100 |
| MAP4_0957 | alanine rich transferase | 386 | Rv2739c | Possible alanine rich transferase | 83.64 | 388 | Mb2759c | transferase | 83.64 | 388 | MAV_3631 | hypothetical protein | 98.45 | 386 | BCG_2753c | alanine rich transferase | 83.64 | 388 | MAP2851c | hypothetical protein | 386 | 100 |
| MAP4_0958 | hypothetical protein | 94 | Rv3333c | Hypothetical proline rich protein | 66.67 | 281 | Mb3366c | hypothetical protein | 66.67 | 281 | MAV_3630 | hypothetical protein | 100 | 94 | BCG_3403c | hypothetical protein | 66.67 | 281 | MAP3461 | hypothetical protein | 203 | 40 |
| MAP4_0959 | hypothetical protein | 68 | Rv2738c | hypothetical protein | 79.41 | 68 | Mb2758c | hypothetical protein | 79.41 | 68 | MAV_3629 | hypothetical protein | 100 | 64 | BCG_2752c | hypothetical protein | 79.41 | 68 | MAP2850c | hypothetical protein | 68 | 100 |
| MAP4_0960 | hypothetical protein | 218 | Rv2737A | Conserved hypothetical cysteine rich | 58.93 | 57 | Mb2757 | hypothetical protein | 58.93 | 57 | MAV_3628 | hypothetical protein | 98.62 | 262 | BCG_2751 | hypothetical protein | 58.93 | 57 | MAP2849 | hypothetical protein | 218 | 100 |
| MAP4_0961 | DNA recombination protein | 350 | Rv2737c | RecA protein (recombinase A) [conta | 96.03 | 790 | Mb2756c | DNA recombination protein R | 96.03 | 790 | MAV_3627 | recombinase A | 100 | 350 | BCG_2750c | DNA recombination protein Re | 96.03 | 790 | MAP2848c | recombinase A | 409 | 100 |
| MAP4_0962 | recombination regulator RecX | 173 | Rv2736c | Regulatory protein RecX | 79.55 | 174 | Mb2755c | recombination regulator RecX | 79.55 | 174 | MAV_3626 | recombination regulator RecX | 99.42 | 173 | BCG_2749c | recombination regulator RecX | 79.55 | 174 | MAP2847c | recombination regulator RecX | 173 | 100 |
| MAP4_0963 | conserved alanine and arginine rich protein | 517 | Rv2733c | Conserved hypothetical alanine, arg | 88.73 | 512 | Mb2752c | (dimethylallyl)adenosine tRN | 88.73 | 512 | MAV_3625 | hypothetical protein | 98.91 | 688 | BCG_2746c | (dimethylallyl)adenosine tRNA | 88.73 | 512 | MAP2846c | (dimethylallyl)adenosine tRNA methylth | 517 | 100 |
| MAP4_0964 | hypothetical protein | 202 | Rv2732c | Probable conserved transmembrane | 73.98 | 204 | Mb2751c | transmembrane protein | 73.98 | 204 | MAV_3625 | hypothetical protein | 98.02 | 688 | BCG_2745c | hypothetical protein | 73.98 | 204 | MAP2845c | hypothetical protein | 202 | 100 |
| MAP4_0965 | conserved alanine and arginine rich protein | 468 | Rv2731 | Conserved alanine and arginine rich | 79.38 | 450 | Mb2750 | hypothetical protein | 79.38 | 450 | MAV_3624 | hypothetical protein | 99.52 | 419 | BCG_2744 | hypothetical protein | 79.38 | 450 | MAP2844 | hypothetical protein | 468 | 100 |
| MAP4_0966 | conserved alanine, valine and leucine rich membrane p | 328 | Rv2729c | Probable conserved integral membr | 52.16 | 301 | Mb2748c | hypothetical protein | 52.94 | 301 | MAV_3622 | hypothetical protein | 99.7 | 328 | BCG_2742c | integral membrane alanine and | 52.94 | 301 | MAP2843c | hypothetical protein | 328 | 100 |
| MAP4_0967 | conserved alanine rich protein | 232 | Rv2728c | Conserved alanine rich protein | 66.67 | 231 | Mb2747c | hypothetical protein | 66.67 | 231 | MAV_3621 | hypothetical protein | 98.28 | 232 | BCG_2741c | hypothetical protein | 66.67 | 231 | MAP2842c | hypothetical protein | 232 | 100 |
| MAP4_0968 | tRNA delta(2)-isopentenyl pyrophosphate transferase | 314 | Rv2727c | Probable tRNA delta(2)-isopentenylp | 82.48 | 314 | Mb2746c | tRNA delta(2)-isopentenylpyr | 82.48 | 314 | MAV_3620 | tRNA delta(2)-isopentenylpyrophos | 98.05 | 307 | BCG_2740c | tRNA delta(2)-isopentenylpyro | 82.48 | 314 | MAP2841c | tRNA delta(2)-isopentenylpyrophosphat | 314 | 100 |
| MAP4_0969 | diaminopimelate epimerase | 294 | Rv2726c | Probable diaminopimelate epimeras | 79.31 | 289 | Mb2745c | diaminopimelate epimerase | 79.31 | 289 | MAV_3619 | diaminopimelate epimerase | 96.6 | 294 | BCG_2739c | diaminopimelate epimerase | 79.31 | 289 | MAP2840c | diaminopimelate epimerase | 294 | 100 |
| MAP4_0970 | GTP-binding protein HflX | 482 | Rv2725c | Probable GTP-binding protein HflX | 87.08 | 495 | Mb2744c | GTP-binding protein HflX | 87.08 | 495 | MAV_3618 | GTPase | 99.59 | 482 | BCG_2738c | GTP-binding protein hflX | 86.88 | 495 | MAP2839c | hypothetical protein | 482 | 100 |
| MAP4_0974 | conserved alanine and glycine rich membrane protein | 733 | Rv2721c | Possible conserved transmembrane | 59.87 | 699 | Mb2740c | hypothetical protein | 59.87 | 699 | MAV_3615 | hypothetical protein | 97.95 | 735 | BCG_2734c | transmembrane alanine and gl | 59.61 | 699 | MAP2837c | hypothetical protein | 786 | 100 |
| MAP4_0975 | SOS-response repressor LexA | 232 | Rv2720 | Repressor LexA | 88.14 | 236 | Mb2739 | LexA repressor | 90.78 | 217 | MAV_3614 | LexA repressor | 99.14 | 232 | BCG_2733 | LexA repressor | 90.78 | 217 | MAP2836 | LexA repressor | 217 | 99.54 |
| MAP4_0976 | hypothetical protein | 164 | Rv2719c | Possible conserved membrane prote | 59.38 | 165 | Mb2738c | hypothetical protein | 59.38 | 165 | MAV_3613 | LysM domain-containing protein | 98.17 | 164 | BCG_2732c | hypothetical protein | 59.38 | 165 | MAP2835c | hypothetical protein | 170 | 100 |
| MAP4_0977 | transcriptional regulator | 154 | Rv2718c | Probable transcriptional regulatory p | 92.72 | 154 | Mb2737c | transcriptional regulator NrdR | 92.72 | 154 | MAV_3612 | NrdR family transcriptional regulat | 100 | 154 | BCG_2731c | transcriptional regulator NrdR | 92.72 | 154 | MAP2834c | transcriptional regulator NrdR | 154 | 100 |
| MAP4_0978 | hypothetical protein | 161 | Rv2717c | hypothetical protein | 75.61 | 164 | Mb2736c | hypothetical protein | 75.61 | 164 | MAV_3611 | hypothetical protein | 98.14 | 161 | BCG_2730c | hypothetical protein | 75.61 | 164 | MAP2833c | hypothetical protein | 161 | 100 |
| MAP4_0979 | putative phenazine biosynthesis-like protein Phz C-Phz | 228 | Rv2716 | hypothetical protein | 75.44 | 228 | Mb2735 | hypothetical protein | 75.44 | 228 | MAV_3610 | thymidylate synthase | 92.98 | 217 | BCG_2729 | hypothetical protein | 75.44 | 228 | MAP1610 | hypothetical protein | 194 | 32.31 |
| MAP4_0980 | putative hydrolase, alphabeta fold family | 343 | Rv2715 | Possible hydrolase | 84.84 | 341 | Mb2734 | hydrolase | 84.84 | 341 | MAV_3609 | hydrolase | 99.71 | 343 | BCG_2728 | hydrolase | 84.84 | 341 | MAP2832 | hypothetical protein | 343 | 100 |
| MAP4_0981 | conserved alanine and leucine rich protein | 323 | Rv2714 | Conserved alanine and leucine rich p | 90.48 | 324 | Mb2733 | hypothetical protein | 91.11 | 324 | MAV_3608 | hypothetical protein | 99.69 | 324 | BCG_2727 | hypothetical protein | 91.11 | 324 | MAP2831 | hypothetical protein | 323 | 100 |
| MAP4_0982 | hypothetical protein | 278 | Rv3237c | hypothetical protein | 32.99 | 160 | Mb3265c | hypothetical protein | 32.99 | 160 | MAV_3607 | hypothetical protein | 99.28 | 278 | BCG_3266c | hypothetical protein | 32.99 | 160 | MAP2830c | hypothetical protein | 278 | 100 |
| MAP4_0983 | soluble pyridine nucleotide transhydrogenase SthA | 471 | Rv2713 | Probable soluble pyridine nucleotide | 91.65 | 468 | Mb2732 | soluble pyridine nucleotide tr | 91.65 | 468 | MAV_3606 | soluble pyridine nucleotide transhy | 100 | 471 | BCG_2726 | soluble pyridine nucleotide tra | 91.65 | 468 | MAP2829 | soluble pyridine nucleotide transhydrog | 471 | 100 |
| MAP4_0984 | hypothetical protein | 353 | Rv2712c | Hypothetical protein | 74.22 | 352 | Mb2731c | hypothetical protein | 74.22 | 352 | MAV_3605 | hypothetical protein | 100 | 353 | BCG_2725c | hypothetical protein | 74.22 | 352 | MAP2828c | hypothetical protein | 353 | 100 |
| MAP4_0985 | iron-dependent repressor and activator IdeR | 229 | Rv2711 | Iron-dependent repressor and activa | 93.04 | 230 | Mb2730 | IRON-dependent repressor ar | 93.04 | 230 | MAV_3604 | iron-dependent repressor IdeR | 99.56 | 229 | BCG_2724 | Iron-dependent repressor and | 93.04 | 230 | MAP2895 | hypothetical protein | 149 | 40.68 |
| MAP4_0986 | RNA polymerase sigma factor SigB | 332 | Rv2710 | RNA polymerase sigma factor SigB | 96.88 | 323 | Mb2729 | RNA polymerase sigma factor | 96.88 | 323 | MAV_3603 | RNA polymerase sigma factor SigB | 100 | 319 | BCG_2723 | RNA polymerase sigma factor S | 96.88 | 323 | MAP2826 | RNA polymerase sigma factor SigB | 332 | 100 |
| MAP4_0987 | hypothetical protein | 153 | Rv2709 | Probable conserved transmembrane | 72.22 | 148 | Mb2728 | transmembrane protein | 71.53 | 148 | MAV_3602 | hypothetical protein | 100 | 147 | BCG_2722 | hypothetical protein | 71.53 | 148 | MAP2825 | hypothetical protein | 153 | 100 |
| MAP4_0988 | hypothetical protein | 79 | Rv2708c | hypothetical protein | 89.87 | 82 | Mb2727c | hypothetical protein | 89.87 | 82 | MAV_3601 | hypothetical protein | 100 | 79 | BCG_2721c | hypothetical protein | 89.87 | 82 | MAP2824c | hypothetical protein | 79 | 100 |
| MAP4_0989 | conserved alanine and leucine rich membrane protein | 333 | Rv2707 | Probable conserved transmembrane | 83.06 | 324 | Mb2726 | hypothetical protein | 83.06 | 324 | MAV_3600 | hypothetical protein | 99.7 | 333 | BCG_2720 | transmembrane alanine and le | 83.06 | 324 | MAP2823 | hypothetical protein | 333 | 100 |
| MAP4_0990 | hypothetical protein | 116 | Rv3395A | Probable membrane protein | 44.44 | 208 | Mb3428 | hypothetical protein | 44.44 | 208 | MAV_1834 | acetyl-CoA hydrolase/transferase | 40 | 396 | BCG_3465 | hypothetical protein | 44.44 | 208 | MAP2822 | hypothetical protein | 116 | 100 |
| MAP4_0991 | putative endoribonuclease L-PSPdomain-containing pr | 135 | Rv2704 | hypothetical protein | 76.8 | 142 | Mb2723 | hypothetical protein | 76.8 | 142 | MAV_3598 | endoribonuclease L-PSP | 96.12 | 129 | BCG_2717 | hypothetical protein | 76.8 | 142 | MAP2821 | hypothetical protein | 135 | 100 |
| MAP4_0992 | RNA polymerase sigma factor SigA | 509 | Rv2703 | RNA polymerase sigma factor SigA (s | 80.64 | 528 | Mb2722 | RNA polymerase sigma factor | 80.64 | 528 | MAV_3595 | RNA polymerase sigma factor | 99.19 | 496 | BCG_2716 | RNA polymerase sigma factor | 80.64 | 528 | MAP2820 | RNA polymerase sigma factor | 509 | 99.8 |
| MAP4_0993 | polyphosphate glucokinase PpgK | 268 | Rv2702 | Polyphosphate glucokinase PpgK (pc | 79.55 | 265 | Mb2721 | polyphosphate glucokinase | 79.93 | 265 | MAV_3594 | polyphosphate glucokinase | 100 | 268 | BCG_2715 | polyphosphate glucokinase pp | 79.93 | 265 | MAP2819 | PpgK | 268 | 100 |
| MAP4_0994 | extragenic suppressor protein SuhB | 292 | Rv2701c | Inositol-1-monophosphatase SuhB | 73.81 | 290 | Mb2720c | extragenic suppressor protein | 73.81 | 290 | MAV_3593 | inositol-1-monophosphatase | 99.3 | 284 | BCG_2714c | extragenic suppressor protein | 73.81 | 290 | MAP2818c | hypothetical protein | 292 | 100 |
| MAP4_0995 | conserved secreted protein | 222 | Rv2700 | Possible conserved secreted alanine | 81.98 | 216 | Mb2719 | secreted alanine rich protein | 81.98 | 216 | MAV_3592 | hypothetical protein | 99.55 | 222 | BCG_2713 | hypothetical protein | 81.98 | 216 | MAP2817 | hypothetical protein | 222 | 100 |
| MAP4_0996 | hypothetical protein | 100 | Rv2699c | hypothetical protein | 98 | 100 | Mb2718c | hypothetical protein | 98 | 100 | MAV_3591 | hypothetical protein | 100 | 100 | BCG_2712c | hypothetical protein | 98 | 100 | MAP2816c | hypothetical protein | 100 | 100 |
| MAP4_0997 | conserved alanine rich membrane protein | 161 | Rv2698 | Probable conserved alanine rich tra | 76.88 | 161 | Mb2717 | hypothetical protein | 76.88 | 161 | MAV_3590 | hypothetical protein | 98.52 | 145 | BCG_2711 | alanine rich transmembrane pr | 76.88 | 161 | MAP2815 | hypothetical protein | 161 | 100 |
| MAP4_0998 | deoxyuridine 5'-triphosphate nucleotidohydrolase Dut | 154 | Rv2697c | Probable deoxyuridine 5'-triphospha | 94.29 | 154 | Mb2716c | deoxyuridine 5'-triphosphate | 94.29 | 154 | MAV_3589 | deoxyuridine 5'-triphosphate nucle | 100 | 154 | BCG_2710c | deoxyuridine 5'-triphosphate n | 94.29 | 154 | MAP2814c | deoxyuridine 5'-triphosphate nucleotid | 154 | 100 |
| MAP4_0999 | conserved alanine, glycine and valine rich protein | 257 | Rv2696c | Conserved alanine and glycine and v | 79.45 | 259 | Mb2715c | hypothetical protein | 77.38 | 259 | MAV_3588 | hypothetical protein | 99.61 | 258 | BCG_2709c | hypothetical protein | 77.38 | 259 | MAP2813c | hypothetical protein | 257 | 100 |
| MAP4_1000 | conserved alanine rich protein | 232 | Rv2695 | Conserved hypothetical alanine rich | 77.16 | 235 | Mb2714 | hypothetical protein | 77.16 | 235 | MAV_3587 | hypothetical protein | 98.28 | 232 | BCG_2708 | hypothetical protein | 77.16 | 235 | MAP2812 | hypothetical protein | 232 | 100 |
| MAP4_1001 | hypothetical protein | 122 | Rv2694c | hypothetical protein | 90.16 | 122 | Mb2713c | hypothetical protein | 89.34 | 122 | MAV_3585 | OB-fold nucleic acid binding domai | 100 | 116 | BCG_2707c | hypothetical protein | 89.34 | 122 | MAP2811c | hypothetical protein | 150 | 100 |
| MAP4_1002 | conserved alanine and leucine rich membrane protein | 213 | Rv2693c | Probable conserved integral membr | 69.81 | 223 | Mb2712c | hypothetical protein | 69.81 | 223 | MAV_3584 | hypothetical protein | 99.53 | 213 | BCG_2706c | integral membrane alanine and | 69.81 | 223 | MAP2810c | hypothetical protein | 213 | 100 |
| MAP4_1003 | trk system potassium uptake protein | 218 | Rv2692 | TRK system potassium uptake protei | 90.32 | 220 | Mb2711 | TRK system potassium uptake | 90.78 | 220 | MAV_3583 | TrkB protein | 100 | 218 | BCG_2705 | TRK system potassium uptake | 90.78 | 220 | MAP2809 | TrkB | 218 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1004 | trk system potassium uptake protein | 221 | Rv2691 | TRK system potassium uptake prote | 89.14 | 227 | Mb2710 | TRK system potassium uptake | 89.59 | 227 | MAV_3582 | TrkA protein | 99.54 | 218 | BCG_2704 | TRK system potassium uptake | 89.59 | 227 | MAP2808 | hypothetical protein | 221 | 100 |
| MAP4_1005 | conserved alanine, valine and leucine rich membrane p | 664 | Rv2690c | Probable conserved integral membr | 82.19 | 657 | Mb2709c | hypothetical protein | 82.23 | 663 | MAV_3581 | amino acid permease | 99.55 | 664 | BCG_2703c | integral membrane alanine and | 82.23 | 663 | MAP2807c | hypothetical protein | 664 | 100 |
| MAP4_1006 | conserved alanine, valine and glycine rich protein | 361 | Rv2689c | Conserved alanine and valine and gl | 74.16 | 405 | Mb2708c | hypothetical protein | 74.16 | 405 | MAV_3580 | RNA methyltransferase | 98.26 | 395 | BCG_2702c | hypothetical protein | 74.16 | 405 | MAP2806c | hypothetical protein | 361 | 100 |
| MAP4_1007 | arsenic-transport integral membrane protein | 429 | Rv2684 | Probable arsenic-transport integral | 73.07 | 429 | Mb2703 | arsenic-transport integral me | 73.07 | 429 | MAV_3579 | citrate transporter | 99.53 | 429 | BCG_2697 | arsenic-transport integral mem | 73.07 | 429 | MAP2805 | hypothetical protein | 429 | 100 |
| MAP4_1008 | hypothetical protein | 160 | Rv2683 | hypothetical protein | 80.14 | 165 | Mb2702 | hypothetical protein | 80.82 | 165 | MAV_3578 | CBS domain-containing protein | 99.32 | 147 | BCG_2696 | hypothetical protein | 80.82 | 165 | MAP2804 | hypothetical protein | 160 | 100 |
| MAP4_1009 | 1-deoxy-D-xylulose 5-phosphate synthase | 641 | Rv2682c | Probable 1-deoxy-D-xylulose 5-phos | 87.54 | 638 | Mb2701c | 1-deoxy-D-xylulose-5-phosph | 87.54 | 638 | MAV_3577 | 1-deoxy-D-xylulose-5-phosphate sy | 99.84 | 641 | BCG_2695c | 1-deoxy-D-xylulose-5-phosphat | 87.54 | 638 | MAP2803c | 1-deoxy-D-xylulose-5-phosphate syntha | 641 | 100 |
| MAP4_1010 | conserved alanine rich protein | 428 | Rv2681 | Conserved hypothetical alanine rich | 75.12 | 438 | Mb2700 | hypothetical protein | 74.88 | 438 | MAV_3576 | ribonuclease D | 99.53 | 428 | BCG_2694 | hypothetical protein | 74.88 | 438 | MAP2802 | hypothetical protein | 428 | 100 |
| MAP4_1011 | hypothetical protein | 211 | Rv2680 | hypothetical protein | 82.59 | 210 | Mb2699 | hypothetical protein | 82.59 | 210 | MAV_3575 | hypothetical protein | 99.48 | 193 | BCG_2693 | hypothetical protein | 82.59 | 210 | MAP2801 | hypothetical protein | 211 | 100 |
| MAP4_1012 | enoyl-CoA hydratase | 273 | Rv2679 | Probable enoyl-CoA hydratase EchA | 84.15 | 276 | Mb2698 | enoyl-CoA hydratase | 84.15 | 276 | MAV_3574 | enoyl-CoA hydratase | 99.63 | 273 | BCG_2692 | enoyl-CoA hydratase | 84.15 | 276 | MAP2800 | enoyl-CoA hydratase | 273 | 100 |
| MAP4_1013 | uroporphyrinogen decarboxylase | 357 | Rv2678c | Probable uroporphyrinogen decarbo | 78.03 | 357 | Mb2697c | uroporphyrinogen decarboxy | 78.03 | 357 | MAV_3573 | uroporphyrinogen decarboxylase | 99.16 | 357 | BCG_2691c | uroporphyrinogen decarboxyla | 78.03 | 357 | MAP2799c | uroporphyrinogen decarboxylase | 357 | 100 |
| MAP4_1014 | protoporphyrinogen oxidase | 451 | Rv2677c | Probable protoporphyrinogen oxida | 73.13 | 452 | Mb2696c | protoporphyrinogen oxidase | 73.13 | 452 | MAV_3890 | dehydrogenase | 35.79 | 509 | BCG_2690c | protoporphyrinogen oxidase | 73.13 | 452 | MAP2798c | protoporphyrinogen oxidase | 451 | 100 |
| MAP4_1015 | chlorite dismutase family protein | 231 | Rv2676c | hypothetical protein | 90.91 | 231 | Mb2695c | hypothetical protein | 90.91 | 231 | MAV_3571 | hypothetical protein | 100 | 231 | BCG_2689c | hypothetical protein | 90.91 | 231 | MAP2797c | hypothetical protein | 231 | 100 |
| MAP4_1016 | putative methyltransferase | 250 | Rv2675c | hypothetical protein | 80 | 250 | Mb2694c | hypothetical protein | 80 | 250 | MAV_3570 | thiopurine S-methyltransferase (tp | 99.2 | 250 | BCG_2688c | hypothetical protein | 80 | 250 | MAP2796c | hypothetical protein | 250 | 100 |
| MAP4_1017 | hypothetical protein | 282 | Rv3714c | hypothetical protein | 60.71 | 296 | Mb3741c | hypothetical protein | 60.71 | 296 | MAV_3567 | hypothetical protein | 98.8 | 173 | BCG_3774c | hypothetical protein | 60.71 | 296 | MAP2795 | hypothetical protein | 282 | 100 |
| MAP4_1018 | putative methionine sulfoxide reductase | 134 | Rv2674 | Probable peptide methionine sulfox | 84.96 | 136 | Mb2693 | hypothetical protein | 84.96 | 136 | MAV_3566 | methionine-R-sulfoxide reductase | 98.51 | 134 | BCG_2687 | hypothetical protein | 84.96 | 136 | MAP2794 | hypothetical protein | 134 | 100 |
| MAP4_1019 | hypothetical protein | 428 | Rv2673 | Possible arabinofuranosyltransferas | 82.56 | 433 | Mb2692 | hypothetical protein | 82.56 | 433 | MAV_3565 | hypothetical protein | 100 | 428 | BCG_2686 | hypothetical protein | 82.56 | 433 | MAP2793 | hypothetical protein | 428 | 100 |
| MAP4_1020 | secreted protease | 526 | Rv2672 | Possible secreted protease | 77.65 | 528 | Mb2691 | protease | 77.84 | 528 | MAV_3564 | alpha/beta hydrolase | 99.81 | 522 | BCG_2685 | protease | 77.84 | 528 | MAP2792 | hypothetical protein | 526 | 100 |
| MAP4_1021 | bifunctional riboflavin biosynthesis protein | 254 | Rv2671 | Possible bifunctional enzyme ribofla | 74.3 | 258 | Mb2690 | hypothetical protein | 74.3 | 258 | MAV_3563 | hypothetical protein | 99.21 | 254 | BCG_2684 | hypothetical protein | 74.3 | 258 | MAP2791 | hypothetical protein | 254 | 100 |
| MAP4_1022 | putative ATPGTP-binding integral membrane protein | 232 | Rv2670c | hypothetical protein | 85.6 | 369 | Mb2689c | hypothetical protein | 85.6 | 369 | MAV_3561 | ATP/GTP-binding integral membra | 98.44 | 361 | BCG_2683c | hypothetical protein | 85.6 | 369 | MAP2790c | hypothetical protein | 361 | 100 |
| MAP4_1023 | acetyltransferase (GNAT) family protein | 173 | Rv2669 | GCN5-related N-acetyltransferase | 64.29 | 156 | Mb2688 | hypothetical protein | 64.29 | 156 | MAV_3562 | acetyltransferase, gnat family prot | 94.8 | 176 | BCG_2682 | hypothetical protein | 64.29 | 156 | MAP2789 | hypothetical protein | 173 | 100 |
| MAP4_1024 | exported alanine and valine rich protein | 175 | Rv2668 | Possible exported alanine and valine | 71.59 | 173 | Mb2687 | hypothetical protein | 72.16 | 173 | MAV_3560 | hypothetical protein | 99.23 | 130 | BCG_2681 | hypothetical protein | 72.16 | 173 | MAP2788 | hypothetical protein | 175 | 100 |
| MAP4_1025 | ATP-dependent protease ATP-binding subunit ClpC2 | 250 | Rv2667 | Possible ATP-dependent protease A | 75.73 | 252 | Mb2686 | ATP-dependent protease ATP | 75.73 | 252 | MAV_3559 | ATP-dependent Clp protease ATP-b | 98 | 250 | BCG_2680 | ATP-dependent protease ATP- | 75.73 | 252 | MAP2787 | ClpX' | 250 | 100 |
| MAP4_1026 | hypothetical protein | 114 | Rv1804c | hypothetical protein | 42.42 | 108 | Mb1833c | hypothetical protein | 42.42 | 108 | MAV_3558 | hypothetical protein | 99.12 | 122 | BCG_1837c | hypothetical protein | 42.42 | 108 | MAP2786c | hypothetical protein | 114 | 100 |
| MAP4_1027 | hypothetical protein | 114 | Rv1804c | hypothetical protein | 43.56 | 108 | Mb1833c | hypothetical protein | 43.56 | 108 | MAV_3557 | hypothetical protein | 100 | 114 | BCG_1837c | hypothetical protein | 43.56 | 108 | MAP2785c | hypothetical protein | 161 | 100 |
| MAP4_1028 | hypothetical protein | 416 | Rv2025c | hypothetical protein | 39.55 | 332 | Mb2050c | hypothetical protein | 39.55 | 332 | MAV_3555 | cation efflux family protein | 100 | 306 | BCG_2044c | hypothetical protein | 39.55 | 332 | MAP2784 | hypothetical protein | 416 | 100 |
| MAP4_1029 | hypothetical protein | 70 | Rv3483c | Possible exported protein | 56.25 | 220 | Mb3513c | hypothetical protein | 56.25 | 220 | MAV_3554 | hypothetical protein | 100 | 70 | BCG_3547c | hypothetical protein | 56.25 | 220 | MAP0026 | long-chain-fatty-acid--ACP ligase | 518 | 40 |
| MAP4_1030 | aldehyde dehydrogenase family protein (betB) | 487 | Rv2858c | Probable aldehyde dehydrogenase A | 41.83 | 455 | Mb2883c | aldehyde dehydrogenase | 41.83 | 455 | MAV_3553 | aldehyde dehydrogenase | 99.79 | 487 | BCG_2880c | aldehyde dehydrogenase aldC | 41.83 | 455 | MAP2782 | hypothetical protein | 487 | 100 |
| MAP4_1031 | carboxymuconolactone decarboxylase family protein | 258 | Rv0771 | Possible 4-carboxymuconolactone d | 36.61 | 144 | Mb0794 | 4-carboxymuconolactone de | 36.61 | 144 | MAV_3552 | hypothetical protein | 98.84 | 271 | BCG_0823 | 4-carboxymuconolactone deca | 36.61 | 144 | MAP2781 | hypothetical protein | 258 | 100 |
| MAP4_1032 | dehydrogenase | 273 | Rv2750 | Probable dehydrogenase | 48.68 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 48.68 | 272 | MAV_3551 | carveol dehydrogenase | 99.27 | 273 | BCG_2766 | 3-ketoacyl-ACP reductase | 48.68 | 272 | MAP2780 | hypothetical protein | 273 | 100 |
| MAP4_1033 | short-chain dehydrogenase-reductase | 276 | Rv2750 | Probable dehydrogenase | 52.75 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 52.75 | 272 | MAV_3550 | short chain dehydrogenase | 98.55 | 276 | BCG_2766 | 3-ketoacyl-ACP reductase | 52.75 | 272 | MAP2779 | short chain dehydrogenase | 276 | 100 |
| MAP4_1034 | Transcriptional regulator, TetR family | 225 | Rv3574 | Transcriptional regulatory protein K | 27.61 | 199 | Mb3605 | transcriptional regulatory pro | 27.61 | 199 | MAV_3548 | TetR family transcriptional regulat | 98.2 | 222 | BCG_3639 | TetR family transcriptional reg | 27.61 | 199 | MAP2778c | hypothetical protein | 225 | 100 |
| MAP4_1035 | hypothetical protein | 245 | Rv0385 | Probable monooxygenase | 40 | 390 | Mb0392 | hypothetical protein | 40 | 390 | MAV_2753 | catalase/peroxidase HPI | 27.43 | 748 | BCG_0423 | monooxygenase | 40 | 390 | MAP2777c | hypothetical protein | 245 | 100 |
| MAP4_1036 | hypothetical protein | 72 | Rv3156 | Probable NADH dehydrogenase I (ch | 75 | 633 | Mb3180 | NADH dehydrogenase subuni | 75 | 633 | MAV_3546 | hypothetical protein | 97.22 | 72 | BCG_3179 | NADH dehydrogenase subunit | 75 | 633 | MAP4084 | Mce2 | 380 | 35 |
| MAP4_1037 | putative amidohydrolase | 424 | Rv3299c | Probable arylsulfatase AtsB (aryl-sul | 24.14 | 970 | Mb3327c | arylsulfatase | 24.14 | 970 | MAV_3544 | amidohydrolase | 99.76 | 424 | BCG_3328c | arylsulfatase atsB | 24.14 | 970 | MAP2776c | hypothetical protein | 417 | 99.76 |
| MAP4_1038 | Transcriptional regulator, IclR family | 295 | Rv2827c | Hypothetical protein | 34.55 | 295 | Mb2596 | hypothetical protein | 31.51 | 597 | MAV_3545 | hypothetical protein | 98.64 | 317 | BCG_2589 | hypothetical protein | 29.29 | 597 | MAP2775 | hypothetical protein | 295 | 100 |
| MAP4_1039 | short-chain type dehydrogenase reductase | 312 | Rv0851c | Probable short-chain type dehydrog | 34.74 | 275 | Mb0874c | short chain dehydrogenase | 34.74 | 275 | MAV_3543 | hypothetical protein | 98.4 | 312 | BCG_0903c | short chain dehydrogenase | 35.09 | 275 | MAP2774c | hypothetical protein | 325 | 100 |
| MAP4_1040 | acetoacetate decarboxylase family protein | 267 | Rv0327c | Possible cytochrome P450 135A1 Cy | 47.62 | 449 | Mb0334c | cytochrome P450 135A1 | 47.62 | 449 | MAV_3542 | acetoacetate decarboxylase | 98.88 | 267 | BCG_0366c | cytochrome P450 135A1 cyp13 | 47.62 | 449 | MAP2773c | hypothetical protein | 267 | 100 |
| MAP4_1041 | putative amidohydrolase | 404 | Rv3198c | Probable ATP-dependent DNA helica | 35.42 | 700 | Mb3222c | DNA helicase II | 35.42 | 700 | MAV_3541 | amidohydrolase | 99.5 | 404 | BCG_3222c | DNA helicase II | 35.42 | 700 | MAP2772c | hypothetical protein | 404 | 100 |
| MAP4_1042 | putative amidohydrolase | 425 | Rv3510c | hypothetical protein | 37.5 | 278 | Mb3540c | hypothetical protein | 37.5 | 278 | MAV_3540 | amidohydrolase | 100 | 425 | BCG_3574c | hypothetical protein | 37.5 | 278 | MAP2771c | hypothetical protein | 425 | 100 |
| MAP4_1043 | hypothetical protein | 185 | Rv0015c | Transmembrane serine/threonine-p | 40.62 | 431 | Mb0015c | Ser/Thr protein kinase | 40.62 | 431 | MAV_3539 | hypothetical protein | 98.27 | 173 | BCG_0045c | Ser/Thr protein kinase | 40.62 | 431 | MAP2770 | hypothetical protein | 185 | 100 |
| MAP4_1044 | hypothetical protein | 100 | Rv3263 | Probable DNA methylase (modificati | 38.89 | 553 | Mb3291 | DNA methylase | 38.89 | 553 | MAV_3538 | hypothetical protein | 99 | 102 | BCG_3292 | DNA methylase | 38.89 | 553 | MAP3610 | hypothetical protein | 213 | 47.83 |
| MAP4_1045 | hypothetical protein | 99 | Rv0214 | Probable fatty-acid-CoA ligase FadD | 40 | 537 | Mb0220 | long-chain-fatty-acid--CoA lig | 40 | 537 | MAV_3537 | hypothetical protein | 100 | 99 | BCG_0251 | long-chain-fatty-acid--CoA liga | 40 | 537 | MAP0244 | hypothetical protein | 398 | 68.75 |
| MAP4_1046 | prophage integrase | 326 | Rv2659c | Probable PhiRv2 prophage integrase | 57.53 | 375 | Mb2776c | type I restriction/modificatio | 68.75 | 91 | MAV_1484 | integrase | 37.63 | 368 | BCG_2771c | type I restriction/modification | 68.75 | 91 | MAP2768c | hypothetical protein | 345 | 99.69 |
| MAP4_1047 | hypothetical protein | 183 | Rv1516c | Probable sugar transferase | 31.58 | 336 | Mb2440c | hypothetical protein | 45.83 | 280 | MAV_4987 | sugar transporter family protein | 27.59 | 411 | BCG_2433c | hypothetical protein | 45.83 | 280 | MAP2767c | hypothetical protein | 183 | 100 |
| MAP4_1048 | putative phiRv1 phage protein | 158 | Rv1583c | Probable PhiRv1 phage protein | 50 | 132 | Mb1609c | phiRv1 phage protein | 50 | 132 | MAV_2437 | cobaltochelatase subunit CobN | 31.58 | 1191 | BCG_3888c | polyketide synthase | 32.84 | 2126 | MAP2766c | hypothetical protein | 158 | 100 |
| MAP4_1049 | hypothetical protein | 396 | Rv0408 | Probable phosphate acetyltransfera | 29.27 | 690 | Mb0416 | phosphate acetyltransferase | 29.27 | 690 | MAV_3847 | D-3-phosphoglycerate dehydrogen | 28.77 | 528 | BCG_0447 | phosphate acetyltransferase | 29.27 | 690 | MAP2765c | hypothetical protein | 396 | 100 |
| MAP4_1050 | hypothetical protein | 149 | Rv2156c | Probable phospho-N-acetylmuramo | 28.57 | 359 | Mb2180c | phospho-N-acetylmuramoyl- | 28.57 | 359 | MAV_2333 | phospho-N-acetylmuramoyl-penta | 28.3 | 359 | BCG_2173c | phospho-N-acetylmuramoyl-pe | 28.57 | 359 | MAP2764c | hypothetical protein | 149 | 100 |
| MAP4_1051 | hypothetical protein | 102 | Rv1173 | Probable F420 biosynthesis protein | 35 | 856 | Mb1206 | FO synthase | 35 | 856 | MAV_3893 | MarR family transcriptional regulat | 39.68 | 188 | BCG_1236 | FO synthase | 35 | 856 | MAP2763c | hypothetical protein | 102 | 100 |
| MAP4_1052 | hypothetical protein | 146 | Rv3750c | Possible excisionase | 23.73 | 130 | Mb3776c | excisionase | 23.73 | 130 | MAV_0282 | DNA binding domain-containing pr | 26.67 | 155 | BCG_3809c | excisionase | 23.73 | 130 | MAP2762c | hypothetical protein | 146 | 100 |
| MAP4_1053 | hypothetical protein | 238 | Rv2438c | Glutamine-dependent NAD(+) synth | 27.37 | 679 | Mb3610c | tRNA/rRNA methyltransferas | 43.24 | 402 | MAV_0811 | hypothetical protein | 32.38 | 421 | BCG_2457c | NAD synthetase | 27.37 | 679 | MAP2761c | hypothetical protein | 238 | 100 |
| MAP4_1054 | hypothetical protein | 141 | Rv3099c | hypothetical protein | 33.33 | 283 | Mb3126c | hypothetical protein | 33.33 | 283 | MAV_0808 | hypothetical protein | 44.07 | 110 | BCG_3124c | hypothetical protein | 33.33 | 283 | MAP2760c | hypothetical protein | 141 | 100 |
| MAP4_1055 | hypothetical protein | 172 | Rv2516c | Hypothetical protein | 67.74 | 267 | Mb2545c | hypothetical protein | 67.74 | 267 | MAV_2450 | erythronolide synthase, modules 3 | 41.94 | 4171 | BCG_2537c | hypothetical protein | 67.74 | 267 | MAP2759 | hypothetical protein | 172 | 100 |
| MAP4_1056 | hypothetical protein | 83 | Rv2517c | hypothetical protein | 69.62 | 83 | Mb2546c | hypothetical protein | 69.62 | 83 | MAV_0458 | alpha/beta hydrolase | 29.79 | 321 | BCG_2538c | hypothetical protein | 69.62 | 83 | MAP2758 | hypothetical protein | 83 | 100 |
| MAP4_1057 | hypothetical protein | 93 | Rv2646 | Probable integrase | 38.64 | 332 | Mb1253 | RNA polymerase sigma factor | 21.21 | 257 | MAV_2555 | short chain dehydrogenase/reduct | 36.11 | 275 | BCG_1281 | RNA polymerase sigma factor | 21.21 | 257 | MAP2757 | hypothetical protein | 93 | 100 |
| MAP4_1058 | phage tail tape measure protein | 1636 | Rv1115 | Possible exported protein | 31.54 | 232 | Mb1145 | hypothetical protein | 33.09 | 232 | MAV_0800 | phage tail tape measure protein, fa | 97.23 | 1659 | BCG_1175 | hypothetical protein | 33.09 | 232 | MAP2756c | hypothetical protein | 1636 | 100 |
| MAP4_1059 | hypothetical protein | 100 | Rv0174 | Mce-family protein Mce1F | 35.71 | 515 | | | | | MAV_1039 | hypothetical protein | 54.72 | 95 | | | | | MAP2755 | hypothetical protein | 100 | 100 |
| MAP4_1060 | hypothetical protein | 85 | Rv1839c | Possible antitoxin VapB13 | 45.71 | 87 | Mb1870c | hypothetical protein | 45.71 | 87 | MAV_3576 | ribonuclease D | 40.74 | 428 | BCG_1874c | hypothetical protein | 45.71 | 87 | MAP2754 | hypothetical protein | 85 | 100 |
| MAP4_1061 | hypothetical protein | 252 | Rv2213 | Probable aminopeptidase PepB | 33.78 | 515 | Mb2236 | leucyl aminopeptidase | 33.78 | 515 | MAV_0781 | hypothetical protein | 33.8 | 217 | BCG_2229 | leucyl aminopeptidase | 33.78 | 515 | MAP2753 | hypothetical protein | 252 | 100 |
| MAP4_1062 | integrase | 381 | Rv2646 | Probable integrase | 34.22 | 332 | Mb1727 | site-specific tyrosine recombi | 28.21 | 311 | MAV_0779 | site-specific recombinase, phage in | 61.73 | 160 | BCG_1739 | site-specific tyrosine recombin | 28.21 | 311 | MAP2752 | hypothetical protein | 381 | 100 |
| MAP4_1063 | hypothetical protein | 193 | Rv2496c | Probable branched-chain keto acid | 42.42 | 348 | Mb2524c | pyruvate dehydrogenase E1 | 42.42 | 348 | MAV_1676 | pyruvate dehydrogenase E1 comp | 45.45 | 351 | BCG_2516c | pyruvate dehydrogenase E1 co | 42.42 | 348 | MAP2751 | hypothetical protein | 193 | 100 |
| MAP4_1064 | hypothetical protein | 145 | Rv1443c | hypothetical protein | 34.41 | 161 | Mb1478c | hypothetical protein | 34.41 | 161 | MAV_3526 | hypothetical protein | 97.73 | 132 | BCG_1504c | hypothetical protein | 34.41 | 161 | MAP2750c | hypothetical protein | 145 | 100 |
| MAP4_1065 | hypothetical protein | 97 | Rv0309 | Possible conserved exported protei | 40.91 | 218 | Mb0317 | hypothetical protein | 40.91 | 218 | MAV_3525 | hypothetical protein | 100 | 97 | BCG_0349 | hypothetical protein | 40.91 | 218 | MAP2749c | hypothetical protein | 97 | 100 |
| MAP4_1066 | enoyl-CoA hydrataseisomerase family protein | 293 | Rv1070c | Probable enoyl-CoA hydratase EchA | 32.55 | 257 | Mb1099c | enoyl-CoA hydratase | 32.55 | 257 | MAV_3524 | enoyl-CoA hydratase/isomerase | 99.25 | 278 | BCG_1128c | enoyl-CoA hydratase | 32.55 | 257 | MAP2748c | hypothetical protein | 293 | 100 |
| MAP4_1067 | fatty-acid--CoA ligase | 515 | Rv0166 | Probable fatty-acid-CoA ligase FadD | 35.6 | 554 | Mb0172 | long-chain-fatty-acid--CoA lig | 35.41 | 554 | MAV_3523 | acyl-CoA synthase | 99.42 | 515 | BCG_0203 | long-chain-fatty-acid--CoA liga | 35.41 | 554 | MAP2747 | hypothetical protein | 515 | 100 |
| MAP4_1068 | hypothetical protein | 172 | Rv3432c | Probable glutamate decarboxylase | 35 | 460 | Mb3462c | glutamate decarboxylase | 35 | 460 | MAV_3522 | hypothetical protein | 98.73 | 157 | BCG_3498c | glutamate decarboxylase gadB | 35 | 460 | MAP2746 | hypothetical protein | 172 | 100 |
| MAP4_1069 | short-chain type dehydrogenase reductase | 266 | Rv2857c | Probable short-chain type dehydrog | 37.16 | 258 | Mb2882c | short chain dehydrogenase | 37.16 | 258 | MAV_3521 | NAD dependent epimerase/dehydr | 98.5 | 266 | BCG_2879c | short chain dehydrogenase | 37.16 | 258 | MAP2745c | hypothetical protein | 266 | 100 |
| MAP4_1070 | catalase | 313 | Rv0998 | hypothetical protein | 32.79 | 333 | Mb1025 | hypothetical protein | 32.79 | 333 | MAV_3520 | catalase | 99.04 | 313 | BCG_1055 | hypothetical protein | 32.79 | 333 | MAP2744c | hypothetical protein | 313 | 100 |
| MAP4_1071 | hypothetical protein | 261 | Rv1176c | hypothetical protein | 34.67 | 189 | Mb1209c | hypothetical protein | 34.67 | 189 | MAV_3519 | hypothetical protein | 99.61 | 256 | BCG_1239c | hypothetical protein | 34.67 | 189 | MAP2743c | hypothetical protein | 261 | 100 |
| MAP4_1072 | putative anti-anti-sigma factor | 145 | Rv2638 | hypothetical protein | 68.35 | 148 | Mb2671 | hypothetical protein | 68.35 | 148 | MAV_3518 | anti-anti-sigma factor | 98.57 | 140 | BCG_2665 | hypothetical protein | 68.35 | 148 | MAP2742 | hypothetical protein | 145 | 100 |
| MAP4_1073 | Transcriptional regulator, TetR family | 205 | Rv3173c | Probable transcriptional regulatory | 33.33 | 200 | Mb3198c | TetR/ACRR family transcripti | 33.33 | 200 | MAV_3517 | TetR family transcriptional regulat | 100 | 205 | BCG_3197c | TetR family transcriptional reg | 33.33 | 200 | MAP2741c | hypothetical protein | 205 | 100 |
| MAP4_1074 | hypothetical protein | 221 | Rv2637 | Possible transmembrane protein De | 84.33 | 218 | Mb2670 | transmembrane protein Ded | 84.33 | 218 | MAV_3516 | integral membrane protein | 99.51 | 204 | BCG_2664 | transmembrane protein dedA | 84.33 | 218 | MAP2740 | hypothetical protein | 221 | 100 |
| MAP4_1075 | GDSL-like lipase family protein | 268 | Rv2940c | Probable multifunctional mycoceros | 26.42 | 2111 | Mb2965c | multifunctional mycocerosic | 26.42 | 2111 | MAV_3515 | hypothetical protein | 98.88 | 268 | BCG_0779 | d-xylulose kinase xylB | 33.71 | 448 | MAP2739 | hypothetical protein | 296 | 99.63 |
| MAP4_1076 | Transcriptional regulator, IclR family | 271 | Rv1719 | Probable transcriptional regulatory | 34.67 | 259 | Mb1748 | transcriptional regulator | 34.67 | 259 | MAV_3513 | IclR family transcriptional regulator | 99.26 | 271 | BCG_1758 | transcriptional regulatory prot | 34.67 | 259 | MAP2738c | hypothetical protein | 271 | 100 |
| MAP4_1077 | class II aldolaseadducin family protein | 240 | Rv0727c | Possible L-fuculose phosphate aldol | 24.35 | 218 | Mb0748c | L-fuculose phosphate aldolas | 24.35 | 218 | MAV_3514 | FliH protein | 97.92 | 240 | BCG_0777c | L-fuculose phosphate aldolase | 24.35 | 218 | MAP2737 | hypothetical protein | 240 | 100 |
| MAP4_1078 | 2,3-dihydroxy-2,3-dihydrophenylpropionate dehydroge | 264 | Rv2002 | Possible 20-beta-hydroxysteroid deh | 32.05 | 260 | Mb2025 | 20-beta-hydroxysteroid dehy | 32.05 | 260 | MAV_3512 | 2,3-dihydroxy-2,3-dihydrophenylpr | 99.24 | 264 | BCG_2019 | 20-beta-hydroxysteroid dehydr | 32.05 | 260 | MAP2736 | 2,3-dihydroxy-2,3-dihydrophenylpropio | 264 | 100 |
| MAP4_1079 | hypothetical protein | 83 | Rv0270 | Probable fatty-acid-CoA ligase FadD | 25 | 560 | Mb0276 | acyl-CoA synthetase | 25 | 560 | MAV_3511 | dihydrodiol dehydrogenase | 97.59 | 83 | BCG_0308 | acyl-CoA synthetase | 25 | 560 | MAP4121 | hypothetical protein | 1407 | 30 |
| MAP4_1080 | aromatic-ring-hydroxylating dioxygenase, beta subunit | 174 | Rv0890c | Probable transcriptional regulatory | 28.3 | 882 | Mb0914c | LuxR family transcriptional re | 28.3 | 882 | MAV_3510 | 3-phenylpropionate dioxygenase s | 100 | 174 | BCG_0942c | LuxR family transcriptional reg | 28.3 | 882 | MAP2735 | 3-phenylpropionate dioxygenase subun | 184 | 100 |
| MAP4_1081 | ring hydroxylating dioxygenase, alpha subunit | 446 | Rv3161c | Possible dioxygenase | 30.77 | 382 | Mb3186c | dioxygenase | 30.77 | 382 | MAV_3509 | phthalate dioxygenase large subun | 99.32 | 453 | BCG_3185c | dioxygenase | 30.77 | 382 | MAP2734 | hypothetical protein | 446 | 100 |
| MAP4_1082 | rieske (2Fe-2S) domain-containing protein | 323 | Rv3526 | Oxygenase component of 3-ketoste | 31.48 | 386 | Mb3556 | oxidoreductase | 31.48 | 386 | MAV_3508 | Rieske (2Fe-2S) domain-containing | 99.69 | 323 | BCG_3590 | oxidoreductase | 31.48 | 386 | MAP2733c | hypothetical protein | 323 | 100 |
| MAP4_1083 | hemerythrin HHE cation bindingdomain-containing pro | 161 | Rv2633c | Hypothetical protein | 76.4 | 161 | Mb2666c | hypothetical protein | 76.4 | 161 | MAV_3507 | hemerythrin HHE cation binding d | 100 | 161 | BCG_2660c | hypothetical protein | 76.4 | 161 | MAP2732c | hypothetical protein | 161 | 100 |
| MAP4_1084 | Protocatechuate 3,4-dioxygenase beta chain | 254 | Rv0814c | Conserved protein SseC2 | 29.51 | 100 | Mb0837c | hypothetical protein | 29.51 | 100 | MAV_3506 | protocatechuate 3,4-dioxygenase, | 99.21 | 254 | BCG_0866c | hypothetical protein | 29.51 | 100 | MAP2731c | PcaH | 254 | 100 |
| MAP4_1085 | protocatechuate 3,4-dioxygenase alpha chain | 187 | Rv0083 | Probable oxidoreductase | 34.62 | 640 | Mb0086 | oxidoreductase | 34.62 | 642 | MAV_3505 | protocatechuate 3,4-dioxygenase, | 98.21 | 168 | BCG_0116 | oxidoreductase | 34.62 | 642 | MAP2730c | PcaG | 187 | 100 |
| MAP4_1086 | 3-carboxy-cis,cis-muconate cyclo-isomerase | 408 | Rv0777 | Probable adenylosuccinate lyase Pu | 23.91 | 472 | Mb0800 | adenylosuccinate lyase | 23.91 | 472 | MAV_3504 | 3-carboxy-cis,cis-muconate cyclois | 96.57 | 408 | BCG_0829 | adenylosuccinate lyase | 23.91 | 472 | MAP2729c | PcaB | 408 | 100 |
| MAP4_1087 | hypothetical protein | 87 | Rv2628 | Hypothetical protein | 64.47 | 120 | Mb2661 | hypothetical protein | 64.47 | 120 | MAV_3503 | hypothetical protein | 98.85 | 87 | BCG_2655 | hypothetical protein | 65.79 | 120 | MAP2728 | hypothetical protein | 87 | 100 |
| MAP4_1088 | hypothetical protein | 78 | Rv2913c | Possible D-amino acid aminohydrola | 39.13 | 611 | Mb2937c | D-amino acid aminohydrolase | 39.13 | 611 | MAV_3502 | hypothetical protein | 100 | 70 | BCG_2934c | D-amino acid aminohydrolase | 39.13 | 611 | MAP2981c | hypothetical protein | 620 | 36.96 |
| MAP4_1089 | methyltransferasemethylase | 281 | Rv2622 | Possible methyltransferase (methyla | 74.35 | 273 | Mb2655 | methyltransferase | 74.35 | 273 | MAV_3501 | SAM-dependent methyltransferase | 99.29 | 281 | BCG_2649 | methyltransferase | 74.35 | 273 | MAP2727 | hypothetical protein | 281 | 100 |
| MAP4_1090 | 4Fe-4S ferredoxin, iron-sulfur binding protein | 118 | Rv2007c | Ferredoxin FdxA | 73.64 | 114 | Mb2030c | ferredoxin FDXA | 73.64 | 114 | MAV_3500 | ferredoxin FdxA | 100 | 118 | BCG_2024c | ferredoxin fdxA | 73.64 | 114 | MAP2726c | FdxA | 118 | 100 |
| MAP4_1091 | transcriptional regulatory protein | 234 | Rv2621c | Possible transcriptional regulatory p | 69.68 | 224 | Mb2654c | transcriptional regulator | 69.23 | 223 | MAV_3499 | hypothetical protein | 99.15 | 234 | BCG_2648c | transcriptional regulatory prot | 69.23 | 223 | MAP2725c | hypothetical protein | 234 | 100 |
| MAP4_1092 | hypothetical protein | 141 | Rv2620c | Probable conserved transmembrane | 75.89 | 141 | Mb2653c | transmembrane protein | 75.89 | 141 | MAV_3498 | hypothetical protein | 100 | 141 | BCG_2647c | hypothetical protein | 75.89 | 141 | MAP2724c | hypothetical protein | 141 | 100 |
| MAP4_1093 | hypothetical protein | 114 | Rv2619c | hypothetical protein | 84.21 | 117 | Mb2652c | hypothetical protein | 84.21 | 117 | MAV_3497 | cupin domain-containing protein | 100 | 114 | BCG_2646c | hypothetical protein | 84.21 | 117 | MAP2723c | hypothetical protein | 114 | 100 |
| MAP4_1094 | oxidoreductase, 2-nitropropane dioxygenase | 313 | Rv0021c | hypothetical protein | 36.36 | 322 | Mb0021c | hypothetical protein | 36.05 | 322 | MAV_3496 | oxidoreductase, 2-nitropropane di | 99.36 | 313 | BCG_0051c | hypothetical protein | 36.05 | 322 | MAP2722c | hypothetical protein | 313 | 100 |
| MAP4_1095 | hypothetical protein | 166 | Rv2616 | hypothetical protein | 71.69 | 166 | Mb2649 | hypothetical protein | 71.08 | 166 | MAV_3495 | hypothetical protein | 98.8 | 166 | BCG_2643 | hypothetical protein | 71.08 | 166 | MAP2721 | hypothetical protein | 166 | 100 |
| MAP4_1096 | putative oxidoreductase | 308 | Rv2298 | hypothetical protein | 30.13 | 323 | Mb2320 | hypothetical protein | 30.13 | 323 | MAV_3494 | oxidoreductase YdbC | 99.66 | 292 | BCG_2314 | hypothetical protein | 30.13 | 323 | MAP2720c | hypothetical protein | 308 | 100 |
| MAP4_1097 | hypothetical protein | 208 | Rv0356c | hypothetical protein | 41.18 | 214 | Mb0363c | hypothetical protein | 41.18 | 214 | MAV_3493 | thioesterase | 99.52 | 208 | BCG_0394c | hypothetical protein | 41.18 | 214 | MAP2719c | hypothetical protein | 208 | 100 |
| MAP4_1098 | N-alpha-acyl-glutamine aminoacylase | 424 | Rv3305c | Possible N-acyl-L-amino acid amido | 38.63 | 389 | Mb3333c | N-acyl-L-amino acid amidohy | 38.63 | 389 | MAV_3492 | N-alpha-acyl-glutamine aminoacyl | 97.34 | 414 | BCG_3370c | N-acyl-L-amino acid amidohyd | 38.63 | 389 | MAP2718c | hypothetical protein | 421 | 100 |
| MAP4_1099 | Na+H+ antiporter | 585 | Rv2287 | Probable conserved integral membr | 34.71 | 542 | Mb2309 | integral membrane transport | 34.71 | 542 | MAV_3491 | Na+/H+ antiporter | 99.46 | 553 | BCG_2303 | integral membrane transport | 34.71 | 542 | MAP2717 | hypothetical protein | 585 | 100 |
| MAP4_1100 | threonyl-tRNA synthetase | 684 | Rv2614c | Probable threonyl-tRNA synthetase | 86.66 | 692 | Mb2646c | threonyl-tRNA synthetase | 86.66 | 692 | MAV_3490 | threonyl-tRNA synthetase | 99.56 | 684 | BCG_2639c | threonyl-tRNA synthetase | 86.66 | 692 | MAP2716c | threonyl-tRNA synthetase | 684 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1101 | histidine triad (HIT) family protein | 194 | Rv2613c | hypothetical protein | 84.02 | 195 | Mb2645c | hypothetical protein | 84.02 | 195 | MAV_3489 | diadenosine tetraphosphate | 100 | 194 | BCG_2638c | hypothetical protein | 84.02 | 195 | MAP2715c | hypothetical protein | 194 | 100 |
| MAP4_1102 | phosphatidylinositol synthase PgsA1 | 213 | Rv2612c | PI synthase PgsA1 (phosphatidylinos | 79.33 | 217 | Mb2644c | CDP-diacylglycerol--inositol 3 | 79.33 | 217 | MAV_3488 | CDP-alcohol phosphatidyltransfera | 99.53 | 213 | BCG_2637c | phosphatidylinositol synthase | 79.33 | 217 | MAP2714c | hypothetical protein | 213 | 100 |
| MAP4_1103 | acyltransferase | 320 | Rv2611c | Probable acyltransferase | 74.83 | 316 | Mb2643c | lipid A biosynthesis lauroyl ac | 75.5 | 316 | MAV_3487 | lipid A biosynthesis lauroyl acyltran | 99.06 | 320 | BCG_2636c | lipid A biosynthesis lauroyl acy | 75.5 | 316 | MAP2713c | lipid A biosynthesis lauroyl acyltransfera | 320 | 100 |
| MAP4_1104 | alpha-mannosyltransferase pimA | 374 | Rv2610c | Alpha-mannosyltransferase PimA | 87.83 | 378 | Mb2642c | alpha-mannosyltransferase P | 87.83 | 378 | MAV_3486 | phosphatidylinositol alpha-mannos | 99.47 | 374 | BCG_2635c | Alpha-mannosyltransferase pir | 87.83 | 378 | MAP2712c | hypothetical protein | 374 | 100 |
| MAP4_1105 | hypothetical protein | 341 | Rv2609c | Probable conserved membrane prot | 77.64 | 351 | Mb2641c | hypothetical protein | 77.64 | 351 | MAV_3485 | hydrolase, nudix family protein | 99.41 | 342 | BCG_2634c | hypothetical protein | 77.64 | 351 | MAP2711c | hypothetical protein | 341 | 100 |
| MAP4_1106 | pyridoxal biosynthesis lyase PdxS | 303 | Rv2606c | Possible pyridoxine biosynthesis pro | 91.58 | 299 | Mb2638c | pyridoxal biosynthesis lyase P | 91.58 | 299 | MAV_3484 | pyridoxal biosynthesis lyase PdxS | 100 | 303 | BCG_2631c | pyridoxal biosynthesis lyase Pd | 91.58 | 299 | MAP2710c | pyridoxal biosynthesis lyase PdxS | 303 | 100 |
| MAP4_1107 | acyl-CoA thioesterase II | 278 | Rv2605c | Probable acyl-CoA thioesterase II Te | 87.36 | 281 | Mb2637c | acyl-CoA thioesterase | 87 | 281 | MAV_3483 | acyl-CoA thioesterase II | 100 | 278 | BCG_2630c | acyl-CoA thioesterase II tesB2 | 87 | 281 | MAP2709c | TesB2 | 278 | 100 |
| MAP4_1108 | glutamine amidotransferase subunit PdxT | 173 | Rv2604c | Probable glutamine amidotransferas | 86.14 | 198 | Mb2636c | glutamine amidotransferase s | 86.14 | 198 | MAV_3482 | glutamine amidotransferase subun | 99.4 | 198 | BCG_2629c | glutamine amidotransferase su | 86.14 | 198 | MAP2708c | hypothetical protein | 173 | 100 |
| MAP4_1109 | hypothetical protein | 106 | Rv1083 | hypothetical protein | 62.77 | 88 | Mb1112 | hypothetical protein | 62.77 | 88 | MAV_1207 | hypothetical protein | 97.17 | 106 | BCG_1141 | hypothetical protein | 62.77 | 88 | MAP2707c | hypothetical protein | 106 | 100 |
| MAP4_1110 | hypothetical protein | 671 | Rv1084 | hypothetical protein | 83.33 | 673 | Mb1113 | hypothetical protein | 83.33 | 673 | MAV_1208 | hypothetical protein | 98.51 | 671 | BCG_1142 | hypothetical protein | 83.33 | 673 | MAP2706c | hypothetical protein | 671 | 100 |
| MAP4_1111 | hypothetical protein | 127 | Rv2042c | hypothetical protein | 29.59 | 265 | Mb2068c | hypothetical protein | 29.59 | 265 | MAV_1209 | steroid delta-isomerase | 100 | 127 | BCG_2061c | hypothetical protein | 29.59 | 265 | MAP2705c | hypothetical protein | 127 | 100 |
| MAP4_1112 | putative hemolysin | 257 | Rv1085c | Possible hemolysin-like protein | 68.29 | 242 | Mb1114c | hemolysin-like protein | 68.29 | 242 | MAV_1210 | channel protein, hemolysin III famil | 100 | 257 | BCG_1143c | hemolysin-like protein | 68.29 | 242 | MAP2704 | hypothetical protein | 257 | 99.61 |
| MAP4_1113 | short-chain Z-isoprenyl diphosphate synthase | 264 | Rv1086 | Short (C15) chain Z-isoprenyl diphos | 89.69 | 262 | Mb1115 | short chain Z-isoprenyl dipho | 90.08 | 262 | MAV_1211 | short chain Z-isoprenyl diphosphat | 100 | 264 | BCG_1144 | Short (C15) chain Z-isoprenyl d | 90.08 | 262 | MAP2703c | hypothetical protein | 264 | 100 |
| MAP4_1114 | hypothetical protein | 456 | Rv0435c | Putative conserved ATPase | 41.03 | 728 | Mb0443c | ATPase | 41.03 | 728 | MAV_1212 | hypothetical protein | 99.78 | 456 | BCG_0474c | atpase | 41.03 | 728 | MAP2702c | hypothetical protein | 456 | 100 |
| MAP4_1115 | hypothetical protein | 141 | Rv2449c | hypothetical protein | 35.9 | 419 | Mb2476c | hypothetical protein | 35.9 | 419 | MAV_1213 | hypothetical protein | 100 | 141 | BCG_2469c | hypothetical protein | 35.9 | 419 | MAP2701c | hypothetical protein | 141 | 100 |
| MAP4_1116 | pantothenate kinase | 312 | Rv1092c | Probable pantothenate kinase CoaA | 94.55 | 312 | Mb1122c | pantothenate kinase | 94.55 | 312 | MAV_1214 | pantothenate kinase | 99.67 | 302 | BCG_1152c | pantothenate kinase | 94.55 | 312 | MAP2700 | pantothenate kinase | 312 | 100 |
| MAP4_1117 | serine hydroxymethyltransferase 1 | 426 | Rv1093 | Serine hydroxymethyltransferase 1 ( | 88.26 | 426 | Mb1123 | serine hydroxymethyltransfer | 88.03 | 426 | MAV_1215 | serine hydroxymethyltransferase | 99.53 | 443 | BCG_1153 | serine hydroxymethyltransfera | 88.03 | 426 | MAP2699c | serine hydroxymethyltransferase | 426 | 100 |
| MAP4_1118 | acyl-ACP desaturase DesA2 | 275 | Rv1094 | Possible acyl-[acyl-carrier protein] d | 78.55 | 275 | Mb1124 | acyl-ACP desaturase | 78.55 | 275 | MAV_1216 | Fatty acid desaturase | 98.91 | 275 | BCG_1154 | acyl-ACP desaturase | 78.55 | 275 | MAP2698c | DesA2 | 275 | 100 |
| MAP4_1119 | phosphate starvation-inducible protein PhoH | 433 | Rv1095 | Probable PHOH-like protein PhoH2 ( | 95.6 | 433 | Mb1125 | PhoH-like protein PhoH2 (pho | 95.6 | 433 | MAV_1217 | PhoH2 protein | 99.54 | 433 | BCG_1155 | phoH-like protein phoH2 | 95.6 | 433 | MAP2697c | PhoH2 | 433 | 100 |
| MAP4_1120 | glycosyl hydrolase | 291 | Rv1096 | Possible glycosyl hydrolase | 83.51 | 291 | Mb1126 | glycosyl hydrolase | 83.16 | 291 | MAV_1218 | carbohydrate degrading enzyme | 98.97 | 291 | BCG_1156 | glycosyl hydrolase | 83.16 | 291 | MAP2696c | hypothetical protein | 291 | 100 |
| MAP4_1121 | hypothetical protein | 477 | Rv3645 | Probable conserved transmembrane | 42.27 | 549 | Mb3669 | transmembrane protein | 42.27 | 549 | MAV_1220 | adenylate cyclase, family protein 3 | 99.37 | 477 | BCG_3703 | hypothetical protein | 42.27 | 549 | MAP2695c | hypothetical protein | 501 | 100 |
| MAP4_1122 | glycine and proline rich membrane protein | 339 | Rv1097c | Probable membrane glycine and pro | 64.96 | 293 | Mb1127c | hypothetical protein | 64.96 | 293 | MAV_1219 | hypothetical protein | 99.12 | 339 | BCG_1157c | membrane glycine and proline | 64.96 | 293 | MAP2694 | hypothetical protein | 351 | 100 |
| MAP4_1123 | fumarate hydratase class II | 470 | Rv1098c | Probable fumarase Fum (fumarate h | 90.85 | 474 | Mb1128c | fumarate hydratase | 90.85 | 474 | MAV_1221 | fumarate hydratase | 100 | 470 | BCG_1158c | fumarate hydratase | 90.85 | 474 | MAP2693 | fumarate hydratase | 470 | 100 |
| MAP4_1124 | fructose-1,6-bisphosphatase, GlpX type | 359 | Rv1099c | Fructose 1,6-bisphosphatase GlpX | 89.5 | 362 | Mb1129c | fructose 1,6-bisphosphatase I | 92.99 | 328 | MAV_1222 | fructose 1,6-bisphosphatase II | 100 | 359 | BCG_1159c | fructose 1,6-bisphosphatase II | 92.99 | 328 | MAP2692 | fructose 1,6-bisphosphatase II | 359 | 100 |
| MAP4_1125 | hypothetical protein | 228 | Rv1100 | hypothetical protein | 75.12 | 233 | Mb1130 | hypothetical protein | 75.12 | 233 | MAV_1223 | hypothetical protein | 98.25 | 228 | BCG_1160 | hypothetical protein | 75.12 | 233 | MAP2691c | hypothetical protein | 247 | 100 |
| MAP4_1126 | dienelactone hydrolase family protein | 267 | Rv2054 | hypothetical protein | 24.77 | 237 | Mb2080 | hypothetical protein | 24.77 | 237 | MAV_1224 | dienelactone hydrolase | 99.63 | 267 | BCG_2073 | hypothetical protein | 24.77 | 237 | MAP2690c | hypothetical protein | 267 | 100 |
| MAP4_1127 | putative para-nitrobenzyl esterase | 514 | Rv1104 | Possible para-nitrobenzyl esterase (f | 76.53 | 229 | Mb1134 | hypothetical protein | 76.53 | 229 | MAV_1226 | carboxylesterase | 98.83 | 514 | BCG_1164 | para-nitrobenzyl esterase | 76.53 | 229 | MAP2689c | hypothetical protein | 514 | 100 |
| MAP4_1128 | cholesterol dehydrogenase | 366 | Rv1106c | 3-beta-hydroxysteroid dehydrogena | 84.97 | 370 | Mb1136c | cholesterol dehydrogenase | 84.97 | 370 | MAV_1225 | 3-beta hydroxysteroid dehydrogen | 99.45 | 366 | BCG_1166c | cholesterol dehydrogenase | 84.97 | 370 | MAP2688 | hypothetical protein | 366 | 100 |
| MAP4_1129 | Exodeoxyribonuclease VII small subunit | 82 | Rv1107c | Probable exodeoxyribonuclease VII ( | 70.89 | 85 | Mb1137c | exodeoxyribonuclease VII sm | 70.89 | 85 | MAV_1227 | exodeoxyribonuclease VII small sub | 100 | 82 | BCG_1167c | exodeoxyribonuclease VII smal | 70.89 | 85 | MAP2687 | exodeoxyribonuclease VII small subunit | 82 | 100 |
| MAP4_1130 | Exodeoxyribonuclease VII large subunit | 415 | Rv1108c | Probable exodeoxyribonuclease VII ( | 85.89 | 415 | Mb1138c | exodeoxyribonuclease VII larg | 85.89 | 415 | MAV_1228 | exodeoxyribonuclease VII large sub | 99.21 | 379 | BCG_1168c | exodeoxyribonuclease VII large | 85.89 | 415 | MAP2686 | exodeoxyribonuclease VII large subunit | 415 | 100 |
| MAP4_1131 | hypothetical protein | 198 | Rv1109c | hypothetical protein | 72.3 | 212 | Mb1139c | hypothetical protein | 72.3 | 212 | MAV_1229 | hypothetical protein | 99.49 | 198 | BCG_1169c | hypothetical protein | 71.83 | 212 | MAP2685 | hypothetical protein | 198 | 100 |
| MAP4_1132 | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | 332 | Rv1110 | Probable LYTB-related protein LytB2 | 89.55 | 335 | Mb1140 | 4-hydroxy-3-methylbut-2-eny | 89.55 | 335 | MAV_1230 | 4-hydroxy-3-methylbut-2-enyl diph | 99.32 | 296 | BCG_1170 | 4-hydroxy-3-methylbut-2-enyl | 89.55 | 335 | MAP2684c | 4-hydroxy-3-methylbut-2-enyl diphosph | 332 | 100 |
| MAP4_1133 | hypothetical protein | 402 | Rv1111c | hypothetical protein | 46.17 | 327 | Mb1141c | hypothetical protein | 46.17 | 327 | MAV_1231 | hypothetical protein | 93.83 | 368 | BCG_1171c | hypothetical protein | 46.17 | 327 | MAP2683 | hypothetical protein | 402 | 100 |
| MAP4_1134 | GTP-dependent nucleic acid-binding protein | 357 | Rv1112 | Probable GTP binding protein | 89.92 | 357 | Mb1142 | GTP-dependent nucleic acid-b | 89.64 | 357 | MAV_1232 | GTP-dependent nucleic acid-bindin | 99.43 | 350 | BCG_1172 | GTP-dependent nucleic acid-bi | 89.64 | 357 | MAP2682c | GTP-dependent nucleic acid-binding pro | 357 | 99.72 |
| MAP4_1135 | HNH endonuclease family protein | 314 | Rv2469c | hypothetical protein | 31.75 | 222 | Mb2496c | hypothetical protein | 31.75 | 222 | MAV_1236 | HNH endonuclease, putative | 98.55 | 69 | BCG_2489c | hypothetical protein | 31.75 | 222 | MAP2681c | hypothetical protein | 314 | 100 |
| MAP4_1136 | hypothetical protein | 123 | Rv1114 | Possible toxin VapC32 Contains PIN | 64.23 | 124 | Mb1144 | hypothetical protein | 64.23 | 124 | MAV_1240 | PilT domain-containing protein | 100 | 123 | BCG_1174 | hypothetical protein | 64.23 | 124 | MAP2680c | hypothetical protein | 123 | 100 |
| MAP4_1137 | hypothetical protein | 135 | Rv1261c | hypothetical protein | 72.93 | 149 | Mb1292c | hypothetical protein | 72.93 | 149 | MAV_1241 | hypothetical protein | 99.26 | 135 | BCG_1320c | hypothetical protein | 72.93 | 149 | MAP2679c | hypothetical protein | 146 | 99.26 |
| MAP4_1139 | glyoxalase-like domain-containing protein | 132 | Rv0546c | hypothetical protein | 26.27 | 128 | Mb0560c | hypothetical protein | 26.27 | 128 | MAV_1244 | glyoxalase | 97.73 | 132 | BCG_0590c | hypothetical protein | 26.27 | 128 | MAP2677c | hypothetical protein | 132 | 100 |
| MAP4_1140 | hypothetical protein | 127 | Rv3312A | Secreted protein antigen | 43.94 | 103 | Mb3341c | hypothetical protein | 43.94 | 103 | MAV_1245 | secreted protein antigen | 97.64 | 127 | BCG_3378c | hypothetical protein | 43.94 | 103 | MAP1972c | hypothetical protein | 123 | 55.17 |
| MAP4_1141 | hypothetical protein | 117 | Rv3762c | Possible hydrolase | 33.8 | 626 | Mb3788c | hydrolase | 33.8 | 626 | MAV_1246 | hypothetical protein | 92.31 | 110 | BCG_3821c | hydrolase | 33.8 | 626 | MAP2676c | hypothetical protein | 117 | 100 |
| MAP4_1142 | hypothetical protein | 167 | Rv1115 | Possible exported protein | 71.61 | 232 | Mb1145 | hypothetical protein | 71.61 | 232 | MAV_1247 | hypothetical protein | 98.8 | 136 | BCG_1175 | hypothetical protein | 71.61 | 232 | MAP2675c | hypothetical protein | 167 | 100 |
| MAP4_1144 | hypothetical protein | 309 | Rv1118c | hypothetical protein | 65.26 | 286 | Mb1149c | hypothetical protein | 65.26 | 286 | MAV_1249 | hypothetical protein | 99.56 | 227 | BCG_1179c | hypothetical protein | 65.26 | 286 | MAP2673 | hypothetical protein | 309 | 100 |
| MAP4_1145 | Putative adenylateguanylate cyclase | 272 | Rv1120c | hypothetical protein | 80.54 | 164 | Mb1151c | hypothetical protein | 79.87 | 164 | MAV_1250 | adenylate and guanylate cyclase ca | 100 | 272 | BCG_1181c | hypothetical protein | 80.54 | 164 | MAP2672 | hypothetical protein | 223 | 99.55 |
| MAP4_1146 | Glucose-6-phosphate 1-dehydrogenase | 469 | Rv1121 | Probable glucose-6-phosphate 1-deh | 78.28 | 466 | Mb1152 | glucose-6-phosphate 1-dehyd | 78.28 | 466 | MAV_1252 | glucose-6-phosphate 1-dehydroger | 99.36 | 469 | BCG_1182 | glucose-6-phosphate 1-dehydr | 78.28 | 466 | MAP2671c | glucose-6-phosphate 1-dehydrogenase | 469 | 100 |
| MAP4_1147 | 6-phosphogluconate dehydrogenase | 340 | Rv1122 | Probable 6-phosphogluconate dehyd | 86.76 | 340 | Mb1153 | 6-phosphogluconate dehydro | 86.76 | 340 | MAV_1253 | 6-phosphogluconate dehydrogenas | 99.41 | 340 | BCG_1183 | 6-phosphogluconate dehydrog | 86.76 | 340 | MAP2670c | 6-phosphogluconate dehydrogenase-lik | 340 | 100 |
| MAP4_1148 | peroxidase bpoB | 309 | Rv1123c | Possible peroxidase BpoB (non-haen | 75.09 | 302 | Mb1154c | peroxidase BpoB | 75.09 | 302 | MAV_1254 | alpha/beta hydrolase | 99.64 | 277 | BCG_1184c | peroxidase bpoB | 75.09 | 302 | MAP2669 | BpoB | 309 | 99.68 |
| MAP4_1149 | 3-demethylubiquinone-9 3-methyltransferase | 157 | Rv1505c | hypothetical protein | 25.86 | 221 | Mb1543c | hypothetical protein | 25.86 | 221 | MAV_1255 | 3-demethylubiquinone-9 3-methylt | 99.36 | 157 | BCG_1568c | hypothetical protein | 25.86 | 221 | MAP2668c | hypothetical protein | 157 | 100 |
| MAP4_1150 | epoxide hydrolase ephC | 284 | Rv1124 | Probable epoxide hydrolase EphC (e | 79.43 | 316 | Mb1155 | epoxide hydrolase | 79.43 | 316 | MAV_1256 | alpha/beta hydrolase | 98.94 | 304 | BCG_1185 | epoxide hydrolase ephC | 79.43 | 316 | MAP2667c | EphC | 284 | 100 |
| MAP4_1151 | hypothetical protein | 413 | Rv1125 | hypothetical protein | 70.94 | 414 | Mb1156 | hypothetical protein | 70.94 | 414 | MAV_1257 | hypothetical protein | 99.26 | 408 | BCG_1186 | hypothetical protein | 70.94 | 414 | MAP2666c | hypothetical protein | 413 | 100 |
| MAP4_1152 | hypothetical protein | 201 | Rv1126c | hypothetical protein | 68.66 | 201 | Mb1157c | hypothetical protein | 68.66 | 201 | MAV_1258 | hypothetical protein | 98.51 | 201 | BCG_1187c | hypothetical protein | 68.66 | 201 | MAP2665 | hypothetical protein | 201 | 100 |
| MAP4_1153 | pyruvate phosphate dikinase | 521 | Rv1127c | Probable pyruvate, phosphate dikina | 77.07 | 490 | Mb1158c | pyruvate phosphate dikinase | 77.28 | 490 | MAV_1259 | pyruvate phosphate dikinase | 99.62 | 521 | BCG_1188c | pyruvate phosphate dikinase | 77.28 | 490 | MAP2664 | pyruvate phosphate dikinase | 560 | 99.81 |
| MAP4_1154 | hypothetical protein, DoxX family | 169 | Rv3005c | hypothetical protein | 36.64 | 279 | Mb3030c | hypothetical protein | 36.64 | 279 | MAV_1260 | DoxX subfamily protein, putative | 100 | 169 | BCG_3027c | hypothetical protein | 36.64 | 279 | MAP2663c | hypothetical protein | 169 | 100 |
| MAP4_1155 | hypothetical protein | 582 | Rv1132 | hypothetical protein | 78.78 | 576 | Mb1163 | hypothetical protein | 78.61 | 576 | MAV_1261 | hypothetical protein | 99.83 | 582 | BCG_1193 | hypothetical protein | 78.78 | 576 | MAP2662c | hypothetical protein | 582 | 100 |
| MAP4_1156 | 5-methyltetrahydropteroyltriglutamate histidine kinase | 756 | Rv1133c | Probable 5-methyltetrahydropteroy | 86.17 | 759 | Mb1164c | 5- methyltetrahydropteroyltr | 86.17 | 759 | MAV_1262 | 5-methyltetrahydropteroyltriglutar | 99.47 | 756 | BCG_1194c | 5- methyltetrahydropteroyltrig | 86.17 | 759 | MAP2661 | 5-methyltetrahydropteroyltriglutamate | 756 | 100 |
| MAP4_1157 | hypothetical protein | 209 | Rv1106c | 3-beta-hydroxysteroid dehydrogena | 29.68 | 370 | Mb1136c | cholesterol dehydrogenase | 29.68 | 370 | MAV_1263 | NAD dependent epimerase/dehydr | 97.13 | 209 | BCG_1166c | cholesterol dehydrogenase | 29.68 | 370 | MAP2660 | hypothetical protein | 209 | 100 |
| MAP4_1160 | Transcriptional regulator, TetR family | 429 | Rv3557c | Transcriptional regulatory protein (p | 33.74 | 200 | Mb3587c | TetR family transcriptional re | 33.74 | 200 | MAV_1265 | TetR family transcriptional regulato | 98.37 | 429 | BCG_3621c | TetR family transcriptional regu | 33.74 | 200 | MAP2658 | hypothetical protein | 429 | 100 |
| MAP4_1161 | oxidoreductase, nitroreductase family protein | 215 | Rv3368c | Possible oxidoreductase | 40 | 214 | Mb3403c | oxidoreductase | 40 | 214 | MAV_1266 | nitroreductase | 99.07 | 215 | BCG_3440c | oxidoreductase | 40 | 214 | MAP2657 | hypothetical protein | 216 | 99.53 |
| MAP4_1162 | acyl-CoA dehydrogenase | 366 | Rv1933c | Probable acyl-CoA dehydrogenase F | 36.74 | 363 | Mb1968c | acyl-CoA dehydrogenase | 36.74 | 363 | MAV_1267 | acyl-CoA dehydrogenase domain-c | 99.18 | 366 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 36.74 | 363 | MAP2656 | hypothetical protein | 366 | 100 |
| MAP4_1163 | acyl-CoA dehydrogenase | 389 | Rv3560c | Probable acyl-CoA dehydrogenase F | 39.74 | 385 | Mb3590c | acyl-CoA dehydrogenase | 39.74 | 385 | MAV_1268 | acyl-CoA dehydrogenase domain-c | 99.49 | 389 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 39.74 | 385 | MAP2655 | hypothetical protein | 389 | 100 |
| MAP4_1164 | hypothetical protein | 585 | Rv1969 | Mce-family protein Mce3D | 35.38 | 423 | Mb0454c | transmembrane protein | 46.88 | 256 | MAV_1269 | von Willebrand factor type A | 98.42 | 571 | BCG_0485c | hypothetical protein | 46.88 | 256 | MAP2654c | hypothetical protein | 607 | 100 |
| MAP4_1165 | denitrification regulatory protein | 280 | Rv2426c | hypothetical protein | 26.14 | 291 | Mb2450c | hypothetical protein | 26.14 | 291 | MAV_1270 | denitrification regulatory protein n | 98.93 | 280 | BCG_2443c | hypothetical protein | 26.14 | 291 | MAP2653c | NirQ | 304 | 100 |
| MAP4_1166 | hypothetical protein | 372 | Rv0408 | Probable phosphate acetyltransfera | 21.95 | 690 | Mb0416 | phosphate acetyltransferase | 21.95 | 690 | MAV_1271 | hypothetical protein | 99.19 | 372 | BCG_0447 | phosphate acetyltransferase | 21.95 | 690 | MAP2652c | hypothetical protein | 372 | 100 |
| MAP4_1167 | hypothetical protein | 381 | Rv2811 | hypothetical protein | 44.83 | 202 | Mb2834 | hypothetical protein | 44.83 | 202 | MAV_1272 | hypothetical protein | 99.74 | 381 | BCG_2829 | hypothetical protein | 44.83 | 202 | MAP2651c | hypothetical protein | 381 | 100 |
| MAP4_1168 | putative short-chain dehydrogenase | 341 | Rv3057c | Probable short chain alcohol dehydr | 36.14 | 287 | Mb3083c | short chain dehydrogenase | 36.14 | 287 | MAV_1273 | NAD dependent epimerase/dehydr | 98.83 | 341 | BCG_3082c | short chain dehydrogenase | 36.14 | 287 | MAP2650c | hypothetical protein | 341 | 100 |
| MAP4_1169 | putative cytochrome P450 hydroxylase | 404 | Rv3518c | Probable cytochrome P450 monoox | 35.53 | 398 | Mb0801 | cytochrome P450 126 | 37.5 | 414 | MAV_1274 | cytochrome P450 superfamily prot | 99.5 | 404 | BCG_0830 | cytochrome P450 126 cyp126 | 37.5 | 414 | MAP2649c | hypothetical protein | 404 | 99.75 |
| MAP4_1172 | acetyl-CoA acetyltransferase | 382 | Rv3556c | Probable acetyl-CoA acetyltransfera | 51.16 | 386 | Mb3586c | acetyl-CoA acetyltransferase | 51.16 | 386 | MAV_1276 | acetyl-CoA acetyltransferase | 100 | 382 | BCG_3620c | acetyl-CoA acetyltransferase | 51.16 | 386 | MAP2646c | FadA6_3 | 382 | 100 |
| MAP4_1173 | Enoyl-CoA hydratase | 263 | Rv0222 | Probable enoyl-CoA hydratase EchA | 47.33 | 262 | Mb1168 | enoyl-CoA hydratase | 80.36 | 113 | MAV_1277 | carnitinyl-CoA dehydratase | 99.62 | 263 | BCG_1198 | enoyl-CoA hydratase | 80.36 | 113 | MAP2645c | EchA1_1 | 263 | 100 |
| MAP4_1174 | oxidoreductase | 338 | Rv1138c | Possible oxidoreductase | 85.76 | 338 | Mb1170c | oxidoreductase | 85.76 | 338 | MAV_1278 | oxidoreductase | 99.11 | 337 | BCG_1200c | oxidoreductase | 85.76 | 338 | MAP2644 | hypothetical protein | 338 | 100 |
| MAP4_1175 | hypothetical protein | 166 | Rv1139c | hypothetical protein | 80.61 | 166 | Mb1171c | hypothetical protein | 80.61 | 166 | MAV_1279 | isoprenylcysteine carboxyl methylt | 99.4 | 166 | BCG_1201c | hypothetical protein | 80.61 | 166 | MAP2643 | hypothetical protein | 166 | 99.4 |
| MAP4_1176 | Chalcone synthase | 349 | Rv1665 | Chalcone synthase Pks11 | 50.14 | 353 | Mb1693 | chalcone synthase | 50.14 | 353 | MAV_1280 | transferase | 99.71 | 349 | BCG_1704 | chalcone synthase pks11 | 50.14 | 353 | MAP2642 | hypothetical protein | 349 | 100 |
| MAP4_1177 | hypothetical protein | 382 | Rv3634c | UDP-glucose 4-epimerase GalE1 (gal | 35 | 314 | Mb3658c | UDP-glucose 4-epimerase | 35 | 314 | MAV_1281 | hypothetical protein | 99.48 | 382 | BCG_3692c | UDP-glucose 4-epimerase | 35 | 314 | MAP2641c | hypothetical protein | 461 | 100 |
| MAP4_1178 | hypothetical protein | 240 | Rv1140 | Probable integral membrane protein | 75 | 282 | Mb1172 | hypothetical protein | 75 | 282 | MAV_1282 | caax amino protease | 99.17 | 240 | BCG_1202 | integral membrane protein | 75 | 282 | MAP2640c | hypothetical protein | 240 | 100 |
| MAP4_1179 | Enoyl-CoA hydratase | 270 | Rv1142c | Probable enoyl-CoA hydratase EchA | 71.85 | 268 | Mb1174c | enoyl-CoA hydratase | 71.85 | 268 | MAV_1283 | enoyl-CoA hydratase | 99.63 | 270 | BCG_1204c | enoyl-CoA hydratase | 71.85 | 268 | MAP2639 | enoyl-CoA hydratase | 270 | 100 |
| MAP4_1180 | Alpha-methylacyl-CoA racemase | 360 | Rv1143 | Probable alpha-methylacyl-CoA race | 84.68 | 360 | Mb1175 | alpha-methylacyl-CoA racema | 84.68 | 360 | MAV_1284 | Mcr protein | 99.72 | 360 | BCG_1205 | alpha-methylacyl-CoA racemas | 84.68 | 360 | MAP2638c | Mcr | 360 | 100 |
| MAP4_1181 | short-chain type CoA dehydrogenase | 254 | Rv1144 | Probable short-chain type dehydrog | 81.1 | 250 | Mb1176 | short-chain type dehydrogena | 81.1 | 250 | MAV_1285 | 3-hydroxyacyl-CoA dehydrogenase | 100 | 254 | BCG_1206 | short-chain type dehydrogenas | 81.1 | 250 | MAP2637c | hypothetical protein | 254 | 100 |
| MAP4_1182 | hypothetical protein | 48 | Rv3003c | Acetolactate synthase (large subunit | 47.37 | 618 | Mb3028c | acetolactate synthase 1 catal | 47.37 | 618 | MAV_1286 | hypothetical protein | 100 | 40 | BCG_3025c | acetolactate synthase 1 catalyt | 47.37 | 618 | MAP2636 | hypothetical protein | 48 | 100 |
| MAP4_1183 | transmembrane transport protein, MMPL family | 780 | Rv1146 | Probable conserved transmembrane | 83.03 | 470 | Mb1177 | transmembrane transport pro | 82.6 | 781 | MAV_1287 | mmpL protein | 99.6 | 808 | BCG_1207 | transmembrane transport prot | 82.6 | 781 | MAP2635c | hypothetical protein | 800 | 100 |
| MAP4_1184 | methyltransferase domain-containing protein | 215 | Rv1147 | hypothetical protein | 72.06 | 216 | Mb1178 | hypothetical protein | 72.06 | 216 | MAV_1288 | hypothetical protein | 99.05 | 211 | BCG_1208 | hypothetical protein | 72.06 | 216 | MAP2634c | hypothetical protein | 215 | 100 |
| MAP4_1185 | NAD-dependent protein deacetylase of SIR2family | 237 | Rv1151c | Transcriptional regulatory protein | 86.08 | 237 | Mb1182c | NAD-dependent deacetylase | 86.08 | 237 | MAV_1289 | NAD-dependent deacetylase | 99.14 | 233 | BCG_1212c | NAD-dependent deacetylase | 86.08 | 237 | MAP2633 | NAD-dependent deacetylase | 237 | 100 |
| MAP4_1186 | Transcriptional regulator, GntR family | 121 | Rv1152 | Probable transcriptional regulatory | 82.64 | 121 | Mb1183 | transcriptional regulator | 82.64 | 121 | MAV_1290 | GntR family transcriptional regulato | 99.17 | 121 | BCG_1213 | transcriptional regulatory prot | 82.64 | 121 | MAP2632c | hypothetical protein | 121 | 100 |
| MAP4_1187 | hypothetical protein | 186 | Rv1154c | Hypothetical protein | 77.9 | 213 | Mb1185c | hypothetical protein | 77.9 | 213 | MAV_1291 | hypothetical protein | 100 | 186 | BCG_1215c | hypothetical protein | 77.9 | 213 | MAP2631 | hypothetical protein | 186 | 100 |
| MAP4_1188 | putative pyridoxamine 5'-phosphate oxidasefamily pro | 147 | Rv1155 | Possible pyridoxamine 5'-phosphate | 91.84 | 147 | Mb1186 | hypothetical protein | 92.52 | 147 | MAV_1292 | pyridoxamine 5'-phosphate oxidase | 100 | 147 | BCG_1216 | hypothetical protein | 92.52 | 147 | MAP2630c | hypothetical protein | 147 | 100 |
| MAP4_1189 | hypothetical protein | 74 | Rv3695 | Possible conserved membrane prote | 55.56 | 310 | Mb3720 | hypothetical protein | 55.56 | 310 | MAV_1293 | hypothetical protein | 95.95 | 74 | BCG_3754 | hypothetical protein | 55.56 | 310 | MAP2629c | hypothetical protein | 74 | 100 |
| MAP4_1190 | hypothetical protein | 191 | Rv1156 | hypothetical protein | 88.46 | 195 | Mb1187 | hypothetical protein | 88.46 | 195 | MAV_1294 | base excision DNA repair protein, H | 100 | 191 | BCG_1217 | hypothetical protein | 88.46 | 195 | MAP2628c | hypothetical protein | 191 | 100 |
| MAP4_1191 | hypothetical protein | 48 | Rv0064A | Possible antitoxin VapB1 | 27.5 | 79 | Mb0467 | aldehyde dehydrogenase | 30.77 | 507 | MAV_1295 | hypothetical protein | 100 | 48 | BCG_0095A | antitoxin | 27.5 | 79 | MAP2627c | hypothetical protein | 48 | 100 |
| MAP4_1192 | conserved alanine and proline rich protein | 363 | Rv1157c | Conserved ala-, pro-rich protein | 88.49 | 371 | Mb1188c | hypothetical protein | 88.49 | 371 | MAV_1296 | hypothetical protein | 100 | 359 | BCG_1218c | hypothetical protein | 87.88 | 347 | MAP2626 | hypothetical protein | 363 | 100 |
| MAP4_1193 | conserved alanine and proline rich protein | 232 | Rv1158c | Conserved hypothetical ala-, pro-ric | 52.8 | 227 | Mb1189c | hypothetical protein | 52.8 | 227 | MAV_1297 | hypothetical protein | 98.78 | 196 | BCG_1219c | hypothetical protein | 52.8 | 227 | MAP2625 | hypothetical protein | 232 | 100 |
| MAP4_1194 | mannosyltransferase | 437 | Rv1159 | Mannosyltransferase PimE | 75.67 | 431 | Mb1190 | mannosyltransferase | 75.67 | 431 | MAV_1298 | mannosyltransferase | 98.22 | 394 | BCG_1220 | mannosyltransferase | 75.67 | 431 | MAP2624c | mannosyltransferase | 437 | 100 |
| MAP4_1195 | Pterin-4-alpha-carbinolamine dehydratase | 94 | Rv1159A | hypothetical protein | 73.4 | 94 | Mb1191c | pterin-4-alpha-carbinolamine | 73.4 | 94 | MAV_1299 | pterin-4-alpha-carbinolamine dehy | 98.94 | 94 | BCG_1221c | pterin-4-alpha-carbinolamine d | 73.4 | 94 | MAP2623 | pterin-4-alpha-carbinolamine dehydrat | 109 | 100 |
| MAP4_1196 | hypothetical protein | 257 | Rv1682 | Probable coiled-coil structural prote | 36.03 | 305 | Mb1709 | coiled-coil structural protein | 36.03 | 305 | MAV_1300 | hypothetical protein | 98.05 | 257 | BCG_1720 | coiled-coil structural protein | 36.03 | 305 | MAP2622 | hypothetical protein | 314 | 100 |
| MAP4_1197 | mutator protein MutT | 130 | Rv1160 | Probable mutator protein MutT2 (7, | 75.38 | 141 | Mb1192 | 7,8-dihydro-8-oxoguanine-tri | 75.38 | 141 | MAV_1301 | hydrolase, NUDIX family protein | 98.46 | 140 | BCG_1222 | mutator protein mutT2 | 75.38 | 141 | MAP2621c | hypothetical protein | 130 | 100 |
| MAP4_1198 | Respiratory nitrate reductase alpha chain | 1228 | Rv1161 | Respiratory nitrate reductase (alpha | 87.09 | 1232 | Mb1193 | respiratory nitrate reductase | 86.93 | 1232 | MAV_1303 | nitrate reductase, alpha subunit | 99.02 | 1230 | BCG_1223 | respiratory nitrate reductase (a | 86.93 | 1232 | MAP2620c | NarG | 1230 | 99.84 |
| MAP4_1199 | Respiratory nitrate reductase beta chain | 538 | Rv1162 | Probable respiratory nitrate reducta | 83.33 | 558 | Mb1194 | respiratory nitrate reductase | 83.33 | 558 | MAV_1304 | nitrate reductase, beta subunit | 99.81 | 538 | BCG_1224 | respiratory nitrate reductase s | 83.33 | 558 | MAP2619c | NarH | 538 | 100 |
| MAP4_1200 | Respiratory nitrate reductase delta chain | 212 | Rv1163 | Probable respiratory nitrate reducta | 75.49 | 201 | Mb1195 | respiratory nitrate reductase | 75.49 | 201 | MAV_1305 | nitrate reductase molybdenum cof | 99.06 | 227 | BCG_1225 | respiratory nitrate reductase (c | 75 | 201 | MAP2618c | NarJ | 212 | 100 |
| MAP4_1201 | Respiratory nitrate reductase gamma chain | 243 | Rv1164 | Probable respiratory nitrate reducta | 65.55 | 246 | Mb1196 | respiratory nitrate reductase | 65.55 | 246 | MAV_1306 | respiratory nitrate reductase, gamr | 100 | 243 | BCG_1226 | respiratory nitrate reductase (g | 65.55 | 246 | MAP2617c | NarI | 243 | 100 |
| MAP4_1202 | GTP-binding translation elongation factor | 629 | Rv1165 | Possible GTP-binding translation elo | 87.28 | 628 | Mb1197 | GTP-binding translation elong | 87.28 | 628 | MAV_1307 | GTP-binding protein TypA/BipA | 99.68 | 629 | BCG_1227 | GTP-binding translation elonga | 87.28 | 628 | MAP2616c | hypothetical protein | 678 | 99.84 |
| MAP4_1203 | lipoprotein LpqW | 647 | Rv1166 | Probable conserved lipoprotein Lpq | 82.73 | 635 | Mb1198 | lipoprotein LPQW | 82.73 | 635 | MAV_1308 | extracellular solute-binding protein | 99.85 | 647 | BCG_1228 | lipoprotein lpqW | 82.73 | 635 | MAP2615c | hypothetical protein | 647 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1204 | Transcriptional regulator, TetR family | 230 | Rv1167c | Probable transcriptional regulatory | 68.89 | 201 | Mb1199c | transcriptional regulator | 68.89 | 201 | MAV_1309 | TetR family transcriptional regulato | 99.13 | 230 | BCG_1229c | transcriptional regulatory prote | 68.89 | 201 | MAP2614 | hypothetical protein | 230 | 100 |
| MAP4_1205 | N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha- D-gl | 300 | Rv1170 | N-acetyl-1-D-myo-inositol-2-amino-2 | 73.42 | 303 | Mb1203 | N-Acetyl-1-D-myo-Inositol-2-a | 73.42 | 303 | MAV_1310 | N-Acetyl-1-D-myo-Inositol-2-amino | 98.33 | 300 | BCG_1233 | N-Acetyl-1-D-myo-Inositol-2-an | 73.42 | 303 | MAP2613c | hypothetical protein | 300 | 100 |
| MAP4_1206 | hypothetical protein | 153 | Rv1171 | hypothetical protein | 67.11 | 146 | Mb1204 | hypothetical protein | 67.11 | 146 | MAV_1311 | hypothetical protein | 100 | 153 | BCG_1234 | hypothetical protein | 67.11 | 146 | MAP2612c | hypothetical protein | 162 | 99.35 |
| MAP4_1207 | F420 biosynthesis protein FbiC | 888 | Rv1173 | Probable F420 biosynthesis protein | 89.44 | 856 | Mb1206 | FO synthase | 89.44 | 856 | MAV_1312 | FO synthase | 99.42 | 867 | BCG_1236 | FO synthase | 89.44 | 856 | MAP2611c | FO synthase | 867 | 99.88 |
| MAP4_1208 | hypothetical protein | 257 | Rv3408 | Possible toxin VapC47 Contains PIN | 45.65 | 136 | Mb3442 | hypothetical protein | 45.65 | 136 | MAV_1313 | hypothetical protein | 98.83 | 257 | BCG_3478 | hypothetical protein | 45.65 | 136 | MAP2070 | hypothetical protein | 206 | 63.16 |
| MAP4_1209 | putative low molecular weight T-cell antigen | 110 | Rv1174c | Low molecular weight T-cell antigen | 61.82 | 110 | Mb1207c | hypothetical protein | 61.82 | 110 | MAV_1314 | hypothetical protein | 100 | 110 | BCG_1237c | hypothetical protein | 61.82 | 110 | MAP2609 | hypothetical protein | 110 | 100 |
| MAP4_1210 | transposase | 329 | Rv2812 | Probable transposase | 32.65 | 469 | Mb2836 | transposase | 32.29 | 265 | MAV_2002 | transposase | 83.28 | 345 | BCG_2830 | transposase | 32.65 | 469 | MAP2608 | hypothetical protein | 329 | 100 |
| MAP4_1211 | 4Fe-4S ferredoxin, iron-sulfur binding protein | 108 | Rv1177 | Probable ferredoxin FdxC | 93.4 | 108 | Mb1210 | ferredoxin FdxC | 93.4 | 108 | MAV_1316 | ferredoxin | 100 | 108 | BCG_1240 | ferredoxin fdxC | 93.4 | 108 | MAP2607c | FdxC_2 | 108 | 100 |
| MAP4_1212 | N-succinyl-L,L-diaminopimelate aminotransferase alter | 372 | Rv1178 | Probable aminotransferase | 83.89 | 362 | Mb1211 | N-succinyldiaminopimelate ai | 83.89 | 362 | MAV_1317 | N-succinyldiaminopimelate aminot | 99.19 | 372 | BCG_1241 | N-succinyldiaminopimelate am | 83.89 | 362 | MAP2606c | N-succinyldiaminopimelate aminotrans | 372 | 100 |
| MAP4_1213 | hypothetical protein | 796 | Rv2690c | Probable conserved integral membr | 34.04 | 657 | Mb2709c | hypothetical protein | 34.04 | 663 | MAV_1318 | OB-fold nucleic acid binding domai | 99.62 | 794 | BCG_2703c | integral membrane alanine and | 34.04 | 663 | MAP2605c | hypothetical protein | 796 | 100 |
| MAP4_1214 | Polyketide synthase | 763 | Rv1527c | Probable polyketide synthase Pks5 | 71.82 | 2108 | Mb1213 | polyketide beta-ketoacyl synt | 81.07 | 2085 | MAV_1321 | mycocerosic acid synthase | 98.22 | 2089 | BCG_1243 | polyketide beta-ketoacyl synth | 81.07 | 2085 | MAP2604c | hypothetical protein | 763 | 100 |
| MAP4_1215 | polyketide beta-ketoacyl synthase PKS4 | 1336 | Rv1181 | Probable polyketide beta-ketoacyl s | 73.91 | 1582 | Mb1213 | polyketide beta-ketoacyl synt | 73.84 | 2085 | MAV_1321 | mycocerosic acid synthase | 98.58 | 2089 | BCG_1243 | polyketide beta-ketoacyl synth | 73.91 | 2085 | MAP2603c | hypothetical protein | 1336 | 100 |
| MAP4_1216 | hypothetical protein | 81 | Rv0974c | Probable acetyl-/propionyl-CoA carb | 31.03 | 529 | Mb0999c | acetyl-/propionyl-CoA carbox | 31.03 | 529 | MAV_1320 | hypothetical protein | 98.77 | 81 | BCG_1028c | acetyl-/propionyl-coa carboxyl | 31.03 | 529 | MAP2602 | hypothetical protein | 81 | 100 |
| MAP4_1217 | hypothetical protein | 67 | Rv0634A | hypothetical protein | 54.1 | 83 | Mb0652 | hypothetical protein | 54.1 | 83 | MAV_1323 | hypothetical protein | 98.51 | 67 | BCG_0682 | hypothetical protein | 54.1 | 83 | MAP4105 | hypothetical protein | 76 | 60 |
| MAP4_1218 | PPE family protein | 357 | Rv1790 | PPE family protein PPE27 | 49.38 | 350 | Mb1818 | PPE family protein | 49.69 | 350 | MAV_1322 | PPE family protein | 98.6 | 363 | BCG_1822 | PPE family protein | 49.38 | 350 | MAP2601 | hypothetical protein | 357 | 100 |
| MAP4_1219 | PPE family protein | 395 | Rv1808 | PPE family protein PPE32 | 46.2 | 409 | Mb1837 | PPE family protein | 46.2 | 409 | MAV_1324 | PPE family protein | 99.24 | 395 | BCG_1841 | PPE family protein | 46.2 | 409 | MAP2600 | hypothetical protein | 395 | 100 |
| MAP4_1220 | bifunctional sulfate adenyltransferase/adenylylsulfate | 230 | Rv1286 | Probable bifunctional enzyme CysN/ | 46.67 | 614 | Mb1317 | bifunctional sulfate adenylylt | 46.67 | 614 | MAV_1325 | adenylylsulfate kinase | 100 | 230 | BCG_1345 | bifunctional sulfate adenylyltra | 46.67 | 614 | MAP2599c | hypothetical protein | 230 | 100 |
| MAP4_1221 | sulfate adenylyltransferase | 419 | Rv3877 | ESX conserved component EccD1 ES | 37.14 | 511 | Mb3907 | transmembrane protein | 37.14 | 511 | MAV_1326 | sulfate adenylyltransferase | 99.52 | 419 | BCG_3155c | two component sensor histidin | 35.19 | 578 | MAP2598c | sulfate adenylyltransferase | 419 | 100 |
| MAP4_1222 | hypothetical protein | 110 | Rv0339c | Possible transcriptional regulatory p | 44.44 | 832 | Mb0346c | transcriptional regulator | 44.44 | 832 | MAV_1327 | hypothetical protein | 100 | 110 | BCG_0378c | transcriptional regulatory prote | 44.44 | 832 | MAP2597c | hypothetical protein | 110 | 99.09 |
| MAP4_1223 | fatty-acid-CoA ligase | 579 | Rv1185c | Probable fatty-acid-AMP ligase FadD | 71.16 | 578 | Mb1217c | acyl-CoA synthetase | 71.16 | 578 | MAV_1328 | acyl-CoA synthetase | 98.1 | 579 | BCG_1247c | acyl-CoA synthetase | 71.16 | 578 | MAP2596 | acyl-CoA synthetase | 579 | 100 |
| MAP4_1224 | PPE family protein | 552 | Rv0256c | PPE family protein PPE2 | 55.22 | 556 | Mb0262c | PPE family protein | 55.22 | 556 | MAV_1329 | PPE family protein | 98.73 | 555 | BCG_0294c | PPE family protein | 55.22 | 556 | MAP2595 | hypothetical protein | 585 | 99.21 |
| MAP4_1225 | hypothetical protein | 530 | Rv1186c | hypothetical protein | 78.13 | 538 | Mb1218c | hypothetical protein | 78.13 | 538 | MAV_1330 | hypothetical protein | 99.43 | 530 | BCG_1248c | hypothetical protein | 78.13 | 538 | MAP2594 | hypothetical protein | 530 | 100 |
| MAP4_1226 | pyrroline-5-carboxylate dehydrogenase | 546 | Rv1187 | Probable pyrroline-5-carboxylate de | 88.64 | 543 | Mb1219 | pyrroline-5-carboxylate dehy | 88.64 | 543 | MAV_1331 | 1-pyrroline-5-carboxylate dehydrog | 99.63 | 555 | BCG_1249 | pyrroline-5-carboxylate dehydr | 88.64 | 543 | MAP2593c | RocA | 546 | 100 |
| MAP4_1227 | Proline dehydrogenase | 320 | Rv1188 | Probable proline dehydrogenase | 73.21 | 329 | Mb1220 | proline dehydrogenase | 73.21 | 329 | MAV_1332 | proline dehydrogenase | 99.38 | 320 | BCG_1250 | proline dehydrogenase | 73.21 | 329 | MAP2592c | hypothetical protein | 320 | 100 |
| MAP4_1228 | Transcriptional regulator, TetR family | 200 | Rv1534 | Probable transcriptional regulator | 32.34 | 225 | Mb1561 | transcriptional regulator | 32.34 | 225 | MAV_1333 | TetR family transcriptional regulato | 99 | 200 | BCG_1586 | transcriptional regulator | 32.34 | 225 | MAP2591 | hypothetical protein | 200 | 100 |
| MAP4_1229 | lipid transfer protein or keto acyl-CoA thiolase ltp2 | 389 | Rv3540c | Probable lipid transfer protein or ke | 66.06 | 386 | Mb3570c | lipid-transfer protein | 66.06 | 386 | MAV_1334 | lipid-transfer protein | 99.49 | 389 | BCG_3604c | lipid-transfer protein | 66.06 | 386 | MAP2590 | lipid-transfer protein | 389 | 100 |
| MAP4_1230 | hypothetical protein | 153 | Rv3541c | hypothetical protein | 46.67 | 129 | Mb3571c | hypothetical protein | 46.67 | 129 | MAV_1335 | hypothetical protein | 100 | 153 | BCG_3605c | hypothetical protein | 46.67 | 129 | MAP2589 | hypothetical protein | 153 | 100 |
| MAP4_1231 | acyl-CoA dehydrogenase | 373 | Rv3505 | Probable acyl-CoA dehydrogenase F | 41.01 | 373 | Mb3535 | acyl-CoA dehydrogenase | 41.27 | 373 | MAV_1336 | acyl-CoA dehydrogenase domain-c | 98.12 | 373 | BCG_3569 | acyl-CoA dehydrogenase fadE2 | 41.27 | 373 | MAP2588 | hypothetical protein | 373 | 100 |
| MAP4_1232 | hypothetical protein | 134 | Rv3542c | hypothetical protein | 47.01 | 311 | Mb3572c | hypothetical protein | 47.01 | 311 | MAV_0619 | hypothetical protein | 42.65 | 317 | BCG_3606c | hypothetical protein | 47.01 | 311 | MAP2587 | hypothetical protein | 134 | 100 |
| MAP4_1233 | hypothetical protein | 181 | Rv3542c | hypothetical protein | 36.26 | 311 | Mb3572c | hypothetical protein | 36.26 | 311 | MAV_0619 | hypothetical protein | 38.75 | 317 | BCG_3606c | hypothetical protein | 36.26 | 311 | MAP2586 | hypothetical protein | 181 | 100 |
| MAP4_1234 | acyl-CoA dehydrogenase | 394 | Rv3504 | Probable acyl-CoA dehydrogenase F | 51.87 | 400 | Mb3534 | acyl-CoA dehydrogenase | 51.87 | 400 | MAV_1338 | acyl-CoA dehydrogenase | 99.75 | 394 | BCG_3568 | acyl-CoA dehydrogenase fadE2 | 51.87 | 400 | MAP2585 | FadE26_2 | 394 | 100 |
| MAP4_1235 | putative cytochrome P450 hydroxylase | 398 | Rv3518c | Probable cytochrome P450 monoox | 40.1 | 398 | Mb3575c | cytochrome P450 125 | 34.32 | 433 | MAV_1339 | cytochrome P450 superfamily prot | 99.75 | 398 | BCG_3609c | cytochrome P450 125 cyp125 | 34.32 | 433 | MAP2584 | hypothetical protein | 398 | 100 |
| MAP4_1236 | aldehyde dehydrogenase | 486 | Rv0768 | Probable aldehyde dehydrogenase N | 44.65 | 489 | Mb0791 | aldehyde dehydrogenase | 44.65 | 489 | MAV_1340 | aldehyde dehydrogenase | 98.97 | 486 | BCG_0820 | aldehyde dehydrogenase AldA | 44.65 | 489 | MAP2583c | hypothetical protein | 486 | 100 |
| MAP4_1237 | CoA-transferase family protein | 763 | Rv1866 | hypothetical protein | 28.33 | 778 | Mb1897 | hypothetical protein | 28.21 | 778 | MAV_1341 | caib/baif family protein | 98.69 | 763 | BCG_1902 | hypothetical protein | 28.21 | 778 | MAP2582c | hypothetical protein | 763 | 99.87 |
| MAP4_1238 | hydrolase, alphabeta hydrolase family protein | 302 | Rv1191 | hypothetical protein | 77.08 | 304 | Mb1223 | hypothetical protein | 77.08 | 304 | MAV_1342 | hydrolase, alpha/beta hydrolase fa | 99.67 | 302 | BCG_1251 | RNA polymerase sigma factor S | 72.06 | 401 | MAP2581c | hypothetical protein | 302 | 100 |
| MAP4_1239 | fatty-acid-CoA ligase | 473 | Rv1193 | Probable fatty-acid-CoA ligase FadD | 83.93 | 473 | Mb1225 | acyl-CoA synthetase | 83.93 | 473 | MAV_1343 | acyl-CoA synthetase | 99.58 | 473 | BCG_1253 | acyl-CoA synthetase | 83.93 | 473 | MAP2580c | acyl-CoA synthetase | 473 | 100 |
| MAP4_1240 | putative conserved membrane transport protein | 444 | Rv1200 | Probable conserved integral membr | 64.93 | 425 | Mb1232 | integral membrane transport | 64.93 | 425 | MAV_1344 | major facilitator family protein tran | 99.55 | 444 | BCG_1260 | integral membrane transport p | 64.93 | 425 | MAP2579c | hypothetical protein | 444 | 100 |
| MAP4_1241 | transferase | 317 | Rv1201c | Tetrahydrodipicolinate N-succinyltra | 88.33 | 317 | Mb1233c | transferase | 88.33 | 317 | MAV_1345 | tetrahydropicolinate succinylase | 100 | 317 | BCG_1261c | transferase | 88.33 | 317 | MAP2578 | hypothetical protein | 317 | 99.68 |
| MAP4_1242 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_1243 | PE family protein | 278 | Rv1788 | PE family protein PE18 | 63.22 | 99 | Mb1816 | PE family protein | 63.22 | 99 | MAV_1346 | PE family protein | 100 | 278 | BCG_1820 | PE family protein | 63.22 | 99 | MAP2576c | hypothetical protein | 278 | 100 |
| MAP4_1244 | PPE family protein | 383 | Rv2768c | PPE family protein PPE43 | 49.49 | 394 | Mb2790c | PPE family protein | 49.49 | 394 | MAV_1347 | PPE family protein | 99.48 | 383 | BCG_2785c | PPE family protein | 49.49 | 394 | MAP2575c | hypothetical protein | 383 | 100 |
| MAP4_1245 | succinyl-diaminopimelate desuccinylase | 354 | Rv1202 | Probable succinyl-diaminopimelate | 85.03 | 354 | Mb1234 | succinyl-diaminopimelate des | 85.03 | 354 | MAV_1349 | succinyl-diaminopimelate desuccin | 98.87 | 354 | BCG_1262 | succinyl-diaminopimelate desu | 85.03 | 354 | MAP2574c | succinyl-diaminopimelate desuccinylase | 354 | 100 |
| MAP4_1246 | hypothetical protein | 712 | Rv1204c | hypothetical protein | 52.27 | 562 | Mb1236c | hypothetical protein | 52.27 | 562 | MAV_1348 | TPR repeat-containing protein | 98.74 | 712 | BCG_1264c | hypothetical protein | 52.27 | 562 | MAP2573 | hypothetical protein | 605 | 100 |
| MAP4_1247 | Lysine decarboxylase family protein | 187 | Rv1205 | hypothetical protein | 68.28 | 187 | Mb1237 | hypothetical protein | 68.28 | 187 | MAV_1350 | hypothetical protein | 100 | 187 | BCG_1265 | hypothetical protein | 68.28 | 187 | MAP2572c | hypothetical protein | 187 | 100 |
| MAP4_1248 | fatty-acid-CoA ligase | 592 | Rv1206 | Probable fatty-acid-CoA ligase FadD | 82.18 | 597 | Mb1238 | long-chain-acyl-CoA syntheta | 82.18 | 597 | MAV_1351 | long-chain-acyl-CoA synthetase | 99.49 | 592 | BCG_1266 | long-chain-acyl-CoA synthetase | 82.18 | 597 | MAP2571c | long-chain-acyl-CoA synthetase | 592 | 100 |
| MAP4_1249 | Dihydropteroate synthase 2 | 307 | Rv1207 | Dihydropteroate synthase 2 FolP2 (D | 88.62 | 318 | Mb1239 | dihydropteroate synthase 2 F | 88.62 | 318 | MAV_1352 | dihydropteroate synthase | 99.66 | 291 | BCG_1267 | dihydropteroate synthase 2 fol | 88.62 | 318 | MAP2570c | FolP2 | 307 | 100 |
| MAP4_1250 | glucosyl-3-phosphoglycerate synthase | 329 | Rv1208 | Probable glucosyl-3-phosphoglycera | 82.07 | 324 | Mb1240 | glucosyl-3-phosphoglycerate | 82.07 | 324 | MAV_1353 | glucosyl-3-phosphoglycerate synth | 99.7 | 329 | BCG_1268 | glucosyl-3-phosphoglycerate sy | 82.07 | 324 | MAP2569c | glucosyl-3-phosphoglycerate synthase | 329 | 100 |
| MAP4_1251 | hypothetical protein | 116 | Rv1209 | hypothetical protein | 72.04 | 122 | Mb1241 | hypothetical protein | 72.04 | 122 | MAV_1354 | hypothetical protein | 99.14 | 116 | BCG_1269 | hypothetical protein | 72.04 | 122 | MAP2568c | hypothetical protein | 116 | 100 |
| MAP4_1252 | DNA-3-methyladenine glycosylase I | 193 | Rv1210 | Probable DNA-3-methyladenine glyc | 77.25 | 204 | Mb1242 | DNA-3-methyladenine glycos | 77.25 | 204 | MAV_1355 | DNA-3-methyladenine glycosylase | 99.48 | 193 | BCG_1270 | DNA-3-methyladenine glycosyl | 77.25 | 204 | MAP2567c | TagA | 193 | 100 |
| MAP4_1253 | hypothetical protein | 77 | Rv1211 | hypothetical protein | 96 | 75 | Mb1243 | hypothetical protein | 96 | 75 | MAV_1356 | hypothetical protein | 98.25 | 57 | BCG_1271 | hypothetical protein | 96 | 75 | MAP4336 | hypothetical protein | 1188 | 29.55 |
| MAP4_1254 | transposase, IS4 family protein | 557 | Rv3386 | Possible transposase | 25.95 | 234 | Mb3418 | transposase | 25.95 | 234 | MAV_3010 | ABC transporter ATP-binding prote | 29.31 | 862 | BCG_3455 | transposase | 25.95 | 234 | MAP0338c | hypothetical protein | 557 | 100 |
| MAP4_1255 | glycosyltransferase | 390 | Rv1212c | Putative glycosyl transferase GlgA | 78.72 | 387 | Mb1244c | glycosyl transferase family pr | 78.46 | 387 | MAV_1357 | glycogen synthase | 99.23 | 426 | BCG_1272c | glycosyl transferase family prot | 78.21 | 387 | MAP2565 | hypothetical protein | 390 | 100 |
| MAP4_1256 | Glucose-1-phosphate adenylyltransferase | 404 | Rv1213 | Glucose-1-phosphate adenylyltransf | 96.53 | 404 | Mb1245 | glucose-1-phosphate adenyly | 96.53 | 404 | MAV_1358 | glucose-1-phosphate adenylyltrans | 99.5 | 398 | BCG_1273 | glucose-1-phosphate adenylylt | 96.53 | 404 | MAP2564c | glucose-1-phosphate adenylyltransfera | 404 | 100 |
| MAP4_1257 | hydrolase, CocENonD family protein | 564 | Rv1215c | hypothetical protein | 77.92 | 561 | Mb1247c | hypothetical protein | 77.92 | 561 | MAV_1359 | hydrolase CocE/NonD family prote | 98.76 | 564 | BCG_1275c | hypothetical protein | 77.92 | 561 | MAP2563 | hypothetical protein | 564 | 100 |
| MAP4_1258 | putative conserved membrane protein | 224 | Rv1216c | Probable conserved integral membr | 64.73 | 224 | Mb1248c | hypothetical protein | 64.73 | 224 | MAV_1360 | isoprenylcysteine carboxyl methylt | 98.66 | 224 | BCG_1276c | integral membrane protein | 64.73 | 224 | MAP2562 | hypothetical protein | 225 | 100 |
| MAP4_1259 | tetronasin-transport membrane protein ABC transport | 547 | Rv1217c | Probable tetronasin-transport integr | 75.73 | 548 | Mb1249c | tetronasin-transport integral | 75.55 | 548 | MAV_1361 | ABC transporter transmembrane p | 98.54 | 547 | BCG_1277c | tetronasin-transport integral m | 75.73 | 548 | MAP2561 | hypothetical protein | 547 | 100 |
| MAP4_1260 | tetronasin-transport ATP-binding protein ABC transpor | 257 | Rv1218c | Probable tetronasin-transport ATP-b | 86.13 | 311 | Mb1250c | tetronasin ABC transporter A | 86.55 | 311 | MAV_1362 | ABC transporter ATP-binding prote | 97.67 | 314 | BCG_1278c | tetronasin-transport atp-bindi | 86.55 | 311 | MAP2560 | hypothetical protein | 257 | 100 |
| MAP4_1261 | Transcriptional regulator, TetR family | 267 | Rv1219c | Probable transcriptional regulatory | 76.56 | 212 | Mb1251c | transcriptional regulator | 76.56 | 212 | MAV_1363 | TetR family transcriptional regulato | 100 | 215 | BCG_1279c | transcriptional regulatory prot | 76.08 | 212 | MAP2559 | hypothetical protein | 267 | 100 |
| MAP4_1262 | methyltransferase | 222 | Rv1220c | Probable methyltransferase | 89.72 | 215 | Mb1252c | methyltransferase | 89.72 | 215 | MAV_1364 | O-methyltransferase, family protei | 99.55 | 222 | BCG_1280c | methyltransferase | 89.72 | 215 | MAP2558 | hypothetical protein | 244 | 100 |
| MAP4_1263 | alternative RNA polymerase sigma factor sigE | 251 | Rv1221 | Alternative RNA polymerase sigma f | 84.3 | 257 | Mb1253 | RNA polymerase sigma factor | 84.3 | 257 | MAV_1365 | RNA polymerase sigma-70 factor | 100 | 424 | BCG_1281 | RNA polymerase sigma factor S | 84.3 | 257 | MAP2557c | RNA polymerase sigma factor SigE | 251 | 100 |
| MAP4_1264 | hypothetical protein | 133 | Rv1222 | Anti-sigma factor RseA | 88.57 | 154 | Mb1254 | hypothetical protein | 88.57 | 154 | MAV_1365 | RNA polymerase sigma-70 factor | 99.25 | 424 | BCG_1282 | hypothetical protein | 88.57 | 154 | MAP2556c | hypothetical protein | 133 | 100 |
| MAP4_1265 | serine protease | 504 | Rv1223 | Probable serine protease HtrA (DEG | 81.55 | 528 | Mb1255 | serine protease HtrA | 81.15 | 528 | MAV_1366 | trypsin | 99.6 | 504 | BCG_1283 | serine protease htrA | 81.15 | 528 | MAP2555c | hypothetical protein | 504 | 100 |
| MAP4_1266 | sec-independent translocase TatB | 131 | Rv1224 | Probable protein TatB | 68.7 | 131 | Mb1256 | sec-independent translocase | 68.7 | 131 | MAV_1367 | sec-independent translocase | 99.24 | 131 | BCG_1284 | sec-independent translocase | 68.7 | 131 | MAP2554c | sec-independent translocase | 131 | 100 |
| MAP4_1267 | MRP family ATP-binding protein | 386 | Rv1229c | Probable Mrp-related protein Mrp | 89.3 | 390 | Mb1261c | MRP family ATP-binding prot | 89.3 | 390 | MAV_1368 | Mrp protein | 100 | 385 | BCG_1289c | MRP-related protein mrp | 89.3 | 390 | MAP2553 | hypothetical protein | 386 | 100 |
| MAP4_1268 | hypothetical protein | 454 | Rv1230c | Possible membrane protein | 73.37 | 411 | Mb1262c | hypothetical protein | 73.1 | 411 | MAV_1369 | hypothetical protein | 99.7 | 413 | BCG_1290c | hypothetical protein | 73.1 | 411 | MAP2552 | hypothetical protein | 454 | 100 |
| MAP4_1269 | hypothetical protein | 180 | Rv1231c | Probable membrane protein | 76.54 | 180 | Mb1263c | hypothetical protein | 76.54 | 180 | MAV_1370 | integral membrane protein | 99.44 | 180 | BCG_1291c | hypothetical protein | 76.54 | 180 | MAP2551 | hypothetical protein | 180 | 100 |
| MAP4_1270 | hypothetical protein | 435 | Rv1232c | hypothetical protein | 85.45 | 435 | Mb1264c | hypothetical protein | 85.68 | 435 | MAV_1371 | Mg/Co/Ni transporter MgtE | 99.53 | 429 | BCG_1292c | hypothetical protein | 85.68 | 435 | MAP2550 | hypothetical protein | 435 | 100 |
| MAP4_1271 | hypothetical protein | 198 | Rv1233c | hypothetical protein | 40.62 | 198 | Mb1265c | hypothetical protein | 42.53 | 198 | MAV_1372 | hypothetical protein | 95.96 | 197 | BCG_1293c | hypothetical protein | 42.53 | 198 | MAP1826c | hypothetical protein | 263 | 37.7 |
| MAP4_1272 | transmembrane protein | 174 | Rv1234 | Probable transmembrane protein | 93.14 | 175 | Mb1266 | hypothetical protein | 93.14 | 175 | MAV_1373 | hypothetical protein | 99.34 | 151 | BCG_1294 | hypothetical protein | 93.14 | 175 | MAP2549c | hypothetical protein | 174 | 100 |
| MAP4_1273 | sugar-binding lipoprotein lpqY | 470 | Rv1235 | Probable sugar-binding lipoprotein L | 75.74 | 468 | Mb1267 | sugar-binding lipoprotein Lpq | 75.74 | 468 | MAV_1374 | extracellular solute-binding protein | 98.3 | 470 | BCG_1295 | sugar-binding lipoprotein lpqY | 75.74 | 468 | MAP2548c | hypothetical protein | 470 | 100 |
| MAP4_1274 | sugar-transport membrane protein ABC transporter su | 311 | Rv1236 | Probable sugar-transport integral m | 85.47 | 307 | Mb1268 | sugar-transport integral mem | 85.47 | 307 | MAV_1375 | ABC transporter permease | 99.32 | 292 | BCG_1296 | sugar-transport integral memb | 85.47 | 307 | MAP2547c | SugA | 311 | 100 |
| MAP4_1275 | sugar-transport membrane protein ABC transporter su | 268 | Rv1237 | Probable sugar-transport integral m | 89.85 | 274 | Mb1269 | sugar-transport integral mem | 89.85 | 274 | MAV_1376 | ABC transporter permease | 99.24 | 264 | BCG_1297 | sugar-transport integral memb | 89.85 | 274 | MAP2546c | SugB | 268 | 100 |
| MAP4_1276 | sugar-transport ATP-binding protein ABC transporter S | 392 | Rv1238 | Probable sugar-transport ATP-bindi | 86.12 | 393 | Mb1270 | sugar-transport ATP-binding | 86.12 | 393 | MAV_1377 | ABC transporter ATP-binding prote | 99.49 | 392 | BCG_1298 | sugar-transport ATP-binding pr | 86.12 | 393 | MAP2545c | SugC | 392 | 100 |
| MAP4_1277 | hypothetical protein | 197 | Rv1005c | Probable para-aminobenzoate synth | 38.3 | 458 | Mb1032c | aminodeoxychorismate synth | 38.3 | 478 | MAV_1378 | hypothetical protein | 98.48 | 197 | BCG_1062c | aminodeoxychorismate syntha | 38.3 | 478 | MAP2544c | hypothetical protein | 140 | 100 |
| MAP4_1278 | hypothetical protein | 248 | Rv2248 | hypothetical protein | 62.25 | 271 | Mb2272 | hypothetical protein | 61.76 | 271 | MAV_1002 | hypothetical protein | 37.37 | 293 | BCG_2266 | hypothetical protein | 68.55 | 234 | MAP2543 | hypothetical protein | 236 | 99.58 |
| MAP4_1279 | magnesium and cobalt transport transmembrane prote | 366 | Rv1239c | Possible magnesium and cobalt tran | 77.6 | 366 | Mb1271c | magnesium/cobalt transporte | 77.6 | 366 | MAV_1379 | magnesium and cobalt transport p | 99.45 | 366 | BCG_1299c | magnesium and cobalt transpo | 77.87 | 366 | MAP2542 | hypothetical protein | 366 | 100 |
| MAP4_1280 | malate dehydrogenase | 329 | Rv1240 | Probable malate dehydrogenase Md | 91.79 | 329 | Mb1272 | malate dehydrogenase | 91.79 | 329 | MAV_1380 | malate dehydrogenase | 99.7 | 329 | BCG_1300 | malate dehydrogenase | 91.79 | 329 | MAP2541c | malate dehydrogenase | 329 | 100 |
| MAP4_1281 | NADP-dependent malic enzyme | 400 | Rv2332 | Probable [NAD] dependent malate d | 28.45 | 548 | Mb2360 | malate dehydrogenase | 28.74 | 548 | MAV_1381 | NAD-dependent malic enzyme | 99.25 | 400 | BCG_2354 | malate dehydrogenase | 28.74 | 548 | MAP2540c | hypothetical protein | 403 | 99.75 |
| MAP4_1282 | putative lipoprotein LPQZ | 289 | Rv1244 | Probable lipoprotein LpqZ | 71.79 | 286 | Mb1276 | lipoprotein LPQZ | 71.43 | 286 | MAV_1383 | LpqZ protein | 97.58 | 289 | BCG_1304 | lipoprotein lpqZ | 71.43 | 286 | MAP2539c | hypothetical protein | 289 | 100 |
| MAP4_1283 | short-chain type dehydrogenasereductase | 283 | Rv1245c | Probable short-chain type dehydrog | 74.11 | 276 | Mb1277c | short-chain type dehydrogen | 74.11 | 276 | MAV_1382 | short chain alcohol dehydrogenase | 100 | 283 | BCG_1305c | short-chain type dehydrogenas | 74.11 | 276 | MAP2538 | hypothetical protein | 283 | 100 |
| MAP4_1284 | short-chain type dehydrogenasereductase | 274 | Rv1245c | Probable short-chain type dehydrog | 84.62 | 276 | Mb1277c | short-chain type dehydrogen | 84.62 | 276 | MAV_1384 | short chain alcohol dehydrogenase | 100 | 274 | BCG_1305c | short-chain type dehydrogenas | 84.62 | 276 | MAP2537 | hypothetical protein | 274 | 100 |
| MAP4_1285 | 2-oxoglutarate dehydrogenase sucA | 1247 | Rv1248c | Multifunctional alpha-ketoglutarate | 88.92 | 1231 | Mb1280c | alpha-ketoglutarate decarbox | 88.92 | 1231 | MAV_2273 | dihydrolipoamide acetyltransferase | 31.63 | 596 | BCG_1308c | alpha-ketoglutarate decarboxy | 88.93 | 1214 | MAP2536 | alpha-ketoglutarate decarboxylase | 1247 | 100 |
| MAP4_1286 | membrane protein | 257 | Rv1249c | Possible membrane protein | 66.03 | 262 | Mb1281c | hypothetical protein | 65.65 | 262 | MAV_1386 | hypothetical protein | 99.22 | 257 | BCG_1309c | hypothetical protein | 65.65 | 262 | MAP2535 | hypothetical protein | 257 | 100 |
| MAP4_1287 | drug-transport membrane protein | 671 | Rv1250 | Probable drug-transport integral me | 69.33 | 579 | Mb1282 | drug-transport integral memb | 69.52 | 579 | MAV_1387 | drug transporter | 98.56 | 626 | BCG_1310 | drug-transport integral membr | 69.52 | 579 | MAP2534c | hypothetical protein | 671 | 100 |
| MAP4_1288 | hypothetical protein | 1137 | Rv1251c | hypothetical protein | 76.87 | 1139 | Mb1283c | hypothetical protein | 76.87 | 1139 | MAV_1388 | ATPase | 99.56 | 1137 | BCG_1311c | hypothetical protein | 76.87 | 1139 | MAP2533 | hypothetical protein | 1140 | 99.91 |
| MAP4_1289 | putative cytochrome P450 hydroxylase | 223 | Rv0766c | Probable cytochrome P450 123 Cyp | 37 | 402 | Mb0789c | cytochrome P450 123 | 37 | 402 | MAV_1389 | NikQ protein | 97.94 | 394 | BCG_0818c | cytochrome P450 123 cyp123 | 39.41 | 541 | MAP2532 | hypothetical protein | 223 | 100 |
| MAP4_1290 | hypothetical protein | 184 | Rv3472 | hypothetical protein | 33.01 | 168 | Mb3501 | hypothetical protein | 33.01 | 168 | MAV_1390 | hypothetical protein | 97.28 | 184 | BCG_3537 | hypothetical protein | 33.01 | 168 | MAP2531 | hypothetical protein | 184 | 100 |
| MAP4_1291 | short-chain dehydrogenase | 256 | Rv3530c | Possible oxidoreductase | 36.61 | 260 | Mb3560c | short chain dehydrogenase | 36.61 | 260 | MAV_1391 | short chain dehydrogenase/reduct | 98.05 | 256 | BCG_3594c | short chain dehydrogenase | 36.61 | 260 | MAP2530 | hypothetical protein | 256 | 100 |
| MAP4_1292 | hypothetical protein | 203 | Rv1531 | hypothetical protein | 28 | 188 | Mb1558 | hypothetical protein | 28 | 188 | MAV_1392 | hypothetical protein | 94.58 | 203 | BCG_1583 | hypothetical protein | 28 | 188 | MAP2529 | hypothetical protein | 203 | 100 |
| MAP4_1293 | short-chain dehydrogenasereductase SDR | 278 | Rv2750 | Probable dehydrogenase | 48.92 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 48.92 | 272 | MAV_1393 | carveol dehydrogenase | 99.28 | 278 | BCG_2766 | 3-ketoacyl-ACP reductase | 48.92 | 272 | MAP2528 | hypothetical protein | 282 | 100 |
| MAP4_1294 | Transcriptional regulator, TetR family | 213 | Rv0775 | hypothetical protein | 41.18 | 207 | Mb0798 | hypothetical protein | 41.18 | 207 | MAV_1394 | hypothetical protein | 97.52 | 161 | BCG_0827 | hypothetical protein | 41.18 | 207 | MAP2527c | hypothetical protein | 213 | 100 |
| MAP4_1295 | dehydrogenase | 247 | Rv0769 | Probable dehydrogenase/reductase | 36.55 | 248 | Mb0792 | short chain dehydrogenase | 36.14 | 248 | MAV_1395 | 2-hydroxycyclohexanecarboxyl-CoA | 97.54 | 244 | BCG_0821 | short chain dehydrogenase | 36.14 | 248 | MAP2526c | hypothetical protein | 247 | 100 |
| MAP4_1296 | ferredoxin | 73 | Rv1786 | Probable ferredoxin | 37.1 | 67 | Mb1814 | ferredoxin | 37.1 | 67 | MAV_1396 | hypothetical protein | 98.63 | 73 | BCG_1818 | ferredoxin | 37.1 | 67 | MAP0753c | hypothetical protein | 66 | 57.81 |
| MAP4_1297 | putative cytochrome P450 hydroxylase | 454 | Rv2266 | Probable cytochrome P450 124 Cyp | 29.75 | 428 | Mb2289 | cytochrome P450 124 CYP124 | 29.75 | 428 | MAV_1397 | cytochrome P450 superfamily prot | 97.79 | 454 | BCG_2283 | cytochrome P450 124 CYP124 | 29.75 | 428 | MAP2525c | hypothetical protein | 454 | 100 |
| MAP4_1298 | luciferase-like monooxygenase | 309 | Rv2893 | Possible oxidoreductase | 34.34 | 325 | Mb2917 | oxidoreductase | 34.34 | 325 | MAV_0923 | hypothetical protein | 38.99 | 318 | BCG_2914 | oxidoreductase | 34.34 | 325 | MAP2524c | hypothetical protein | 309 | 100 |
| MAP4_1299 | hypothetical protein | 347 | Rv1059 | hypothetical protein | 32.76 | 354 | Mb1088 | hypothetical protein | 32.76 | 354 | MAV_1399 | homoserine dehydrogenase | 98.85 | 347 | BCG_1117 | hypothetical protein | 32.76 | 354 | MAP2523c | hypothetical protein | 347 | 100 |
| MAP4_1300 | Putative lipoprotein lprE | 202 | Rv1252c | Probable lipoprotein LprE | 66.01 | 202 | Mb1284c | lipoprotein LprE | 66.01 | 202 | MAV_1400 | LprE protein | 98.97 | 195 | BCG_1312c | lipoprotein lprE | 66.01 | 202 | MAP2522 | hypothetical protein | 202 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1301 | cold-shock DEAD-box protein A | 566 | Rv1253 | Probable cold-shock DeaD-box prote | 81.48 | 563 | Mb1285 | cold-shock DEAD-box protein | 81.66 | 563 | MAV_1401 | ATP-dependent rna helicase, dead/ | 99.65 | 566 | BCG_1313 | cold-shock dead-box protein a | 81.66 | 563 | MAP2521c | DeaD | 566 | 100 |
| MAP4_1302 | putative acyltransferase | 379 | Rv1254 | Probable acyltransferase | 79.63 | 383 | Mb1286 | acyltransferase | 79.63 | 383 | MAV_1402 | acyltransferase, putative | 98.42 | 379 | BCG_1314 | acyltransferase | 79.63 | 383 | MAP2520c | hypothetical protein | 379 | 99.74 |
| MAP4_1303 | Transcriptional regulator, TetR family | 197 | Rv1255c | Probable transcriptional regulatory | 75 | 202 | Mb1805c | transcriptional regulator | 30.37 | 186 | MAV_1403 | TetR family transcriptional regulato | 100 | 197 | BCG_1809c | transcriptional regulatory prote | 30.37 | 186 | MAP2519 | hypothetical protein | 197 | 100 |
| MAP4_1304 | putative cytochrome P450 hydroxylase | 409 | Rv1256c | Probable cytochrome P450 130 Cyp | 83.86 | 405 | Mb0789c | cytochrome P450 123 | 34.68 | 402 | MAV_1404 | cytochrome P450 130 | 99.76 | 409 | BCG_2283 | cytochrome P450 124 CYP124 | 34.9 | 428 | MAP2518 | hypothetical protein | 409 | 100 |
| MAP4_1305 | putative oxidoreductase | 455 | Rv1257c | Probable oxidoreductase | 87.47 | 455 | Mb2301 | dehydrogenase | 34.57 | 459 | MAV_1405 | oxidoreductase, FAD-binding | 100 | 455 | BCG_2295 | dehydrogenase | 34.57 | 459 | MAP2517 | hypothetical protein | 455 | 100 |
| MAP4_1306 | conserved membrane transport protein | 415 | Rv1258c | Probable conserved integral membr | 71.36 | 419 | Mb1288c | integral membrane transport | 71.36 | 419 | MAV_1406 | transporter, major facilitator family | 99.01 | 405 | BCG_1316c | integral membrane transport p | 71.36 | 419 | MAP2516 | hypothetical protein | 415 | 100 |
| MAP4_1307 | Uracil-DNA glycosylase superfamily protein | 275 | Rv1259 | Probable uracil DNA glycosylase, Ud | 80.36 | 299 | Mb1289 | hypothetical protein | 80.36 | 299 | MAV_1407 | uracil-DNA glycosylase | 99.64 | 275 | BCG_1317 | hypothetical protein | 80.36 | 299 | MAP2515c | hypothetical protein | 314 | 100 |
| MAP4_1308 | oxidoreductase | 375 | Rv1260 | Probable oxidoreductase | 81.33 | 372 | Mb1290 | hypothetical protein | 79.09 | 274 | MAV_1408 | hypothetical protein | 99.47 | 375 | BCG_1318 | oxidoreductase | 79.09 | 274 | MAP2514c | hypothetical protein | 375 | 100 |
| MAP4_1309 | luciferase family oxidoreductase | 343 | Rv3618 | Possible monooxygenase | 38.32 | 395 | Mb1971 | monooxygenase | 30.09 | 369 | MAV_1409 | alkanal monooxygenase alpha chai | 99.71 | 343 | BCG_1975 | monooxygenase | 30.09 | 369 | MAP2513c | hypothetical protein | 343 | 100 |
| MAP4_1312 | hypothetical protein | 144 | Rv1262c | Hypothetical hit-like protein | 86.36 | 144 | Mb1293c | HIT-like protein | 87.12 | 144 | MAV_1411 | HIT family protein | 100 | 147 | BCG_1321c | HIT family protein | 87.12 | 144 | MAP2510 | hypothetical protein | 144 | 100 |
| MAP4_1313 | amidase | 461 | Rv1263 | Probable amidase AmiB2 (aminohyd | 82.35 | 462 | Mb1294 | amidase | 82.35 | 462 | MAV_1414 | amidase | 99.78 | 461 | BCG_1322 | amidase | 82.35 | 462 | MAP2509c | amidase | 461 | 100 |
| MAP4_1314 | G:TU mismatch-specific uracil thymine DNA-glycosylase | 165 | Rv2692 | TRK system potassium uptake prote | 29.41 | 220 | Mb2711 | TRK system potassium uptake | 29.41 | 220 | MAV_1413 | T/U mismatch-specific DNA glycosy | 98.79 | 165 | BCG_2705 | TRK system potassium uptake | 29.41 | 220 | MAP2508 | hypothetical protein | 165 | 100 |
| MAP4_1315 | adenylate cyclase | 385 | Rv1264 | Adenylyl cyclase (ATP pyrophosphat | 78.13 | 397 | Mb1295 | adenylyl cyclase | 77.87 | 397 | MAV_1415 | chain A, Myco adenylyl cyclase, hol | 100 | 385 | BCG_1323 | adenylyl cyclase | 77.87 | 397 | MAP2507c | hypothetical protein | 385 | 100 |
| MAP4_1316 | hypothetical protein | 191 | Rv1265 | hypothetical protein | 84.9 | 226 | Mb1296 | hypothetical protein | 84.9 | 226 | MAV_1416 | hypothetical protein | 98.95 | 191 | BCG_1324 | hypothetical protein | 84.9 | 226 | MAP2506c | hypothetical protein | 191 | 100 |
| MAP4_1319 | transcriptional regulatory protein EMBR | 380 | Rv1267c | Probable transcriptional regulatory | 73.73 | 388 | Mb1298c | transcriptional regulator Emb | 73.73 | 388 | MAV_1418 | transcriptional regulator | 99.74 | 381 | BCG_1326c | transcriptional regulatory prote | 73.73 | 388 | MAP2503 | EmbR_2 | 380 | 100 |
| MAP4_1320 | transposase, IS4 family protein | 557 | Rv3386 | Possible transposase | 25.95 | 234 | Mb3418 | transposase | 25.95 | 234 | MAV_3010 | ABC transporter ATP-binding prote | 29.31 | 862 | BCG_3455 | transposase | 25.95 | 234 | MAP0338c | hypothetical protein | 557 | 100 |
| MAP4_1321 | conserved secreted protein | 111 | Rv1271c | Conserved hypothetical secreted pr | 48.62 | 113 | Mb1302c | hypothetical protein | 48.62 | 113 | MAV_1419 | hypothetical protein | 98.18 | 110 | BCG_1330c | hypothetical protein | 48.62 | 113 | MAP2501 | hypothetical protein | 114 | 100 |
| MAP4_1322 | drugs-transport transmembrane ATP-binding protein A | 634 | Rv1272c | Probable drugs-transport transmem | 79.65 | 631 | Mb1303c | drugs-transport transmembra | 79.65 | 631 | MAV_1420 | ABC transporter | 96.87 | 638 | BCG_1331c | drugs-transport transmembran | 79.65 | 631 | MAP2500 | hypothetical protein | 634 | 100 |
| MAP4_1323 | drugs-transport transmembrane ATP-binding protein A | 585 | Rv1273c | Probable drugs-transport transmem | 79.38 | 582 | Mb1304c | drugs-transport transmembra | 79.38 | 582 | MAV_1421 | ABC transporter ATP-binding prote | 99.15 | 585 | BCG_1332c | drugs-transport transmembran | 79.38 | 582 | MAP2499 | hypothetical protein | 585 | 100 |
| MAP4_1324 | lipoprotein LprB | 185 | Rv1274 | Possible lipoprotein LprB | 81.62 | 185 | Mb1305 | lipoprotein LPRB | 82.16 | 185 | MAV_1423 | LprB protein | 99.42 | 171 | BCG_1333 | lipoprotein lprB | 82.16 | 185 | MAP2498c | hypothetical protein | 185 | 100 |
| MAP4_1325 | lipoprotein LprC | 189 | Rv1275 | Possible lipoprotein LprC | 85.64 | 180 | Mb1306 | lipoprotein LPRC | 85.64 | 180 | MAV_1424 | LprC protein | 100 | 189 | BCG_1334 | lipoprotein lprC | 85.64 | 180 | MAP2497c | hypothetical protein | 189 | 100 |
| MAP4_1326 | putative histidine phosphatase superfamily (branch 1) | 167 | Rv1276c | hypothetical protein | 68.35 | 158 | Mb1307c | hypothetical protein | 67.72 | 158 | MAV_1425 | phosphoglycerate mutase | 98.2 | 167 | BCG_1335c | hypothetical protein | 67.72 | 158 | MAP2496 | hypothetical protein | 158 | 100 |
| MAP4_1327 | REP13E12 repeat protein | 483 | Rv1702c | hypothetical protein | 63.97 | 454 | Mb1159c | hypothetical protein | 64.78 | 451 | MAV_1426 | hypothetical protein | 91.72 | 472 | BCG_1189c | hypothetical protein | 64.78 | 451 | MAP2495 | hypothetical protein | 472 | 96.69 |
| MAP4_1328 | hypothetical protein | 383 | Rv1277 | hypothetical protein | 82.77 | 417 | Mb1308 | hypothetical protein | 82.77 | 417 | MAV_1427 | DNA repair exonuclease | 98.17 | 383 | BCG_1336 | hypothetical protein | 82.77 | 417 | MAP2494c | hypothetical protein | 383 | 100 |
| MAP4_1329 | hypothetical protein | 876 | Rv1278 | Hypothetical protein | 72.15 | 875 | Mb1309 | hypothetical protein | 72.15 | 875 | MAV_1428 | hypothetical protein | 98.4 | 876 | BCG_1337 | hypothetical protein | 72.15 | 875 | MAP2493c | hypothetical protein | 876 | 100 |
| MAP4_1330 | hydrolase, alphabeta fold family protein | 414 | Rv1938 | Probable epoxide hydrolase EphB (e | 31.46 | 356 | Mb1973 | epoxide hydrolase | 31.46 | 356 | MAV_1430 | alpha/beta hydrolase | 98.79 | 414 | BCG_1977 | epoxide hydrolase ephB | 31.46 | 356 | MAP2492c | hypothetical protein | 326 | 100 |
| MAP4_1331 | periplasmic oligopeptide-binding lipoprotein oppA | 558 | Rv1280c | Probable periplasmic oligopeptide-b | 81.82 | 591 | Mb1311c | periplasmic oligopeptide-bind | 81.82 | 591 | MAV_1429 | extracellular solute-binding protein | 99.46 | 558 | BCG_1339c | periplasmic oligopeptide-bindi | 81.82 | 591 | MAP2491 | hypothetical protein | 543 | 99.82 |
| MAP4_1332 | oligopeptide-transport ATP-binding protein ABC transp | 611 | Rv1281c | Probable oligopeptide-transport AT | 84.31 | 612 | Mb1312c | oligopeptide-transport ATP-b | 84.31 | 612 | MAV_1431 | ABC transporter ATP-binding prote | 99.02 | 611 | BCG_1340c | oligopeptide-transport ATP-bin | 84.31 | 612 | MAP2490 | OppD | 611 | 100 |
| MAP4_1333 | oligopeptide-transport membrane protein ABC transpo | 291 | Rv1282c | Probable oligopeptide-transport int | 86.6 | 291 | Mb1313c | oligopeptide-transport integr | 86.6 | 291 | MAV_1432 | ABC transporter permease | 99.31 | 308 | BCG_1341c | oligopeptide-transport integral | 86.6 | 291 | MAP2489 | hypothetical protein | 291 | 100 |
| MAP4_1334 | oligopeptide-transport membrane protein ABC transpo | 324 | Rv1283c | Probable oligopeptide-transport int | 84.92 | 325 | Mb1314c | oligopeptide-transport integr | 84.92 | 325 | MAV_1433 | ABC transporter permease | 99.69 | 324 | BCG_1342c | oligopeptide-transport integral | 84.92 | 325 | MAP2488 | hypothetical protein | 324 | 100 |
| MAP4_1335 | putative carbonic anhydrase | 163 | Rv1284 | Beta-carbonic anhydrase | 80.98 | 163 | Mb1315 | hypothetical protein | 80.98 | 163 | MAV_1434 | carbonic anhydrase | 99.39 | 163 | BCG_1343 | beta-carbonic anhydrase | 80.98 | 163 | MAP2487c | hypothetical protein | 163 | 100 |
| MAP4_1336 | hypothetical protein | 148 | Rv1532c | hypothetical protein | 34.62 | 144 | Mb1559c | hypothetical protein | 34.62 | 144 | MAV_1435 | hypothetical protein | 99.22 | 129 | BCG_1584c | hypothetical protein | 34.62 | 144 | MAP2486 | hypothetical protein | 148 | 100 |
| MAP4_1337 | sulfate adenylyltransferase subunit 2 | 314 | Rv1285 | Probable sulfate adenylyltransferase | 89.42 | 332 | Mb1316 | sulfate adenylyltransferase | 89.42 | 332 | MAV_1436 | sulfate adenylyltransferase subunit | 100 | 314 | BCG_1344 | sulfate adenylyltransferase sub | 89.42 | 332 | MAP2485c | sulfate adenylyltransferase subunit 2 | 314 | 100 |
| MAP4_1338 | bifunctional sulfate adenyltransferase/adenylylsulfate | 616 | Rv1286 | Probable bifunctional enzyme CysN/ | 88.38 | 614 | Mb1317 | bifunctional sulfate adenylylt | 88.22 | 614 | MAV_1437 | bifunctional sulfate adenylyltransfe | 99.51 | 616 | BCG_1345 | bifunctional sulfate adenylyltra | 88.38 | 614 | MAP2484c | bifunctional sulfate adenylyltransferase | 616 | 100 |
| MAP4_1339 | putative transcriptional regulator, Rrf2 family | 161 | Rv1287 | hypothetical protein | 89.44 | 161 | Mb1318 | hypothetical protein | 89.44 | 161 | MAV_1439 | StaS protein | 99.37 | 159 | BCG_1346 | hypothetical protein | 89.44 | 161 | MAP2483c | hypothetical protein | 161 | 100 |
| MAP4_1340 | hypothetical protein | 131 | Rv3100c | Probable SSRA-binding protein Smp | 40.91 | 160 | Mb3127c | SsrA-binding protein | 40.91 | 160 | MAV_1438 | glyoxalase/bleomycin resistance pr | 100 | 131 | BCG_3125c | SsrA-binding protein | 40.91 | 160 | MAP2482 | hypothetical protein | 131 | 100 |
| MAP4_1341 | glyoxalasebleomycin resistanceprotein/dioxygenase | 137 | Rv0274 | hypothetical protein | 25.32 | 193 | Mb0280 | hypothetical protein | 25.32 | 193 | MAV_1440 | glyoxalase/bleomycin resistance pr | 99.27 | 137 | BCG_0312 | hypothetical protein | 25.32 | 193 | MAP2029c | hypothetical protein | 150 | 35.42 |
| MAP4_1342 | putative oxidoreductase, luciferase family protein | 292 | Rv0953c | Possible oxidoreductase | 35.33 | 282 | Mb0978c | oxidoreductase | 35.33 | 282 | MAV_1441 | hypothetical protein | 98.29 | 292 | BCG_1007c | oxidoreductase | 35.33 | 282 | MAP2481c | hypothetical protein | 324 | 100 |
| MAP4_1343 | hypothetical protein | 290 | Rv1783 | ESX conserved component EccC5 ES | 29.85 | 1391 | Mb1812 | hypothetical protein | 29.85 | 1391 | MAV_1442 | hypothetical protein | 99.66 | 290 | BCG_1816 | hypothetical protein | 29.85 | 1391 | MAP2480c | hypothetical protein | 206 | 99.51 |
| MAP4_1344 | putative ion transport protein | 581 | Rv3200c | Possible transmembrane cation tran | 28.81 | 355 | Mb3225c | transmembrane cation transp | 28.81 | 355 | MAV_1443 | TrkA domain-containing protein | 99.83 | 581 | BCG_3225c | transmembrane cation transpo | 28.81 | 355 | MAP2479 | hypothetical protein | 581 | 100 |
| MAP4_1345 | hypothetical protein | 123 | Rv2042c | hypothetical protein | 46.88 | 265 | Mb2068c | hypothetical protein | 46.88 | 265 | MAV_1444 | steroid delta-isomerase | 99.19 | 123 | BCG_2061c | hypothetical protein | 46.88 | 265 | MAP2478 | hypothetical protein | 123 | 100 |
| MAP4_1346 | putative phosphohydrolase, NUDIX family | 201 | Rv1700 | NUDIX hydrolase | 35.2 | 207 | Mb1726 | hypothetical protein | 35.2 | 207 | MAV_1446 | nudix hydrolase | 99.5 | 201 | BCG_1738 | hypothetical protein | 35.2 | 207 | MAP2477c | hypothetical protein | 208 | 99.5 |
| MAP4_1347 | hypothetical protein | 95 | Rv1271c | Conserved hypothetical secreted pr | 31.08 | 113 | Mb1302c | hypothetical protein | 31.08 | 113 | MAV_1445 | hypothetical protein | 100 | 95 | BCG_1330c | hypothetical protein | 31.08 | 113 | MAP2476 | hypothetical protein | 162 | 100 |
| MAP4_1348 | hypothetical protein | 233 | Rv1728c | hypothetical protein | 65.94 | 256 | Mb1757c | hypothetical protein | 65.94 | 256 | MAV_1447 | hypothetical protein | 100 | 233 | BCG_1767c | hypothetical protein | 65.94 | 256 | MAP2475 | hypothetical protein | 233 | 100 |
| MAP4_1349 | hypothetical protein | 168 | Rv3547 | Deazaflavin-dependent nitroreducta | 41.18 | 151 | Mb3577 | hypothetical protein | 41.18 | 151 | MAV_1448 | hypothetical protein | 98.21 | 168 | BCG_3611 | hypothetical protein | 41.18 | 151 | MAP2474c | hypothetical protein | 154 | 99.35 |
| MAP4_1350 | hypothetical protein | 145 | Rv1829 | hypothetical protein | 25.71 | 164 | Mb2303c | LysR family transcriptional re | 34.15 | 312 | MAV_1478 | hypothetical protein | 63.64 | 156 | BCG_1864 | hypothetical protein | 25.71 | 164 | MAP2473 | hypothetical protein | 145 | 100 |
| MAP4_1351 | putative conserved membrane protein | 362 | Rv2077c | Possible conserved transmembrane | 59.51 | 323 | Mb2102c | transmembrane protein | 59.51 | 323 | MAV_1479 | hypothetical protein | 96.41 | 362 | BCG_2095c | hypothetical protein | 59.51 | 323 | MAP2472 | hypothetical protein | 362 | 100 |
| MAP4_1352 | hypothetical protein | 97 | Rv2077A | hypothetical protein | 48.48 | 99 | Mb2103c | hypothetical protein | 48.48 | 99 | MAV_1451 | hypothetical protein | 97.94 | 97 | BCG_2096c | hypothetical protein | 48.48 | 99 | MAP2471 | hypothetical protein | 97 | 100 |
| MAP4_1353 | Arginyl-tRNA synthetase | 550 | Rv1292 | Probable arginyl-tRNA synthetase A | 89.82 | 550 | Mb1324 | arginyl-tRNA synthetase | 89.82 | 550 | MAV_1724 | valyl-tRNA synthetase | 27.42 | 882 | BCG_1352 | arginyl-tRNA synthetase | 89.82 | 550 | MAP2470c | arginyl-tRNA synthetase | 550 | 100 |
| MAP4_1354 | Diaminopimelate decarboxylase | 472 | Rv1293 | Diaminopimelate decarboxylase Lys | 85.65 | 447 | Mb1325 | diaminopimelate decarboxyla | 85.65 | 447 | MAV_1508 | diaminopimelate decarboxylase | 99.58 | 472 | BCG_1353 | diaminopimelate decarboxylas | 85.65 | 447 | MAP2469c | LysA_2 | 472 | 100 |
| MAP4_1355 | homoserine dehydrogenase | 441 | Rv1294 | Probable homoserine dehydrogenas | 90.7 | 441 | Mb1326 | homoserine dehydrogenase | 90.7 | 441 | MAV_1509 | homoserine dehydrogenase | 99.77 | 441 | BCG_1354 | homoserine dehydrogenase | 90.7 | 441 | MAP2468c | homoserine dehydrogenase | 441 | 100 |
| MAP4_1356 | threonine synthase | 360 | Rv1295 | Threonine synthase ThrC (ts) | 89.72 | 360 | Mb1327 | threonine synthase | 89.72 | 360 | MAV_1510 | threonine synthase | 99.72 | 360 | BCG_1355 | threonine synthase | 89.72 | 360 | MAP2467c | threonine synthase | 360 | 100 |
| MAP4_1357 | homoserine kinase | 315 | Rv1296 | Probable homoserine kinase ThrB | 78.8 | 316 | Mb1328 | homoserine kinase | 78.8 | 316 | MAV_1511 | homoserine kinase | 99.36 | 311 | BCG_1356 | homoserine kinase | 78.8 | 316 | MAP2466c | homoserine kinase | 315 | 100 |
| MAP4_1358 | hypothetical protein | 101 | Rv3644c | Possible DNA polymerase | 40 | 401 | Mb3668c | DNA polymerase III subunit d | 40 | 401 | MAV_1512 | hypothetical protein | 97.92 | 48 | BCG_3702c | DNA polymerase III subunit del | 40 | 401 | MAP2465c | hypothetical protein | 101 | 100 |
| MAP4_1359 | Transcription termination factor Rho | 620 | Rv1297 | Probable transcription termination f | 80.19 | 602 | Mb1329 | transcription termination fact | 80.19 | 602 | MAV_1514 | transcription termination factor Rh | 99 | 596 | BCG_1357 | transcription termination facto | 80.19 | 602 | MAP2464c | transcription termination factor Rho | 620 | 100 |
| MAP4_1360 | 50S ribosomal protein L31 rpmE | 80 | Rv1298 | 50S ribosomal protein L31 RpmE | 87.5 | 80 | Mb1330 | 50S ribosomal protein L31 | 87.5 | 80 | MAV_1515 | 50S ribosomal protein L31 | 100 | 80 | BCG_1358 | 50S ribosomal protein L31 | 87.5 | 80 | MAP2463c | 50S ribosomal protein L31 | 80 | 100 |
| MAP4_1361 | Peptide chain release factor 1 | 357 | Rv1299 | Probable peptide chain release facto | 88.8 | 357 | Mb1331 | peptide chain release factor 1 | 88.8 | 357 | MAV_1516 | peptide chain release factor 1 | 99.72 | 357 | BCG_1359 | peptide chain release factor 1 | 88.8 | 357 | MAP2462c | peptide chain release factor 1 | 357 | 100 |
| MAP4_1362 | putative modification methylase, HemK family | 300 | Rv1300 | Probable HemK protein homolog He | 72.51 | 325 | Mb1332 | hypothetical protein | 72.51 | 325 | MAV_1517 | modification methylase, HemK fam | 97.98 | 312 | BCG_1360 | hemk protein hemK | 72.51 | 325 | MAP2461c | hypothetical protein | 300 | 100 |
| MAP4_1363 | hypothetical protein, YrdCSua5 family | 219 | Rv1301 | hypothetical protein | 82.33 | 217 | Mb1333 | hypothetical protein | 81.86 | 217 | MAV_1518 | Sua5/YciO/YrdC/YwlC family protei | 98.63 | 219 | BCG_1361 | hypothetical protein | 81.86 | 217 | MAP2460c | hypothetical protein | 219 | 100 |
| MAP4_1364 | UDP-phosphatealpha-N-acetylglucosaminyl transferase | 407 | Rv1302 | Probable undecapaprenyl-phosphat | 93.97 | 404 | Mb1334 | undecapaprenyl-phosphate a | 93.72 | 404 | MAV_1519 | glycosyl transferase, group 4 family | 100 | 407 | BCG_1362 | undecapaprenyl-phosphate alp | 93.72 | 404 | MAP2459c | hypothetical protein | 407 | 100 |
| MAP4_1365 | hypothetical protein | 160 | Rv1303 | hypothetical protein | 73.75 | 161 | Mb1335 | hypothetical protein | 73.75 | 161 | MAV_1520 | hypothetical protein | 98.75 | 160 | BCG_1363 | hypothetical protein | 73.75 | 161 | MAP2458c | hypothetical protein | 160 | 100 |
| MAP4_1366 | ATP synthase A chain | 252 | Rv1304 | Probable ATP synthase a chain AtpB | 84.46 | 250 | Mb1336 | ATP synthase F0F1 subunit A | 84.46 | 250 | MAV_1521 | F0F1 ATP synthase subunit A | 99.6 | 252 | BCG_1364 | F0F1 ATP synthase subunit A | 84.46 | 250 | MAP2457c | F0F1 ATP synthase subunit A | 252 | 100 |
| MAP4_1367 | ATP synthase C chain | 84 | Rv1305 | Probable ATP synthase C chain AtpE | 90 | 81 | Mb1337 | ATP synthase F0F1 subunit C | 90 | 81 | MAV_1522 | F0F1 ATP synthase subunit C | 100 | 84 | BCG_1365 | F0F1 ATP synthase subunit C | 90 | 81 | MAP2456c | F0F1 ATP synthase subunit C | 84 | 100 |
| MAP4_1368 | ATP synthase B chain atpF | 177 | Rv1306 | Probable ATP synthase B chain AtpF | 77.65 | 171 | Mb1338 | ATP synthase F0F1 subunit B | 77.65 | 171 | MAV_1523 | F0F1 ATP synthase subunit B | 100 | 178 | BCG_1366 | F0F1 ATP synthase subunit B | 77.65 | 171 | MAP2455c | F0F1 ATP synthase subunit B | 177 | 100 |
| MAP4_1369 | ATP synthase delta chain | 446 | Rv1307 | Probable ATP synthase delta chain A | 76.68 | 446 | Mb1339 | ATP synthase F0F1 subunit de | 76.68 | 446 | MAV_1524 | F0F1 ATP synthase subunit delta | 99.78 | 446 | BCG_1367 | F0F1 ATP synthase subunit delt | 76.68 | 446 | MAP2454c | F0F1 ATP synthase subunit delta | 446 | 100 |
| MAP4_1370 | ATP synthase alpha chain | 554 | Rv1308 | Probable ATP synthase alpha chain | 91.6 | 549 | Mb1340 | ATP synthase F0F1 subunit al | 91.6 | 549 | MAV_1525 | F0F1 ATP synthase subunit alpha | 100 | 554 | BCG_1368 | F0F1 ATP synthase subunit alp | 91.6 | 549 | MAP2453c | F0F1 ATP synthase subunit alpha | 554 | 100 |
| MAP4_1371 | ATP synthase gamma chain | 304 | Rv1309 | Probable ATP synthase gamma chai | 87.87 | 305 | Mb1341 | ATP synthase F0F1 subunit ga | 87.87 | 305 | MAV_1526 | F0F1 ATP synthase subunit gamma | 100 | 304 | BCG_1369 | F0F1 ATP synthase subunit gam | 87.87 | 305 | MAP2452c | F0F1 ATP synthase subunit gamma | 304 | 100 |
| MAP4_1372 | ATP synthase beta chain | 485 | Rv1310 | Probable ATP synthase beta chain A | 94.8 | 486 | Mb1342 | ATP synthase F0F1 subunit be | 94.8 | 486 | MAV_1527 | F0F1 ATP synthase subunit beta | 99.79 | 485 | BCG_1370 | F0F1 ATP synthase subunit bet | 94.8 | 486 | MAP2451c | F0F1 ATP synthase subunit beta | 402 | 99.75 |
| MAP4_1373 | ATP synthase epsilon chain | 121 | Rv1311 | Probable ATP synthase epsilon chai | 89.26 | 121 | Mb1343 | ATP synthase F0F1 subunit ep | 89.26 | 121 | MAV_1528 | F0F1 ATP synthase subunit epsilon | 100 | 121 | BCG_1371 | F0F1 ATP synthase subunit eps | 89.26 | 121 | MAP2450c | F0F1 ATP synthase subunit epsilon | 121 | 100 |
| MAP4_1374 | putative conserved secreted protein | 147 | Rv1312 | Conserved hypothetical secreted pr | 91.85 | 147 | Mb1344 | hypothetical protein | 90.85 | 144 | MAV_1530 | hypothetical protein | 100 | 143 | BCG_1372 | hypothetical protein | 90.85 | 144 | MAP2449c | hypothetical protein | 147 | 100 |
| MAP4_1375 | putative coblalamin adenosyl transferase | 195 | Rv1314c | hypothetical protein | 82.45 | 193 | Mb1347c | hypothetical protein | 82.45 | 193 | MAV_1529 | ATP:cob(I)alamin adenosyltransfera | 99.49 | 195 | BCG_1375c | hypothetical protein | 82.45 | 193 | MAP2448 | hypothetical protein | 199 | 99.49 |
| MAP4_1376 | UDP-N-acetylglucosamine1-carboxyvinyl transferase | 417 | Rv1315 | Probable UDP-N-acetylglucosamine | 97.6 | 418 | Mb1348 | UDP-N-acetylglucosamine 1-c | 97.6 | 418 | MAV_1531 | UDP-N-acetylglucosamine 1-carbox | 100 | 417 | BCG_1376 | UDP-N-acetylglucosamine 1-ca | 97.6 | 418 | MAP2447c | UDP-N-acetylglucosamine 1-carboxyvin | 417 | 100 |
| MAP4_1377 | hypothetical protein | 165 | Rv3008 | Hypothetical protein | 37.25 | 207 | Mb3033 | hypothetical protein | 37.25 | 207 | MAV_1535 | pyridoxamine 5'-phosphate oxidase | 98.18 | 165 | BCG_3030 | hypothetical protein | 37.25 | 207 | MAP2446c | hypothetical protein | 165 | 100 |
| MAP4_1378 | methylated-DNA--protein-cysteinemethyl transferase | 165 | Rv1316c | Methylated-DNA--protein-cysteine | 80 | 165 | Mb1349c | methylated-DNA--protein-cys | 80 | 165 | MAV_1536 | methylated-DNA--protein-cysteine | 100 | 165 | BCG_1377c | methylated-DNA--protein-cyste | 80 | 165 | MAP2445 | Ogt | 165 | 100 |
| MAP4_1379 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_1380 | ada regulatory protein alkA | 507 | Rv1317c | Probable bifunctional regulatory pr | 82.15 | 496 | Mb1350c | methylated-DNA--protein-cys | 79.9 | 416 | MAV_1537 | AraC family transcriptional regulato | 98.59 | 499 | BCG_1378c | ada regulatory protein alkA | 82.35 | 496 | MAP2443 | hypothetical protein | 507 | 100 |
| MAP4_1381 | putative transcriptional regulator | 294 | Rv2282c | Probable transcription regulator (Ly | 29.11 | 312 | Mb2303c | LysR family transcriptional re | 29.11 | 312 | MAV_1538 | LysR family transcriptional regulato | 98.98 | 294 | BCG_2297c | LysR family transcriptional regu | 29.11 | 312 | MAP2442 | hypothetical protein | 294 | 99.66 |
| MAP4_1382 | putative transport protein, major facilitator superfamil | 420 | Rv1902c | Probable sialic acid-transport integr | 28.27 | 422 | Mb1937c | sialic acid-transport integral | 28.27 | 422 | MAV_1539 | major facilitator family protein tran | 97.34 | 414 | BCG_1941c | sialic acid-transport integral me | 28.27 | 422 | MAP2441c | hypothetical protein | 420 | 100 |
| MAP4_1383 | Adenylate cyclase | 544 | Rv1318c | Possible adenylate cyclase (ATP pyr | 76.26 | 541 | Mb1352c | adenylate cyclase | 76.26 | 541 | MAV_1540 | HAMP domain-containing protein | 99.82 | 544 | BCG_1379c | adenylate cyclase | 76.26 | 541 | MAP2440 | hypothetical protein | 544 | 100 |
| MAP4_1384 | hypothetical protein | 226 | Rv1321 | hypothetical protein | 93.36 | 226 | Mb1355 | hypothetical protein | 93.81 | 226 | MAV_1541 | hypothetical protein | 99.09 | 220 | BCG_1382 | hypothetical protein | 93.81 | 226 | MAP2439c | hypothetical protein | 226 | 100 |
| MAP4_1385 | hypothetical protein | 98 | Rv1322 | hypothetical protein | 74.49 | 98 | Mb1356 | hypothetical protein | 74.49 | 98 | MAV_1542 | hypothetical protein | 96.05 | 76 | BCG_1383 | hypothetical protein | 74.49 | 98 | MAP2438c | hypothetical protein | 98 | 100 |
| MAP4_1386 | putative methylmalonyl-CoA epimerase | 154 | Rv1322A | hypothetical protein | 78.43 | 152 | Mb1357c | hypothetical protein | 78.43 | 152 | MAV_1543 | methylmalonyl-CoA epimerase | 100 | 154 | BCG_1384c | hypothetical protein | 78.43 | 152 | MAP2437 | hypothetical protein | 154 | 100 |
| MAP4_1387 | Acetyl-CoA acetyltransferase | 393 | Rv1323 | Probable acetyl-CoA acetyltransfera | 90.75 | 389 | Mb1358 | acetyl-CoA acetyltransferase | 90.75 | 389 | MAV_1544 | acetyl-CoA acetyltransferase | 99.75 | 393 | BCG_1385 | acetyl-CoA acetyltransferase | 90.75 | 389 | MAP2436c | acetyl-CoA acetyltransferase | 389 | 99.74 |
| MAP4_1388 | thioredoxin | 303 | Rv1324 | Possible thioredoxin | 76.64 | 304 | Mb1359 | thioredoxin | 76.64 | 304 | MAV_1545 | thioredoxin | 99.67 | 303 | BCG_1386 | thioredoxin | 76.64 | 304 | MAP2435c | hypothetical protein | 303 | 100 |
| MAP4_1389 | 1,4-alpha-glucan (glycogen) branching enzyme | 731 | Rv1326c | 1,4-alpha-glucan branching enzyme | 88.9 | 731 | Mb1361c | glycogen branching protein | 89.32 | 731 | MAV_3212 | malto-oligosyltrehalose trehalohyd | 27.01 | 590 | BCG_1388c | glycogen branching protein | 89.32 | 731 | MAP2434 | glycogen branching enzyme | 731 | 100 |
| MAP4_1390 | Putative glucanase glgE | 694 | Rv1327c | Probable glucanase GlgE | 85.45 | 701 | Mb1362c | glucanase GLGE | 85.45 | 701 | MAV_1547 | alpha-amylase | 99.42 | 694 | BCG_1389c | glucanase glgE | 85.45 | 701 | MAP2433 | hypothetical protein | 712 | 99.86 |
| MAP4_1391 | Glycogen phosphorylase | 871 | Rv1328 | Probable glycogen phosphorylase G | 83.39 | 863 | Mb1363 | glycogen phosphorylase GlgP | 83.16 | 863 | MAV_1549 | alpha-glucan phosphorylase | 99.66 | 871 | BCG_1390 | glycogen phosphorylase glgP | 83.16 | 863 | MAP2432c | hypothetical protein | 871 | 100 |
| MAP4_1392 | ATP-dependent helicase DinG | 663 | Rv1329c | Probable ATP-dependent helicase D | 82.04 | 664 | Mb1364c | ATP-dependent helicase dinG | 82.04 | 664 | MAV_1548 | DeaD/DeaH family protein helicase | 99.55 | 663 | BCG_1391c | atp-dependent helicase dinG-li | 82.04 | 664 | MAP2431 | DinG | 663 | 100 |
| MAP4_1393 | Nicotinate phosphoribosyltransferase | 444 | Rv1330c | Nicotinic acid phosphoribosyltransfe | 81.11 | 448 | Mb1365c | nicotinate phosphoribosyltra | 80.88 | 448 | MAV_1550 | nicotinate phosphoribosyltransfera | 99.55 | 444 | BCG_1392c | nicotinate phosphoribosyltrans | 81.11 | 448 | MAP2430 | nicotinate phosphoribosyltransferase | 467 | 100 |
| MAP4_1394 | ATP-dependent Clp protease adaptor protein ClpS | 105 | Rv1331 | hypothetical protein | 85.71 | 101 | Mb1366 | ATP-dependent Clp protease | 85.71 | 101 | MAV_1551 | ATP-dependent Clp protease adapt | 100 | 105 | BCG_1393 | ATP-dependent Clp protease a | 85.71 | 101 | MAP2429c | ATP-dependent Clp protease adaptor p | 105 | 100 |
| MAP4_1395 | transcriptional regulatory protein | 195 | Rv1332 | Probable transcriptional regulatory | 80.1 | 218 | Mb1367 | transcriptional regulator | 80.1 | 218 | MAV_1552 | hypothetical protein | 98.97 | 195 | BCG_1394 | transcriptional regulatory prote | 80.1 | 218 | MAP2428c | hypothetical protein | 195 | 100 |
| MAP4_1396 | putative hydrolase | 347 | Rv1333 | Probable hydrolase | 78.61 | 344 | Mb1368 | hydrolase | 78.61 | 344 | MAV_1553 | peptidase T4 | 97.41 | 346 | BCG_1395 | hydrolase | 78.61 | 344 | MAP2427c | hypothetical protein | 347 | 100 |
| MAP4_1399 | Glutamate racemase | 275 | Rv1338 | Probable glutamate racemase MurI | 86.86 | 271 | Mb1373 | glutamate racemase | 86.86 | 271 | MAV_1555 | glutamate racemase | 99.64 | 275 | BCG_1400 | glutamate racemase | 86.5 | 271 | MAP2424c | glutamate racemase | 275 | 100 |
| MAP4_1400 | Beta-lactamase superfamily protein | 275 | Rv1339 | hypothetical protein | 86.4 | 273 | Mb1374 | hypothetical protein | 86.4 | 273 | MAV_1556 | metal-dependent hydrolase of the | 99.61 | 254 | BCG_1401 | hypothetical protein | 86.4 | 273 | MAP2423c | hypothetical protein | 275 | 100 |
| MAP4_1401 | Ribonuclease PH | 259 | Rv1340 | Probable ribonuclease RphA (RNase | 91.12 | 259 | Mb1375 | ribonuclease PH | 90.73 | 259 | MAV_1557 | ribonuclease PH | 99.61 | 259 | BCG_1402 | ribonuclease PH | 91.12 | 259 | MAP2422c | ribonuclease PH | 259 | 100 |
| MAP4_1402 | hypothetical protein | 72 | Rv2605c | Probable acyl-CoA thioesterase II Te | 42.86 | 281 | Mb2637c | acyl-CoA thioesterase | 46.43 | 281 | MAV_2645 | carveol dehydrogenase | 32.5 | 240 | BCG_2630c | acyl-CoA thioesterase II tesB2 | 46.43 | 281 | MAP2421c | hypothetical protein | 101 | 100 |
| MAP4_1403 | putative non-canonical purine NTP pyrophosphatase, R | 204 | Rv1341 | hypothetical protein | 85.19 | 204 | Mb1376 | deoxyribonucleotide triphosp | 85.19 | 204 | MAV_1558 | deoxyribonucleotide triphosphate | 98.53 | 204 | BCG_1403 | deoxyribonucleotide triphosph | 85.19 | 204 | MAP2420c | deoxyribonucleotide triphosphate pyro | 204 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1404 | hypothetical protein | 116 | Rv1342c | hypothetical protein | 70.83 | 120 | Mb1377c | hypothetical protein | 70.83 | 120 | MAV_1559 | hypothetical protein | 100 | 116 | BCG_1404c | hypothetical protein | 70.83 | 120 | MAP2419 | hypothetical protein | 116 | 100 |
| MAP4_1405 | putative conserved lipoprotein LPRD | 130 | Rv1343c | Probable conserved lipoprotein LprD | 82.64 | 126 | Mb1378c | lipoprotein LprD | 81.82 | 126 | MAV_1560 | hypothetical protein | 97.32 | 112 | BCG_1405c | lipoprotein lprD | 81.82 | 126 | MAP2418 | hypothetical protein | 130 | 100 |
| MAP4_1406 | putative lipoprotein | 174 | Rv2080 | Lipoprotein LppJ | 31.89 | 187 | Mb2106 | lipoprotein LppJ | 32.89 | 187 | MAV_1563 | LppJ protein | 97.33 | 150 | BCG_2099 | lipoprotein LppJ | 32.89 | 187 | MAP2417c | hypothetical protein | 174 | 100 |
| MAP4_1407 | transposase, IS4 family protein | 557 | Rv3386 | Possible transposase | 25.95 | 234 | Mb3418 | transposase | 25.95 | 234 | MAV_3010 | ABC transporter ATP-binding prote | 29.31 | 862 | BCG_3455 | transposase | 25.95 | 234 | MAP0338c | hypothetical protein | 557 | 100 |
| MAP4_1408 | hypothetical protein | 120 | Rv0275c | Possible transcriptional regulatory p | 29.03 | 241 | Mb1285 | cold-shock DEAD-box protein | 36.54 | 563 | MAV_1565 | hypothetical protein | 99.09 | 110 | BCG_1313 | cold-shock dead-box protein a | 36.54 | 563 | MAP2415c | hypothetical protein | 120 | 100 |
| MAP4_1409 | ABC transporter ATP-binding protein | 869 | Rv1348 | Iron-regulated transporter IrtA | 79.33 | 859 | Mb1383 | drugs-transport transmembra | 79.33 | 859 | MAV_1566 | ABC transporter ATP-binding prote | 97.68 | 862 | BCG_1410 | drugs-transport transmembran | 79.33 | 859 | MAP2414c | hypothetical protein | 869 | 100 |
| MAP4_1410 | ABC transporter ATP-binding protein | 578 | Rv1349 | Iron-regulated transporter IrtB | 77.08 | 579 | Mb1384 | drugs-transport transmembra | 77.08 | 579 | MAV_1567 | ABC transporter ATP-binding prote | 98.96 | 578 | BCG_1411 | drugs-transport transmembran | 77.08 | 579 | MAP2413c | hypothetical protein | 578 | 100 |
| MAP4_1411 | phosphotransferase enzyme family protein | 358 | Rv3168 | Putative aminoglycoside phosphotra | 26.71 | 378 | Mb3193 | hypothetical protein | 26.62 | 378 | MAV_1568 | phosphotransferase enzyme family | 98.59 | 355 | BCG_3192 | hypothetical protein | 26.71 | 378 | MAP2412c | hypothetical protein | 358 | 100 |
| MAP4_1412 | pyridoxamine 5'-phosphate oxidase family protein | 142 | Rv1911c | Probable lipoprotein LppC | 50 | 201 | Mb1946c | lipoprotein LppC | 50 | 201 | MAV_1569 | pyridoxamine 5'-phosphate oxidase | 99.3 | 142 | BCG_1950c | lipoprotein lppC | 50 | 201 | MAP2411 | hypothetical protein | 142 | 100 |
| MAP4_1413 | short-chain dehydrogenase | 273 | Rv0687 | Probable short-chain type dehydrog | 48.35 | 275 | Mb0706 | 3-ketoacyl-ACP reductase | 48.35 | 275 | MAV_1570 | carveol dehydrogenase | 99.27 | 273 | BCG_0736 | 3-ketoacyl-ACP reductase | 48.35 | 275 | MAP2410 | hypothetical protein | 273 | 100 |
| MAP4_1414 | acyl-CoA dehydrogenase | 397 | Rv3274c | Probable acyl-CoA dehydrogenase F | 34.31 | 389 | Mb0221c | acyl-CoA dehydrogenase | 35.98 | 388 | MAV_1571 | acyl-CoA dehydrogenase | 98.74 | 397 | BCG_0252c | acyl-CoA dehydrogenase fadE3 | 35.98 | 388 | MAP2409 | FadE25_3 | 397 | 100 |
| MAP4_1415 | 3-oxyacyl-ACP reductase | 249 | Rv1350 | Probable 3-oxoacyl-[acyl-carrier pro | 86.94 | 247 | Mb1385 | 3-ketoacyl-ACP reductase | 86.94 | 247 | MAV_1572 | short chain dehydrogenase | 99.59 | 246 | BCG_1412 | 3-ketoacyl-ACP reductase | 86.94 | 247 | MAP2408c | 3-ketoacyl-ACP reductase | 249 | 99.6 |
| MAP4_1416 | Acetyl-CoA acetyltransferase | 406 | Rv1074c | Probable beta-ketoacyl CoA thiolase | 39.57 | 405 | Mb1103c | acetyl-CoA acetyltransferase | 39.57 | 405 | MAV_1573 | acetyl-CoA acetyltransferase | 99.26 | 406 | BCG_1132c | acetyl-CoA acetyltransferase | 39.57 | 405 | MAP2407c | acetyl-CoA acetyltransferase | 406 | 100 |
| MAP4_1417 | CoA-transferase family III protein | 399 | Rv3272 | hypothetical protein | 27.53 | 394 | Mb3300 | hypothetical protein | 27.53 | 394 | MAV_1574 | L-carnitine dehydratase/bile acid-ir | 100 | 399 | BCG_3301 | hypothetical protein | 27.53 | 394 | MAP2406c | hypothetical protein | 399 | 100 |
| MAP4_1418 | acyl-CoA dehydrogenase | 397 | Rv0215c | Probable acyl-CoA dehydrogenase F | 45.68 | 357 | Mb0221c | acyl-CoA dehydrogenase | 46.25 | 388 | MAV_1575 | acyl-CoA dehydrogenase | 100 | 397 | BCG_0252c | acyl-CoA dehydrogenase fadE3 | 45.99 | 388 | MAP2405c | FadE3_1 | 397 | 100 |
| MAP4_1419 | putative regulator PutR for prolineutilization, GntR fam | 230 | Rv0165c | Probable transcriptional regulatory | 40.51 | 223 | Mb0170c | GntR family transcriptional re | 42.05 | 271 | MAV_1576 | GntR family transcriptional regulato | 99.13 | 230 | BCG_0201c | GntR family transcriptional reg | 42.05 | 271 | MAP2404c | hypothetical protein | 230 | 100 |
| MAP4_1420 | hypothetical protein | 120 | Rv1352 | hypothetical protein | 43.22 | 123 | Mb1387 | hypothetical protein | 43.22 | 123 | MAV_1578 | hypothetical protein | 96.67 | 120 | BCG_1414 | hypothetical protein | 43.22 | 123 | MAP2403c | hypothetical protein | 120 | 100 |
| MAP4_1421 | AMP-binding enzyme family protein | 518 | Rv2505c | Probable fatty-acid-CoA ligase FadD | 30.17 | 547 | Mb2533c | AMP-binding protein | 30.17 | 547 | MAV_1577 | AMP-binding enzyme | 97.68 | 518 | BCG_2525c | AMP-binding protein | 30.17 | 547 | MAP2402 | hypothetical protein | 518 | 100 |
| MAP4_1422 | fatty-acid-CoA ligase | 524 | Rv2505c | Probable fatty-acid-CoA ligase FadD | 30.45 | 547 | Mb2533c | AMP-binding protein | 30.45 | 547 | MAV_1579 | acyl-CoA dehydrogenase | 99.05 | 524 | BCG_2525c | AMP-binding protein | 30.64 | 547 | MAP2401 | FadD35 | 524 | 100 |
| MAP4_1423 | Long-chain-fatty-acid--CoA ligase | 485 | Rv1427c | Possible long-chain-fatty-acid--CoA l | 26.12 | 535 | Mb1462c | acyl-CoA synthetase | 26.12 | 535 | MAV_1580 | AMP-dependent synthetase and lig | 98.14 | 485 | BCG_1488c | acyl-CoA synthetase | 26.12 | 535 | MAP2400 | hypothetical protein | 485 | 100 |
| MAP4_1424 | enoyl-CoA hydratase | 266 | Rv2831 | Probable enoyl-CoA hydratase EchA | 34.21 | 249 | Mb2855 | enoyl-CoA hydratase | 34.21 | 249 | MAV_1581 | enoyl-CoA hydratase/isomerase | 100 | 268 | BCG_2851 | enoyl-CoA hydratase | 34.21 | 249 | MAP2399 | EchA16_1 | 270 | 100 |
| MAP4_1425 | Enoyl-CoA hydratase | 270 | Rv3516 | Possible enoyl-CoA hydratase EchA1 | 34.36 | 263 | Mb3545 | enoyl-CoA hydratase | 34.36 | 263 | MAV_1582 | enoyl-CoA hydratase/isomerase | 100 | 270 | BCG_3579 | enoyl-CoA hydratase | 34.36 | 263 | MAP2398 | hypothetical protein | 270 | 100 |
| MAP4_1426 | Enoyl-CoA hydratase | 273 | Rv1142c | Probable enoyl-CoA hydratase EchA | 35 | 268 | Mb1174c | enoyl-CoA hydratase | 35 | 268 | MAV_1583 | enoyl-CoA hydratase/isomerase | 99.23 | 260 | BCG_1204c | enoyl-CoA hydratase | 35 | 268 | MAP2397 | EchA10 | 286 | 99.63 |
| MAP4_1427 | hypothetical protein | 231 | Rv0356c | hypothetical protein | 27.83 | 214 | Mb0363c | hypothetical protein | 27.83 | 214 | MAV_1584 | hypothetical protein | 100 | 231 | BCG_0394c | hypothetical protein | 27.83 | 214 | MAP2396c | hypothetical protein | 231 | 100 |
| MAP4_1428 | Enoyl-CoA hydratase | 296 | Rv0673 | Possible enoyl-CoA hydratase EchA4 | 29.97 | 312 | Mb0692 | enoyl-CoA hydratase | 29.97 | 312 | MAV_1585 | enoyl-CoA hydratase/isomerase | 99.32 | 296 | BCG_0722 | enoyl-CoA hydratase | 29.97 | 312 | MAP2395c | hypothetical protein | 296 | 100 |
| MAP4_1429 | Transcriptional regulator, TetR family | 268 | Rv1353c | Probable transcriptional regulatory | 79.12 | 261 | Mb1388c | transcriptional regulator | 79.12 | 261 | MAV_1586 | TetR family transcriptional regulato | 99.62 | 262 | BCG_1415c | transcriptional regulatory prote | 79.12 | 261 | MAP2394 | hypothetical protein | 268 | 100 |
| MAP4_1430 | Short chain dehydrogenase | 265 | Rv1483 | 3-oxoacyl-[acyl-carrier protein] redu | 28.17 | 247 | Mb1519 | 3-oxoacyl-ACP reductase | 28.17 | 247 | MAV_1587 | oxidoreductase, short chain dehydr | 99.62 | 265 | BCG_1545 | 3-oxoacyl-ACP reductase | 28.17 | 247 | MAP2393c | hypothetical protein | 265 | 100 |
| MAP4_1431 | dihydrodipicolinate synthetase | 338 | Rv1989c | Hypothetical protein | 35.71 | 186 | Mb2011c | hypothetical protein | 35.71 | 186 | MAV_1588 | dihydrodipicolinate synthetase | 99.11 | 338 | BCG_2005c | hypothetical protein | 35.71 | 186 | MAP2392c | hypothetical protein | 338 | 100 |
| MAP4_1432 | hypothetical protein | 80 | Rv0101 | Probable peptide synthetase Nrp (pe | 41.38 | 2512 | Mb0104 | peptide synthetase | 41.38 | 2512 | MAV_1589 | hypothetical protein | 100 | 80 | BCG_0134 | peptide synthetase nrp | 41.38 | 2512 | MAP2391 | hypothetical protein | 111 | 100 |
| MAP4_1433 | Enoyl-CoA hydratase | 274 | Rv1070c | Probable enoyl-CoA hydratase EchA | 33.71 | 257 | Mb1099c | enoyl-CoA hydratase | 33.71 | 257 | MAV_1590 | enoyl-CoA hydratase | 98.54 | 274 | BCG_1128c | enoyl-CoA hydratase | 33.71 | 257 | MAP2390c | enoyl-CoA hydratase | 275 | 100 |
| MAP4_1434 | amidohydrolase family protein | 400 | Rv1142c | Probable enoyl-CoA hydratase EchA | 32.79 | 268 | Mb1174c | enoyl-CoA hydratase | 32.79 | 268 | MAV_1591 | amidohydrolase | 100 | 400 | BCG_1204c | enoyl-CoA hydratase | 32.79 | 268 | MAP2389c | hypothetical protein | 400 | 100 |
| MAP4_1435 | fatty-acid-CoA ligase | 545 | Rv3515c | Fatty-acid-CoA ligase FadD19 (fatty- | 35.56 | 548 | Mb3544c | acyl-CoA synthetase | 35.56 | 548 | MAV_1592 | acyl-CoA synthetase | 98.9 | 545 | BCG_3578c | acyl-CoA synthetase | 35.56 | 548 | MAP2388c | acyl-CoA synthetase | 545 | 100 |
| MAP4_1436 | amidohydrolase family protein | 276 | Rv3510c | hypothetical protein | 32.78 | 278 | Mb3540c | hypothetical protein | 32.78 | 278 | MAV_1593 | amidohydrolase | 98.91 | 276 | BCG_3574c | hypothetical protein | 32.78 | 278 | MAP2387c | hypothetical protein | 276 | 100 |
| MAP4_1437 | putative acyl-CoA dehydrogenase | 348 | Rv1933c | Probable acyl-CoA dehydrogenase F | 27.25 | 363 | Mb1968c | acyl-CoA dehydrogenase | 27.25 | 363 | MAV_1594 | acyl-CoA dehydrogenase | 100 | 348 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 27.25 | 363 | MAP2386c | hypothetical protein | 348 | 100 |
| MAP4_1438 | putative acyl-CoA dehydrogenase | 397 | Rv3543c | Probable acyl-CoA dehydrogenase F | 32.77 | 387 | Mb3573c | acyl-CoA dehydrogenase | 32.77 | 387 | MAV_1595 | acyl-CoA dehydrogenase | 99.24 | 397 | BCG_3607c | acyl-CoA dehydrogenase fadE2 | 32.77 | 387 | MAP2385c | hypothetical protein | 397 | 100 |
| MAP4_1439 | putative thiolase | 381 | Rv1627c | Probable nonspecific lipid-transfer p | 31.5 | 402 | Mb1653c | lipid-transfer protein | 31.5 | 402 | MAV_1596 | thiolase | 99.48 | 381 | BCG_1665c | lipid-transfer protein | 31.5 | 402 | MAP2384 | hypothetical protein | 381 | 100 |
| MAP4_1440 | putative acyl-CoA transferasecarnitinedehydratase | 408 | Rv3272 | hypothetical protein | 30.1 | 394 | Mb3300 | hypothetical protein | 29.85 | 394 | MAV_1597 | L-carnitine dehydratase/bile acid-ir | 99.26 | 404 | BCG_3301 | hypothetical protein | 29.25 | 394 | MAP2383 | hypothetical protein | 408 | 100 |
| MAP4_1441 | putative cytochrome P450 hydroxylase | 400 | Rv3518c | Probable cytochrome P450 monoox | 35.23 | 398 | Mb0789c | cytochrome P450 123 | 30.13 | 402 | MAV_1598 | cytochrome P450 superfamily prot | 99.25 | 400 | BCG_0830 | cytochrome P450 126 cyp126 | 32.33 | 414 | MAP2382 | hypothetical protein | 400 | 100 |
| MAP4_1442 | short-chain type dehydrogenasereductase | 280 | Rv3085 | Probable short-chain type dehydrog | 46.62 | 276 | Mb3112 | short-chain type dehydrogen | 46.62 | 276 | MAV_1599 | oxidoreductase, short chain dehydr | 99.64 | 280 | BCG_3110 | short-chain type dehydrogenas | 46.62 | 276 | MAP2381 | hypothetical protein | 280 | 100 |
| MAP4_1443 | fatty-acid-CoA ligase fadD19 | 550 | Rv3515c | Fatty-acid-CoA ligase FadD19 (fatty- | 40.51 | 548 | Mb3544c | acyl-CoA synthetase | 40.51 | 548 | MAV_1600 | acyl-CoA synthetase | 99.09 | 550 | BCG_3578c | acyl-CoA synthetase | 40.51 | 548 | MAP2380 | acyl-CoA synthetase | 550 | 100 |
| MAP4_1444 | hypothetical protein | 210 | Rv0356c | hypothetical protein | 53.81 | 214 | Mb0363c | hypothetical protein | 53.81 | 214 | MAV_1601 | thioesterase | 98.57 | 210 | BCG_0394c | hypothetical protein | 53.81 | 214 | MAP2379 | hypothetical protein | 210 | 100 |
| MAP4_1445 | hydrolase, isochorismatase family | 209 | Rv2043c | Pyrazinamidase/nicotinamidase Pnc | 30.43 | 186 | Mb2069c | pyrazinamidase | 30.43 | 186 | MAV_1602 | isochorismatase | 99.52 | 209 | BCG_2062c | pyrazinamidase/nicotinamidas | 30.43 | 186 | MAP2378 | hypothetical protein | 209 | 100 |
| MAP4_1446 | Rieske (2Fe-2S) domain-containing protein | 337 | Rv3526 | Oxygenase component of 3-ketoster | 26.91 | 386 | Mb3556 | oxidoreductase | 26.91 | 386 | MAV_1603 | Rieske (2Fe-2S) domain-containing | 99.41 | 337 | BCG_3590 | oxidoreductase | 26.91 | 386 | MAP2377 | hypothetical protein | 337 | 100 |
| MAP4_1447 | monooxygenase | 540 | Rv1393c | Probable monoxygenase | 31.69 | 492 | Mb1428c | monoxygenase | 31.69 | 492 | MAV_1604 | steroid monooxygenase | 98.33 | 540 | BCG_1454c | monoxygenase | 31.69 | 492 | MAP2376c | hypothetical protein | 542 | 100 |
| MAP4_1448 | hypothetical protein | 373 | Rv2627c | hypothetical protein | 32.33 | 413 | Mb2660c | hypothetical protein | 32.33 | 413 | MAV_1605 | hypothetical protein | 98.12 | 373 | BCG_2654c | hypothetical protein | 32.33 | 413 | MAP2375c | hypothetical protein | 373 | 100 |
| MAP4_1449 | hypothetical protein | 126 | Rv0119 | Probable fatty-acid-CoA ligase FadD | 24.19 | 525 | Mb0123 | acyl-CoA synthetase | 24.19 | 525 | MAV_1606 | hypothetical protein | 100 | 126 | BCG_0153 | acyl-CoA synthetase | 24.19 | 525 | MAP2374c | hypothetical protein | 117 | 99.15 |
| MAP4_1450 | oxidoreductase | 346 | Rv2951c | Possible oxidoreductase | 29.63 | 381 | Mb2975c | oxidoreductase | 29.63 | 381 | MAV_1607 | hypothetical protein | 98.83 | 342 | BCG_2972c | oxidoreductase | 29.63 | 381 | MAP2373c | hypothetical protein | 346 | 100 |
| MAP4_1451 | Propionyl-CoA carboxylase beta chain | 498 | Rv3799c | Probable propionyl-CoA carboxylase | 36.05 | 522 | Mb3829c | propionyl-CoA carboxylase su | 36.05 | 522 | MAV_1608 | carboxyl transferase domain-conta | 99.6 | 498 | BCG_3861c | propionyl-CoA carboxylase bet | 36.05 | 522 | MAP2372 | AccD4_2 | 498 | 100 |
| MAP4_1452 | putative cytochrome P450 hydroxylase | 411 | Rv2266 | Probable cytochrome P450 124 Cyp | 35.09 | 428 | Mb2289 | cytochrome P450 124 CYP124 | 35.09 | 428 | MAV_1609 | cytochrome P450 family protein | 100 | 411 | BCG_2283 | cytochrome P450 124 CYP124 | 35.09 | 428 | MAP2371c | hypothetical protein | 411 | 100 |
| MAP4_1453 | short-chain dehydrogenase | 274 | Rv0439c | Probable dehydrogenase/reductase | 34.98 | 311 | Mb0447c | short chain dehydrogenase | 34.98 | 311 | MAV_1610 | NAD dependent epimerase/dehydr | 100 | 274 | BCG_0478c | short chain dehydrogenase | 34.98 | 311 | MAP2370c | hypothetical protein | 274 | 100 |
| MAP4_1454 | Transcriptional regulator, TetR family | 205 | Rv1534 | Probable transcriptional regulator | 41.46 | 225 | Mb1561 | transcriptional regulator | 41.46 | 225 | MAV_1611 | TetR family transcriptional regulato | 99.51 | 205 | BCG_1586 | transcriptional regulator | 41.46 | 225 | MAP2369c | hypothetical protein | 201 | 100 |
| MAP4_1455 | hypothetical protein | 225 | Rv1349 | Iron-regulated transporter IrtB | 36.05 | 579 | Mb1384 | drugs-transport transmembra | 36.05 | 579 | MAV_1612 | hypothetical protein | 98.67 | 225 | BCG_1411 | drugs-transport transmembran | 36.05 | 579 | MAP2368c | hypothetical protein | 225 | 100 |
| MAP4_1456 | ABC-2 family transporter protein | 634 | Rv0180c | Probable conserved transmembrane | 26.11 | 452 | Mb0186c | transmembrane protein | 26.11 | 452 | MAV_1613 | ABC transporter | 99.53 | 634 | BCG_0217c | hypothetical protein | 26.11 | 452 | MAP2367c | hypothetical protein | 634 | 100 |
| MAP4_1457 | zinc-type alcohol dehydrogenase | 529 | Rv3086 | Probable zinc-type alcohol dehydrog | 45.3 | 368 | Mb3113 | zinc-type alcohol dehydrogen | 45.3 | 368 | MAV_1614 | alcohol dehydrogenase B | 99.17 | 385 | BCG_3111 | zinc-type alcohol dehydrogena | 45.3 | 368 | MAP2366 | hypothetical protein | 529 | 100 |
| MAP4_1458 | cytochrome P450 | 410 | Rv3518c | Probable cytochrome P450 monoox | 31.49 | 398 | Mb0789c | cytochrome P450 123 | 30.71 | 402 | MAV_1615 | cytochrome P450 superfamily prot | 99.76 | 410 | BCG_2283 | cytochrome P450 124 CYP124 | 29.95 | 428 | MAP2365 | hypothetical protein | 410 | 100 |
| MAP4_1459 | alphabeta hydrolase domain-containing protein | 319 | Rv1400c | Probable lipase LipH | 36.89 | 320 | Mb1435c | lipase LipH | 36.89 | 320 | MAV_1617 | alpha/beta hydrolase | 99.69 | 319 | BCG_1461c | lipase lipH | 36.89 | 320 | MAP2364c | hypothetical protein | 314 | 99.68 |
| MAP4_1460 | Acyl-CoA dehydrogenase | 382 | Rv1933c | Probable acyl-CoA dehydrogenase F | 31.64 | 363 | Mb1968c | acyl-CoA dehydrogenase | 31.64 | 363 | MAV_1618 | acyl-CoA dehydrogenase domain-c | 98.95 | 382 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 31.64 | 363 | MAP2363c | hypothetical protein | 382 | 100 |
| MAP4_1461 | Acyl-CoA dehydrogenase | 413 | Rv3560c | Probable acyl-CoA dehydrogenase F | 30.58 | 385 | Mb3590c | acyl-CoA dehydrogenase | 30.58 | 385 | MAV_1620 | acyl-CoA dehydrogenase middle do | 99.27 | 413 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 30.58 | 385 | MAP2362c | hypothetical protein | 413 | 100 |
| MAP4_1462 | putative regulator of sigma subunit | 655 | Rv1364c | Possible sigma factor regulatory pro | 76.45 | 653 | Mb1399c | hypothetical protein | 76.45 | 653 | MAV_1619 | anti-anti-sigma factor | 99.69 | 655 | BCG_1426c | hypothetical protein | 76.45 | 653 | MAP2361 | hypothetical protein | 655 | 100 |
| MAP4_1463 | hypothetical protein | 169 | Rv3817 | Possible phosphotransferase | 31.03 | 251 | Mb3847 | phosphotransferase | 31.03 | 251 | MAV_1621 | hypothetical protein | 98.22 | 169 | BCG_3879 | phosphotransferase | 31.03 | 251 | MAP2360c | hypothetical protein | 177 | 99.41 |
| MAP4_1464 | oxidoreductase | 496 | Rv0218 | Probable conserved transmembrane | 36.81 | 442 | Mb0224 | transmembrane protein | 36.81 | 442 | MAV_1622 | oxidoreductase molybdopterin bin | 99.4 | 496 | BCG_0255 | hypothetical protein | 36.81 | 442 | MAP2359c | hypothetical protein | 496 | 100 |
| MAP4_1465 | hypothetical protein | 100 | Rv2831 | Probable enoyl-CoA hydratase EchA | 44 | 249 | Mb2855 | enoyl-CoA hydratase | 44 | 249 | MAV_1624 | hypothetical protein | 98 | 100 | BCG_2851 | enoyl-CoA hydratase | 44 | 249 | MAP2358c | hypothetical protein | 100 | 100 |
| MAP4_1466 | amidohydrolase domain-containing protein | 402 | Rv2303c | Probable antibiotic-resistance prote | 28.95 | 307 | Mb2325c | antibiotic-resistance protein | 28.95 | 307 | MAV_1625 | amidohydrolase | 99.75 | 402 | BCG_2319c | antibiotic-resistance protein | 28.95 | 307 | MAP2357 | hypothetical protein | 402 | 100 |
| MAP4_1467 | Transcriptional regulator, TetR family | 343 | Rv0135c | Possible transcriptional regulatory p | 30.56 | 201 | Mb0140c | transcriptional regulator | 30.56 | 201 | MAV_1626 | hypothetical protein | 98.54 | 343 | BCG_0171c | transcriptional regulatory prote | 30.56 | 201 | MAP2356 | hypothetical protein | 343 | 100 |
| MAP4_1470 | Acyl-CoA dehydrogenase | 311 | Rv3544c | Probable acyl-CoA dehydrogenase F | 34.95 | 339 | Mb3574c | acyl-CoA dehydrogenase | 34.95 | 339 | MAV_1628 | acyl-CoA dehydrogenase | 99.04 | 311 | BCG_3608c | acyl-CoA dehydrogenase fadE2 | 34.95 | 339 | MAP2353 | hypothetical protein | 311 | 100 |
| MAP4_1471 | Acyl-CoA dehydrogenase | 382 | Rv1934c | Probable acyl-CoA dehydrogenase F | 35.24 | 409 | Mb1969c | acyl-CoA dehydrogenase | 35.24 | 409 | MAV_1629 | acyl-CoA dehydrogenase | 99.48 | 382 | BCG_1973c | acyl-CoA dehydrogenase fadE1 | 35.24 | 409 | MAP2352 | hypothetical protein | 382 | 100 |
| MAP4_1472 | acyl-CoA dehydrogenase | 375 | Rv0271c | Probable acyl-CoA dehydrogenase F | 39.41 | 731 | Mb0277c | acyl-CoA dehydrogenase | 39.41 | 731 | MAV_1630 | acyl-CoA dehydrogenase | 99.18 | 365 | BCG_0309c | acyl-CoA dehydrogenase fadE6 | 39.41 | 731 | MAP2351 | hypothetical protein | 375 | 100 |
| MAP4_1473 | acyl-CoA dehydrogenase | 356 | Rv1933c | Probable acyl-CoA dehydrogenase F | 33.97 | 363 | Mb1968c | acyl-CoA dehydrogenase | 33.97 | 363 | MAV_1631 | acyl-CoA dehydrogenase | 98.88 | 356 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 33.97 | 363 | MAP2350 | hypothetical protein | 377 | 100 |
| MAP4_1474 | hypothetical protein | 283 | Rv0791c | hypothetical protein | 29.17 | 347 | Mb0815c | hypothetical protein | 29.17 | 347 | MAV_1632 | hypothetical protein | 98.94 | 283 | BCG_0844c | hypothetical protein | 29.17 | 347 | MAP2349c | hypothetical protein | 283 | 100 |
| MAP4_1475 | short-chain dehydrogenasereductase | 238 | Rv0484c | Probable short-chain type oxidoredu | 32.44 | 251 | Mb0494c | short-chain type oxidoreduct | 32.44 | 251 | MAV_1633 | NAD dependent epimerase/dehydr | 98.32 | 238 | BCG_0525c | short-chain type oxidoreductas | 32.44 | 251 | MAP2348 | hypothetical protein | 238 | 100 |
| MAP4_1476 | Transcriptional regulator, GntR family | 273 | Rv3060c | Probable transcriptional regulatory | 27.27 | 490 | Mb3086c | GntR family transcriptional re | 27.27 | 490 | MAV_1634 | GntR family transcriptional regulato | 100 | 273 | BCG_3085c | GntR family transcriptional reg | 27.27 | 490 | MAP2347 | hypothetical protein | 273 | 100 |
| MAP4_1477 | putative CoA-transferase family protein | 807 | Rv1866 | hypothetical protein | 28.16 | 778 | Mb1897 | hypothetical protein | 28.04 | 778 | MAV_1635 | caib/baif family protein | 99.38 | 806 | BCG_1902 | hypothetical protein | 28.04 | 778 | MAP2346c | hypothetical protein | 816 | 99.88 |
| MAP4_1478 | ferredoxin | 63 | Rv3503c | Probable ferredoxin FdxD | 42.37 | 63 | Mb3533c | ferredoxin FdxD | 42.37 | 63 | MAV_1636 | hypothetical protein | 100 | 63 | BCG_3567c | ferredoxin fdxD | 42.37 | 63 | MAP2345c | hypothetical protein | 63 | 100 |
| MAP4_1479 | putative cytochrome P450 hydroxylase | 431 | Rv2266 | Probable cytochrome P450 124 Cyp | 36.08 | 428 | Mb2289 | cytochrome P450 124 CYP124 | 36.08 | 428 | MAV_1637 | cytochrome P450 superfamily prot | 98.61 | 431 | BCG_2283 | cytochrome P450 124 CYP124 | 36.08 | 428 | MAP2344 | hypothetical protein | 431 | 100 |
| MAP4_1480 | oxidoreductase, Rieske 2Fe-2S domain protein | 384 | Rv3526 | Oxygenase component of 3-ketoster | 24.62 | 386 | Mb3556 | oxidoreductase | 24.62 | 386 | MAV_1638 | Rieske (2Fe-2S) domain-containing | 99.47 | 375 | BCG_3590 | oxidoreductase | 24.62 | 386 | MAP2343c | hypothetical protein | 384 | 100 |
| MAP4_1481 | putative AMP-binding enzyme | 521 | Rv1058 | Probable medium chain fatty-acid-C | 27.67 | 543 | Mb1087 | long-chain-fatty-acid--CoA lig | 27.67 | 543 | MAV_1639 | AMP-binding enzyme, putative | 98.66 | 521 | BCG_1116 | long-chain-fatty-acid--CoA ligas | 27.67 | 543 | MAP2342c | hypothetical protein | 521 | 100 |
| MAP4_1482 | hypothetical protein | 141 | Rv3472 | hypothetical protein | 27.87 | 168 | Mb3501 | hypothetical protein | 27.87 | 168 | MAV_1640 | hypothetical protein | 99.29 | 141 | BCG_3537 | hypothetical protein | 27.87 | 168 | MAP2341c | hypothetical protein | 141 | 100 |
| MAP4_1483 | hypothetical protein | 176 | Rv3542c | hypothetical protein | 25.44 | 311 | Mb3572c | hypothetical protein | 25.44 | 311 | MAV_1641 | hypothetical protein | 98.3 | 176 | BCG_3606c | hypothetical protein | 25.44 | 311 | MAP2340c | hypothetical protein | 176 | 100 |
| MAP4_1484 | hypothetical protein | 145 | Rv3541c | hypothetical protein | 37.89 | 129 | Mb3571c | hypothetical protein | 37.89 | 129 | MAV_1642 | MaoC like domain-containing prote | 99.29 | 140 | BCG_3605c | hypothetical protein | 37.89 | 129 | MAP2339c | hypothetical protein | 145 | 100 |
| MAP4_1485 | Aldehyde dehydrogenase | 488 | Rv0223c | Probable aldehyde dehydrogenase | 48.2 | 487 | Mb0791 | aldehyde dehydrogenase | 41.77 | 489 | MAV_1643 | aldehyde dehydrogenase | 99.39 | 488 | BCG_0820 | aldehyde dehydrogenase AldA | 41.77 | 489 | MAP2338 | hypothetical protein | 525 | 100 |
| MAP4_1486 | hypothetical protein | 450 | Rv0988 | Possible conserved exported protein | 24.61 | 386 | Mb1015 | hypothetical protein | 23.14 | 386 | MAV_1645 | hypothetical protein | 99.33 | 450 | BCG_1043 | hypothetical protein | 23.14 | 386 | MAP2337c | hypothetical protein | 455 | 100 |
| MAP4_1487 | putative dioxygenase, Rieske (2Fe-2S) domain-containi | 381 | Rv3161c | Possible dioxygenase | 28.69 | 382 | Mb3186c | dioxygenase | 29.08 | 382 | MAV_1644 | Rieske (2Fe-2S) domain-containing | 99.48 | 381 | BCG_3185c | dioxygenase | 29.08 | 382 | MAP2336 | hypothetical protein | 381 | 100 |
| MAP4_1488 | transcriptional regulator, MerR family protein | 302 | Rv3334 | Probable transcriptional regulatory | 29.85 | 146 | Mb3367 | MerR family transcriptional re | 29.85 | 146 | MAV_1646 | MerR family transcriptional regulat | 99.34 | 302 | BCG_3405 | MerR family transcriptional reg | 29.85 | 146 | MAP2335c | hypothetical protein | 302 | 100 |
| MAP4_1489 | Putative secreted protein | 240 | Rv2525c | Conserved hypothetical protein Secr | 85.71 | 240 | Mb2554c | hypothetical protein | 85.71 | 240 | MAV_1648 | secreted protein | 99.17 | 240 | BCG_2546c | hypothetical protein | 85.71 | 240 | MAP2334c | hypothetical protein | 240 | 100 |
| MAP4_1490 | hypothetical protein | 101 | Rv2221c | Glutamate-ammonia-ligase adenylyl | 39.29 | 994 | Mb2245c | bifunctional glutamine-synthe | 39.29 | 994 | MAV_1647 | hypothetical protein | 96.43 | 101 | BCG_2238c | bifunctional glutamine-synthet | 39.29 | 994 | MAP2333 | hypothetical protein | 101 | 100 |
| MAP4_1491 | fatty acid synthase | 3092 | Rv2524c | Probable fatty acid synthase Fas (fat | 88.47 | 3069 | Mb2553c | fatty acid synthase | 88.5 | 3069 | MAV_1650 | fatty acid synthase | 99.71 | 3092 | BCG_2545c | fatty acid synthase fas | 88.5 | 3069 | MAP2332c | Fas | 3092 | 100 |
| MAP4_1492 | Holo-ACP synthase | 130 | Rv2523c | holo-[acyl-carrier protein] synthase | 93.08 | 130 | Mb2552c | 4'-phosphopantetheinyl trans | 93.08 | 130 | MAV_1651 | 4'-phosphopantetheinyl transferase | 99.2 | 125 | BCG_2544c | 4'-phosphopantetheinyl transfe | 93.08 | 130 | MAP2331c | 4'-phosphopantetheinyl transferase | 130 | 100 |
| MAP4_1493 | Peptidase family M20M25M40 protein | 473 | Rv2522c | hypothetical protein | 84.7 | 470 | Mb2551c | hypothetical protein | 84.7 | 470 | MAV_1652 | hypothetical protein | 97.76 | 446 | BCG_2543c | hypothetical protein | 84.7 | 470 | MAP2330c | hypothetical protein | 473 | 100 |
| MAP4_1494 | bacterioferritin comigratory protein | 164 | Rv2521 | Probable bacterioferritin comigrator | 82.8 | 157 | Mb2550 | bacterioferritin comigratory p | 82.17 | 157 | MAV_1653 | alkyl hydroperoxide reductase/ Thi | 98.09 | 157 | BCG_2542 | bacterioferritin comigratory pr | 82.8 | 157 | MAP2329 | hypothetical protein | 164 | 100 |
| MAP4_1495 | putative conserved membrane protein | 86 | Rv2520c | Possible conserved membrane prote | 65.33 | 75 | Mb2549c | hypothetical protein | 65.33 | 75 | MAV_1655 | hypothetical protein | 96.43 | 75 | BCG_2541c | hypothetical protein | 65.33 | 75 | MAP2328c | hypothetical protein | 86 | 100 |
| MAP4_1496 | putative conserved membrane protein | 579 | Rv1132 | hypothetical protein | 63.6 | 576 | Mb1163 | hypothetical protein | 63.6 | 576 | MAV_1654 | hypothetical protein | 98.96 | 579 | BCG_1193 | hypothetical protein | 63.6 | 576 | MAP2327 | hypothetical protein | 579 | 100 |
| MAP4_1497 | hypothetical protein | 88 | Rv0245 | Possible oxidoreductase | 30.43 | 162 | Mb0251 | oxidoreductase | 30.43 | 162 | MAV_1656 | hypothetical protein | 98.86 | 88 | BCG_0283 | oxidoreductase | 30.43 | 162 | MAP2326 | hypothetical protein | 88 | 100 |
| MAP4_1498 | hypothetical protein | 412 | Rv2416c | Enhanced intracellular survival prote | 34.9 | 402 | Mb2439c | hypothetical protein | 34.63 | 408 | MAV_1658 | hypothetical protein | 98.79 | 412 | BCG_2432c | hypothetical protein | 34.88 | 408 | MAP2325 | hypothetical protein | 412 | 100 |
| MAP4_1499 | transmembrane transport protein MmpL13B | 784 | Rv1146 | Probable conserved transmembrane | 69.27 | 470 | Mb1177 | transmembrane transport pro | 68.16 | 781 | MAV_1659 | mmpl family protein | 99.23 | 784 | BCG_1207 | transmembrane transport prot | 68.16 | 781 | MAP2324c | hypothetical protein | 784 | 100 |
| MAP4_1500 | alanine, valine and leucine rich membrane protein | 297 | Rv2729c | Probable conserved integral membr | 49.14 | 301 | Mb2748c | hypothetical protein | 49.57 | 301 | MAV_1660 | hypothetical protein | 98.99 | 297 | BCG_2742c | integral membrane alanine and | 49.57 | 301 | MAP2323c | hypothetical protein | 297 | 100 |
| MAP4_1501 | conserved lipoprotein LPPS | 407 | Rv2518c | Probable L,D-transpeptidase LdtB | 84.26 | 408 | Mb2547c | lipoprotein LppS | 84.26 | 408 | MAV_1661 | ErfK/YbiS/YcfS/YnhG family protein | 99.74 | 379 | BCG_2539c | lipoprotein lppS | 84.26 | 408 | MAP2322c | hypothetical protein | 407 | 100 |
| MAP4_1502 | hypothetical protein | 112 | Rv1906c | hypothetical protein | 45.12 | 156 | Mb1941c | hypothetical protein | 45.12 | 156 | MAV_1662 | hypothetical protein | 99.11 | 141 | BCG_1945c | hypothetical protein | 45.12 | 156 | MAP2321 | hypothetical protein | 112 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1503 | 3'-to-5' oligoribonuclease (orn) | 215 | Rv2511 | Oligoribonuclease Orn | 83.72 | 215 | Mb2539 | oligoribonuclease | 83.72 | 215 | MAV_1664 | oligoribonuclease | 99.53 | 215 | BCG_2531 | oligoribonuclease | 83.72 | 215 | MAP2320 | oligoribonuclease | 215 | 100 |
| MAP4_1504 | hypothetical protein | 521 | Rv2510c | hypothetical protein | 73.56 | 533 | Mb2538c | hypothetical protein | 73.56 | 533 | MAV_1665 | ATP-binding protein | 97.89 | 521 | BCG_2530c | hypothetical protein | 73.56 | 533 | MAP2319c | hypothetical protein | 521 | 100 |
| MAP4_1505 | putative short-chain dehydrogenase | 268 | Rv2509 | Probable short-chain type dehydrog | 86.89 | 268 | Mb2537 | short-chain type dehydrogen | 86.89 | 268 | MAV_1666 | short chain dehydrogenase | 99.63 | 268 | BCG_2529 | short-chain type dehydrogenas | 86.89 | 268 | MAP2318 | hypothetical protein | 268 | 100 |
| MAP4_1506 | putative conserved alanine and leucine rich membrane | 446 | Rv2508c | Probable conserved integral membr | 75.85 | 445 | Mb2536c | hypothetical protein | 75.85 | 445 | MAV_1667 | permease of the major facilitator su | 99.77 | 431 | BCG_2528c | integral membrane leucine and | 75.85 | 445 | MAP2317c | hypothetical protein | 449 | 100 |
| MAP4_1507 | putative conserved proline rich membrane protein | 253 | Rv2507 | Possible conserved proline rich mem | 57.14 | 273 | Mb2535 | hypothetical protein | 57.14 | 273 | MAV_1668 | hypothetical protein | 99.21 | 253 | BCG_2527 | proline rich membrane protein | 57.14 | 273 | MAP2316 | hypothetical protein | 253 | 100 |
| MAP4_1508 | Transcriptional regulator, TetR family | 218 | Rv2506 | Probable transcriptional regulatory | 80.18 | 215 | Mb2534 | TetR family transcriptional re | 80.18 | 215 | MAV_1669 | TetR family transcriptional regulato | 98.98 | 197 | BCG_2526 | TetR family transcriptional regu | 80.18 | 215 | MAP2315 | hypothetical protein | 218 | 100 |
| MAP4_1509 | acetyl-propionyl-CoA carboxylase subunit beta | 533 | Rv2502c | Probable acetyl-/propionyl-CoA carb | 90.74 | 529 | Mb2530c | acetyl-/propionyl-CoA carbox | 90.55 | 529 | MAV_1670 | carboxyl transferase | 99.25 | 533 | BCG_2522c | acetyl-/propionyl-coa carboxyl | 90.55 | 529 | MAP2314c | AccD1 | 559 | 100 |
| MAP4_1510 | acetyl-coenzyme A carboxylase subunit alpha | 671 | Rv2501c | Probable acetyl-/propionyl-coenzym | 82.6 | 654 | Mb2529c | acetyl-/propionyl-coenzyme A | 82.6 | 654 | MAV_1671 | acetyl-/propionyl-coenzyme A carb | 98.66 | 671 | BCG_2521c | acetyl-/propionyl-coenzyme A | 82.6 | 654 | MAP2313c | AccA1 | 671 | 100 |
| MAP4_1511 | acyl-CoA dehydrogenase | 388 | Rv2500c | Possible acyl-CoA dehydrogenase Fa | 90.93 | 394 | Mb2528c | acyl-CoA dehydrogenase | 90.93 | 394 | MAV_1672 | acyl-CoA dehydrogenase | 99.74 | 388 | BCG_2520c | acyl-CoA dehydrogenase fadE1 | 90.93 | 394 | MAP2312c | FadE19 | 388 | 100 |
| MAP4_1512 | oxidase regulatory-related protein | 166 | Rv2499c | Possible oxidase regulatory-related | 91.56 | 185 | Mb2527c | oxidase regulatory-like protei | 91.56 | 185 | MAV_1673 | MoaC domain-containing protein | 100 | 166 | BCG_2519c | oxidase regulatory-related prot | 91.56 | 185 | MAP2311c | hypothetical protein | 166 | 100 |
| MAP4_1513 | citrate (Pro-3S)-lyase beta subunit | 273 | Rv2498c | Probable citrate (pro-3S)-lyase (beta | 80.67 | 273 | Mb2526c | citrate (Pro-3S)-lyase subunit | 80.67 | 273 | MAV_1674 | CitE protein | 98.9 | 273 | BCG_2518c | citrate (pro-3s)-lyase subunit b | 80.67 | 273 | MAP2310c | hypothetical protein | 273 | 100 |
| MAP4_1514 | pyruvate dehydrogenase E1 component alpha subunit | 363 | Rv2497c | Probable branched-chain keto acid d | 81.97 | 367 | Mb2525c | pyruvate dehydrogenase E1 c | 81.97 | 367 | MAV_1675 | pyruvate dehydrogenase E1 compo | 98.9 | 363 | BCG_2517c | pyruvate dehydrogenase E1 co | 81.97 | 367 | MAP2309c | PdhA | 363 | 100 |
| MAP4_1515 | pyruvate dehydrogenase E1 subunit beta | 351 | Rv2496c | Probable branched-chain keto acid d | 84.05 | 348 | Mb2524c | pyruvate dehydrogenase E1 c | 83.76 | 348 | MAV_1676 | pyruvate dehydrogenase E1 compo | 99.15 | 351 | BCG_2516c | pyruvate dehydrogenase E1 co | 83.76 | 348 | MAP2308c | hypothetical protein | 351 | 100 |
| MAP4_1516 | dihydrolipoamide S-acetyltransferase E2 component p | 388 | Rv2495c | Probable branched-chain keto acid d | 72.05 | 393 | Mb2523c | branched-chain alpha-keto ac | 72.05 | 393 | MAV_1677 | branched-chain alpha-keto acid deh | 99.23 | 388 | BCG_2515c | branched-chain alpha-keto acid | 72.05 | 393 | MAP2307c | branched-chain alpha-keto acid dehydr | 388 | 100 |
| MAP4_1517 | Enoyl-CoA hydratase | 256 | Rv2486 | Probable enoyl-CoA hydratase EchA | 81.64 | 256 | Mb2511 | enoyl-CoA hydratase | 81.64 | 256 | MAV_1678 | enoyl-CoA hydratase | 100 | 256 | BCG_2504 | enoyl-CoA hydratase | 81.64 | 256 | MAP2306 | enoyl-CoA hydratase | 256 | 100 |
| MAP4_1518 | hypothetical protein | 136 | Rv1590 | hypothetical protein | 47.83 | 79 | Mb1616 | hypothetical protein | 47.83 | 79 | MAV_1679 | hypothetical protein | 98.53 | 136 | BCG_1628 | hypothetical protein | 47.83 | 79 | MAP2305 | hypothetical protein | 136 | 100 |
| MAP4_1519 | cutinase precursor | 219 | Rv1984c | Probable cutinase precursor CFP21 | 52.68 | 217 | Mb2006c | cutinase CFP21 | 52.68 | 217 | MAV_1682 | serine esterase cutinase | 99.09 | 219 | BCG_1798 | cutinase cut1 | 46.93 | 218 | MAP2304 | hypothetical protein | 213 | 100 |
| MAP4_1520 | hypothetical protein | 102 | Rv1969 | Mce-family protein Mce3D | 27.69 | 423 | Mb2977 | hypothetical protein | 35.71 | 418 | MAV_1683 | hypothetical protein | 100 | 102 | BCG_2974 | hypothetical protein | 35.71 | 418 | MAP2303c | hypothetical protein | 102 | 100 |
| MAP4_1521 | transposase, ISMav2 | 395 | Rv0755A | Putative transposase (fragment) | 83.02 | 61 | Mb0778c | transposase | 83.02 | 61 | MAV_0752 | transposase | 29.57 | 345 | BCG_0807c | transposase | 83.02 | 61 | MAP0664c | hypothetical protein | 395 | 100 |
| MAP4_1522 | carboxylesterase | 423 | Rv2485c | Probable carboxylesterase LipQ | 70.91 | 421 | Mb2510c | carboxylesterase LipQ | 70.91 | 421 | MAV_1685 | alpha/beta hydrolase | 99.28 | 415 | BCG_2503c | carboxylesterase lipQ | 70.91 | 421 | MAP2301c | hypothetical protein | 423 | 100 |
| MAP4_1523 | acyltransferase, wsdgatmgat subfamily protein | 489 | Rv2484c | Possible triacylglycerol synthase (dia | 85.54 | 491 | Mb2509c | hypothetical protein | 85.74 | 491 | MAV_1686 | acyltransferase, ws/dgat/mgat sub | 99.39 | 491 | BCG_2502c | hypothetical protein | 85.74 | 491 | MAP2300c | hypothetical protein | 489 | 100 |
| MAP4_1524 | bifunctional phospholipid biosynthesis enzyme plsC | 609 | Rv2483c | Possible transmembrane phospholip | 84.95 | 580 | Mb2508c | bifunctional L-3-phosphoseri | 85.14 | 580 | MAV_1687 | acyltransferase | 96.42 | 583 | BCG_2501c | transmembrane phospholipid b | 85.14 | 580 | MAP2299c | hypothetical protein | 357 | 99.72 |
| MAP4_1525 | Glycerol-3-phosphate acyltransferase | 784 | Rv2482c | Probable glycerol-3-phosphate acylt | 79.59 | 789 | Mb2507c | glycerol-3-phosphate acyltra | 79.59 | 789 | MAV_3220 | glycerol-3-phosphate acyltransfera | 35.4 | 633 | BCG_2500c | glycerol-3-phosphate acyltrans | 79.72 | 789 | MAP2298c | glycerol-3-phosphate acyltransferase | 784 | 100 |
| MAP4_1526 | putative conserved membrane protein | 689 | Rv0102 | Probable conserved integral membr | 52.4 | 661 | Mb0105 | hypothetical protein | 52.4 | 661 | MAV_1692 | ABC transporter permease | 98.98 | 689 | BCG_0135 | integral membrane protein | 52.4 | 661 | MAP2297c | hypothetical protein | 689 | 99.85 |
| MAP4_1527 | hypothetical protein, single-strand DNA binding protei | 160 | Rv2478c | hypothetical protein | 88.79 | 161 | Mb2505c | hypothetical protein | 88.79 | 161 | MAV_1694 | hypothetical protein | 99.38 | 160 | BCG_2498 | hypothetical protein | 88.79 | 161 | MAP2296c | hypothetical protein | 160 | 100 |
| MAP4_1528 | macrolide-transport ATP-binding protein ABC transport | 558 | Rv2477c | Probable macrolide-transport ATP-b | 94.97 | 558 | Mb2504c | ABC transporter ATP-binding | 94.97 | 558 | MAV_1695 | ABC transporter ATP-binding prote | 100 | 558 | BCG_2497c | ABC transporter ATP-binding p | 94.97 | 558 | MAP2295c | ABC transporter ATP-binding protein | 558 | 100 |
| MAP4_1529 | NAD-dependent glutamate dehydrogenase | 1616 | Rv2476c | Probable NAD-dependent glutamate | 83.68 | 1624 | Mb2503c | NAD-dependent glutamate de | 83.8 | 1623 | MAV_1696 | NAD-glutamate dehydrogenase | 99.51 | 1632 | BCG_2496c | NAD-dependent glutamate deh | 83.8 | 1623 | MAP2294c | hypothetical protein | 1616 | 100 |
| MAP4_1531 | hypothetical protein | 223 | Rv2474c | hypothetical protein | 77.17 | 217 | Mb2501c | hypothetical protein | 76.71 | 217 | MAV_1698 | hypothetical protein | 100 | 223 | BCG_2494c | hypothetical protein | 77.17 | 217 | MAP4150c | hypothetical protein | 347 | 48.15 |
| MAP4_1532 | Alpha-glucosidase | 773 | Rv2471 | Probable alpha-glucosidase AglA (m | 81.8 | 546 | Mb2498 | alpha-glucosidase | 81.58 | 546 | MAV_1700 | alpha-amylase | 95.48 | 538 | BCG_2491 | alpha-glucosidase aglA | 81.58 | 546 | MAP2292 | hypothetical protein | 773 | 100 |
| MAP4_1533 | oxygen-binding protein globin glbO | 129 | Rv2470 | Globin (oxygen-binding protein) Glb | 86.4 | 128 | Mb2497 | globin GlbO | 86.4 | 128 | MAV_1701 | hypothetical protein | 100 | 129 | BCG_2490 | globin (oxygen-binding protein | 86.4 | 128 | MAP2291 | GlbO | 129 | 100 |
| MAP4_1534 | putative HNH endonuclease family protein | 215 | Rv2469c | hypothetical protein | 82.59 | 222 | Mb2496c | hypothetical protein | 81.7 | 222 | MAV_1702 | HNH endonuclease | 100 | 215 | BCG_2489c | hypothetical protein | 81.7 | 222 | MAP2290c | hypothetical protein | 215 | 100 |
| MAP4_1535 | hypothetical protein | 79 | Rv2468A | hypothetical protein | 82.05 | 77 | Mb0362c | PPE family protein | 41.67 | 3507 | MAV_1703 | hypothetical protein | 100 | 76 | BCG_0393c | PPE family protein | 41.67 | 3507 | MAP2289c | hypothetical protein | 79 | 100 |
| MAP4_1536 | hypothetical protein | 155 | Rv2468c | hypothetical protein | 83.12 | 167 | Mb2495c | hypothetical protein | 83.12 | 167 | MAV_1705 | hypothetical protein | 100 | 155 | BCG_2488c | hypothetical protein | 83.12 | 167 | MAP2288c | hypothetical protein | 158 | 99.35 |
| MAP4_1537 | aminopeptidase N | 863 | Rv2467 | Probable aminopeptidase N PepN (L | 85.63 | 861 | Mb2494 | aminopeptidase | 85.63 | 861 | MAV_1704 | aminopeptidase N | 98.49 | 863 | BCG_2487 | aminopeptidase N pepN | 85.63 | 861 | MAP2287 | hypothetical protein | 863 | 100 |
| MAP4_1538 | hypothetical protein | 207 | Rv2466c | hypothetical protein | 81.64 | 207 | Mb2493c | hypothetical protein | 81.64 | 207 | MAV_1706 | hypothetical protein | 99.03 | 207 | BCG_2486c | hypothetical protein | 81.64 | 207 | MAP2286c | hypothetical protein | 207 | 100 |
| MAP4_1539 | isomerase | 159 | Rv2465c | Ribose-5-phosphate isomerase | 91.08 | 162 | Mb2492c | ribose-5-phosphate isomeras | 91.08 | 162 | MAV_1707 | ribose-5-phosphate isomerase B | 100 | 159 | BCG_2485c | ribose-5-phosphate isomerase | 91.08 | 162 | MAP2285c | ribose-5-phosphate isomerase B | 159 | 100 |
| MAP4_1540 | DNA glycosylase | 268 | Rv2464c | Possible DNA glycosylase | 81.65 | 268 | Mb2491c | DNA glycosylase | 81.65 | 268 | MAV_1708 | endonuclease VIII and DNA n-glyco | 99.25 | 268 | BCG_2484c | DNA glycosylase | 81.65 | 268 | MAP2284c | hypothetical protein | 268 | 100 |
| MAP4_1541 | esteraselipase lipP | 396 | Rv2463 | Probable esterase/lipase LipP | 82.9 | 394 | Mb2490 | esterase | 82.9 | 394 | MAV_1709 | carboxylesterase, putative | 100 | 396 | BCG_2483 | esterase/lipase lipP | 82.9 | 394 | MAP2283 | hypothetical protein | 396 | 100 |
| MAP4_1542 | trigger factor protein | 464 | Rv2462c | Probable trigger factor (TF) protein T | 77.38 | 466 | Mb2489c | trigger factor | 77.6 | 466 | MAV_1712 | trigger factor | 100 | 464 | BCG_2482c | trigger factor | 77.6 | 466 | MAP2282c | trigger factor | 464 | 100 |
| MAP4_1543 | ATP-dependent clp protease proteolytic subunit1 c lpP | 199 | Rv2461c | Probable ATP-dependent CLP protea | 92.46 | 200 | Mb2488c | ATP-dependent Clp protease | 92.46 | 200 | MAV_1713 | ATP-dependent Clp protease prote | 100 | 199 | BCG_2481c | ATP-dependent Clp protease p | 92.46 | 200 | MAP2281c | ATP-dependent Clp protease proteolyti | 199 | 100 |
| MAP4_1544 | ATP-dependent clp protease proteolytic subunit2 c lpP | 211 | Rv2460c | Probable ATP-dependent CLP protea | 97.62 | 214 | Mb2487c | ATP-dependent Clp protease | 97.62 | 214 | MAV_1714 | ATP-dependent Clp protease prote | 100 | 211 | BCG_2480c | ATP-dependent Clp protease p | 97.62 | 214 | MAP2280c | ATP-dependent Clp protease proteolyti | 211 | 100 |
| MAP4_1545 | Homocysteine S-methyltransferase | 306 | Rv2458 | Probable homocysteine S-methyltra | 76.03 | 302 | Mb2485 | homocysteine methyltransfer | 76.03 | 302 | MAV_1715 | homocysteine methyltransferase | 91.47 | 291 | BCG_2478 | homocysteine methyltransfera | 76.03 | 302 | MAP2279 | homocysteine methyltransferase | 306 | 100 |
| MAP4_1546 | ATP-dependent Clp protease ATP-binding subunit ClpX | 426 | Rv2457c | Probable ATP-dependent CLP protea | 98.59 | 426 | Mb2484c | ATP-dependent protease ATP | 98.59 | 426 | MAV_1716 | ATP-dependent protease ATP-bindi | 100 | 426 | BCG_2477c | ATP-dependent protease ATP-b | 98.36 | 426 | MAP2278c | ATP-dependent protease ATP-binding s | 426 | 100 |
| MAP4_1547 | oxidoreductase subunit alpha | 656 | Rv2455c | Probable oxidoreductase (alpha sub | 88.96 | 653 | Mb2482c | oxidoreductase subunit alpha | 88.96 | 653 | MAV_1717 | pyruvate synthase | 100 | 656 | BCG_2475c | oxidoreductase subunit alpha | 88.96 | 653 | MAP2277c | hypothetical protein | 656 | 100 |
| MAP4_1548 | oxidoreductase beta subunit | 363 | Rv2454c | Probable oxidoreductase (beta subu | 89.26 | 373 | Mb2481c | 2-oxoglutarate ferredoxin oxi | 89.26 | 373 | MAV_1718 | 2-oxoglutarate ferredoxin oxidored | 99.45 | 363 | BCG_2474c | 2-oxoglutarate ferredoxin oxid | 89.26 | 373 | MAP2276c | 2-oxoglutarate ferredoxin oxidoreducta | 363 | 100 |
| MAP4_1549 | Molybdopterin-guanine dinucleotide biosynthesis prot | 197 | Rv2453c | Probable molybdopterin-guanine di | 67.71 | 201 | Mb2480c | molybdopterin-guanine dinuc | 67.71 | 201 | MAV_1719 | molybdopterin-guanine dinucleoti | 98.98 | 197 | BCG_2473c | molybdopterin-guanine dinucle | 67.71 | 201 | MAP2275c | molybdopterin-guanine dinucleotide bi | 197 | 100 |
| MAP4_1550 | Transposase | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 99.76 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0028c | hypothetical protein | 411 | 100 |
| MAP4_1551 | resuscitation-promoting factor RpfE | 216 | Rv2450c | Probable resuscitation-promoting fa | 60.11 | 172 | Mb2477c | resuscitation-promoting facto | 60.64 | 172 | MAV_1722 | secreted protein | 80.14 | 146 | BCG_2470c | resuscitation-promoting factor | 60.64 | 172 | MAP2273c | hypothetical protein | 216 | 100 |
| MAP4_1552 | saccharopine dehydrogenase family protein | 419 | Rv2449c | hypothetical protein | 80.14 | 419 | Mb2476c | hypothetical protein | 80.14 | 419 | MAV_1723 | saccharopine dehydrogenase | 98.81 | 419 | BCG_2469c | hypothetical protein | 79.9 | 419 | MAP2272c | hypothetical protein | 419 | 100 |
| MAP4_1553 | Valyl-tRNA synthetase | 882 | Rv2448c | Probable valyl-tRNA synthase protei | 88.11 | 876 | Mb2475c | valyl-tRNA synthetase | 88.11 | 876 | MAV_1724 | valyl-tRNA synthetase | 99.32 | 882 | BCG_2468c | valyl-tRNA synthetase | 88.11 | 876 | MAP2271c | valyl-tRNA synthetase | 882 | 100 |
| MAP4_1554 | folylpolyglutamate synthase protein folC | 485 | Rv2447c | Probable folylpolyglutamate synthas | 84.19 | 487 | Mb2474c | bifunctional folylpolyglutama | 84.19 | 487 | MAV_1725 | FolC protein | 99.79 | 485 | BCG_2467c | folylpolyglutamate synthase fo | 84.19 | 487 | MAP2270c | hypothetical protein | 485 | 100 |
| MAP4_1555 | hypothetical protein | 125 | Rv2446c | Probable conserved integral membr | 79.82 | 123 | Mb2473c | hypothetical protein | 79.82 | 123 | MAV_1726 | hypothetical protein | 100 | 125 | BCG_2466c | integral membrane protein | 79.82 | 123 | MAP2269c | hypothetical protein | 125 | 100 |
| MAP4_1556 | nucleoside diphosphate kinase | 136 | Rv2445c | Probable nucleoside diphosphate ki | 83.82 | 136 | Mb2472c | nucleoside diphosphate kinas | 83.82 | 136 | MAV_1727 | nucleoside diphosphate kinase | 99.26 | 136 | BCG_2465c | nucleoside diphosphate kinase | 83.82 | 136 | MAP2268c | nucleoside diphosphate kinase | 136 | 100 |
| MAP4_1557 | ribonuclease E | 946 | Rv2444c | Possible ribonuclease E Rne | 78.08 | 953 | Mb2471c | ribonuclease E | 78.08 | 953 | MAV_1728 | Rne protein | 99.64 | 949 | BCG_2464c | ribonuclease E rne | 78.08 | 953 | MAP2267c | Rne | 946 | 100 |
| MAP4_1558 | 50S ribosomal protein L21 | 103 | Rv2442c | 50S ribosomal protein L21 RplU | 91.18 | 104 | Mb2469c | 50S ribosomal protein L21 | 91.18 | 104 | MAV_1729 | 50S ribosomal protein L21 | 100 | 103 | BCG_2462c | 50S ribosomal protein L21 | 91.18 | 104 | MAP2266c | 50S ribosomal protein L21 | 103 | 100 |
| MAP4_1559 | 50S ribosomal protein L27 | 88 | Rv2441c | 50S ribosomal protein L27 RpmA | 87.21 | 86 | Mb2468c | 50S ribosomal protein L27 | 87.21 | 86 | MAV_1730 | 50S ribosomal protein L27 | 100 | 88 | BCG_2461c | 50S ribosomal protein L27 | 87.21 | 86 | MAP2265c | 50S ribosomal protein L27 | 88 | 100 |
| MAP4_1560 | GTP1obg-family GTP-binding protein obg | 492 | Rv2440c | Probable GTP1/Obg-family GTP-bind | 87.29 | 479 | Mb2467c | GTPase ObgE | 87.29 | 479 | MAV_1731 | GTPase ObgE | 99.8 | 492 | BCG_2460c | GTPase ObgE | 87.29 | 479 | MAP2264c | GTPase ObgE | 492 | 100 |
| MAP4_1561 | glutamate 5-kinase protein proB | 367 | Rv2439c | Probable glutamate 5-kinase protein | 87.36 | 376 | Mb2466c | gamma-glutamyl kinase | 87.64 | 376 | MAV_1732 | gamma-glutamyl kinase | 99.46 | 367 | BCG_2459c | gamma-glutamyl kinase | 87.64 | 376 | MAP2263c | gamma-glutamyl kinase | 367 | 100 |
| MAP4_1562 | Transcriptional regulator, TetR family | 216 | Rv3855 | Transcriptional regulatory repressor | 28.5 | 216 | Mb3885 | TetR family transcriptional re | 28.5 | 216 | MAV_1733 | TetR family transcriptional regulato | 99.07 | 216 | BCG_3918 | TetR family transcriptional regu | 28.5 | 216 | MAP2262 | hypothetical protein | 216 | 100 |
| MAP4_1563 | putative cytochrome P450 hydroxylase | 436 | Rv2266 | Probable cytochrome P450 124 Cyp1 | 39.25 | 428 | Mb2289 | cytochrome P450 124 CYP124 | 39.25 | 428 | MAV_1734 | cytochrome P450 124 | 98.59 | 425 | BCG_2283 | cytochrome P450 124 CYP124 | 39.25 | 428 | MAP2261c | hypothetical protein | 436 | 100 |
| MAP4_1564 | NAD-dependent protein deacetylase, SIR2 family | 282 | Rv1151c | Transcriptional regulatory protein | 33.46 | 237 | Mb1182c | NAD-dependent deacetylase | 33.46 | 237 | MAV_1735 | NAD-dependent deacetylase 1 | 98.23 | 282 | BCG_1212c | NAD-dependent deacetylase | 33.46 | 237 | MAP2260 | hypothetical protein | 282 | 99.65 |
| MAP4_1565 | isochorismatase | 180 | Rv0389 | Probable phosphoribosylglycinamide | 26.88 | 419 | Mb0395 | phosphoribosylglycinamide fo | 26.88 | 419 | MAV_1736 | isochorismatase | 98.86 | 175 | BCG_0426 | phosphoribosylglycinamide for | 26.88 | 419 | MAP2259 | EntB | 180 | 100 |
| MAP4_1566 | glutamine-dependent NAD(+) synthetase nadE | 680 | Rv2438c | Glutamine-dependent NAD(+) synth | 84.68 | 679 | Mb2464c | NAD synthetase | 84.68 | 679 | MAV_1737 | NAD synthetase | 99.71 | 680 | BCG_2457c | NAD synthetase | 84.68 | 679 | MAP2258c | NAD synthetase | 680 | 100 |
| MAP4_1567 | hypothetical protein | 146 | Rv1401 | Possible membrane protein | 41.03 | 200 | Mb1436 | hypothetical protein | 41.03 | 200 | MAV_1738 | hypothetical protein | 99.26 | 135 | BCG_1462 | hypothetical protein | 41.03 | 200 | MAP2257 | hypothetical protein | 165 | 99.32 |
| MAP4_1568 | 3-isopropylmalate dehydratase small subunit | 183 | Rv2987c | Probable 3-isopropylmalate dehydra | 29.59 | 198 | Mb3011c | isopropylmalate isomerase sm | 29.59 | 198 | MAV_1739 | 3-isopropylmalate dehydratase sma | 100 | 189 | BCG_3008c | isopropylmalate isomerase sma | 29.59 | 198 | MAP2256 | hypothetical protein | 183 | 100 |
| MAP4_1569 | isopropylmalate isomerase large subunit | 415 | Rv2988c | Probable 3-isopropylmalate dehydra | 31.29 | 473 | Mb3012c | isopropylmalate isomerase la | 31.29 | 473 | MAV_1740 | 3-isopropylmalate dehydratase larg | 99.52 | 413 | BCG_3009c | isopropylmalate isomerase larg | 31.29 | 473 | MAP2255 | hypothetical protein | 415 | 99.76 |
| MAP4_1570 | carboxyvinyl-carboxyphosphonatephosphorylmutase | 295 | Rv0467 | Isocitrate lyase Icl (isocitrase) (isocit | 34.83 | 428 | Mb0476 | isocitrate lyase | 34.83 | 428 | MAV_0345 | methylisocitrate lyase | 45.1 | 300 | BCG_0507 | isocitrate lyase icl | 34.83 | 428 | MAP2254 | hypothetical protein | 295 | 100 |
| MAP4_1571 | hypothetical protein | 476 | Rv3343c | PPE family protein PPE54 | 30.56 | 2523 | Mb3829c | propionyl-CoA carboxylase su | 26.87 | 522 | MAV_1742 | MmgE/PrpD family protein | 99.16 | 476 | BCG_3861c | propionyl-CoA carboxylase bet | 26.87 | 522 | MAP2253 | hypothetical protein | 476 | 100 |
| MAP4_1572 | Transcriptional regulator, GntR family | 267 | Rv0792c | Probable transcriptional regulatory | 32.56 | 269 | Mb0816c | GntR family transcriptional re | 32.56 | 269 | MAV_1744 | GntR family transcriptional regulato | 99.63 | 267 | BCG_0845c | GntR family transcriptional reg | 32.56 | 269 | MAP2252c | hypothetical protein | 257 | 99.61 |
| MAP4_1573 | Ribokinase | 292 | Rv2436 | Ribokinase RbsK | 71.53 | 304 | Mb2462 | ribokinase RBSK | 71.53 | 304 | MAV_1743 | kinase, pfkB family protein | 99.65 | 283 | BCG_2455 | ribokinase rbsK | 71.53 | 304 | MAP2251 | hypothetical protein | 322 | 100 |
| MAP4_1574 | cyclase | 731 | Rv2435c | Probable cyclase (adenylyl-or guany | 65.12 | 730 | Mb2461c | cyclase | 65.12 | 730 | MAV_1745 | adenylate and guanylate cyclase ca | 99.32 | 731 | BCG_2454c | cyclase | 65.12 | 730 | MAP2250c | hypothetical protein | 731 | 100 |
| MAP4_1577 | Gamma-glutamyl phosphate reductase | 435 | Rv2427c | Probable gamma-glutamyl phosphat | 83.13 | 415 | Mb2451c | gamma-glutamyl phosphate r | 83.13 | 415 | MAV_1747 | gamma-glutamyl phosphate reduct | 99.77 | 435 | BCG_2444c | gamma-glutamyl phosphate re | 83.13 | 415 | MAP2247c | gamma-glutamyl phosphate reductase | 435 | 100 |
| MAP4_1578 | putative ATPases, AAA5 domain-containing protein | 291 | Rv2426c | hypothetical protein | 94.85 | 291 | Mb2450c | hypothetical protein | 94.5 | 291 | MAV_1748 | ATPase | 100 | 291 | BCG_2443c | hypothetical protein | 94.5 | 291 | MAP2246c | hypothetical protein | 291 | 100 |
| MAP4_1579 | hypothetical protein | 482 | Rv2425c | hypothetical protein | 89.83 | 480 | Mb2449c | hypothetical protein | 89.83 | 480 | MAV_1749 | hypothetical protein | 99.38 | 482 | BCG_2442c | hypothetical protein | 89.83 | 480 | MAP2245c | hypothetical protein | 482 | 100 |
| MAP4_1580 | Nicotinate-nucleotide adenylyltransferase | 222 | Rv2421c | Probable nicotinate-nucleotide ade | 81.9 | 211 | Mb2444c | nicotinic acid mononucleotid | 81.43 | 211 | MAV_1750 | nicotinic acid mononucleotide ade | 98.12 | 213 | BCG_2437c | nicotinic acid mononucleotide | 81.43 | 211 | MAP2244c | nicotinic acid mononucleotide adenylyl | 222 | 100 |
| MAP4_1581 | hypothetical protein | 131 | Rv2420c | hypothetical protein | 88.98 | 126 | Mb2443c | hypothetical protein | 88.98 | 126 | MAV_1751 | hypothetical protein | 97.71 | 131 | BCG_2436c | hypothetical protein | 82.44 | 127 | MAP2243c | hypothetical protein | 131 | 100 |
| MAP4_1582 | Phosphoglycerate mutase | 224 | Rv2419c | Glucosyl-3-phosphoglycerate phosp | 83.48 | 223 | Mb2442c | phosphoglycerate mutase | 83.04 | 223 | MAV_1752 | phosphoglycerate mutase | 100 | 224 | BCG_2435c | phosphoglycerate mutase | 83.48 | 223 | MAP2242c | hypothetical protein | 224 | 100 |
| MAP4_1583 | hypothetical protein | 249 | Rv2418c | hypothetical protein | 88.66 | 247 | Mb2441c | hypothetical protein | 88.66 | 247 | MAV_1753 | hypothetical protein | 99.6 | 249 | BCG_2434c | hypothetical protein | 88.66 | 247 | MAP2241c | hypothetical protein | 249 | 100 |
| MAP4_1584 | hypothetical protein | 277 | Rv2417c | hypothetical protein | 75.37 | 280 | Mb2440c | hypothetical protein | 75.37 | 280 | MAV_1754 | DegV family protein | 99.28 | 277 | BCG_2433c | hypothetical protein | 75.37 | 280 | MAP2240c | hypothetical protein | 277 | 100 |
| MAP4_1585 | transmembrane transport protein | 968 | Rv0450c | Probable conserved transmembrane | 58.02 | 967 | Mb0458c | transmembrane transport pr | 57.92 | 967 | MAV_1755 | MmpL4 protein | 99.79 | 968 | BCG_0489c | transmembrane transport prot | 58.02 | 967 | MAP2239 | hypothetical protein | 968 | 100 |
| MAP4_1586 | membrane protein, MmpS family | 128 | Rv0677c | Possible conserved membrane prote | 45.74 | 142 | Mb0696c | hypothetical protein | 45.74 | 142 | MAV_1756 | Mmps1 protein | 99.22 | 130 | BCG_0726c | membrane protein mmpS5 | 45.74 | 142 | MAP2238 | hypothetical protein | 164 | 99.22 |
| MAP4_1587 | hypothetical protein | 351 | Rv1059 | hypothetical protein | 33.24 | 354 | Mb1088 | hypothetical protein | 33.24 | 354 | MAV_1757 | dihydrodipicolinate reductase N-te | 99.43 | 361 | BCG_1117 | hypothetical protein | 33.24 | 354 | MAP2237 | hypothetical protein | 364 | 100 |
| MAP4_1588 | putative conserved membrane protein | 216 | Rv3821 | Probable conserved integral membr | 44.96 | 237 | Mb3851 | hypothetical protein | 45.38 | 237 | MAV_1758 | hypothetical protein | 100 | 216 | BCG_3883 | integral membrane protein | 45.38 | 237 | MAP2236 | hypothetical protein | 216 | 100 |
| MAP4_1589 | fatty-acid-CoA ligase fadD21 | 578 | Rv1185c | Probable fatty-acid-AMP ligase FadD | 63.67 | 578 | Mb1217c | acyl-CoA synthetase | 63.67 | 578 | MAV_1759 | acyl-CoA synthetase | 99.3 | 570 | BCG_1247c | acyl-CoA synthetase | 63.67 | 578 | MAP2235 | acyl-CoA synthetase | 578 | 100 |
| MAP4_1590 | hypothetical protein | 376 | Rv1184c | Possible exported protein | 46.39 | 359 | Mb1216c | hypothetical protein | 46.39 | 359 | MAV_1760 | hypothetical protein | 99.47 | 376 | BCG_1246c | hypothetical protein | 46.39 | 359 | MAP2234 | hypothetical protein | 376 | 100 |
| MAP4_1591 | hypothetical protein | 169 | Rv1183 | Probable conserved transmembrane | 74.69 | 1002 | Mb1215 | transmembrane transport pr | 74.69 | 1002 | MAV_1761 | MmpL10 protein | 98.74 | 1014 | BCG_1245 | transmembrane transport prot | 74.69 | 1002 | MAP2233 | hypothetical protein | 169 | 100 |
| MAP4_1592 | membrane protein, MmpL family, putative | 836 | Rv1183 | Probable conserved transmembrane | 56.97 | 1002 | Mb1215 | transmembrane transport pr | 56.97 | 1002 | MAV_1761 | MmpL10 protein | 99.52 | 1014 | BCG_1245 | transmembrane transport prot | 56.97 | 1002 | MAP2232 | hypothetical protein | 822 | 99.88 |
| MAP4_1593 | polyketide synthase associated protein papA3 | 473 | Rv1182 | Probable conserved polyketide synt | 59.62 | 472 | Mb1214 | polyketide synthase | 59.62 | 472 | MAV_1762 | condensation domain-containing p | 99.58 | 473 | BCG_1244 | polyketide synthase associated | 59.62 | 472 | MAP2231 | PapA3_1 | 473 | 100 |
| MAP4_1594 | polyketide synthase | 3679 | Rv2048c | Polyketide synthase Pks12 | 36.5 | 4151 | Mb2074c | polyketide synthase | 36.67 | 4151 | MAV_1763 | tylactone synthase modules 4 & 5 | 99.4 | 3679 | BCG_2067c | polyketide synthase | 36.57 | 4151 | MAP2230c | hypothetical protein | 3679 | 100 |
| MAP4_1595 | pyridoxamine 5'-phosphate oxidase family protein | 140 | Rv2991 | hypothetical protein | 31.07 | 163 | Mb3015 | hypothetical protein | 30.1 | 163 | MAV_1764 | pyridoxamine 5'-phosphate oxidase | 99.29 | 140 | BCG_3012 | hypothetical protein | 30.1 | 163 | MAP2229 | hypothetical protein | 140 | 100 |
| MAP4_1596 | Acyl-CoA dehydrogenase family protein | 368 | Rv1933c | Probable acyl-CoA dehydrogenase F | 29.81 | 363 | Mb1968c | acyl-CoA dehydrogenase | 29.81 | 363 | MAV_1765 | pimeloyl-CoA dehydrogenase | 99.73 | 368 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 29.81 | 363 | MAP2228 | hypothetical protein | 368 | 100 |
| MAP4_1597 | acyl-CoA dehydrogenase | 386 | Rv1934c | Probable acyl-CoA dehydrogenase F | 34.73 | 409 | Mb1969c | acyl-CoA dehydrogenase | 34.73 | 409 | MAV_1766 | acyl-CoA dehydrogenase domain-c | 100 | 386 | BCG_1973c | acyl-CoA dehydrogenase fadE1 | 34.73 | 409 | MAP2227 | FadE17 | 386 | 100 |
| MAP4_1598 | hypothetical protein | 286 | Rv2415c | hypothetical protein | 71.91 | 297 | Mb2438c | hypothetical protein | 72.24 | 297 | MAV_1767 | competence protein ComEA | 98.6 | 286 | BCG_2431c | hypothetical protein | 72.24 | 297 | MAP2226c | hypothetical protein | 286 | 100 |
| MAP4_1599 | hypothetical protein | 325 | Rv2413c | hypothetical protein | 84.01 | 316 | Mb2436c | hypothetical protein | 84.01 | 316 | MAV_1769 | hypothetical protein | 99.69 | 325 | BCG_2429c | hypothetical protein | 84.01 | 316 | MAP2225c | hypothetical protein | 325 | 100 |
| MAP4_1600 | 30S ribosomal protein S20 rpsT | 86 | Rv2412 | 30S ribosomal protein S20 RpsT | 95.35 | 86 | Mb2435 | 30S ribosomal protein S20 | 95.35 | 86 | MAV_1770 | 30S ribosomal protein S20 | 100 | 86 | BCG_2428 | 30S ribosomal protein S20 | 95.35 | 86 | MAP2224 | 30S ribosomal protein S20 | 86 | 100 |
| MAP4_1601 | hypothetical protein | 558 | Rv2411c | hypothetical protein | 89.75 | 551 | Mb2434c | hypothetical protein | 89.75 | 551 | MAV_3438 | hypothetical protein | 32.39 | 887 | BCG_2427c | hypothetical protein | 89.75 | 551 | MAP2223c | hypothetical protein | 558 | 100 |
| MAP4_1602 | hypothetical protein | 325 | Rv2410c | hypothetical protein | 88.82 | 325 | Mb2433c | hypothetical protein | 88.82 | 325 | MAV_1772 | hypothetical protein | 99.38 | 325 | BCG_2426c | hypothetical protein | 88.82 | 325 | MAP2222c | hypothetical protein | 325 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1603 | hypothetical protein | 510 | Rv2409c | hypothetical protein | 79.42 | 279 | Mb2432c | hypothetical protein | 79.42 | 279 | MAV_1773 | hypothetical protein | 89.91 | 350 | BCG_2425c | hypothetical protein | 79.42 | 279 | MAP2221c | hypothetical protein | 510 | 100 |
| MAP4_1604 | hypothetical protein | 280 | Rv2407 | hypothetical protein | 78.62 | 273 | Mb2430 | ribonuclease Z | 80.07 | 280 | MAV_1774 | ribonuclease Z | 98.21 | 280 | BCG_2423 | ribonuclease Z | 80.07 | 280 | MAP2220 | ribonuclease Z | 280 | 100 |
| MAP4_1605 | conserved hypothetical protein, CBS domain protein | 142 | Rv2406c | hypothetical protein | 90.14 | 142 | Mb2429c | hypothetical protein | 90.14 | 142 | MAV_1776 | CBS domain-containing protein | 100 | 142 | BCG_2422c | hypothetical protein | 90.14 | 142 | MAP2219c | hypothetical protein | 142 | 100 |
| MAP4_1606 | hypothetical protein | 204 | Rv2405 | hypothetical protein | 78.19 | 189 | Mb2428 | hypothetical protein | 78.19 | 189 | MAV_1777 | hypothetical protein | 99.48 | 200 | BCG_2421 | hypothetical protein | 78.19 | 189 | MAP2218 | hypothetical protein | 204 | 100 |
| MAP4_1607 | GTP-binding protein LepA | 660 | Rv2404c | Probable GTP-binding protein LepA | 88.99 | 653 | Mb2427c | GTP-binding protein LepA | 88.99 | 653 | MAV_1778 | GTP-binding protein LepA | 99.53 | 644 | BCG_2420c | GTP-binding protein LepA | 88.99 | 653 | MAP2217c | GTP-binding protein LepA | 660 | 100 |
| MAP4_1608 | putative conserved lipoprotein LPPR | 252 | Rv2403c | Probable conserved lipoprotein Lpp | 47.9 | 251 | Mb2426c | lipoprotein LppR | 47.48 | 251 | MAV_1779 | LppR protein | 99.21 | 252 | BCG_2419c | lipoprotein lppR | 47.48 | 251 | MAP2216c | hypothetical protein | 252 | 100 |
| MAP4_1609 | putative glycosyl hydrolase, Glycosylhydrolases family | 679 | Rv2402 | hypothetical protein | 94.53 | 642 | Mb2425 | hypothetical protein | 94.53 | 642 | MAV_1780 | glycoside hydrolase | 99.85 | 679 | BCG_2418 | hypothetical protein | 94.53 | 642 | MAP2215 | hypothetical protein | 652 | 100 |
| MAP4_1610 | hypothetical protein | 67 | Rv2401A | Possible conserved membrane prote | 67.74 | 67 | Mb2424c | hypothetical protein | 67.74 | 67 | MAV_1781 | hypothetical protein | 98.44 | 64 | BCG_2417c | hypothetical protein | 67.74 | 67 | MAP2214c | hypothetical protein | 67 | 100 |
| MAP4_1611 | sulfate-binding lipoprotein subI | 343 | Rv2400c | Probable sulfate-binding lipoprotein | 77.39 | 356 | Mb2422c | sulfate-binding lipoprotein | 77.39 | 356 | MAV_1782 | sulfate ABC transporter sulfate-bin | 99.71 | 343 | BCG_2415c | sulfate-binding lipoprotein sub | 77.39 | 356 | MAP2213c | SubI | 343 | 100 |
| MAP4_1612 | sulfate-transport membrane protein ABC transporter c | 290 | Rv2399c | Probable sulfate-transport integral | 87.36 | 283 | Mb2421c | sulfate-transport integral me | 87.36 | 283 | MAV_1783 | sulfate ABC transporter permease | 100 | 290 | BCG_2414c | sulfate-transport integral mem | 87.36 | 283 | MAP2212c | CysT | 290 | 100 |
| MAP4_1613 | sulfate-transport membrane protein ABC transporter c | 272 | Rv2398c | Probable sulfate-transport integral | 85.61 | 272 | Mb2420c | sulfate-transport integral me | 85.61 | 272 | MAV_1784 | sulfate ABC transporter permease | 99.26 | 272 | BCG_2413c | sulfate-transport integral mem | 85.98 | 272 | MAP2211c | CysW | 272 | 100 |
| MAP4_1614 | sulfate-transport ATP-binding protein ABC transporter | 362 | Rv2397c | Sulfate-transport ATP-binding prote | 91.04 | 351 | Mb2419c | sulfate-transport ABC transp | 91.04 | 351 | MAV_1785 | sulfate/thiosulfate import ATP-bin | 99.17 | 362 | BCG_2412c | sulfate-transport ATP-binding | 91.04 | 351 | MAP2210c | hypothetical protein | 362 | 100 |
| MAP4_1615 | 3-phosphoadenosine 5-phosphosulfate reductasecysH | 247 | Rv2392 | Probable 3'-phosphoadenosine 5'-p | 78.35 | 254 | Mb2413 | phosphoadenosine phosphos | 78.35 | 254 | MAV_1786 | phosphoadenosine phosphosulfate | 100 | 247 | BCG_2406 | phosphoadenosine phosphosu | 78.35 | 254 | MAP2209 | phosphoadenosine phosphosulfate red | 247 | 100 |
| MAP4_1616 | ferredoxin-dependent nitrite reductase | 555 | Rv2391 | Ferredoxin-dependent sulfite reduct | 87.93 | 563 | Mb2412 | ferredoxin-dependent nitrite | 87.93 | 563 | MAV_1787 | sulfite reductase [ferredoxin] 2 | 99.64 | 569 | BCG_2405 | ferredoxin-dependent nitrite r | 87.93 | 563 | MAP2208 | NirA_2 | 555 | 100 |
| MAP4_1617 | oxygen-independent coproporphyrinogen III oxidase h | 390 | Rv2388c | Probable oxygen-independent copro | 80.16 | 375 | Mb2409c | coproporphyrinogen III oxida | 79.89 | 375 | MAV_1789 | coproporphyrinogen III oxidase | 98.46 | 390 | BCG_2402c | coproporphyrinogen III oxidase | 79.89 | 375 | MAP2207c | coproporphyrinogen III oxidase | 390 | 100 |
| MAP4_1618 | hypothetical protein | 413 | Rv2387 | hypothetical protein | 78.1 | 417 | Mb2408 | hypothetical protein | 78.1 | 417 | MAV_1790 | hypothetical protein | 99.76 | 413 | BCG_2401 | hypothetical protein | 78.1 | 417 | MAP2206 | hypothetical protein | 413 | 100 |
| MAP4_1619 | isochorismate synthase mbtI | 450 | Rv2386c | Isochorismate synthase MbtI | 74 | 450 | Mb2407c | salicylate synthase MbtI | 74 | 450 | MAV_1792 | salicylate synthase MbtI | 99.56 | 450 | BCG_2400c | salicylate synthase MbtI | 74 | 450 | MAP2205c | salicylate synthase MbtI | 450 | 100 |
| MAP4_1620 | acyl-ACP desaturase | 338 | Rv0824c | Probable acyl-[acyl-carrier protein] | 74.78 | 338 | Mb0847c | acyl-ACP desaturase | 74.78 | 338 | MAV_1793 | Fatty acid desaturase | 100 | 338 | BCG_0877c | acyl-ACP desaturase | 74.78 | 338 | MAP0658c | DesA1 | 340 | 75.81 |
| MAP4_1621 | putative transcription regulator protein | 308 | Rv3334 | Probable transcriptional regulatory | 33.33 | 146 | Mb3367 | MerR family transcriptional r | 33.33 | 146 | MAV_1794 | MerR family transcriptional regulat | 98.96 | 288 | BCG_3405 | MerR family transcriptional reg | 33.33 | 146 | MAP2201 | hypothetical protein | 308 | 99.68 |
| MAP4_1622 | monooxygenase | 498 | Rv3049c | Probable monooxygenase | 41.58 | 524 | Mb3075c | monooxygenase | 41.58 | 524 | MAV_1795 | flavin-binding monooxygenase | 100 | 498 | BCG_3073c | monooxygenase | 41.58 | 524 | MAP2200 | hypothetical protein | 527 | 100 |
| MAP4_1623 | hypothetical protein | 306 | Rv0767c | hypothetical protein | 26.11 | 213 | Mb1193 | respiratory nitrate reductase | 24.59 | 1232 | MAV_1796 | hypothetical protein | 100 | 306 | BCG_1223 | respiratory nitrate reductase ( | 24.59 | 1232 | MAP2199 | hypothetical protein | 306 | 100 |
| MAP4_1624 | Oxidoreductase, short chaindehydrogenase/reductase | 282 | Rv0851c | Probable short-chain type dehydrog | 31.97 | 275 | Mb0874c | short chain dehydrogenase | 31.97 | 275 | MAV_1797 | oxidoreductase, short chain dehyd | 98.58 | 282 | BCG_0903c | short chain dehydrogenase | 31.97 | 275 | MAP2198 | hypothetical protein | 282 | 100 |
| MAP4_1625 | acetyl hydrolase | 334 | Rv2385 | Putative acetyl hydrolase MbtJ | 69.23 | 306 | Mb2406 | acetyl hydrolase MBTJ | 69.23 | 306 | MAV_1798 | alpha/beta hydrolase | 98.36 | 305 | BCG_2399 | acetyl hydrolase mbtJ | 69.23 | 306 | MAP2197 | hypothetical protein | 334 | 100 |
| MAP4_1627 | hypothetical protein | 448 | Rv0311 | hypothetical protein | 57.14 | 409 | Mb0319 | hypothetical protein | 57.14 | 409 | MAV_4850 | hypothetical protein | 55.12 | 408 | BCG_0351 | hypothetical protein | 57.14 | 409 | MAP2195 | hypothetical protein | 448 | 100 |
| MAP4_1628 | MCE-family protein | 526 | Rv1971 | Mce-family protein Mce3F | 41.77 | 437 | Mb0610 | MCE-family protein MCE2F | 36.55 | 516 | MAV_0953 | mce-family protein mce1f | 62.65 | 575 | BCG_0640 | mce-family protein mce2F | 36.55 | 516 | MAP2194 | hypothetical protein | 526 | 99.81 |
| MAP4_1629 | MCE-family lipoprotein | 401 | Rv1970 | Possible Mce-family lipoprotein Lpr | 44.88 | 377 | Mb3525c | MCE-family lipoprotein LprN | 38.15 | 384 | MAV_2536 | virulence factor Mce | 46.86 | 386 | BCG_3559c | mce family lipoprotein LprN | 38.15 | 384 | MAP0764 | hypothetical protein | 426 | 68.92 |
| MAP4_1630 | MCE-family protein | 444 | Rv3496c | Mce-family protein Mce4D | 37.8 | 451 | Mb3526c | MCE-family protein MCE4D | 37.8 | 451 | MAV_0951 | virulence factor Mce | 64.62 | 475 | BCG_3560c | Mce-family protein mce4D | 37.8 | 451 | MAP2192 | hypothetical protein | 444 | 100 |
| MAP4_1631 | MCE-family protein | 354 | Rv3497c | Mce-family protein Mce4C | 38.56 | 357 | Mb3527c | MCE-family protein MCE4C | 38.56 | 357 | MAV_0950 | virulence factor Mce | 63.69 | 372 | BCG_3561c | Mce-family protein mce4C | 38.56 | 357 | MAP2191 | hypothetical protein | 359 | 99.72 |
| MAP4_1632 | MCE-family protein | 341 | Rv3498c | Mce-family protein Mce4B | 40.35 | 350 | Mb3528c | MCE-family protein MCE4B | 40.35 | 350 | MAV_0949 | virulence factor Mce | 63.17 | 340 | BCG_3562c | Mce-family protein mce4B | 40.35 | 350 | MAP2190 | hypothetical protein | 341 | 100 |
| MAP4_1633 | MCE-family protein | 411 | Rv1966 | Mce-family protein Mce3A | 38.7 | 425 | Mb3529c | MCE-family protein MCE4A | 37.32 | 400 | MAV_0948 | virulence factor Mce | 58.82 | 420 | BCG_3563c | Mce-family protein mce4A | 37.32 | 400 | MAP2189 | hypothetical protein | 411 | 100 |
| MAP4_1634 | AMP-dependent synthetase and ligase | 514 | Rv2505c | Probable fatty-acid-CoA ligase FadD | 32.32 | 547 | Mb2533c | AMP-binding protein | 32.32 | 547 | MAV_2638 | AMP-dependent synthetase and lig | 39.09 | 533 | BCG_2525c | AMP-binding protein | 32.32 | 547 | MAP2188c | hypothetical protein | 514 | 100 |
| MAP4_1637 | putative amidohydrolase | 409 | Rv3181c | hypothetical protein | 28.12 | 150 | Mb3207c | hypothetical protein | 28.12 | 150 | MAV_1837 | amidohydrolase | 39.69 | 383 | BCG_3207c | hypothetical protein | 28.12 | 150 | MAP2185c | hypothetical protein | 409 | 100 |
| MAP4_1638 | Short-chain dehydrogenasereductase | 261 | Rv1928c | Probable short-chain type dehydrog | 38.22 | 255 | Mb1963c | short chain dehydrogenase | 38.22 | 255 | MAV_0886 | short chain dehydrogenase/reduct | 43.77 | 268 | BCG_1967c | short chain dehydrogenase | 38.22 | 255 | MAP2184c | hypothetical protein | 261 | 100 |
| MAP4_1639 | putative cytochrome P450 hydroxylase | 416 | Rv0778 | Possible cytochrome P450 126 Cyp1 | 33.67 | 414 | Mb0801 | cytochrome P450 126 | 33.67 | 414 | MAV_1274 | cytochrome P450 superfamily prot | 39.67 | 404 | BCG_0830 | cytochrome P450 126 cyp126 | 33.33 | 414 | MAP2183c | hypothetical protein | 416 | 100 |
| MAP4_1640 | hypothetical protein | 144 | Rv3547 | Deazaflavin-dependent nitroreducta | 43.9 | 151 | Mb3577 | hypothetical protein | 43.9 | 151 | MAV_0613 | AclJ protein | 43.44 | 142 | BCG_3611 | hypothetical protein | 43.9 | 151 | MAP2182c | hypothetical protein | 144 | 100 |
| MAP4_1641 | Transcriptional regulator, TetR family | 228 | Rv3557c | Transcriptional regulatory protein ( | 25.16 | 200 | Mb3587c | TetR family transcriptional re | 25.16 | 200 | MAV_1626 | hypothetical protein | 26.63 | 343 | BCG_3621c | TetR family transcriptional reg | 25.16 | 200 | MAP2181c | hypothetical protein | 228 | 100 |
| MAP4_1642 | hypothetical protein | 141 | Rv1367c | hypothetical protein | 40.74 | 377 | Mb1402c | hypothetical protein | 40.74 | 377 | MAV_3631 | hypothetical protein | 40 | 386 | BCG_1429c | hypothetical protein | 40.74 | 377 | MAP2180c | hypothetical protein | 141 | 100 |
| MAP4_1643 | hypothetical protein | 153 | Rv0117 | Oxidative stress response regulatory | 44.83 | 314 | Mb0121 | oxidative stress response reg | 44.83 | 314 | MAV_0939 | hypothetical protein | 42.86 | 138 | BCG_0151 | oxidative stress response regul | 44.83 | 314 | MAP2179 | hypothetical protein | 153 | 100 |
| MAP4_1644 | MbtA | 400 | Rv2384 | Bifunctional enzyme MbtA: salicyl-A | 77.48 | 565 | Mb2405 | bifunctional salicyl-AMP liga | 77.48 | 565 | MAV_2008 | 2,3-dihydroxybenzoate-AMP ligase | 98.81 | 551 | BCG_2398 | bifunctional salicyl-AMP ligase/ | 77.48 | 565 | MAP2178 | hypothetical protein | 400 | 100 |
| MAP4_1645 | phenyloxazoline synthase | 1165 | Rv2383c | Phenyloxazoline synthase MbtB (ph | 71.66 | 1414 | Mb2404c | phenyloxazoline synthase | 71.58 | 1414 | MAV_2009 | MbtB protein | 98.63 | 1164 | BCG_2397c | phenyloxazoline synthase mbt | 71.58 | 1414 | MAP2177c | hypothetical protein | 1165 | 100 |
| MAP4_1646 | phenyloxazoline synthase | 254 | Rv2383c | Phenyloxazoline synthase MbtB (ph | 56.38 | 1414 | Mb2404c | phenyloxazoline synthase | 56.38 | 1414 | MAV_2010 | phenyloxazoline synthase mbtb | 98.64 | 220 | BCG_2397c | phenyloxazoline synthase mbt | 56.38 | 1414 | MAP2176c | hypothetical protein | 254 | 100 |
| MAP4_1647 | polyketide synthase | 442 | Rv2382c | Polyketide synthetase MbtC (polyke | 71.69 | 444 | Mb2403c | polyketide synthase | 71.69 | 444 | MAV_2011 | erythronolide synthase, modules 1 | 99.1 | 442 | BCG_2396c | polyketide synthase | 71.69 | 444 | MAP2175c | hypothetical protein | 442 | 100 |
| MAP4_1648 | polyketide synthase mbtD | 1013 | Rv2381c | Polyketide synthetase MbtD (polyke | 47.17 | 1004 | Mb2402c | polyketide synthase | 47.17 | 1004 | MAV_2012 | MbtD protein | 98.22 | 1013 | BCG_2395c | polyketide synthase | 47.17 | 1004 | MAP2174c | hypothetical protein | 1013 | 100 |
| MAP4_1649 | peptide synthetase | 1759 | Rv2380c | Peptide synthetase MbtE (peptide s | 65.14 | 1682 | Mb2401c | peptide synthetase mbtE | 65.14 | 1682 | MAV_2013 | linear gramicidin synthetase subun | 96.78 | 2190 | BCG_2394c | peptide synthetase mbtE | 65.14 | 1682 | MAP2173c | hypothetical protein | 1759 | 100 |
| MAP4_1650 | peptide synthetase | 421 | Rv2380c | Peptide synthetase MbtE (peptide s | 41.27 | 1682 | Mb2401c | peptide synthetase mbtE | 41.27 | 1682 | MAV_2013 | linear gramicidin synthetase subun | 99.29 | 2190 | BCG_2394c | peptide synthetase mbtE | 41.27 | 1682 | MAP2172c | hypothetical protein | 421 | 100 |
| MAP4_1651 | peptide synthetase | 1412 | Rv2379c | Peptide synthetase MbtF (peptide s | 60.49 | 1461 | Mb2400c | peptide synthetase mbtF | 60.41 | 1461 | MAV_2014 | sulfotransferase | 98.37 | 1480 | BCG_2393c | peptide synthetase mbtF | 60.41 | 1461 | MAP2171c | hypothetical protein | 1412 | 100 |
| MAP4_1652 | lysine-N-oxygenase mbtG | 428 | Rv2378c | Lysine-N-oxygenase MbtG (L-lysine | 87.82 | 431 | Mb2399c | lysine-N-oxygenase | 87.82 | 431 | MAV_2015 | MbtG protein | 99.53 | 428 | BCG_2392c | lysine-N-oxygenase mbtG | 87.82 | 431 | MAP2170c | hypothetical protein | 428 | 100 |
| MAP4_1653 | conserved hypothetical protein, MbtH | 71 | Rv2377c | Putative conserved protein MbtH | 70.59 | 71 | Mb2398c | protein MbtH | 71.01 | 71 | MAV_2016 | hypothetical protein | 100 | 71 | BCG_2391c | protein mbtH | 71.01 | 71 | MAP2169c | hypothetical protein | 71 | 100 |
| MAP4_1654 | putative low molecular weight antigen | 178 | Rv2376c | Low molecular weight antigen CFP2 | 46.29 | 168 | Mb2397c | low molecular weight antige | 46.29 | 168 | MAV_2017 | low molecular weight antigen MTB | 98.31 | 178 | BCG_2390c | low molecular weight antigen | 46.29 | 168 | MAP2168c | hypothetical protein | 178 | 100 |
| MAP4_1655 | low molecular weight antigen | 172 | Rv2376c | Low molecular weight antigen CFP2 | 74.81 | 168 | Mb2397c | low molecular weight antige | 74.81 | 168 | MAV_2019 | low molecular weight antigen MTB | 99.42 | 172 | BCG_2390c | low molecular weight antigen | 74.81 | 168 | MAP2167c | hypothetical protein | 172 | 100 |
| MAP4_1656 | putative RNA polymerase sigma factor | 296 | Rv3328c | Probable alternative RNA polymeras | 39.2 | 312 | Mb3361c | RNA polymerase sigma facto | 39.2 | 312 | MAV_2018 | RNA polymerase ECF-subfamily pro | 98.99 | 296 | BCG_3398c | RNA polymerase sigma factor | 39.2 | 312 | MAP2166 | hypothetical protein | 296 | 100 |
| MAP4_1657 | hypothetical protein | 198 | Rv3327 | Probable transposase fusion protein | 32.67 | 570 | Mb3360 | transposase | 32.67 | 570 | MAV_2020 | hypothetical protein | 99.49 | 198 | BCG_3397 | transposase fusion protein | 32.67 | 570 | MAP2165 | hypothetical protein | 198 | 100 |
| MAP4_1658 | hypothetical protein | 104 | Rv2375 | hypothetical protein | 91.09 | 105 | Mb2396 | hypothetical protein | 91.09 | 105 | MAV_2021 | hypothetical protein | 100 | 104 | BCG_2389 | hypothetical protein | 91.09 | 105 | MAP2164 | hypothetical protein | 104 | 100 |
| MAP4_1659 | heat shock protein transcriptional repressorhrcA | 343 | Rv2374c | Probable heat shock protein transcr | 92.13 | 343 | Mb2395c | heat-inducible transcription | 92.13 | 343 | MAV_2022 | heat-inducible transcription repres | 99.42 | 343 | BCG_2388c | heat-inducible transcription re | 91.84 | 343 | MAP2163c | heat-inducible transcription repressor | 343 | 100 |
| MAP4_1660 | chaperone protein dnaJ2 | 381 | Rv2373c | Probable chaperone protein DnaJ2 | 91.62 | 382 | Mb2394c | molecular chaperone DnaJ | 91.62 | 382 | MAV_2023 | chaperone protein DnaJ | 99.48 | 381 | BCG_2387c | chaperone protein DnaJ | 91.62 | 382 | MAP2162c | molecular chaperone DnaJ | 381 | 100 |
| MAP4_1661 | 16S ribosomal RNA small subunitmethyl transferase E | 253 | Rv2372c | hypothetical protein | 76.98 | 262 | Mb2393c | 16S ribosomal RNA methyltra | 76.98 | 262 | MAV_2024 | 16S ribosomal RNA methyltransfer | 99.6 | 253 | BCG_2386c | 16S ribosomal RNA methyltran | 76.98 | 262 | MAP2161c | 16S ribosomal RNA methyltransferase | 253 | 100 |
| MAP4_1662 | Phosphate starvation-inducible protein PhoH, predicte | 352 | Rv2368c | Probable PHOH-like protein PhoH1 ( | 87.91 | 352 | Mb2389c | phosphate starvation-inducib | 87.91 | 352 | MAV_2025 | PhoH family protein | 99.72 | 352 | BCG_2382c | phoH-like protein phoH1 | 87.91 | 352 | MAP2160c | hypothetical protein | 352 | 100 |
| MAP4_1663 | putative metalloprotease | 177 | Rv2367c | hypothetical protein | 93.75 | 182 | Mb2388c | metalloprotease | 93.75 | 182 | MAV_2026 | metalloprotease | 99.44 | 177 | BCG_2381c | metalloprotease | 93.75 | 182 | MAP2159c | metalloprotease | 177 | 100 |
| MAP4_1664 | hypothetical protein | 193 | Rv2997 | Possible alanine rich dehydrogenase | 28.57 | 480 | Mb0117 | phosphoheptose isomerase | 34.55 | 196 | MAV_4420 | MarR family transcriptional regulat | 60 | 168 | BCG_0146 | phosphoheptose isomerase | 34.55 | 196 | MAP2158 | hypothetical protein | 193 | 100 |
| MAP4_1665 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion s | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_1666 | putative transposase | 320 | Rv0796 | Putative transposase for insertion s | 47.63 | 328 | Mb2838c | transposase | 49.11 | 278 | MAV_1473 | transposase | 44.12 | 305 | BCG_2832c | transposase | 49.11 | 278 | MAP2156 | hypothetical protein | 320 | 100 |
| MAP4_1667 | hypothetical protein | 103 | Rv0795 | Putative transposase for insertion s | 42.86 | 108 | Mb2839c | transposase | 42.86 | 108 | MAV_1689 | ISAfe7, transposase OrfA | 38.61 | 114 | BCG_2833c | transposase | 42.86 | 108 | MAP2155 | hypothetical protein | 103 | 100 |
| MAP4_1668 | hypothetical protein | 191 | Rv0949 | Probable ATP-dependent DNA helic | 48 | 771 | Mb0974 | ATP dependent DNA helicase | 48 | 771 | MAV_3389 | carbamoyl phosphate synthase lar | 45.45 | 1117 | BCG_1003 | ATP dependent DNA helicase | 48 | 771 | MAP2154c | hypothetical protein | 191 | 100 |
| MAP4_1669 | hypothetical protein | 350 | Rv0676c | Probable conserved transmembrane | 23.4 | 964 | Mb0695c | transmembrane transport pr | 23.4 | 964 | MAV_4968 | MmpL3 protein | 45.95 | 949 | BCG_0725c | transmembrane transport prot | 23.4 | 964 | MAP2153 | hypothetical protein | 350 | 100 |
| MAP4_1670 | hypothetical protein | 124 | Rv0731c | Possible S-adenosylmethionine-dep | 36.36 | 318 | Mb0752c | hypothetical protein | 36.36 | 318 | MAV_4445 | hypothetical protein | 43.33 | 308 | BCG_0781c | hypothetical protein | 36.36 | 318 | MAP2152c | hypothetical protein | 124 | 100 |
| MAP4_1671 | hypothetical protein | 145 | Rv1427c | Possible long-chain-fatty-acid--CoA | 31.37 | 535 | Mb1462c | acyl-CoA synthetase | 31.37 | 535 | MAV_3056 | linear gramicidin synthetase subun | 29.17 | 10421 | BCG_1488c | acyl-CoA synthetase | 31.37 | 535 | MAP2151 | hypothetical protein | 145 | 100 |
| MAP4_1672 | Transposase, IS1311 | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family prote | 99.76 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0028c | hypothetical protein | 411 | 100 |
| MAP4_1673 | hypothetical protein | 214 | Rv2349c | Probable phospholipase C 3 PlcC | 35.71 | 508 | Mb2508c | bifunctional L-3-phosphoseri | 31.82 | 580 | MAV_0071 | transglycosylase | 38.24 | 877 | BCG_2501c | transmembrane phospholipid | 31.82 | 580 | MAP2149c | hypothetical protein | 214 | 100 |
| MAP4_1674 | phage integrase family protein | 227 | Rv2894c | Probable integrase/recombinase Xe | 32.59 | 298 | Mb2918c | site-specific tyrosine recombi | 32.59 | 298 | MAV_3070 | site-specific tyrosine recombinase | 32.62 | 313 | BCG_2915c | site-specific tyrosine recombin | 32.59 | 298 | MAP2148 | hypothetical protein | 227 | 100 |
| MAP4_1675 | hypothetical protein | 425 | Rv0941c | hypothetical protein | 40.43 | 257 | Mb0966c | hypothetical protein | 40.43 | 257 | MAV_2027 | hypothetical protein | 99.53 | 425 | BCG_0995c | hypothetical protein | 40.43 | 257 | MAP2147c | hypothetical protein | 425 | 100 |
| MAP4_1676 | hypothetical protein | 436 | Rv2366c | Probable conserved transmembrane | 84.33 | 435 | Mb2387c | transmembrane protein | 84.33 | 435 | MAV_2028 | CBS domain-containing protein | 100 | 436 | BCG_2380c | hypothetical protein | 84.33 | 435 | MAP2146c | hypothetical protein | 436 | 100 |
| MAP4_1677 | GTP-binding protein Era | 299 | Rv2364c | Probable GTP-binding protein Era | 88.67 | 300 | Mb2385c | GTP-binding protein Era | 88.67 | 300 | MAV_2029 | GTP-binding protein Era | 99.67 | 299 | BCG_2378c | GTP-binding protein Era | 88.67 | 300 | MAP2145c | GTP-binding protein Era | 299 | 100 |
| MAP4_1678 | putative decarboxylase, OrnLysArgdecarboxylase dom | 485 | Rv2531c | Probable amino acid decarboxylase | 22.93 | 947 | Mb2560c | amino acid decarboxylase | 22.93 | 947 | MAV_2031 | Orn/Lys/Arg decarboxylase | 99.38 | 485 | BCG_2553c | amino acid decarboxylase | 22.93 | 947 | MAP2144 | hypothetical protein | 485 | 100 |
| MAP4_1679 | amidase | 503 | Rv2363 | Probable amidase AmiA2 (aminohy | 87.24 | 484 | Mb2384 | amidase | 87.24 | 484 | MAV_2032 | amidase | 99.78 | 459 | BCG_2377 | amidase | 87.24 | 484 | MAP2143 | amidase | 503 | 100 |
| MAP4_1680 | putative DNA repair protein RecO | 265 | Rv2362c | Possible DNA repair protein RecO | 87.17 | 265 | Mb2383c | DNA repair protein RecO | 87.17 | 265 | MAV_2033 | DNA repair protein RecO | 99.61 | 256 | BCG_2376c | DNA repair protein RecO | 87.17 | 265 | MAP2142c | DNA repair protein RecO | 265 | 100 |
| MAP4_1681 | long-chain (C50)-Z-isoprenyl diphosphate synthase | 296 | Rv2361c | Long (C50) chain Z-isoprenyl dipho | 86.49 | 296 | Mb2382c | undecaprenyl pyrophosphate | 86.49 | 296 | MAV_2034 | undecaprenyl pyrophosphate synt | 99.66 | 296 | BCG_2375c | UDP pyrophosphate synthase | 86.49 | 296 | MAP2141c | UDP pyrophosphate synthase | 296 | 100 |
| MAP4_1682 | hypothetical protein | 142 | Rv2360c | hypothetical protein | 72.14 | 142 | Mb2381c | hypothetical protein | 72.14 | 142 | MAV_2035 | hypothetical protein | 98.59 | 142 | BCG_2374c | hypothetical protein | 72.14 | 142 | MAP2140c | hypothetical protein | 142 | 100 |
| MAP4_1683 | ferric uptake regulation protein | 135 | Rv2359 | Probable zinc uptake regulation pro | 89.84 | 130 | Mb2380 | ferric uptake regulation prot | 90.62 | 130 | MAV_2036 | FurB protein | 99.26 | 135 | BCG_2373 | ferric uptake regulation protei | 90.62 | 130 | MAP2139 | FurB | 135 | 100 |
| MAP4_1684 | ArsR family transcriptional regulator | 141 | Rv2358 | Probable transcriptional regulatory | 74.44 | 135 | Mb2379 | ArsR family transcriptional re | 74.44 | 135 | MAV_2037 | ArsR family transcriptional regulat | 99.29 | 143 | BCG_2372 | ArsR family transcriptional reg | 74.44 | 135 | MAP2138 | hypothetical protein | 141 | 100 |
| MAP4_1685 | Glycyl-tRNA synthetase | 463 | Rv2357c | Probable glycyl-tRNA synthetase Gl | 89.2 | 463 | Mb2378c | glycyl-tRNA synthetase | 89.2 | 463 | MAV_2038 | glycyl-tRNA synthetase | 99.35 | 459 | BCG_2371c | glycyl-tRNA synthetase | 89.2 | 463 | MAP2137c | glycyl-tRNA synthetase | 463 | 100 |
| MAP4_1686 | PPE family protein | 410 | Rv3125c | PPE family protein PPE49 | 46.02 | 391 | Mb3148c | PPE family protein | 45.74 | 391 | MAV_2746 | PPE family protein | 55.17 | 461 | BCG_3147c | PPE family protein | 50.59 | 282 | MAP2136c | hypothetical protein | 410 | 100 |
| MAP4_1687 | hypothetical protein | 143 | Rv2348c | Hypothetical protein | 52.58 | 108 | Mb1829 | PPE family protein | 36.99 | 423 | MAV_2040 | hypothetical protein | 98.63 | 73 | BCG_1833 | PPE family protein | 36.99 | 423 | MAP2135c | hypothetical protein | 143 | 100 |
| MAP4_1690 | Deoxyguanosinetriphosphate triphosphohydrolase | 423 | Rv2344c | Probable deoxyguanosine triphosph | 87.26 | 431 | Mb2373c | deoxyguanosinetriphosphate | 87.26 | 431 | MAV_2042 | deoxyguanosinetriphosphate triph | 100 | 423 | BCG_2367c | deoxyguanosinetriphosphate t | 87.26 | 431 | MAP2132c | deoxyguanosinetriphosphate triphosph | 423 | 100 |
| MAP4_1691 | periplasmic superoxide dismutase | 205 | Rv0432 | Periplasmic superoxide dismutase [ | 54.71 | 240 | Mb0440 | periplasmic superoxide dism | 54.71 | 240 | MAV_2043 | [Cu-Zn] superoxide dismutase | 99.51 | 205 | BCG_0471 | periplasmic superoxide dismut | 54.71 | 240 | MAP2131c | hypothetical protein | 205 | 100 |
| MAP4_1692 | DNA primase | 650 | Rv2343c | Probable DNA primase DnaG | 86.44 | 639 | Mb2372c | DNA primase | 86.44 | 639 | MAV_2045 | DNA primase | 99.54 | 650 | BCG_2366c | DNA primase | 86.28 | 639 | MAP2130c | DNA primase | 650 | 100 |
| MAP4_1693 | hypothetical protein | 101 | Rv2342 | hypothetical protein | 76.92 | 85 | Mb2371 | hypothetical protein | 76.92 | 85 | MAV_2044 | hypothetical protein | 97.8 | 91 | BCG_2365 | hypothetical protein | 76.92 | 85 | MAP2129 | hypothetical protein | 101 | 100 |
| MAP4_1694 | Muconolactone isomerase | 211 | Rv0316 | Possible muconolactone isomerase | 59.31 | 204 | Mb0324 | muconolactone isomerase | 59.31 | 204 | MAV_2047 | muconolactone delta-isomerase | 98.1 | 211 | BCG_0356 | muconolactone isomerase | 59.31 | 204 | MAP2128c | hypothetical protein | 211 | 100 |
| MAP4_1695 | oxidoreductase | 463 | Rv1855c | Possible oxidoreductase | 29.38 | 307 | Mb1886c | oxidoreductase | 29.38 | 307 | MAV_2048 | fmnh2-utilizing oxygenase | 99.35 | 463 | BCG_1891c | oxidoreductase | 29.38 | 307 | MAP2127 | hypothetical protein | 463 | 100 |
| MAP4_1696 | putative monooxygenase, luciferase-like monooxygena | 373 | Rv3618 | Possible monooxygenase | 30.11 | 395 | Mb1971 | monooxygenase | 28.89 | 369 | MAV_2049 | hypothetical protein | 98.93 | 373 | BCG_1975 | monooxygenase | 28.89 | 369 | MAP2126 | hypothetical protein | 373 | 100 |
| MAP4_1697 | putative monooxygenase, luciferase-like monooxygena | 373 | Rv0407 | F420-dependent glucose-6-phospha | 25.62 | 336 | Mb0415 | F420-dependent glucose-6-p | 25.62 | 336 | MAV_2050 | fmnh2-utilizing oxygenase | 98.12 | 373 | BCG_0446 | glucose-6-phosphate dehydrog | 25.62 | 336 | MAP2125 | hypothetical protein | 373 | 100 |
| MAP4_1698 | Serine acetyltransferase | 229 | Rv2335 | Probable serine acetyltransferase C | 78.17 | 229 | Mb2363 | serine acetyltransferase CysE | 78.17 | 229 | MAV_2051 | serine O-acetyltransferase | 99.56 | 229 | BCG_2357 | serine acetyltransferase cysE | 78.17 | 229 | MAP2124 | hypothetical protein | 229 | 100 |
| MAP4_1699 | Cysteine synthase A | 310 | Rv2334 | Cysteine synthase a CysK1 (O-acety | 88.39 | 310 | Mb2362 | cysteine synthase A CysK1 | 88.39 | 310 | MAV_2052 | cysteine synthase A | 100 | 310 | BCG_2356 | cysteine synthase A cysK1 | 88.39 | 310 | MAP2123 | hypothetical protein | 310 | 100 |
| MAP4_1700 | hypothetical protein | 430 | Rv2005c | Universal stress protein family prote | 32.31 | 295 | Mb2028c | hypothetical protein | 32.31 | 295 | MAV_2053 | hypothetical protein | 98.6 | 430 | BCG_2022c | hypothetical protein | 32.31 | 295 | MAP2122 | hypothetical protein | 430 | 100 |
| MAP4_1701 | major membrane protein I | 307 | Rv3347c | PPE family protein PPE55 | 59.09 | 3157 | Mb3380c | hypothetical protein | 59.09 | 2096 | MAV_2054 | major membrane protein 1 | 100 | 307 | BCG_3417c | PPE family protein | 59.09 | 2096 | MAP2121c | hypothetical protein | 307 | 100 |
| MAP4_1702 | Cysteine desulfurase | 670 | Rv1464 | Probable cysteine desulfurase Csd | 44.44 | 417 | Mb1499 | cysteine desulfurase | 44.44 | 417 | MAV_2055 | cysteine desulphurases, SufS | 99.4 | 670 | BCG_1525 | cysteine desulfurase csd | 44.44 | 417 | MAP2120c | hypothetical protein | 670 | 100 |
| MAP4_1703 | hypothetical protein | 378 | Rv0522 | Probable GABA permease GabP (4-a | 23.33 | 434 | Mb0535 | GABA permease GabP | 23.33 | 434 | MAV_2056 | hypothetical protein | 99.73 | 377 | BCG_0565 | 4-amino butyrate transport ca | 23.33 | 434 | MAP2119 | hypothetical protein | 412 | 99.74 |
| MAP4_1704 | hypothetical protein | 52 | Rv2742c | Conserved hypothetical arginine rich | 32.08 | 277 | Mb2763c | hypothetical protein | 32.08 | 195 | MAV_2057 | hypothetical protein | 98.08 | 52 | BCG_2758c | hypothetical protein | 32.08 | 195 | MAP1274 | adenosylmethionine--8-amino-7-oxono | 438 | 38.89 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1705 | hypothetical protein | 267 | Rv0295c | hypothetical protein | 74.53 | 267 | Mb0303c | hypothetical protein | 74.53 | 267 | MAV_2058 | sulfotransferase | 99.61 | 258 | BCG_0335c | hypothetical protein | 74.53 | 267 | MAP2118 | hypothetical protein | 267 | 100 |
| MAP4_1706 | hypothetical protein | 255 | Rv3501c | Conserved integral membrane prote | 58.8 | 254 | Mb3531c | hypothetical protein | 58.8 | 254 | MAV_2059 | TrnB1 protein | 99.61 | 255 | BCG_3565c | integral membrane protein Yrb | 58.8 | 254 | MAP2117c | hypothetical protein | 255 | 100 |
| MAP4_1707 | MCE-family protein | 422 | Rv1966 | Mce-family protein Mce3A | 52.97 | 425 | Mb3529c | MCE-family protein MCE4A | 35.04 | 400 | MAV_2061 | virulence factor Mce | 99.53 | 422 | BCG_3563c | Mce-family protein mce4A | 35.04 | 400 | MAP2116c | Mce3 | 422 | 100 |
| MAP4_1708 | MCE-family protein | 342 | Rv1967 | Mce-family protein Mce3B | 57.89 | 342 | Mb0605 | MCE-family protein MCE2B | 48.1 | 343 | MAV_2062 | virulence factor Mce | 99.42 | 342 | BCG_0635 | mce-family protein mce2B | 48.1 | 343 | MAP2115c | hypothetical protein | 342 | 100 |
| MAP4_1709 | MCE-family protein | 392 | Rv1968 | Mce-family protein Mce3C | 51.32 | 410 | Mb3527c | MCE-family protein MCE4C | 39.48 | 357 | MAV_2063 | virulence factor Mce | 99.73 | 377 | BCG_3561c | Mce-family protein mce4C | 39.48 | 357 | MAP2114c | hypothetical protein | 392 | 100 |
| MAP4_1710 | MCE-family protein | 444 | Rv1969 | Mce-family protein Mce3D | 55.95 | 423 | Mb0178 | MCE-family protein MCE1D | 40.31 | 530 | MAV_2064 | virulence factor Mce | 99.1 | 444 | BCG_0209 | MCE-family protein mce1D | 40.31 | 530 | MAP2113c | hypothetical protein | 444 | 100 |
| MAP4_1711 | MCE-family lipoprotein | 373 | Rv1970 | Possible Mce-family lipoprotein LprM | 60.49 | 377 | Mb0179 | MCE-family lipoprotein LprK | 42.17 | 390 | MAV_2536 | virulence factor Mce | 60 | 386 | BCG_0210 | mce family lipoprotein LprK | 42.17 | 390 | MAP2112c | hypothetical protein | 373 | 100 |
| MAP4_1712 | MCE-family protein | 489 | Rv1971 | Mce-family protein Mce3F | 55.68 | 437 | Mb0180 | MCE-family protein MCE1F | 36.7 | 515 | MAV_2069 | virulence factor Mce | 98.97 | 486 | BCG_0211 | MCE-family protein mce1F | 36.7 | 515 | MAP2111c | hypothetical protein | 489 | 100 |
| MAP4_1713 | MCE associated membrane protein | 203 | Rv1972 | Probable conserved Mce associated | 51.11 | 191 | Mb1398c | hypothetical protein | 35.59 | 261 | MAV_2070 | hypothetical protein | 99.01 | 203 | BCG_1425c | hypothetical protein | 36.16 | 261 | MAP2110c | hypothetical protein | 203 | 100 |
| MAP4_1715 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_1717 | hypothetical protein | 155 | Rv1975 | hypothetical protein | 72.93 | 221 | Mb2886c | methionine aminopeptidase | 36.36 | 285 | MAV_2072 | hypothetical protein | 100 | 166 | BCG_2883c | methionine aminopeptidase | 36.36 | 285 | MAP2106c | hypothetical protein | 155 | 100 |
| MAP4_1718 | hypothetical protein | 92 | Rv2642 | Possible transcriptional regulatory p | 26.67 | 126 | Mb2675 | ArsR family transcriptional re | 26.67 | 126 | MAV_2073 | hypothetical protein | 95.45 | 66 | BCG_0637 | mce-family protein mce2Da | 47.62 | 516 | MAP2105 | hypothetical protein | 92 | 100 |
| MAP4_1719 | putative nitratesulfite reductase | 1411 | Rv2900c | Possible formate dehydrogenase H F | 29.33 | 779 | Mb2924c | formate dehydrogenase H | 29.33 | 779 | MAV_2075 | FdhF protein | 99.43 | 1405 | BCG_2921c | formate dehydrogenase H fdhF | 29.33 | 779 | MAP2104 | FdhF | 1411 | 100 |
| MAP4_1720 | putative lipoprotein LPPP | 160 | Rv2330c | Probable lipoprotein LppP | 74.51 | 175 | Mb2357c | lipoprotein LppP | 74.51 | 175 | MAV_2076 | LppP protein | 99.35 | 155 | BCG_2351c | lipoprotein lppP | 73.86 | 175 | MAP2103c | hypothetical protein | 160 | 100 |
| MAP4_1721 | membrane nitrite extrusion protein narK3 | 485 | Rv0261c | Probable integral membrane nitrite | 60.22 | 469 | Mb0267c | integral membrane nitrite ext | 60.22 | 469 | MAV_2079 | transporter, major facilitator family | 99.78 | 472 | BCG_0299c | integral membrane nitrite extr | 60.22 | 469 | MAP2102c | NarK3_1 | 485 | 100 |
| MAP4_1722 | Acyl-coenzyme A dehydrogenaseoxidase | 650 | Rv0215c | Probable acyl-CoA dehydrogenase F | 29.03 | 357 | Mb0221c | acyl-CoA dehydrogenase | 26.5 | 388 | MAV_2078 | acyl-CoA oxidase | 99.69 | 650 | BCG_0252c | acyl-CoA dehydrogenase fadE3 | 26.5 | 388 | MAP2101 | hypothetical protein | 650 | 99.85 |
| MAP4_1723 | transmembrane ABC transporter ATP-binding protein | 775 | Rv1747 | Probable conserved transmembrane | 44.73 | 865 | Mb1776 | ABC transporter ATP-binding | 44.73 | 865 | MAV_3010 | ABC transporter ATP-binding prote | 43.96 | 862 | BCG_1786 | transmembrane ABC transport | 44.73 | 865 | MAP2100 | hypothetical protein | 586 | 100 |
| MAP4_1724 | Transcriptional regulator, MarR family | 162 | Rv2327 | hypothetical protein | 84.14 | 163 | Mb2354 | hypothetical protein | 84.14 | 163 | MAV_2081 | MarR family transcriptional regulat | 98.77 | 175 | BCG_2348 | hypothetical protein | 84.14 | 163 | MAP2099 | hypothetical protein | 162 | 99.38 |
| MAP4_1725 | transmembrane ATP-binding protein ABC transporter | 714 | Rv2326c | Possible transmembrane ATP-bindin | 72.03 | 697 | Mb2353c | transmembrane ATP-binding | 72.03 | 697 | MAV_2082 | ABC transporter | 99.39 | 653 | BCG_2347c | transmembrane ABC transport | 72.03 | 697 | MAP2098c | hypothetical protein | 714 | 100 |
| MAP4_1726 | Cobalt transport family protein | 284 | Rv2325c | hypothetical protein | 73.65 | 282 | Mb2352c | hypothetical protein | 73.65 | 282 | MAV_2083 | cobalt transport protein | 99.3 | 284 | BCG_2346c | hypothetical protein | 73.65 | 282 | MAP2097c | hypothetical protein | 284 | 100 |
| MAP4_1727 | Transcriptional regulator, AsnC family | 148 | Rv2324 | Probable transcriptional regulatory p | 91.22 | 148 | Mb2351 | AsnC family transcriptional re | 91.22 | 148 | MAV_2084 | AsnC family transcriptional regulato | 97.97 | 148 | BCG_2345 | AsnC family transcriptional reg | 91.22 | 148 | MAP2096 | hypothetical protein | 148 | 100 |
| MAP4_1728 | Amidinotransferase family protein | 289 | Rv2323c | hypothetical protein | 74.74 | 302 | Mb2350c | hypothetical protein | 74.39 | 302 | MAV_2085 | amidinotransferase | 98.59 | 284 | BCG_2344c | hypothetical protein | 74.39 | 302 | MAP2095c | hypothetical protein | 289 | 100 |
| MAP4_1729 | Ornithine aminotransferase | 412 | Rv2322c | Probable ornithine aminotransferase | 72.06 | 221 | Mb2349c | ornithine aminotransferase | 72.06 | 221 | MAV_2086 | ornithine--oxo-acid transaminase | 99.51 | 412 | BCG_2343c | ornithine aminotransferase (N- | 72.06 | 221 | MAP2094c | RocD1 | 412 | 100 |
| MAP4_1730 | cationic amino acid transport membrane protein rocE | 483 | Rv2320c | Probable cationic amino acid transp | 80.97 | 476 | Mb2347c | cationic amino acid transport | 80.97 | 476 | MAV_2087 | amino acid transporter | 98.92 | 461 | BCG_2341c | cationic amino acid transport i | 80.97 | 476 | MAP2093c | RocE | 483 | 100 |
| MAP4_1731 | periplasmic sugar-binding lipoprotein UspC | 445 | Rv2318 | Probable periplasmic sugar-binding l | 77.6 | 440 | Mb2345 | periplasmic sugar-binding lipo | 77.37 | 440 | MAV_2088 | extracellular solute-binding protein | 98.43 | 446 | BCG_2339 | periplasmic sugar-binding lipop | 77.37 | 440 | MAP2092 | UspC | 445 | 100 |
| MAP4_1732 | sugar-transport membrane protein ABC transporter us | 275 | Rv2317 | Probable sugar-transport integral m | 85.82 | 274 | Mb2344 | sugar-transport integral mem | 85.82 | 274 | MAV_2089 | ABC transporter permease | 99.64 | 275 | BCG_2338 | sugar-transport integral memb | 85.82 | 274 | MAP2091 | UspE | 275 | 100 |
| MAP4_1733 | sugar-transport membrane protein ABC transporter us | 294 | Rv2316 | Probable sugar-transport integral m | 84.78 | 290 | Mb2343 | sugar-transport integral mem | 85.12 | 290 | MAV_2090 | ABC transporter permease | 99.66 | 294 | BCG_2337 | sugar-transport integral memb | 85.12 | 290 | MAP2090 | hypothetical protein | 294 | 100 |
| MAP4_1734 | Putative modulator of DNA gyrase | 505 | Rv2315c | hypothetical protein | 85.15 | 505 | Mb2342c | hypothetical protein | 85.15 | 505 | MAV_2091 | modulator of DNA gyrase | 99.6 | 505 | BCG_2336c | hypothetical protein | 85.15 | 505 | MAP2089c | hypothetical protein | 505 | 100 |
| MAP4_1735 | hypothetical protein | 457 | Rv2314c | hypothetical protein | 81.62 | 457 | Mb2341c | hypothetical protein | 81.62 | 457 | MAV_2092 | CalR5 protein | 97.81 | 457 | BCG_2335c | hypothetical protein | 81.62 | 457 | MAP2088c | hypothetical protein | 457 | 100 |
| MAP4_1736 | hypothetical protein | 288 | Rv2313c | Hypothetical protein | 73.52 | 284 | Mb2340c | hypothetical protein | 73.52 | 284 | MAV_2093 | hypothetical protein | 98.26 | 288 | BCG_2334c | hypothetical protein | 73.52 | 284 | MAP2087c | hypothetical protein | 288 | 100 |
| MAP4_1737 | hypothetical protein | 166 | Rv2333c | Integral membrane drug efflux prote | 37.5 | 537 | Mb2361c | integral membrane transport | 37.5 | 523 | MAV_2094 | hypothetical protein | 100 | 140 | BCG_2355c | integral membrane transport p | 37.5 | 523 | MAP2086c | hypothetical protein | 166 | 100 |
| MAP4_1738 | hypothetical protein | 166 | | | | | | | | | MAV_2095 | hypothetical protein | 99.13 | 115 | | | | | MAP2086c | hypothetical protein | 166 | 71.83 |
| MAP4_1739 | hypothetical protein | 41 | Rv3368c | Possible oxidoreductase | 30.3 | 214 | Mb3403c | oxidoreductase | 30.3 | 214 | MAV_2272 | hypothetical protein | 38.1 | 307 | BCG_3440c | oxidoreductase | 30.3 | 214 | MAP0852 | hypothetical protein | 181 | 48 |
| MAP4_1740 | Aldehyde dehydrogenase | 484 | Rv0223c | Probable aldehyde dehydrogenase | 41.34 | 487 | Mb2883c | aldehyde dehydrogenase | 40 | 455 | MAV_2101 | aldehyde dehydrogenase | 99.36 | 468 | BCG_2880c | aldehyde dehydrogenase aldC | 40 | 455 | MAP2084 | hypothetical protein | 484 | 100 |
| MAP4_1741 | hypothetical protein | 304 | Rv2345 | Possible conserved transmembrane | 47.71 | 660 | Mb2374 | transmembrane protein | 47.71 | 660 | MAV_2102 | hypothetical protein | 96.07 | 305 | BCG_2368 | hypothetical protein | 47.71 | 660 | MAP2083c | hypothetical protein | 304 | 100 |
| MAP4_1742 | hypothetical protein | 479 | Rv2004c | hypothetical protein | 33.41 | 498 | Mb2027c | hypothetical protein | 33.41 | 498 | MAV_3416 | shikimate kinase | 46.15 | 176 | BCG_2021c | hypothetical protein | 33.41 | 498 | MAP2082 | hypothetical protein | 479 | 100 |
| MAP4_1743 | putative major facilitator superfamily protein | 576 | Rv1250 | Probable drug-transport integral me | 29.34 | 579 | Mb1282 | drug-transport integral memb | 29.34 | 579 | MAV_2104 | major facilitator superfamily protei | 99.8 | 538 | BCG_1310 | drug-transport integral membr | 29.34 | 579 | MAP2081 | hypothetical protein | 558 | 92.5 |
| MAP4_1744 | hypothetical protein | 231 | Rv3415c | hypothetical protein | 27.78 | 275 | Mb3449c | hypothetical protein | 27.78 | 275 | MAV_2105 | hypothetical protein | 97.82 | 229 | BCG_3485c | hypothetical protein | 27.78 | 275 | MAP2080 | hypothetical protein | 231 | 99.57 |
| MAP4_1745 | hypothetical protein | 3051 | Rv1267c | Probable transcriptional regulatory p | 37.46 | 388 | Mb1298c | transcriptional regulator Emb | 37.46 | 388 | MAV_0226 | EmbR protein | 38.1 | 384 | BCG_1326c | transcriptional regulatory prot | 37.46 | 388 | MAP2079 | hypothetical protein | 3051 | 100 |
| MAP4_1746 | putative multi-sensor signal transduction histidine kina | 855 | Rv2027c | Two component sensor histidine kin | 35.29 | 573 | Mb2052c | histidine kinase response regu | 34.97 | 573 | MAV_2108 | stage II sporulation protein E (SpoII | 99.16 | 835 | BCG_2046c | histidine kinase response regul | 34.97 | 573 | MAP2078c | hypothetical protein | 891 | 100 |
| MAP4_1747 | hypothetical protein | 109 | Rv3687c | Anti-anti-sigma factor RsfB (anti-sigr | 35.94 | 122 | Mb2671 | hypothetical protein | 27.96 | 148 | MAV_2109 | StaS domain-containing protein | 98.17 | 109 | BCG_2665 | hypothetical protein | 27.96 | 148 | MAP2077c | hypothetical protein | 109 | 100 |
| MAP4_1748 | Methyltransferase, Leucine carboxylmethyl transferase | 310 | Rv3787c | hypothetical protein | 63.48 | 308 | Mb3816c | hypothetical protein | 63.48 | 308 | MAV_2110 | methyltransferase, putative, family | 99.35 | 310 | BCG_3849c | hypothetical protein | 63.48 | 308 | MAP2076c | hypothetical protein | 310 | 100 |
| MAP4_1749 | putative methyltransferase | 212 | Rv3342 | Possible methyltransferase (methyla | 36.54 | 243 | Mb3374 | methyltransferase | 36.54 | 243 | MAV_2111 | methyltransferase, UbiE/COQ5 fam | 99.06 | 212 | BCG_3412 | methyltransferase | 36.54 | 243 | MAP2075c | hypothetical protein | 212 | 100 |
| MAP4_1750 | hypothetical protein | 197 | Rv0494 | Probable transcriptional regulatory p | 32.5 | 242 | Mb0505 | GntR family transcriptional re | 32.5 | 242 | MAV_2113 | hypothetical protein | 94.21 | 121 | BCG_0536 | GntR family transcriptional reg | 32.5 | 242 | MAP2074c | hypothetical protein | 197 | 100 |
| MAP4_1751 | hypothetical protein | 237 | Rv1526c | Probable glycosyltransferase | 29.55 | 426 | Mb1553c | glycosyltransferase | 29.55 | 426 | MAV_2114 | mebrane associated protein | 100 | 237 | BCG_1578c | glycosyltransferase | 29.55 | 426 | MAP2073c | hypothetical protein | 237 | 100 |
| MAP4_1752 | hypothetical protein | 285 | Rv3248c | Probable adenosylhomocysteinase S | 25.89 | 495 | Mb3276c | S-adenosyl-L-homocysteine h | 25.89 | 495 | MAV_2115 | hypothetical protein | 98.21 | 283 | BCG_3277c | S-adenosyl-L-homocysteine hy | 25.89 | 495 | MAP2072c | hypothetical protein | 285 | 100 |
| MAP4_1753 | AMP-binding protein | 510 | Rv2505c | Probable fatty-acid-CoA ligase FadD | 33.14 | 547 | Mb2533c | AMP-binding protein | 33.14 | 547 | MAV_2116 | AMP-binding enzyme, putative | 99.22 | 510 | BCG_2525c | AMP-binding protein | 33.14 | 547 | MAP2071c | hypothetical protein | 510 | 100 |
| MAP4_1754 | hypothetical protein | 206 | Rv1929c | hypothetical protein | 34.69 | 214 | Mb1964c | hypothetical protein | 34.69 | 214 | MAV_2117 | hypothetical protein | 98.06 | 206 | BCG_1968c | hypothetical protein | 34.69 | 214 | MAP2070 | hypothetical protein | 206 | 100 |
| MAP4_1755 | chaperone protein htpG | 644 | Rv2299c | Probable chaperone protein HtpG (h | 85.69 | 647 | Mb2321c | heat shock protein 90 | 85.69 | 647 | MAV_2118 | heat shock protein 90 | 99.53 | 644 | BCG_2315c | heat shock protein 90 | 85.69 | 647 | MAP2069c | heat shock protein 90 | 644 | 100 |
| MAP4_1756 | hypothetical protein | 71 | Rv1075c | Conserved exported protein | 33.33 | 314 | Mb1104c | hypothetical protein | 33.33 | 314 | MAV_2119 | hypothetical protein | 97.18 | 71 | BCG_1133c | hypothetical protein | 33.33 | 314 | MAP2068c | hypothetical protein | 71 | 100 |
| MAP4_1757 | hypothetical protein | 341 | Rv3192 | Conserved hypothetical alanine and | 66.67 | 153 | Mb3214 | hypothetical protein | 66.67 | 153 | MAV_2121 | hypothetical protein | 99.41 | 341 | BCG_3214 | hypothetical protein | 66.67 | 153 | MAP2067c | hypothetical protein | 341 | 99.71 |
| MAP4_1758 | putative manganese transport transmembrane protein | 551 | Rv0924c | Divalent cation-transport integral m | 26.18 | 428 | Mb0948c | manganese transport protein | 26.18 | 684 | MAV_2120 | Mn2+/Fe2+ transporter | 99.27 | 551 | BCG_0976c | manganese transport protein M | 25.75 | 428 | MAP2066 | hypothetical protein | 551 | 100 |
| MAP4_1759 | magnesium transporter MgtE intracellular domain-con | 440 | Rv1232c | hypothetical protein | 30.77 | 435 | Mb1264c | hypothetical protein | 30.54 | 435 | MAV_2122 | MgtE intracellular domain-contain | 99.55 | 440 | BCG_1292c | hypothetical protein | 30.54 | 435 | MAP2065 | hypothetical protein | 440 | 100 |
| MAP4_1760 | putative lipoprotein | 247 | Rv3576 | Possible conserved lipoprotein LppH | 34.32 | 237 | Mb3607 | lipoprotein LppH | 34.45 | 237 | MAV_2123 | PknM protein | 98.31 | 247 | BCG_3641 | lipoprotein lppH | 34.45 | 237 | MAP2064 | hypothetical protein | 247 | 100 |
| MAP4_1761 | hypothetical protein | 122 | Rv0546c | hypothetical protein | 29.41 | 128 | Mb0560c | hypothetical protein | 29.41 | 128 | MAV_2124 | glyoxalase | 97.48 | 119 | BCG_0590c | hypothetical protein | 29.41 | 128 | MAP2063c | hypothetical protein | 122 | 100 |
| MAP4_1762 | putative conserved alanine, valine and leucine rich me | 298 | Rv2729c | Probable conserved integral membr | 52.16 | 301 | Mb2748c | hypothetical protein | 52.55 | 301 | MAV_2125 | hypothetical protein | 98.32 | 298 | BCG_2742c | integral membrane alanine and | 52.55 | 301 | MAP2062 | hypothetical protein | 317 | 99.66 |
| MAP4_1763 | hypothetical protein | 130 | Rv1511 | GDP-D-mannose dehydratase GmdA | 40 | 340 | Mb3087c | acyl-CoA dehydrogenase | 33.33 | 600 | MAV_2126 | membrane protein | 99.23 | 130 | BCG_3086c | acyl-CoA dehydrogenase fadE2 | 33.33 | 721 | MAP2061 | hypothetical protein | 130 | 100 |
| MAP4_1764 | putative thiolase | 391 | Rv1074c | Probable beta-ketoacyl CoA thiolase | 35.85 | 405 | Mb1103c | acetyl-CoA acetyltransferase | 35.85 | 405 | MAV_2127 | acetyl-CoA C-acyltransferase | 99.23 | 391 | BCG_1132c | acetyl-CoA acetyltransferase | 35.85 | 405 | MAP2060c | hypothetical protein | 391 | 100 |
| MAP4_1765 | hypothetical protein | 204 | Rv0859 | Possible acyl-CoA thiolase FadA | 29.85 | 403 | Mb0882 | acetyl-CoA acetyltransferase | 29.85 | 403 | MAV_2128 | hypothetical protein | 98.37 | 184 | BCG_0911 | acetyl-CoA acetyltransferase | 29.85 | 403 | MAP2059 | hypothetical protein | 204 | 100 |
| MAP4_1766 | monophosphatase CysQ | 242 | Rv2131c | Monophosphatase CysQ | 54.94 | 267 | Mb2155c | hypothetical protein | 54.94 | 267 | MAV_2129 | 3'(2'),5'-bisphosphate nucleotidase | 99.59 | 242 | BCG_2148c | hypothetical protein | 54.94 | 267 | MAP2058c | CysQ_2 | 242 | 100 |
| MAP4_1767 | haloalkane dehalogenase, alphabeta fold family protei | 301 | Rv2296 | Probable haloalkane dehalogenase | 82.94 | 300 | Mb2318 | haloalkane dehalogenase | 82.94 | 300 | MAV_2130 | haloalkane dehalogenase | 100 | 310 | BCG_2312 | haloalkane dehalogenase | 82.94 | 300 | MAP2057 | haloalkane dehalogenase | 301 | 100 |
| MAP4_1768 | hypothetical protein | 242 | Rv2562 | hypothetical protein | 58.73 | 129 | Mb2591 | hypothetical protein | 62.81 | 245 | MAV_2131 | hypothetical protein | 100 | 242 | BCG_2584 | hypothetical protein | 62.81 | 245 | MAP2056c | hypothetical protein | 242 | 100 |
| MAP4_1769 | aminotransferase | 401 | Rv2294 | Probable aminotransferase | 77.34 | 407 | Mb2316 | aminotransferase | 77.34 | 407 | MAV_2132 | transferase | 98.5 | 401 | BCG_2310 | aminotransferase | 77.34 | 407 | MAP2055 | hypothetical protein | 401 | 100 |
| MAP4_1770 | hypothetical protein | 325 | Rv0953c | Possible oxidoreductase | 28.21 | 282 | Mb0978c | oxidoreductase | 28.21 | 282 | MAV_2133 | hypothetical protein | 99.69 | 325 | BCG_1007c | oxidoreductase | 28.21 | 282 | MAP2054c | hypothetical protein | 325 | 100 |
| MAP4_1771 | hypothetical protein | 261 | Rv0401 | Probable conserved transmembrane | 50 | 123 | Mb0407 | transmembrane protein | 50 | 123 | MAV_2134 | hypothetical protein | 98.44 | 257 | BCG_0438 | hypothetical protein | 50 | 123 | MAP2053 | hypothetical protein | 261 | 100 |
| MAP4_1772 | hypothetical protein | 47 | Rv0402c | Probable conserved transmembrane | 37.14 | 958 | Mb0408c | transmembrane transport pro | 37.14 | 367 | MAV_2135 | hypothetical protein | 100 | 47 | BCG_0439c | transmembrane transport prot | 37.14 | 367 | MAP1240c | hypothetical protein | 963 | 38.89 |
| MAP4_1773 | Transcriptional regulator, TetR family | 219 | Rv1019 | Probable transcriptional regulatory p | 23.44 | 197 | Mb1047 | TetR family transcriptional re | 23.44 | 197 | MAV_2137 | hypothetical protein | 97.2 | 143 | BCG_1076 | TetR family transcriptional regu | 23.44 | 197 | MAP2052c | hypothetical protein | 219 | 100 |
| MAP4_1774 | putative cytochrome P450 hydroxylase | 402 | Rv0766c | Probable cytochrome P450 123 Cyp1 | 40.66 | 402 | Mb0789c | cytochrome P450 123 | 40.66 | 402 | MAV_2138 | cytochrome P450 superfamily prot | 99 | 402 | BCG_0818c | cytochrome P450 123 cyp123 | 39.6 | 541 | MAP2051c | hypothetical protein | 404 | 100 |
| MAP4_1775 | transposase | 407 | Rv2014 | Transposase | 31.65 | 196 | Mb2037 | transposase | 31.65 | 196 | MAV_0496 | transposase IS116/IS110/IS902 | 46.4 | 404 | BCG_2031 | transposase | 31.65 | 196 | MAP0832c | IS1601_B_1 transposase | 407 | 100 |
| MAP4_1776 | putative hydrolase, alphabeta hydrolase family protein | 329 | Rv1834 | Probable hydrolase | 32.01 | 288 | Mb1865 | hydrolase | 32.01 | 288 | MAV_2139 | alpha/beta hydrolase | 98.48 | 329 | BCG_1869 | hydrolase | 32.01 | 288 | MAP2049 | hypothetical protein | 329 | 100 |
| MAP4_1777 | lipoprotein LppO | 180 | Rv2290 | Probable conserved lipoprotein Lpp( | 54.27 | 171 | Mb2313 | lipoprotein lppOb | 55.37 | 121 | MAV_2140 | LppO protein | 98.26 | 172 | BCG_2307 | lipoprotein lppOb | 55.37 | 121 | MAP2048 | hypothetical protein | 180 | 100 |
| MAP4_1778 | hypothetical protein | 242 | Rv3350c | PPE family protein PPE56 | 27.45 | 3716 | Mb1647c | cytochrome assembly ABC tra | 55 | 527 | MAV_2141 | hypothetical protein | 97.52 | 242 | BCG_1659c | cytochrome assembly ABC tran | 55 | 527 | MAP2047 | hypothetical protein | 242 | 99.59 |
| MAP4_1779 | thiosulfate sulfurtransferase | 284 | Rv2291 | Probable thiosulfate sulfurtransfera | 70.07 | 284 | Mb2314 | thiosulfate sulfurtransferase | 69.14 | 256 | MAV_2142 | thiosulfate sulfurtransferase | 97.89 | 284 | BCG_2308 | thiosulfate sulfurtransferase Ss | 70.42 | 284 | MAP2046 | SseB | 284 | 99.65 |
| MAP4_1780 | glycosyl transferase | 381 | Rv0557 | Mannosyltransferase MgtA | 30.05 | 378 | Mb1785c | hypothetical protein | 77.97 | 394 | MAV_2143 | glycosyl transferase | 99.21 | 381 | BCG_1795c | hypothetical protein | 77.97 | 394 | MAP2045 | hypothetical protein | 381 | 100 |
| MAP4_1781 | hypothetical protein | 394 | Rv1747 | Probable conserved transmembrane | 41.18 | 865 | Mb1776 | ABC transporter ATP-binding | 41.18 | 865 | MAV_2144 | hypothetical protein | 98.73 | 402 | BCG_1786 | transmembrane ABC transport | 41.18 | 865 | MAP2044 | hypothetical protein | 394 | 100 |
| MAP4_1782 | membrane transport protein yjcE | 536 | Rv2287 | Probable conserved integral membr | 71.76 | 542 | Mb2309 | integral membrane transport | 71.76 | 542 | MAV_2145 | Na+/H+ antiporter | 99.63 | 536 | BCG_2303 | integral membrane transport p | 71.76 | 542 | MAP2043 | YjcE | 536 | 100 |
| MAP4_1783 | hypothetical protein | 144 | Rv2335 | Probable serine acetyltransferase Cy | 30 | 229 | Mb2363 | serine acetyltransferase CysE | 30 | 229 | MAV_2147 | hypothetical protein | 100 | 144 | BCG_2357 | serine acetyltransferase cysE | 30 | 229 | MAP2042c | hypothetical protein | 144 | 100 |
| MAP4_1784 | membrane-bound esterase LipM | 430 | Rv2284 | Probable esterase LipM | 77.51 | 431 | Mb2305 | esterase | 77.51 | 431 | MAV_2146 | alpha/beta hydrolase | 99.07 | 430 | BCG_2299 | esterase LipM | 77.51 | 431 | MAP2041 | hypothetical protein | 430 | 100 |
| MAP4_1785 | hypothetical protein | 118 | Rv2063 | Antitoxin MazE7 | 30.3 | 77 | Mb2089 | hypothetical protein | 30.3 | 77 | MAV_2148 | HicB family protein | 96.81 | 98 | BCG_2082 | hypothetical protein | 30.3 | 77 | MAP2040c | hypothetical protein | 118 | 100 |
| MAP4_1786 | ferredoxin FdxC | 108 | Rv1177 | Probable ferredoxin FdxC | 82.08 | 108 | Mb1210 | ferredoxin FdxC | 82.08 | 108 | MAV_2150 | ferredoxin | 98.15 | 108 | BCG_1240 | ferredoxin fdxC | 82.08 | 108 | MAP2039 | FdxC_1 | 108 | 100 |
| MAP4_1787 | LysR-family protein transcriptional regulator | 315 | Rv2282c | Probable transcription regulator (Lys | 80.39 | 312 | Mb2303c | LysR family transcriptional re | 80.39 | 312 | MAV_2151 | LysR family transcriptional regulato | 99.37 | 315 | BCG_2297c | LysR family transcriptional regu | 80.39 | 312 | MAP2038c | hypothetical protein | 315 | 100 |
| MAP4_1789 | 3-phosphoadenosine 5-phosphosulfate reductase cysH | 247 | Rv2392 | Probable 3'-phosphoadenosine 5'-ph | 74.02 | 254 | Mb2413 | phosphoadenosine phosphos | 74.02 | 254 | MAV_2153 | phosphoadenosine phosphosulfate | 98.79 | 247 | BCG_2406 | phosphoadenosine phosphosul | 74.02 | 254 | MAP2036 | phosphoadenosine phosphosulfate red | 247 | 100 |
| MAP4_1790 | ferredoxin-dependent nitrite reductase NIRA | 555 | Rv2391 | Ferredoxin-dependent sulfite reduct | 77.66 | 563 | Mb2412 | ferredoxin-dependent nitrite | 77.66 | 563 | MAV_2154 | sulfite reductase [ferredoxin] 1 | 98.74 | 555 | BCG_2405 | ferredoxin-dependent nitrite re | 77.66 | 563 | MAP2035 | NirA_1 | 555 | 100 |
| MAP4_1791 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_1792 | putative cytochrome P450 hydroxylase | 437 | Rv1880c | Probable cytochrome P450 140 Cyp1 | 45.22 | 438 | Mb1912c | cytochrome p450 140 CYP140 | 45.22 | 438 | MAV_2156 | P450 heme-thiolate protein | 98.17 | 437 | BCG_1917c | cytochrome p450 140 CYP140 | 45.22 | 438 | MAP2033 | hypothetical protein | 437 | 100 |
| MAP4_1793 | Transcriptional regulator, TetR family | 220 | Rv0067c | Possible transcriptional regulatory p | 46.15 | 189 | Mb0068c | TetR family transcriptional re | 46.15 | 189 | MAV_2157 | TetR family transcriptional regulato | 97.73 | 220 | BCG_0098c | TetR family transcriptional regu | 46.15 | 189 | MAP2032c | hypothetical protein | 211 | 99.53 |
| MAP4_1794 | putative protein kinase | 485 | Rv1266c | Probable transmembrane serine/thr | 51.09 | 626 | Mb1297c | Ser/Thr protein kinase | 51.09 | 596 | MAV_2158 | serine/threonine protein kinase | 96.84 | 486 | BCG_1325c | transmembrane serine/threoni | 51.09 | 596 | MAP2031c | hypothetical protein | 485 | 100 |
| MAP4_1795 | cytochrome P450 | 422 | Rv3121 | Probable cytochrome P450 141 Cyp1 | 28.85 | 400 | Mb3575c | cytochrome P450 125 | 29.85 | 433 | MAV_2159 | cytochrome P450 superfamily prot | 96.64 | 415 | BCG_3609c | cytochrome P450 125 cyp125 | 29.85 | 433 | MAP2030 | hypothetical protein | 422 | 100 |
| MAP4_1796 | hypothetical protein | 150 | Rv0274 | hypothetical protein | 37.5 | 193 | Mb0280 | hypothetical protein | 37.5 | 193 | MAV_2566 | glyoxalase | 25 | 319 | BCG_0312 | hypothetical protein | 37.5 | 193 | MAP2029c | hypothetical protein | 150 | 100 |
| MAP4_1797 | hypothetical protein | 86 | Rv0626 | Possible antitoxin VapB5 | 86.05 | 86 | Mb0642 | hypothetical protein | 86.05 | 86 | MAV_5277 | amidohydrolase | 33.33 | 588 | BCG_0672 | hypothetical protein | 86.05 | 86 | MAP2028c | hypothetical protein | 86 | 100 |
| MAP4_1798 | hypothetical protein | 135 | Rv0627 | Possible toxin VapC5 | 82.22 | 135 | Mb0643 | hypothetical protein | 82.22 | 135 | MAV_1892 | L-carnitine dehydratase/bile acid-ir | 33.33 | 398 | BCG_0673 | hypothetical protein | 82.22 | 135 | MAP2027c | hypothetical protein | 135 | 100 |
| MAP4_1799 | putative protein kinase | 514 | Rv1266c | Probable transmembrane serine/thr | 58.39 | 626 | Mb1297c | Ser/Thr protein kinase | 51.9 | 596 | MAV_1417 | serine/threonine protein kinase | 60.22 | 604 | BCG_1325c | transmembrane serine/threoni | 51.9 | 596 | MAP2026 | hypothetical protein | 514 | 100 |
| MAP4_1800 | hypothetical protein | 173 | Rv1531 | hypothetical protein | 20.81 | 188 | Mb1558 | hypothetical protein | 20.81 | 188 | MAV_2164 | hypothetical protein | 93.06 | 173 | BCG_1583 | hypothetical protein | 20.81 | 188 | MAP2025c | hypothetical protein | 154 | 99.35 |
| MAP4_1801 | hypothetical protein | 181 | Rv1531 | hypothetical protein | 29.05 | 188 | Mb1558 | hypothetical protein | 29.05 | 188 | MAV_2165 | hypothetical protein | 97.79 | 181 | BCG_1583 | hypothetical protein | 29.05 | 188 | MAP2024c | hypothetical protein | 163 | 99.39 |
| MAP4_1802 | Transcriptional regulator, TetR family | 193 | Rv3173c | Probable transcriptional regulatory p | 35.62 | 200 | Mb3198c | TetR/ACRR family transcriptio | 35.62 | 200 | MAV_2167 | TetR family transcriptional regulato | 98.3 | 176 | BCG_3197c | TetR family transcriptional regu | 35.62 | 200 | MAP2023c | hypothetical protein | 193 | 100 |
| MAP4_1803 | hypothetical protein | 391 | Rv3570c | Possible oxidoreductase Possible 3-h | 33.42 | 394 | Mb3601c | oxidoreductase | 33.42 | 394 | MAV_2166 | acyl-CoA dehydrogenase domain-co | 97.67 | 387 | BCG_3635c | oxidoreductase | 33.42 | 394 | MAP2022 | hypothetical protein | 391 | 100 |
| MAP4_1804 | putative N-acetylmuramoyl-L-alanine amidase | 249 | Rv3717 | hypothetical protein | 60.26 | 241 | Mb3744 | hypothetical protein | 60.26 | 241 | MAV_2168 | N-acetylmuramoyl-L-alanine amida | 98.8 | 258 | BCG_3777 | hypothetical protein | 60.26 | 241 | MAP2021c | hypothetical protein | 249 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1805 | cutinase | 252 | Rv1758 | Probable cutinase Cut1 | 52.94 | 174 | Mb1788 | cutinase | 55.73 | 218 | MAV_2169 | serine esterase cutinase | 99.6 | 252 | BCG_1798 | cutinase cut1 | 55.73 | 218 | MAP2020 | hypothetical protein | 267 | 97.3 |
| MAP4_1806 | hypothetical protein | 80 | Rv0773c | Probable bifunctional acylase GgtA: | 42.86 | 512 | Mb0796c | bifunctional cephalosporin ac | 42.86 | 512 | MAV_2170 | acyl carrier protein | 100 | 80 | BCG_0825c | bifunctional acylase ggtA: ceph | 42.86 | 512 | MAP2019c | hypothetical protein | 80 | 100 |
| MAP4_1807 | putative monooxygenase | 495 | Rv1393c | Probable monooxygenase | 41.88 | 492 | Mb1428c | monoxygenase | 41.88 | 492 | MAV_2172 | FAD dependent oxidoreductase, pu | 99.39 | 495 | BCG_1454c | monoxygenase | 41.88 | 492 | MAP2018c | hypothetical protein | 495 | 100 |
| MAP4_1808 | lipoprotein LppN | 158 | Rv2270 | Probable lipoprotein LppN | 65.67 | 175 | Mb2293 | lipoprotein LppN | 64.93 | 175 | MAV_2171 | LppN protein | 94.94 | 155 | BCG_2287 | lipoprotein lppN | 65.67 | 175 | MAP2017 | hypothetical protein | 158 | 100 |
| MAP4_1809 | hypothetical protein | 180 | Rv2221c | Glutamate-ammonia-ligase adenylyl | 31.58 | 994 | Mb2245c | bifunctional glutamine-synthe | 31.58 | 994 | MAV_2173 | hypothetical protein | 96.67 | 180 | BCG_2238c | bifunctional glutamine-synthet | 31.58 | 994 | MAP2016 | hypothetical protein | 170 | 99.41 |
| MAP4_1810 | putative cytochrome P450 hydroxylase | 435 | Rv2266 | Probable cytochrome P450 124 Cyp1 | 83.29 | 428 | Mb2289 | cytochrome P450 124 CYP124 | 83.29 | 428 | MAV_2174 | P450 heme-thiolate protein | 99.77 | 435 | BCG_2283 | cytochrome P450 124 CYP124 | 83.29 | 428 | MAP2015 | hypothetical protein | 435 | 100 |
| MAP4_1811 | hypothetical protein | 115 | Rv0506 | Probable conserved membrane prot | 36.76 | 147 | Mb0518 | hypothetical protein | 36.76 | 147 | MAV_2175 | hypothetical protein | 98.26 | 115 | BCG_0549 | membrane protein mmpS2 | 36.76 | 147 | MAP2014 | hypothetical protein | 115 | 100 |
| MAP4_1812 | hypothetical protein | 361 | Rv0926c | hypothetical protein | 37.01 | 358 | Mb0949c | hypothetical protein | 37.01 | 358 | MAV_2176 | dihydrodipicolinate reductase N-te | 99.72 | 365 | BCG_0978c | hypothetical protein | 37.01 | 358 | MAP2013c | hypothetical protein | 361 | 100 |
| MAP4_1813 | conserved proline rich protein | 555 | Rv2264c | Conserved hypothetical proline rich | 55.53 | 592 | Mb2287c | hypothetical protein | 55.53 | 592 | MAV_2177 | hypothetical protein | 97.84 | 555 | BCG_2281c | hypothetical protein | 55.53 | 592 | MAP2012c | hypothetical protein | 555 | 100 |
| MAP4_1814 | hypothetical protein | 115 | Rv1079 | Cystathionine gamma-synthase Met | 33.33 | 388 | Mb1108 | cystathionine gamma-synthas | 33.33 | 388 | MAV_2178 | hypothetical protein | 100 | 115 | BCG_1137 | cystathionine gamma-synthase | 33.33 | 388 | MAP2011 | hypothetical protein | 115 | 100 |
| MAP4_1815 | SAM dependent carboxyl methyltransferase family pro | 355 | Rv3907c | Probable poly(A) polymerase PcnA ( | 34.35 | 480 | Mb3937c | poly(A) polymerase | 34.35 | 480 | MAV_2179 | hypothetical protein | 99.15 | 355 | BCG_3964c | poly(A) polymerase | 34.35 | 480 | MAP2010 | hypothetical protein | 355 | 100 |
| MAP4_1816 | metallo-beta-lactamase superfamily protein | 207 | Rv2260 | hypothetical protein | 83.41 | 211 | Mb2284 | hypothetical protein | 83.41 | 211 | MAV_2180 | metallo-beta-lactamase | 100 | 208 | BCG_2278 | hypothetical protein | 83.41 | 211 | MAP2009 | hypothetical protein | 207 | 100 |
| MAP4_1817 | zinc-type alcohol dehydrogenase adhE2 | 361 | Rv2259 | S-nitrosomycothiol reductase MscR | 88.92 | 361 | Mb2283 | zinc-dependent alcohol dehy | 88.92 | 361 | MAV_5022 | zinc-binding dehydrogenase | 36.9 | 363 | BCG_2277 | zinc-dependent alcohol dehydr | 88.92 | 361 | MAP2008 | AdhE2 | 361 | 100 |
| MAP4_1818 | putative transcriptional regulatory protein | 353 | Rv2258c | Possible transcriptional regulatory p | 74.86 | 353 | Mb2282c | transcriptional regulator | 74.86 | 353 | MAV_2182 | transcriptional regulator | 97.45 | 353 | BCG_2276c | transcriptional regulatory prote | 74.86 | 353 | MAP2007c | hypothetical protein | 353 | 100 |
| MAP4_1819 | putative Beta-lactamase | 272 | Rv2257c | hypothetical protein | 75.74 | 272 | Mb2281c | hypothetical protein | 75.74 | 272 | MAV_2183 | beta-lactamase | 98.9 | 272 | BCG_2275c | hypothetical protein | 75.74 | 272 | MAP2006c | hypothetical protein | 272 | 100 |
| MAP4_1820 | Diacylglycerol kinase-related protein | 526 | Rv2252 | Diacylglycerol kinase | 78.91 | 309 | Mb2276 | diacylglycerol kinase | 78.91 | 309 | MAV_2184 | diacylglycerol kinase | 97.67 | 310 | BCG_2270 | diacylglycerol kinase | 78.91 | 309 | MAP2005 | hypothetical protein | 526 | 100 |
| MAP4_1821 | flavoprotein | 526 | Rv2251 | Possible flavoprotein | 81.37 | 475 | Mb2275 | flavoprotein | 79.21 | 529 | MAV_2186 | flavoprotein | 98.86 | 536 | BCG_2269 | flavoprotein | 79.21 | 529 | MAP2004 | hypothetical protein | 526 | 100 |
| MAP4_1822 | Transcriptional regulator, TetR family | 193 | Rv2250c | Possible transcriptional regulatory p | 72.92 | 189 | Mb2274c | transcriptional regulator | 72.4 | 189 | MAV_2187 | TetR family transcriptional regulatc | 98.45 | 193 | BCG_2268c | transcriptional regulatory prote | 72.92 | 189 | MAP2003c | hypothetical protein | 230 | 100 |
| MAP4_1823 | Glycerol-3-phosphate dehydrogenase | 513 | Rv2249c | Probable glycerol-3-phosphate dehy | 82.14 | 516 | Mb2273c | glycerol-3-phosphate dehydr | 82.14 | 516 | MAV_2188 | glycerol-3-phosphate dehydrogena | 98.64 | 513 | BCG_2267c | glycerol-3-phosphate dehydrog | 82.14 | 516 | MAP2002c | GlpD1 | 513 | 100 |
| MAP4_1824 | FAD binding domain-containing protein | 506 | Rv1751 | Probable oxidoreductase | 23.6 | 460 | Mb1780 | hypothetical protein | 23.6 | 460 | MAV_2189 | FAD binding domain-containing pro | 98.22 | 506 | BCG_1790 | hypothetical protein | 23.6 | 460 | MAP2001c | hypothetical protein | 506 | 100 |
| MAP4_1825 | acetylpropionyl CoA carboxylase beta subunit | 473 | Rv2247 | Acetyl/propionyl-CoA carboxylase (b | 95.77 | 473 | Mb2271 | acetyl-/propionyl-CoA carbox | 95.77 | 473 | MAV_2190 | propionyl-CoA carboxylase beta cha | 99.79 | 473 | BCG_2264 | acetyl/propionyl CoA carboxyla | 95.77 | 473 | MAP2000 | AccD6 | 473 | 100 |
| MAP4_1826 | 3-oxoacyl-ACP synthase 2 | 440 | Rv2246 | 3-oxoacyl-[acyl-carrier protein] synt | 88.26 | 438 | Mb2270 | 3-oxoacyl-ACP synthase | 88.26 | 438 | MAV_2191 | 3-oxoacyl-(acyl carrier protein) syn | 99.77 | 440 | BCG_2263 | 3-oxoacyl-ACP synthase | 88.26 | 438 | MAP1999 | 3-oxoacyl-ACP synthase II | 440 | 100 |
| MAP4_1827 | 3-oxoacyl-ACP synthase 1 | 416 | Rv2245 | 3-oxoacyl-[acyl-carrier protein] synt | 91.11 | 416 | Mb2269 | 3-oxoacyl-ACP synthase | 91.11 | 416 | MAV_2192 | 3-oxoacyl-(acyl carrier protein) syn | 99.76 | 416 | BCG_2262 | 3-oxoacyl-ACP synthase | 91.11 | 416 | MAP1998 | 3-oxoacyl-ACP synthase II | 416 | 99.76 |
| MAP4_1828 | meromycolate extension acyl carrier protein acpM | 115 | Rv2244 | Meromycolate extension acyl carrie | 92.17 | 115 | Mb2268 | acyl carrier protein | 92.17 | 115 | MAV_2193 | acyl carrier protein | 100 | 115 | BCG_2261 | acyl carrier protein | 92.17 | 115 | MAP1997 | acyl carrier protein | 115 | 100 |
| MAP4_1829 | malonyl CoA-acyl carrier protein transacylase fabD | 302 | Rv2243 | Malonyl CoA-acyl carrier protein tra | 85.76 | 302 | Mb2267 | ACP S-malonyltransferase | 85.76 | 302 | MAV_2194 | malonyl CoA-acyl carrier protein tra | 100 | 302 | BCG_2260 | malonyl CoA-ACP transacylase | 85.76 | 302 | MAP1996 | ACP S-malonyltransferase | 302 | 100 |
| MAP4_1830 | hypothetical protein | 441 | Rv2242 | hypothetical protein | 88.89 | 414 | Mb2266 | hypothetical protein | 88.89 | 414 | MAV_2195 | hypothetical protein | 99.77 | 441 | BCG_2259 | hypothetical protein | 88.65 | 414 | MAP1995 | hypothetical protein | 441 | 99.77 |
| MAP4_1831 | Pyruvate dehydrogenase E1 component | 929 | Rv2241 | Pyruvate dehydrogenase E1 compor | 92.65 | 901 | Mb2265 | pyruvate dehydrogenase subu | 92.54 | 901 | MAV_2196 | pyruvate dehydrogenase subunit E | 99.78 | 929 | BCG_2258 | pyruvate dehydrogenase subur | 92.65 | 901 | MAP1994 | pyruvate dehydrogenase subunit E1 | 929 | 100 |
| MAP4_1832 | hypothetical protein | 247 | Rv2240c | hypothetical protein | 71.13 | 196 | Mb2264c | hypothetical protein | 71.65 | 265 | MAV_2197 | hypothetical protein | 99.41 | 169 | BCG_2257c | hypothetical protein | 71.65 | 265 | MAP1993c | hypothetical protein | 247 | 100 |
| MAP4_1833 | hypothetical protein | 147 | Rv2239c | hypothetical protein | 90.41 | 158 | Mb2263c | hypothetical protein | 90.41 | 158 | MAV_2198 | hypothetical protein | 99.29 | 140 | BCG_2256c | hypothetical protein | 90.41 | 158 | MAP1992c | hypothetical protein | 147 | 100 |
| MAP4_1834 | peroxiredoxin AhpE | 153 | Rv2238c | Probable peroxiredoxin AhpE | 87.58 | 153 | Mb2262c | peroxiredoxin AhpE | 87.58 | 153 | MAV_2199 | alkyl hydroperoxide reductase/ Thi | 99.35 | 153 | BCG_2255c | peroxiredoxin AhpE | 87.58 | 153 | MAP1991c | AhpE | 153 | 100 |
| MAP4_1835 | Adenosylcobinamide amidohydrolase family protein | 266 | Rv0826 | hypothetical protein | 41.46 | 351 | Mb0849 | hypothetical protein | 43.59 | 351 | MAV_2200 | adenosylcobinamide amidohydrola | 95.82 | 263 | BCG_0879 | hypothetical protein | 41.46 | 351 | MAP1990 | hypothetical protein | 266 | 100 |
| MAP4_1836 | Epoxide hydrolase domain-containing protein | 372 | Rv1833c | Possible haloalkane dehalogenase | 28.28 | 286 | Mb1864c | haloalkane dehalogenase | 28.28 | 286 | MAV_2202 | epoxide hydrolase | 98.66 | 372 | BCG_1868c | haloalkane dehalogenase | 28.28 | 286 | MAP1989c | hypothetical protein | 401 | 99.73 |
| MAP4_1837 | hypothetical protein | 271 | Rv2237 | hypothetical protein | 83.86 | 255 | Mb2261 | hypothetical protein | 83.86 | 255 | MAV_2203 | hypothetical protein | 98.15 | 271 | BCG_2254 | hypothetical protein | 83.86 | 255 | MAP1988 | hypothetical protein | 271 | 100 |
| MAP4_1838 | cobalamin biosynthesis transmembrane protein cobD | 313 | Rv2236c | Probable cobalamin biosynthesis tra | 72.03 | 313 | Mb2260c | cobalamin biosynthesis prote | 72.03 | 313 | MAV_2205 | cobalamin biosynthesis protein | 96.81 | 314 | BCG_2253c | cobalamin biosynthesis protein | 72.03 | 313 | MAP1987c | cobalamin biosynthesis protein | 313 | 100 |
| MAP4_1839 | hypothetical protein | 275 | Rv2235 | Probable conserved transmembrane | 74.28 | 271 | Mb2259 | transmembrane protein | 74.28 | 271 | MAV_2204 | hypothetical protein | 98.91 | 276 | BCG_2252 | hypothetical protein | 74.28 | 271 | MAP1986 | hypothetical protein | 275 | 100 |
| MAP4_1840 | phosphotyrosine protein phosphatase | 163 | Rv2234 | Phosphotyrosine protein phosphata | 81.6 | 163 | Mb2258 | phosphotyrosine protein pho | 81.6 | 163 | MAV_2206 | low molecular weight protein-tyros | 99.39 | 163 | BCG_2251 | phosphotyrosine protein phosp | 81.6 | 163 | MAP1985 | PtpA | 163 | 100 |
| MAP4_1841 | HAD superfamily hydrolase | 222 | Rv2232 | Protein tyrosine kinase transcription | 75.47 | 291 | Mb2257 | hypothetical protein | 75.47 | 291 | MAV_2207 | hypothetical protein | 98.2 | 222 | BCG_2250 | hypothetical protein | 75.47 | 291 | MAP1984 | hypothetical protein | 222 | 100 |
| MAP4_1842 | aminotransferase CobD | 356 | Rv2231c | Possible aminotransferase CobC | 74.16 | 364 | Mb2256c | hypothetical protein | 74.16 | 364 | MAV_2208 | hypothetical protein | 98.83 | 342 | BCG_2249c | hypothetical protein | 74.16 | 364 | MAP1983c | hypothetical protein | 356 | 100 |
| MAP4_1843 | hypothetical protein | 377 | Rv2230c | hypothetical protein | 80.59 | 379 | Mb2255c | hypothetical protein | 80.59 | 379 | MAV_2209 | hypothetical protein | 96.55 | 378 | BCG_2248c | hypothetical protein | 80.59 | 379 | MAP1982c | hypothetical protein | 377 | 100 |
| MAP4_1844 | hypothetical protein | 245 | Rv2229c | hypothetical protein | 68.6 | 245 | Mb2254c | hypothetical protein | 68.18 | 245 | MAV_2210 | hypothetical protein | 97.96 | 245 | BCG_2247c | hypothetical protein | 68.18 | 245 | MAP1981c | hypothetical protein | 245 | 100 |
| MAP4_1845 | bifunctional RNase Hacid phosphatase | 377 | Rv2228c | Multifunctional protein Has RNASE H | 74.01 | 364 | Mb2253c | bifunctional RNase H/acid ph | 74.01 | 364 | MAV_2211 | bifunctional RNase H/acid phospha | 96.34 | 383 | BCG_2246c | bifunctional RNase H/acid phos | 74.01 | 364 | MAP1980c | bifunctional RNase H/acid phosphatase | 377 | 100 |
| MAP4_1846 | putative Ferredoxin | 69 | Rv3503c | Probable ferredoxin FdxD | 35.59 | 63 | Mb3533c | ferredoxin FdxD | 35.59 | 63 | MAV_1949 | hypothetical protein | 48.39 | 64 | BCG_3567c | ferredoxin fdxD | 35.59 | 63 | MAP0560 | FdxD | 63 | 35.59 |
| MAP4_1847 | cytochrome P450 superfamily protein | 389 | Rv1785c | Probable cytochrome P450 143 Cyp1 | 37.87 | 393 | Mb1813c | cytochrome P450 143 | 37.87 | 393 | MAV_2213 | cytochrome P450 superfamily prot | 98.71 | 389 | BCG_1817c | cytochrome P450 143 cyp143 | 37.87 | 393 | MAP1979 | hypothetical protein | 389 | 100 |
| MAP4_1848 | transcriptional regulator, Cro-CI family,putative | 189 | Rv3833 | Transcriptional regulatory protein (p | 54.17 | 263 | Mb3863 | AraC family transcriptional re | 54.17 | 263 | MAV_2214 | regulatory protein | 99.47 | 189 | BCG_3896 | AraC family transcriptional regu | 54.17 | 263 | MAP1978 | hypothetical protein | 189 | 100 |
| MAP4_1849 | putative methyltransferase | 216 | Rv0560c | Possible benzoquinone methyltrans | 34.21 | 241 | Mb0575c | benzoquinone methyltransfer | 34.21 | 241 | MAV_2216 | CheR methyltransferase SAM bindi | 98.61 | 216 | BCG_0605c | benzoquinone methyltransfera | 34.21 | 241 | MAP1977c | hypothetical protein | 216 | 100 |
| MAP4_1850 | hypothetical protein | 236 | Rv2227 | hypothetical protein | 78.57 | 233 | Mb2252 | hypothetical protein | 86.29 | 124 | MAV_2215 | hypothetical protein | 99.15 | 239 | BCG_2245 | hypothetical protein | 86.29 | 124 | MAP1976 | hypothetical protein | 236 | 100 |
| MAP4_1851 | hypothetical protein | 110 | Rv2331A | Hypothetical protein | 45.83 | 112 | Mb2359 | hypothetical protein | 45.83 | 112 | MAV_2480 | phospholipase, patatin family prote | 40 | 318 | BCG_2353 | hypothetical protein | 45.83 | 112 | MAP1975 | hypothetical protein | 110 | 100 |
| MAP4_1852 | conserved hypothetical protein, CHAD domain containi | 539 | Rv2226 | hypothetical protein | 66.73 | 513 | Mb2250 | hypothetical protein | 66.54 | 513 | MAV_2235 | adenylate cyclase, putative | 97.8 | 546 | BCG_2243 | hypothetical protein | 66.73 | 513 | MAP1974 | hypothetical protein | 539 | 100 |
| MAP4_1853 | hypothetical protein | 150 | Rv2744c | Conserved 35 kDa alanine rich prote | 42.31 | 270 | Mb2765c | hypothetical protein | 42.31 | 270 | MAV_2236 | hypothetical protein | 100 | 83 | BCG_2760c | hypothetical protein | 42.31 | 270 | MAP1973 | hypothetical protein | 150 | 100 |
| MAP4_1854 | hypothetical protein | 123 | Rv0203 | Possible exported protein | 38.95 | 136 | Mb0209 | hypothetical protein | 38.95 | 136 | MAV_2237 | hypothetical protein | 98.37 | 134 | BCG_0240 | hypothetical protein | 37.89 | 136 | MAP1972c | hypothetical protein | 123 | 100 |
| MAP4_1855 | hypothetical protein | 391 | Rv3096 | hypothetical protein | 73.23 | 379 | Mb3123 | hypothetical protein | 73.23 | 379 | MAV_0332 | hypothetical protein | 71.88 | 377 | BCG_3121 | hypothetical protein | 73.23 | 379 | MAP1971 | hypothetical protein | 391 | 100 |
| MAP4_1856 | 3-methyl-2-oxobutanoatehydroxy methyltransferase | 285 | Rv2225 | 3-methyl-2-oxobutanoate hydroxym | 88.07 | 281 | Mb2249 | 3-methyl-2-oxobutanoate hyd | 88.07 | 281 | MAV_2239 | 3-methyl-2-oxobutanoate hydroxyn | 99.3 | 285 | BCG_2242 | 3-methyl-2-oxobutanoate hydr | 88.07 | 281 | MAP1970 | 3-methyl-2-oxobutanoate hydroxymeth | 285 | 100 |
| MAP4_1857 | acyltransferase, wsdgatmgat subfamily protein | 463 | Rv1760 | Possible triacylglycerol synthase (dia | 57.64 | 502 | Mb1791 | hypothetical protein | 58.01 | 509 | MAV_2240 | acyltransferase, ws/dgat/mgat sub | 97.41 | 466 | BCG_1801 | hypothetical protein | 58.01 | 509 | MAP1969c | hypothetical protein | 463 | 100 |
| MAP4_1858 | putative exported protease | 520 | Rv2224c | Probable carboxylesterase CaeA | 84.23 | 520 | Mb2248c | exported protease | 84.23 | 520 | MAV_2241 | alpha/beta hydrolase | 100 | 520 | BCG_2241c | protease | 84.23 | 520 | MAP1968c | hypothetical protein | 520 | 100 |
| MAP4_1859 | putative exported protease | 522 | Rv2223c | Probable exported protease | 78.81 | 520 | Mb2247c | exported protease | 78.81 | 520 | MAV_2243 | alpha/beta hydrolase | 99.81 | 519 | BCG_2240c | protease | 78.6 | 520 | MAP1967c | hypothetical protein | 522 | 100 |
| MAP4_1860 | Glutamine synthetase | 446 | Rv2222c | Probable glutamine synthetase GlnA | 94.17 | 446 | Mb2246c | glutamine synthetase | 94.17 | 446 | MAV_2244 | glutamine synthetase, type I | 100 | 446 | BCG_2239c | glutamine synthetase glnA2 | 94.17 | 446 | MAP1966c | GlnA2 | 446 | 100 |
| MAP4_1861 | glutamate-ammonia-ligase adenylyltransferas eglnE | 998 | Rv2221c | Glutamate-ammonia-ligase adenylyl | 84.97 | 994 | Mb2245c | bifunctional glutamine-synthe | 84.97 | 994 | MAV_2245 | bifunctional glutamine-synthetase | 99.6 | 998 | BCG_2238c | bifunctional glutamine-synthet | 84.97 | 994 | MAP1965c | bifunctional glutamine-synthetase aden | 998 | 99.9 |
| MAP4_1862 | hypothetical protein | 214 | Rv0356c | hypothetical protein | 33.33 | 214 | Mb0363c | hypothetical protein | 33.33 | 214 | MAV_2246 | thioesterase | 98.55 | 207 | BCG_0394c | hypothetical protein | 33.33 | 214 | MAP1964c | hypothetical protein | 185 | 99.46 |
| MAP4_1865 | Glutamine synthetase | 478 | Rv2220 | Glutamine synthetase GlnA1 (glutan | 90.38 | 478 | Mb2244 | glutamine synthetase | 90.38 | 478 | MAV_2267 | glutamine synthetase, type I | 100 | 478 | BCG_2237 | glutamine synthetase glnA1 | 90.38 | 478 | MAP1962 | GlnA1 | 478 | 100 |
| MAP4_1866 | hypothetical protein | 140 | Rv2219A | Probable conserved membrane prot | 67.86 | 140 | Mb2243c | hypothetical protein | 67.86 | 140 | MAV_2268 | RDD family protein, putative | 97.14 | 140 | BCG_2236c | hypothetical protein | 67.86 | 140 | MAP1961c | hypothetical protein | 176 | 100 |
| MAP4_1867 | hypothetical protein | 250 | Rv2219 | Probable conserved transmembrane | 85.6 | 250 | Mb2242 | transmembrane protein | 85.6 | 250 | MAV_2269 | integral membrane protein | 99.6 | 250 | BCG_2235 | hypothetical protein | 85.6 | 250 | MAP1960 | hypothetical protein | 250 | 100 |
| MAP4_1868 | lipoate biosynthesis protein A lipA | 307 | Rv2218 | Probable lipoate biosynthesis protei | 90.88 | 311 | Mb2241 | lipoyl synthase | 90.88 | 311 | MAV_2270 | lipoyl synthase | 99.35 | 307 | BCG_2234 | lipoyl synthase | 90.88 | 311 | MAP1959 | lipoyl synthase | 307 | 100 |
| MAP4_1869 | lipoate biosynthesis protein B lipB | 233 | Rv2217 | Probable lipoate biosynthesis protei | 78.54 | 230 | Mb2240 | lipoate-protein ligase B | 78.11 | 230 | MAV_2271 | lipoate-protein ligase B | 98.71 | 233 | BCG_2233 | lipoate-protein ligase B | 78.11 | 230 | MAP1958 | lipoate-protein ligase B | 233 | 100 |
| MAP4_1870 | hypothetical protein | 307 | Rv2216 | hypothetical protein | 84.23 | 301 | Mb2239 | hypothetical protein | 84.23 | 301 | MAV_2272 | hypothetical protein | 99.67 | 307 | BCG_2232 | hypothetical protein | 84.23 | 301 | MAP1957 | hypothetical protein | 307 | 100 |
| MAP4_1871 | pyruvate dehydrogenase E2 component sucB | 590 | Rv2215 | DlaT, dihydrolipoamide acyltransfera | 75.76 | 553 | Mb2238 | dihydrolipoamide acetyltrans | 75.76 | 553 | MAV_2273 | dihydrolipoamide acetyltransferase | 95 | 596 | BCG_2231 | dihydrolipoamide acetyltransfe | 75.59 | 553 | MAP1956 | dihydrolipoamide acetyltransferase | 590 | 100 |
| MAP4_1872 | short-chain type dehydrogenase ephD | 592 | Rv2214c | Possible short-chain dehydrogenase | 78.96 | 592 | Mb2237c | short chain dehydrogenase | 78.96 | 592 | MAV_2275 | short chain dehydrogenase | 99.32 | 592 | BCG_2230c | short chain dehydrogenase | 78.96 | 592 | MAP1955c | short chain dehydrogenase | 592 | 100 |
| MAP4_1873 | hypothetical protein | 113 | Rv0420c | Possible transmembrane protein | 29.52 | 136 | Mb0428c | transmembrane protein | 29.52 | 136 | MAV_2276 | hypothetical protein | 100 | 113 | BCG_0459c | hypothetical protein | 29.52 | 136 | MAP0118 | hypothetical protein | 122 | 32.63 |
| MAP4_1874 | hypothetical protein | 149 | Rv3076 | hypothetical protein | 28.89 | 158 | Mb3103 | hypothetical protein | 28.89 | 158 | MAV_2277 | hypothetical protein | 97.99 | 149 | BCG_3101 | hypothetical protein | 28.89 | 158 | MAP1954c | hypothetical protein | 149 | 100 |
| MAP4_1875 | aminopeptidase pepB | 515 | Rv2213 | Probable aminopeptidase PepB | 83.11 | 515 | Mb2236 | leucyl aminopeptidase | 82.91 | 515 | MAV_2279 | leucyl aminopeptidase | 99.22 | 518 | BCG_2229 | leucyl aminopeptidase | 82.91 | 515 | MAP1953 | leucyl aminopeptidase | 515 | 100 |
| MAP4_1876 | putative transposase | 367 | Rv0797 | Putative transposase for insertion se | 71.79 | 364 | Mb0820 | IS1547 transposase | 72.08 | 364 | MAV_1059 | transposase | 86 | 350 | BCG_0849 | transposase for insertion seque | 72.08 | 364 | MAP1952c | IS1547_1 transposase | 367 | 100 |
| MAP4_1877 | aminomethyltransferase gcvT | 367 | Rv2211c | Probable aminomethyltransferase G | 83.92 | 379 | Mb2234c | glycine cleavage system amin | 83.92 | 379 | MAV_2280 | glycine cleavage system aminomet | 98.91 | 367 | BCG_2227c | glycine cleavage system amino | 83.92 | 379 | MAP1951c | glycine cleavage system aminomethyltr | 367 | 100 |
| MAP4_1878 | branched-chain amino acid transaminase ilvE | 371 | Rv2210c | Branched-chain amino acid transam | 87.6 | 368 | Mb2233c | branched-chain amino acid ar | 87.33 | 368 | MAV_2281 | branched-chain amino acid aminot | 99.46 | 371 | BCG_2226c | branched-chain amino acid am | 87.33 | 368 | MAP1950c | branched-chain amino acid aminotrans | 371 | 100 |
| MAP4_1879 | cobalamin 5-phosphate synthase cobS | 251 | Rv2208 | Probable cobalamin 5'-phosphate sy | 68.9 | 249 | Mb2231 | cobalamin synthase | 68.9 | 249 | MAV_2282 | cobalamin synthase | 98.41 | 251 | BCG_2224 | cobalamin synthase | 68.9 | 249 | MAP1949 | cobalamin synthase | 251 | 100 |
| MAP4_1880 | Nicotinate-nucleotide--dimethylbenzimidazole phosph | 349 | Rv2207 | Probable nicotinate-nucleotide-dime | 83.14 | 361 | Mb2230 | nicotinate-nucleotide--dimet | 83.14 | 361 | MAV_2283 | nicotinate-nucleotide--dimethylber | 99.43 | 349 | BCG_2223 | nicotinate-nucleotide--dimethy | 83.14 | 361 | MAP1948 | nicotinate-nucleotide--dimethylbenzimi | 349 | 100 |
| MAP4_1881 | bifunctional cobalamin biosynthesis protein cobU | 178 | Rv0254c | Probable bifunctional cobalamin bio | 43.89 | 174 | Mb0260c | bifunctional cobalamin biosyr | 43.89 | 174 | MAV_2284 | cobinamide kinase / cobinamide ph | 97.19 | 178 | BCG_0292c | bifunctional cobalamin biosynt | 43.89 | 174 | MAP1947 | hypothetical protein | 178 | 100 |
| MAP4_1882 | hypothetical protein | 230 | Rv2206 | Probable conserved transmembrane | 68.51 | 236 | Mb2229 | transmembrane protein | 68.51 | 236 | MAV_2285 | hypothetical protein | 99.57 | 230 | BCG_2222 | hypothetical protein | 68.51 | 236 | MAP1946 | hypothetical protein | 230 | 100 |
| MAP4_1883 | putative glycerate kinase | 383 | Rv2205c | hypothetical protein | 82.96 | 358 | Mb2228c | hypothetical protein | 82.96 | 358 | MAV_2286 | glycerate kinase subfamily protein | 99.72 | 354 | BCG_2221c | hypothetical protein | 82.96 | 358 | MAP1945c | hypothetical protein | 383 | 100 |
| MAP4_1884 | putative iron-sulfur cluster biosynthesis protein | 125 | Rv2204c | hypothetical protein | 94.07 | 118 | Mb2227c | hypothetical protein | 94.07 | 118 | MAV_2287 | HesB/YadR/YfhF family protein | 100 | 118 | BCG_2220c | hypothetical protein | 94.07 | 118 | MAP1944c | hypothetical protein | 125 | 100 |
| MAP4_1885 | hypothetical protein | 225 | Rv2203 | Possible conserved membrane prote | 66.53 | 230 | Mb2226 | hypothetical protein | 66.53 | 230 | MAV_2288 | hypothetical protein | 100 | 225 | BCG_2219 | hypothetical protein | 66.53 | 230 | MAP1943 | hypothetical protein | 225 | 100 |
| MAP4_1886 | carbohydrate kinase CbhK | 324 | Rv2202c | Adenosine kinase | 86.42 | 324 | Mb2225c | carbohydrate kinase CbhK | 86.42 | 324 | MAV_2289 | adenosine kinase | 99.38 | 324 | BCG_2218c | adenosine kinase | 86.42 | 324 | MAP1942c | CbhK | 324 | 100 |
| MAP4_1887 | asparagine synthetase AsnB | 643 | Rv2201 | Probable asparagine synthetase Asn | 88.04 | 652 | Mb2224 | asparagine synthetase AsnB | 88.04 | 652 | MAV_2290 | asparagine synthase (glutamine-hy | 98.76 | 643 | BCG_2217 | asparagine synthetase AsnB | 88.04 | 652 | MAP1941 | AsnB_2 | 643 | 100 |
| MAP4_1888 | transmembrane cytochrome C oxidase subunit II CtaC | 360 | Rv2200c | Probable transmembrane cytochron | 79.17 | 363 | Mb2223c | transmembrane cytochrome | 79.17 | 363 | MAV_2291 | cytochrome C oxidase, subunit 2 | 99.7 | 336 | BCG_2216c | transmembrane cytochrome C | 79.17 | 363 | MAP1940c | CtaC | 360 | 100 |
| MAP4_1889 | hypothetical protein | 139 | Rv2199c | Possible conserved integral membra | 86.33 | 139 | Mb2222c | hypothetical protein | 86.33 | 139 | MAV_2292 | cytochrome C oxidase polypeptide | 99.28 | 139 | BCG_2215c | hypothetical protein | 86.33 | 139 | MAP1939c | hypothetical protein | 139 | 99.28 |
| MAP4_1890 | membrane protein MMPS3 | 266 | Rv2198c | Probable conserved membrane prot | 56.63 | 299 | Mb2221c | hypothetical protein | 56.63 | 299 | MAV_2293 | MmpS3 protein | 100 | 266 | BCG_2214c | membrane protein mmpS3 | 56.63 | 299 | MAP1938c | hypothetical protein | 266 | 100 |
| MAP4_1891 | hypothetical protein | 210 | Rv2197c | Probable conserved transmembrane | 65.42 | 214 | Mb2220c | transmembrane protein | 65.42 | 214 | MAV_2294 | hypothetical protein | 97.14 | 210 | BCG_2213c | hypothetical protein | 65.42 | 214 | MAP1937c | hypothetical protein | 210 | 100 |
| MAP4_1892 | hypothetical protein | 171 | Rv3791 | Decaprenylphosphoryl-D-2-keto ery | 36.59 | 254 | Mb3820 | short chain dehydrogenase | 36.59 | 254 | MAV_2295 | hypothetical protein | 99.32 | 147 | BCG_3853 | short chain dehydrogenase | 36.59 | 254 | MAP1936c | hypothetical protein | 171 | 100 |
| MAP4_1893 | Ubiquinol-cytochrome c reductase, cytochrome B subu | 566 | Rv2196 | Probable ubiquinol-cytochrome C re | 88.53 | 549 | Mb2219 | ubiquinol-cytochrome C redu | 88.53 | 549 | MAV_2296 | cytochrome b6 | 100 | 566 | BCG_2212 | ubiquinol-cytochrome C reduct | 88.53 | 549 | MAP1935 | QcrB | 566 | 100 |
| MAP4_1894 | Rieske iron-sulfur protein QcrA | 422 | Rv2195 | Probable rieske iron-sulfur protein C | 78.69 | 429 | Mb2218 | Rieske iron-sulfur protein Qcr | 78.69 | 429 | MAV_2297 | ubiquinol-cytochrome C reductase, | 99.25 | 401 | BCG_2211 | Rieske iron-sulfur protein QcrA | 78.69 | 429 | MAP1934 | QcrA | 422 | 99.76 |
| MAP4_1895 | ubiquinol-cytochrome C reductase QcrC | 286 | Rv2194 | Probable ubiquinol-cytochrome C re | 88.63 | 280 | Mb2217 | ubiquinol-cytochrome C redu | 88.63 | 280 | MAV_2298 | cytochrome C | 99.64 | 275 | BCG_2210 | ubiquinol-cytochrome C reduct | 88.63 | 280 | MAP1933 | QcrC | 286 | 100 |
| MAP4_1896 | cytochrome C oxidase subunit III | 203 | Rv2193 | Probable cytochrome C oxidase (sub | 92.61 | 203 | Mb2216 | cytochrome C oxidase subuni | 92.61 | 203 | MAV_2299 | cytochrome C oxidase, subunit 3 | 99.44 | 180 | BCG_2209 | cytochrome C oxidase (subunit | 92.61 | 203 | MAP1932 | CtaE | 203 | 100 |
| MAP4_1897 | anthranilate phosphoribosyltransferase TrpD | 367 | Rv2192c | Probable anthranilate phosphoribos | 85.22 | 370 | Mb2215c | anthranilate phosphoribosylt | 85.22 | 370 | MAV_2301 | anthranilate phosphoribosyltransfe | 99.46 | 407 | BCG_2208c | anthranilate phosphoribosyltra | 85.22 | 370 | MAP1931c | anthranilate phosphoribosyltransferase | 367 | 100 |
| MAP4_1898 | Exonuclease family protein | 640 | Rv2191 | hypothetical protein | 74.81 | 645 | Mb2214 | hypothetical protein | 74.65 | 645 | MAV_2300 | hypothetical protein | 98.28 | 643 | BCG_2207 | hypothetical protein | 74.65 | 645 | MAP1930 | hypothetical protein | 643 | 99.84 |
| MAP4_1899 | hypothetical protein | 91 | Rv3825c | Polyketide synthase Pks2 | 35.19 | 2126 | Mb3855c | polyketide synthase | 35.19 | 2126 | MAV_2303 | hypothetical protein | 96.88 | 64 | BCG_3888c | polyketide synthase | 35.19 | 2126 | MAP1929c | hypothetical protein | 91 | 100 |
| MAP4_1900 | hypothetical protein | 385 | Rv2190c | hypothetical protein | 72.68 | 385 | Mb2213c | hypothetical protein | 72.68 | 385 | MAV_2304 | NLP/P60 family protein | 99.71 | 342 | BCG_2206c | hypothetical protein | 72.68 | 385 | MAP1928c | hypothetical protein | 385 | 100 |
| MAP4_1901 | hypothetical protein | 270 | Rv2189c | hypothetical protein | 73.39 | 257 | Mb2212c | hypothetical protein | 73.39 | 257 | MAV_2305 | hypothetical protein | 99.26 | 276 | BCG_2205c | hypothetical protein | 73.39 | 257 | MAP1927c | hypothetical protein | 270 | 100 |
| MAP4_1902 | mannosyltransferase PimB | 377 | Rv2188c | Mannosyltransferase PimB | 81.22 | 385 | Mb2211c | hypothetical protein | 81.22 | 385 | MAV_2306 | glycosyl transferase, group 1 | 98.94 | 377 | BCG_2204c | hypothetical protein | 81.22 | 385 | MAP1926c | hypothetical protein | 377 | 100 |
| MAP4_1903 | Long-chain-fatty-acid--CoA ligase | 600 | Rv2187 | Long-chain-fatty-acid-CoA ligase Fad | 80.67 | 600 | Mb2210 | long-chain-fatty-acid-CoA liga | 80.51 | 508 | MAV_2307 | acyl-CoA dehydrogenase | 98.67 | 600 | BCG_2203 | long-chain-fatty-acid-CoA ligas | 80.51 | 508 | MAP1925 | FadD15 | 600 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_1904 | hypothetical protein | 132 | Rv2186c | hypothetical protein | 83.33 | 129 | Mb2208c | hypothetical protein | 83.33 | 129 | MAV_2308 | hypothetical protein | 99.24 | 134 | BCG_2201c | hypothetical protein | 83.33 | 129 | MAP1924c | hypothetical protein | 132 | 100 |
| MAP4_1905 | hypothetical protein | 145 | Rv2185c | Conserved protein TB16.3 | 75.69 | 144 | Mb2207c | hypothetical protein | 75.69 | 144 | MAV_2309 | cyclase/dehydrase | 99.31 | 145 | BCG_2200c | hypothetical protein | 75.69 | 144 | MAP1923c | hypothetical protein | 145 | 100 |
| MAP4_1906 | Anion-transporting ATPase family prtoin | 383 | Rv2184c | hypothetical protein | 80.37 | 379 | Mb2206c | hypothetical protein | 80.37 | 379 | MAV_2310 | anion-transporting ATPase | 99.48 | 392 | BCG_2199c | hypothetical protein | 80.37 | 379 | MAP1922c | hypothetical protein | 383 | 100 |
| MAP4_1907 | hypothetical protein | 129 | Rv2183c | hypothetical protein | 67.18 | 131 | Mb2205c | hypothetical protein | 67.18 | 131 | MAV_2311 | hypothetical protein | 98.45 | 129 | BCG_2198c | hypothetical protein | 67.18 | 131 | MAP1921c | hypothetical protein | 129 | 100 |
| MAP4_1908 | 1-acylglycerol-3-phosphate O-acyltransferase | 241 | Rv2182c | 1-acylglycerol-3-phosphate O-acyltra | 83.4 | 247 | Mb2204c | 1-acylglycerol-3-phosphate O | 83.4 | 247 | MAV_2313 | 1-acylglycerol-3-phosphate O-acylt | 99.59 | 241 | BCG_2197c | 1-acylglycerol-3-phosphate O-a | 83.4 | 247 | MAP1920c | hypothetical protein | 241 | 100 |
| MAP4_1909 | hypothetical protein | 429 | Rv2181 | Alpha(1->2)mannosyltransferase | 75.76 | 427 | Mb2203 | hypothetical protein | 75.76 | 427 | MAV_2312 | hypothetical protein | 99.74 | 390 | BCG_2196 | integral membrane protein | 75.76 | 427 | MAP1919 | hypothetical protein | 429 | 100 |
| MAP4_1910 | hypothetical protein | 294 | Rv2180c | Probable conserved integral membr | 76.39 | 295 | Mb2202c | hypothetical protein | 76.04 | 295 | MAV_2314 | hypothetical protein | 99.31 | 289 | BCG_2195c | integral membrane protein | 76.04 | 295 | MAP1918c | hypothetical protein | 268 | 100 |
| MAP4_1911 | hypothetical protein | 162 | Rv2179c | hypothetical protein | 82.61 | 168 | Mb2201c | hypothetical protein | 82.61 | 168 | MAV_2315 | hypothetical protein | 99.38 | 162 | BCG_2194c | hypothetical protein | 82.61 | 168 | MAP1917c | hypothetical protein | 162 | 100 |
| MAP4_1912 | 3-deoxy-D-arabino-heptulosonate 7-phosphate syntha | 462 | Rv2178c | 3-deoxy-D-arabino-heptulosonate 7- | 93.51 | 462 | Mb2200c | 3-deoxy-D-arabinoheptuloso | 93.29 | 462 | MAV_2317 | 3-deoxy-7-phosphoheptulonate syn | 100 | 462 | BCG_2193c | 3-deoxy-D-arabinoheptulosona | 93.29 | 462 | MAP1916c | AroG | 462 | 100 |
| MAP4_1913 | hypothetical protein | 481 | Rv3254 | hypothetical protein | 34.75 | 462 | Mb3282 | hypothetical protein | 34.75 | 462 | MAV_2316 | hypothetical protein | 98.13 | 481 | BCG_3283 | hypothetical protein | 34.75 | 462 | MAP1915 | hypothetical protein | 481 | 100 |
| MAP4_1914 | transmembrane serinethreonine-protein kinase LpknL | 396 | Rv2176 | Probable transmembrane serine/thr | 73.05 | 399 | Mb2198 | Ser/Thr protein kinase | 73.05 | 399 | MAV_2318 | serine/threonine protein kinase | 98.48 | 428 | BCG_2191 | transmembrane serine/threoni | 73.05 | 399 | MAP1914 | hypothetical protein | 396 | 100 |
| MAP4_1915 | regulatory protein, probable DNA-binding protein | 154 | Rv2175c | Conserved regulatory protein | 87.41 | 146 | Mb2197c | regulatory protein | 86.71 | 146 | MAV_2320 | hypothetical protein | 99.2 | 125 | BCG_2190c | regulatory protein | 86.71 | 146 | MAP1913c | hypothetical protein | 154 | 100 |
| MAP4_1916 | hypothetical protein | 505 | Rv2174 | Alpha(1->6)mannosyltransferase Po | 80.48 | 516 | Mb2196 | hypothetical protein | 80.68 | 516 | MAV_2319 | integral membrane protein | 99.8 | 505 | BCG_2189 | hypothetical protein | 80.4 | 567 | MAP1912 | hypothetical protein | 505 | 100 |
| MAP4_1917 | Geranylgeranyl pyrophosphate synthetase | 348 | Rv2173 | Probable geranylgeranyl pyrophosph | 76.99 | 352 | Mb2195 | geranylgeranyl pyrophosphat | 76.99 | 352 | MAV_2321 | polyprenyl synthetase | 99.71 | 349 | BCG_2188 | geranylgeranyl pyrophosphate | 76.99 | 352 | MAP1911 | IdsA2_1 | 348 | 100 |
| MAP4_1918 | hypothetical protein | 302 | Rv2172c | hypothetical protein | 81.63 | 301 | Mb2194c | hypothetical protein | 81.63 | 301 | MAV_2322 | hypothetical protein | 99.66 | 297 | BCG_2187c | hypothetical protein | 81.63 | 301 | MAP1910c | hypothetical protein | 302 | 100 |
| MAP4_1919 | lipoprotein lppM | 243 | Rv2171 | Probable conserved lipoprotein LppI | 84 | 227 | Mb2193 | lipoprotein LppM | 84 | 227 | MAV_2323 | LppM protein | 100 | 226 | BCG_2186 | lipoprotein lppM | 84 | 227 | MAP1909 | hypothetical protein | 243 | 100 |
| MAP4_1920 | hypothetical protein | 200 | Rv2170 | GCN5-related N-acetyltransferase | 80.1 | 206 | Mb2192 | hypothetical protein | 80.1 | 206 | MAV_2324 | acetyltransferase, gnat family prote | 99 | 200 | BCG_2185 | hypothetical protein | 80.1 | 206 | MAP1908 | hypothetical protein | 200 | 100 |
| MAP4_1921 | hypothetical protein | 133 | Rv2169c | Probable conserved transmembrane | 83.58 | 134 | Mb2191c | transmembrane protein | 83.58 | 134 | MAV_2325 | hypothetical protein | 98.5 | 133 | BCG_2184c | hypothetical protein | 83.58 | 134 | MAP1907c | hypothetical protein | 133 | 100 |
| MAP4_1922 | putative cell division protein MraZ | 143 | Rv2166c | hypothetical protein | 94.41 | 143 | Mb2190c | cell division protein MraZ | 94.41 | 143 | MAV_2327 | cell division protein MraZ | 100 | 143 | BCG_2183c | cell division protein MraZ | 94.41 | 143 | MAP1906c | cell division protein MraZ | 143 | 100 |
| MAP4_1923 | S-adenosyl-methyltransferase MraW | 335 | Rv2165c | hypothetical protein | 81.38 | 396 | Mb2189c | S-adenosyl-methyltransferase | 81.38 | 344 | MAV_2328 | S-adenosyl-methyltransferase Mra\ | 99.1 | 335 | BCG_2182c | S-adenosyl-methyltransferase | 81.38 | 396 | MAP1905c | S-adenosyl-methyltransferase MraW | 335 | 100 |
| MAP4_1924 | conserved proline rich membrane protein | 424 | Rv2164c | Probable conserved proline rich mer | 71.81 | 384 | Mb2188c | hypothetical protein | 71.43 | 384 | MAV_2329 | hypothetical protein | 97.17 | 424 | BCG_2181c | proline rich membrane protein | 71.81 | 384 | MAP1904c | hypothetical protein | 425 | 99.76 |
| MAP4_1925 | penicillin-binding membrane protein pbpB | 663 | Rv2163c | Probable penicillin-binding membra | 80.12 | 679 | Mb2187c | penicillin-binding membrane | 80.12 | 679 | MAV_2330 | penicillin binding protein transpept | 99.37 | 639 | BCG_2180c | penicillin-binding membrane p | 80.12 | 679 | MAP1903c | PbpB | 663 | 100 |
| MAP4_1926 | UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diamin | 520 | Rv2158c | Probable UDP-N-acetylmuramoylala | 79 | 535 | Mb2182c | UDP-N-acetylmuramoylalanyl | 79 | 535 | MAV_2331 | UDP-N-acetylmuramoylalanyl-D-glu | 99.42 | 520 | BCG_2175c | UDP-N-acetylmuramoylalanyl-I | 79 | 535 | MAP1902c | UDP-N-acetylmuramoylalanyl-D-glutam | 520 | 100 |
| MAP4_1927 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diamino | 519 | Rv2157c | Probable UDP-N-acetylmuramoylala | 80.73 | 510 | Mb2181c | UDP-N-acetylmuramoylalanyl | 80.73 | 510 | MAV_2332 | UDP-N-acetylmuramoyl-tripeptide- | 96.44 | 533 | BCG_2174c | UDP-N-acetylmuramoylalanyl-I | 80.73 | 510 | MAP1901c | hypothetical protein | 519 | 100 |
| MAP4_1928 | Phospho-N-acetylmuramoyl-pentapeptide- transferase | 359 | Rv2156c | Probable phospho-N-acetylmuramo | 90.25 | 359 | Mb2180c | phospho-N-acetylmuramoyl-p | 90.25 | 359 | MAV_2333 | phospho-N-acetylmuramoyl-penta | 99.44 | 359 | BCG_2173c | phospho-N-acetylmuramoyl-pe | 90.25 | 359 | MAP1900c | phospho-N-acetylmuramoyl-pentapept | 359 | 100 |
| MAP4_1929 | UDP-N-acetylmuramoylalanine--D-glutamate ligase | 489 | Rv2155c | Probable UDP-N-acetylmuramoylala | 78.97 | 486 | Mb2179c | UDP-N-acetylmuramoyl-L-ala | 79.18 | 486 | MAV_2334 | UDP-N-acetylmuramoyl-L-alanyl-D- | 98.98 | 489 | BCG_2172c | UDP-N-acetylmuramoyl-L-alany | 79.18 | 486 | MAP1899c | UDP-N-acetylmuramoyl-L-alanyl-D-gluta | 489 | 100 |
| MAP4_1930 | Cell division protein FtsW | 606 | Rv2154c | FtsW-like protein FtsW | 70.71 | 524 | Mb2178c | FtsW-like protein FtsW | 70.71 | 524 | MAV_2335 | cell division protein FtsW | 96.89 | 610 | BCG_2171c | FtsW-like protein FtsW | 70.71 | 524 | MAP1898c | hypothetical protein | 606 | 100 |
| MAP4_1931 | UDP-N-acetylglucosamine-N-acetylmuramyl- (pentape | 408 | Rv2153c | Probable UPD-N-acetylglucosamine- | 78.5 | 410 | Mb2177c | undecaprenyldiphospho-mur | 78.25 | 410 | MAV_2336 | undecaprenyldiphospho-muramoyl | 98.53 | 408 | BCG_2170c | UDPdiphospho-muramoylpent | 78.25 | 410 | MAP1897c | UDPdiphospho-muramoylpentapeptide | 408 | 100 |
| MAP4_1932 | UDP-N-acetylmuramate--alanine ligase | 496 | Rv2152c | Probable UDP-N-acetylmuramate-al | 83.67 | 494 | Mb2176c | UDP-N-acetylmuramate--L-ala | 83.67 | 494 | MAV_2337 | UDP-N-acetylmuramate--L-alanine | 98.99 | 496 | BCG_2169c | UDP-N-acetylmuramate--L-alar | 83.67 | 494 | MAP1896c | UDP-N-acetylmuramate--L-alanine ligas | 496 | 100 |
| MAP4_1933 | Cell division protein FtsQ | 314 | Rv2151c | Possible cell division protein FtsQ | 76.18 | 314 | Mb2175c | cell division protein FtsQ | 76.18 | 314 | MAV_2338 | cell division protein FtsQ-like prote | 99.36 | 314 | BCG_2168c | cell division protein ftsQ | 76.18 | 314 | MAP1927c | hypothetical protein | 270 | 30.16 |
| MAP4_1934 | Cell division protein FtsZ | 386 | Rv2150c | Cell division protein FtsZ | 95.34 | 379 | Mb2174c | cell division protein FtsZ | 95.34 | 379 | MAV_2340 | cell division protein FtsZ | 100 | 386 | BCG_2167c | cell division protein FtsZ | 95.34 | 379 | MAP1894c | cell division protein FtsZ | 386 | 100 |
| MAP4_1935 | multicopper oxidase family protein | 251 | Rv2149c | Conserved protein YfiH | 83.68 | 250 | Mb2173c | hypothetical protein | 83.68 | 250 | MAV_2341 | hypothetical protein | 98.3 | 235 | BCG_2166c | hypothetical protein | 83.68 | 250 | MAP1893c | YfiH | 251 | 99.6 |
| MAP4_1936 | hypothetical protein | 261 | Rv2148c | hypothetical protein | 72.29 | 258 | Mb2172c | hypothetical protein | 72.29 | 258 | MAV_2342 | hypothetical protein | 99.62 | 261 | BCG_2165c | hypothetical protein | 72.29 | 258 | MAP1892c | hypothetical protein | 264 | 100 |
| MAP4_1937 | hypothetical protein | 214 | Rv2147c | hypothetical protein | 86.49 | 241 | Mb2171c | hypothetical protein | 86.49 | 241 | MAV_2343 | hypothetical protein | 99.5 | 199 | BCG_2164c | hypothetical protein | 86.49 | 241 | MAP1891c | hypothetical protein | 214 | 100 |
| MAP4_1938 | hypothetical protein | 96 | Rv2146c | Possible conserved transmembrane | 93.75 | 96 | Mb2170c | transmembrane protein | 93.75 | 96 | MAV_2344 | transmembrane protein | 97.92 | 115 | BCG_2163c | hypothetical protein | 93.75 | 96 | MAP1890c | hypothetical protein | 96 | 100 |
| MAP4_1939 | hypothetical protein Wag31 | 260 | Rv2145c | Diviva family protein Wag31 | 88.55 | 260 | Mb2169c | hypothetical protein | 88.55 | 260 | MAV_2345 | Wag31 protein | 99.6 | 250 | BCG_2162c | hypothetical protein | 88.55 | 260 | MAP1889c | Wag31 | 260 | 100 |
| MAP4_1940 | putative transmembrane protein | 130 | Rv2144c | Probable transmembrane protein | 69.23 | 118 | Mb2168c | transmembrane protein | 69.23 | 118 | MAV_2346 | hypothetical protein | 93.23 | 131 | BCG_2161c | hypothetical protein | 69.23 | 118 | MAP1888c | hypothetical protein | 131 | 100 |
| MAP4_1941 | hypothetical protein | 238 | Rv2143 | hypothetical protein | 76.42 | 352 | Mb2167 | hypothetical protein | 76.42 | 352 | MAV_2347 | phosphoribosyltransferase | 99.54 | 217 | BCG_2160 | hypothetical protein | 76.42 | 352 | MAP1887 | hypothetical protein | 238 | 100 |
| MAP4_1942 | Putative peptidase | 451 | Rv2141c | hypothetical protein | 84.04 | 448 | Mb2165c | hypothetical protein | 84.04 | 448 | MAV_2350 | hypothetical protein | 100 | 451 | BCG_2158c | hypothetical protein | 84.04 | 448 | MAP1886c | hypothetical protein | 451 | 100 |
| MAP4_1943 | Phospholipid-binding protein | 176 | Rv2140c | Conserved protein TB18.6 | 82.95 | 176 | Mb2164c | hypothetical protein | 82.95 | 176 | MAV_2351 | hypothetical protein | 100 | 176 | BCG_2157c | hypothetical protein | 82.95 | 176 | MAP1885c | hypothetical protein | 176 | 100 |
| MAP4_1944 | REP13E12 repeat protein | 468 | Rv1128c | hypothetical protein | 69.96 | 451 | Mb1159c | hypothetical protein | 69.96 | 451 | MAV_2352 | hypothetical protein | 97.98 | 468 | BCG_1189c | hypothetical protein | 69.96 | 451 | MAP1884c | hypothetical protein | 468 | 100 |
| MAP4_1945 | dihydroorotate dehydrogenase pyrD | 370 | Rv2139 | Probable dihydroorotate dehydroge | 81.36 | 357 | Mb2163 | dihydroorotate dehydrogena | 81.36 | 357 | MAV_2353 | dihydroorotate dehydrogenase 2 | 98.02 | 353 | BCG_2156 | dihydroorotate dehydrogenase | 81.07 | 357 | MAP1883 | dihydroorotate dehydrogenase 2 | 370 | 100 |
| MAP4_1946 | hypothetical protein | 89 | Rv1719 | Probable transcriptional regulatory | 40.62 | 259 | Mb1748 | transcriptional regulator | 40.62 | 259 | MAV_2354 | hypothetical protein | 100 | 89 | BCG_1758 | transcriptional regulatory prot | 40.62 | 259 | MAP1882 | hypothetical protein | 89 | 100 |
| MAP4_1947 | conserved lipoprotein LppL | 375 | Rv2138 | Probable conserved lipoprotein LppI | 71.07 | 358 | Mb2162 | lipoprotein LppL | 70.25 | 358 | MAV_2355 | LppL protein | 97.05 | 339 | BCG_2155 | lipoprotein LppL | 71.07 | 358 | MAP1881 | hypothetical protein | 375 | 100 |
| MAP4_1948 | hypothetical protein | 100 | Rv2137c | hypothetical protein | 86.27 | 137 | Mb2161c | hypothetical protein | 86.27 | 137 | MAV_2356 | hypothetical protein | 100 | 100 | BCG_2154c | hypothetical protein | 86.27 | 137 | MAP3312 | RhlE | 505 | 27.91 |
| MAP4_1949 | putative phosphomutase, histidine phosphatase superf | 264 | Rv2135c | hypothetical protein | 70.08 | 236 | Mb2159c | hypothetical protein | 70.08 | 236 | MAV_2357 | hypothetical protein | 98.11 | 264 | BCG_2152c | hypothetical protein | 70.08 | 236 | MAP1880c | hypothetical protein | 264 | 100 |
| MAP4_1950 | hypothetical protein | 195 | Rv2134c | hypothetical protein | 92.75 | 195 | Mb2158c | hypothetical protein | 92.75 | 195 | MAV_2358 | hypothetical protein | 100 | 195 | BCG_2151c | hypothetical protein | 92.75 | 195 | MAP1879c | hypothetical protein | 195 | 100 |
| MAP4_1951 | hypothetical protein | 272 | Rv2133c | hypothetical protein | 78.68 | 262 | Mb2157c | hypothetical protein | 78.68 | 262 | MAV_2359 | hypothetical protein | 99.26 | 281 | BCG_2150c | hypothetical protein | 78.68 | 262 | MAP1878c | hypothetical protein | 272 | 100 |
| MAP4_1952 | monophosphatase CysQ | 263 | Rv2131c | Monophosphatase CysQ | 79.07 | 267 | Mb2155c | hypothetical protein | 79.07 | 267 | MAV_2360 | inositol monophosphatase | 99.24 | 264 | BCG_2148c | hypothetical protein | 79.07 | 267 | MAP1877c | CysQ_1 | 263 | 100 |
| MAP4_1953 | cysteinyl-tRNA synthetase | 415 | Rv2130c | Cysteine:1D-myo-inositol 2-amino-2 | 82.06 | 414 | Mb2154c | cysteinyl-tRNA synthetase | 82.06 | 414 | MAV_2361 | cysteinyl-tRNA synthetase | 98.96 | 384 | BCG_2147c | cysteinyl-tRNA synthetase | 82.06 | 414 | MAP1876c | cysteinyl-tRNA synthetase | 415 | 100 |
| MAP4_1954 | ATPase Transcriptional regulator, LuxR family | 901 | Rv1204c | hypothetical protein | 34.84 | 562 | Mb1236c | hypothetical protein | 34.84 | 562 | MAV_2362 | TPR repeat-containing protein | 98.54 | 891 | BCG_1264c | hypothetical protein | 34.84 | 562 | MAP1875c | hypothetical protein | 901 | 100 |
| MAP4_1955 | ATPase Transcriptional regulator, LuxR family | 854 | Rv1204c | hypothetical protein | 33.45 | 562 | Mb1236c | hypothetical protein | 33.45 | 562 | MAV_2364 | TPR repeat-containing protein | 97.91 | 863 | BCG_1264c | hypothetical protein | 33.45 | 562 | MAP1874c | hypothetical protein | 854 | 100 |
| MAP4_1956 | putative thiaminepyrophosphate-dependent enzyme | 575 | Rv3470c | Probable acetolactate synthase (larg | 26.42 | 552 | Mb3499c | acetolactate synthase large su | 26.25 | 552 | MAV_2365 | acetolactate synthase | 98.43 | 575 | BCG_3535c | acetolactate synthase large sul | 26.42 | 552 | MAP1873c | hypothetical protein | 575 | 100 |
| MAP4_1957 | MbtH-like protein | 77 | Rv2377c | Putative conserved protein MbtH | 78.26 | 71 | Mb2398c | protein MbtH | 79.71 | 71 | MAV_2366 | hypothetical protein | 100 | 77 | BCG_2391c | protein mbtH | 79.71 | 71 | MAP1872c | hypothetical protein | 77 | 100 |
| MAP4_1958 | peptide synthetase | 2151 | Rv0101 | Probable peptide synthetase Nrp (pe | 56.55 | 2512 | Mb0104 | peptide synthetase | 56.55 | 2512 | MAV_3056 | linear gramicidin synthetase subun | 60.22 | 10421 | BCG_0134 | peptide synthetase nrp | 56.48 | 2512 | MAP1870c | hypothetical protein | 1458 | 99.93 |
| MAP4_1959 | hypothetical protein | 201 | Rv3800c | Polyketide synthase Pks13 | 44.23 | 1733 | Mb3830c | polyketide synthase | 44.23 | 1733 | MAV_3056 | linear gramicidin synthetase subun | 43.15 | 10421 | BCG_3862c | polyketide synthase | 44.23 | 1733 | MAP1869c | hypothetical protein | 201 | 100 |
| MAP4_1960 | putative membrane efflux protein efpA | 494 | Rv2846c | Possible integral membrane efflux p | 68.17 | 530 | Mb2871c | integral membrane efflux pro | 68.17 | 530 | MAV_2368 | transporter, major facilitator family | 99.6 | 495 | BCG_2866c | integral membrane efflux prote | 68.17 | 530 | MAP1868c | EfpA_1 | 494 | 100 |
| MAP4_1961 | Polyketide synthase Pks5 | 2073 | Rv1527c | Probable polyketide synthase Pks5 | 69.49 | 2108 | Mb1554c | polyketide synthase | 69.54 | 2108 | MAV_2370 | mycocerosic acid synthase | 98.32 | 2098 | BCG_1579c | polyketide synthase pks5 | 69.54 | 2108 | MAP1867c | hypothetical protein | 2073 | 100 |
| MAP4_1962 | cytochrome P450 | 423 | Rv1256c | Probable cytochrome P450 130 Cyp1 | 33.02 | 405 | Mb1806 | cytochrome p450 144 CYP144 | 31.78 | 434 | MAV_2371 | cytochrome p450 | 98.8 | 416 | BCG_1810 | cytochrome p450 144 CYP144 | 31.78 | 434 | MAP1866c | hypothetical protein | 423 | 100 |
| MAP4_1963 | hypothetical protein | 121 | Rv1174c | Low molecular weight T-cell antigen | 52.34 | 110 | Mb1207c | hypothetical protein | 52.34 | 110 | MAV_2372 | hypothetical protein | 99.1 | 111 | BCG_1237c | hypothetical protein | 52.34 | 110 | MAP1865c | hypothetical protein | 121 | 100 |
| MAP4_1964 | siderophore-interacting protein | 255 | Rv1348 | Iron-regulated transporter IrtA | 25.32 | 859 | Mb1383 | drugs-transport transmembra | 25.32 | 859 | MAV_2373 | siderophore-interacting protein | 96.86 | 255 | BCG_1410 | drugs-transport transmembran | 25.32 | 859 | MAP1864c | hypothetical protein | 222 | 100 |
| MAP4_1967 | putative oxidoreductase | 299 | Rv2129c | Probable oxidoreductase | 74.39 | 293 | Mb2153c | short chain dehydrogenase | 74.39 | 293 | MAV_2376 | short chain dehydrogenase | 99.33 | 299 | BCG_2146c | short chain dehydrogenase | 74.39 | 293 | MAP1861c | short chain dehydrogenase | 299 | 100 |
| MAP4_1968 | hypothetical protein | 300 | Rv2125 | hypothetical protein | 85.02 | 292 | Mb2149 | hypothetical protein | 85.37 | 292 | MAV_2378 | hypothetical protein | 100 | 300 | BCG_2142 | hypothetical protein | 85.37 | 292 | MAP1860 | hypothetical protein | 300 | 100 |
| MAP4_1969 | 5-methyltetrahydrofolate--homocysteine methyltransf | 1262 | Rv2124c | 5-methyltetrahydrofolate--homocys | 34.08 | 1192 | Mb2148c | 5-methyltetrahydrofolate--hc | 34.16 | 1192 | MAV_2379 | B12-dependent methionine syntha | 99.52 | 1257 | BCG_2141c | 5-methyltetrahydrofolate--hon | 34.16 | 1192 | MAP1859c | B12-dependent methionine synthase | 1262 | 99.92 |
| MAP4_1970 | hypothetical protein | 255 | Rv1980c | Immunogenic protein Mpt64 (antige | 23.21 | 228 | Mb2002c | hypothetical protein | 23.21 | 228 | MAV_2381 | hypothetical protein | 99.22 | 255 | BCG_0545 | hypothetical protein | 27.27 | 358 | MAP1858 | hypothetical protein | 255 | 100 |
| MAP4_1971 | hypothetical protein | 227 | Rv2390c | hypothetical protein | 50.31 | 185 | Mb2411c | hypothetical protein | 53.62 | 185 | MAV_0098 | hypothetical protein | 51.2 | 229 | BCG_2404c | hypothetical protein | 50.31 | 185 | MAP1857 | hypothetical protein | 227 | 100 |
| MAP4_1972 | MCE-family protein | 419 | Rv0174 | Mce-family protein Mce1F | 27.62 | 515 | Mb0180 | MCE-family protein MCE1F | 27.62 | 515 | MAV_2383 | mce related protein | 99.76 | 419 | BCG_0211 | MCE-family protein mce1F | 27.62 | 515 | MAP1856 | hypothetical protein | 419 | 100 |
| MAP4_1973 | putative MCE-family lipoprotein | 409 | Rv1970 | Possible Mce-family lipoprotein LprI | 28.4 | 377 | Mb0609 | MCE-family lipoprotein LprL | 33.13 | 188 | MAV_2384 | mce related protein | 96.73 | 405 | BCG_0639 | mce family lipoprotein LprL | 29.52 | 402 | MAP1855 | hypothetical protein | 409 | 100 |
| MAP4_1974 | MCE-family protein | 371 | Rv3496c | Mce-family protein Mce4D | 34.29 | 451 | Mb3526c | MCE-family protein MCE4D | 34.29 | 451 | MAV_2385 | virulence factor Mce | 99.19 | 371 | BCG_3560c | Mce-family protein mce4D | 34.29 | 451 | MAP1854 | hypothetical protein | 371 | 100 |
| MAP4_1975 | MCE-family protein | 359 | Rv3497c | Mce-family protein Mce4C | 25.78 | 357 | Mb3527c | MCE-family protein MCE4C | 25.78 | 357 | MAV_2386 | virulence factor Mce | 99.42 | 346 | BCG_3561c | Mce-family protein mce4C | 25.78 | 357 | MAP1853 | hypothetical protein | 359 | 100 |
| MAP4_1976 | MCE-family protein | 351 | Rv1967 | Mce-family protein Mce3B | 33.44 | 342 | Mb0605 | MCE-family protein MCE2B | 32.52 | 343 | MAV_2387 | virulence factor Mce | 99.72 | 351 | BCG_0635 | mce-family protein mce2B | 32.52 | 343 | MAP1852 | hypothetical protein | 351 | 100 |
| MAP4_1977 | mce related protein | 530 | Rv3494c | Mce-family protein Mce4F | 26.92 | 564 | Mb3524c | MCE-family protein MCE4F | 26.92 | 564 | MAV_2388 | mce related protein | 99.62 | 530 | BCG_3558c | Mce-family protein mce4F | 26.92 | 564 | MAP1851 | hypothetical protein | 530 | 100 |
| MAP4_1978 | hypothetical protein | 287 | Rv1965 | Conserved hypothetical integral mer | 41.6 | 271 | Mb3530c | hypothetical protein | 36.46 | 280 | MAV_2389 | ABC-transporter integral membran | 100 | 287 | BCG_3564c | integral membrane protein Yrb | 36.46 | 280 | MAP1850 | hypothetical protein | 287 | 100 |
| MAP4_1979 | hypothetical protein | 286 | Rv3501c | Conserved integral membrane prote | 38.29 | 254 | Mb3531c | hypothetical protein | 38.29 | 254 | MAV_2390 | hypothetical protein | 99.65 | 286 | BCG_3565c | integral membrane protein Yrb | 38.29 | 254 | MAP1849 | hypothetical protein | 286 | 100 |
| MAP4_1980 | Transcriptional regulator, TetR family | 222 | Rv2506 | Probable transcriptional regulatory | 40.54 | 215 | Mb2534 | TetR family transcriptional re | 40.54 | 215 | MAV_2391 | TetR family transcriptional regulato | 98.57 | 210 | BCG_2526 | TetR family transcriptional regu | 40.54 | 215 | MAP1848c | hypothetical protein | 222 | 100 |
| MAP4_1981 | Phosphoribosyl-ATP pyrophosphatase | 93 | Rv2122c | Phosphoribosyl-AMP pyrophosphata | 89.25 | 93 | Mb2146c | phosphoribosyl-ATP pyrophos | 89.25 | 93 | MAV_2392 | phosphoribosyl-ATP pyrophosphata | 98.92 | 93 | BCG_2139c | phosphoribosyl-ATP pyrophosp | 89.25 | 93 | MAP1847c | phosphoribosyl-ATP pyrophosphatase | 93 | 100 |
| MAP4_1982 | ATP phosphoribosyltransferase | 284 | Rv2121c | ATP phosphoribosyltransferase HisG | 89.82 | 284 | Mb2145c | ATP phosphoribosyltransfera | 89.82 | 284 | MAV_2393 | ATP phosphoribosyltransferase | 100 | 284 | BCG_2138c | ATP phosphoribosyltransferase | 89.82 | 284 | MAP1846c | ATP phosphoribosyltransferase | 284 | 100 |
| MAP4_1983 | hypothetical protein | 184 | Rv2120c | Probable conserved integral membr | 69.48 | 160 | Mb2144c | hypothetical protein | 69.48 | 160 | MAV_2394 | hypothetical protein | 98.24 | 170 | BCG_2137c | integral membrane protein | 69.48 | 160 | MAP1845c | hypothetical protein | 184 | 100 |
| MAP4_1984 | putative pyridine nucleotide-disulfide oxido reductase | 456 | Rv0462 | Dihydrolipoamide dehydrogenase Lp | 30 | 464 | Mb0471 | dihydrolipoamide dehydroge | 30 | 464 | MAV_2396 | mercuric reductase | 98.9 | 456 | BCG_0502 | dihydrolipoamide dehydrogena | 30 | 464 | MAP1844c | mercuric reductase | 456 | 100 |
| MAP4_1985 | RecB family exonuclease | 301 | Rv2119 | hypothetical protein | 81.99 | 278 | Mb2143 | hypothetical protein | 81.99 | 278 | MAV_2395 | RecB family protein exonuclease | 98.67 | 301 | BCG_2136 | hypothetical protein | 81.99 | 278 | MAP1843 | hypothetical protein | 301 | 100 |
| MAP4_1986 | RNA methyltransferase | 281 | Rv2118c | RNA methyltransferase | 84.7 | 280 | Mb2142c | RNA methyltransferase | 84.7 | 280 | MAV_2397 | PimT protein | 98.93 | 281 | BCG_2135c | RNA methyltransferase | 84.7 | 280 | MAP1842c | hypothetical protein | 281 | 100 |
| MAP4_1987 | hypothetical protein | 99 | Rv2117 | hypothetical protein | 90.72 | 97 | Mb2141 | hypothetical protein | 90.72 | 97 | MAV_2398 | hypothetical protein | 100 | 99 | BCG_2134 | hypothetical protein | 90.72 | 97 | MAP1841 | hypothetical protein | 99 | 100 |
| MAP4_1988 | putative conserved lipoprotein lppK | 204 | Rv2116 | Conserved lipoprotein LppK | 61.99 | 189 | Mb2140 | lipoprotein LppK | 61.99 | 189 | MAV_2399 | LppK protein | 98.98 | 196 | BCG_2133 | lipoprotein lppK | 61.99 | 189 | MAP1840 | hypothetical protein | 204 | 100 |
| MAP4_1989 | ATPase | 609 | Rv2115c | Mycobacterial proteasome ATPase M | 93.92 | 609 | Mb2139c | ATPase | 93.92 | 609 | MAV_2400 | ATPase AAA | 100 | 646 | BCG_2132c | ATPase | 93.92 | 609 | MAP3928c | hypothetical protein | 722 | 36.76 |
| MAP4_1990 | hypothetical protein | 214 | Rv2114 | hypothetical protein | 77.57 | 207 | Mb2138 | hypothetical protein | 77.57 | 207 | MAV_2401 | hypothetical protein | 99.07 | 214 | BCG_2131 | hypothetical protein | 77.57 | 207 | MAP1838 | hypothetical protein | 214 | 100 |
| MAP4_1991 | putative Pup ligase | 502 | Rv2112c | Deamidase of pup Dop | 96.41 | 554 | Mb2136c | hypothetical protein | 96.41 | 535 | MAV_2406 | proteasome component | 39.18 | 452 | BCG_2129c | hypothetical protein | 96.41 | 535 | MAP1837c | hypothetical protein | 502 | 100 |
| MAP4_1992 | conserved hypothetical protein, Pup-like protein family | 64 | Rv2111c | Prokaryotic ubiquitin-like protein Pu | 90.62 | 64 | Mb2135c | hypothetical protein | 90.62 | 64 | MAV_2403 | hypothetical protein | 100 | 64 | BCG_2128c | hypothetical protein | 90.62 | 64 | MAP1836c | hypothetical protein | 64 | 100 |
| MAP4_1993 | proteasome beta subunit prcB | 303 | Rv2110c | Proteasome beta subunit PrcB; asse | 81.52 | 291 | Mb2134c | proteasome subunit beta | 81.52 | 291 | MAV_2404 | PcrB protein | 99.67 | 303 | BCG_2127c | proteasome subunit beta PrcB | 81.52 | 291 | MAP1835c | PrcB | 303 | 100 |
| MAP4_1994 | proteasome alpha subunit prcA | 256 | Rv2109c | Proteasome alpha subunit PrcA; ass | 86.48 | 248 | Mb2133c | proteasome subunit alpha | 86.48 | 248 | MAV_2405 | peptidase, T1 family protein | 100 | 256 | BCG_2126c | proteasome subunit alpha PrcA | 86.48 | 248 | MAP1834c | PrcA | 256 | 100 |
| MAP4_1995 | proteasome accessory factor A PafA | 452 | Rv2097c | Proteasome accessory factor a PafA | 96.9 | 452 | Mb2124c | hypothetical protein | 96.9 | 452 | MAV_2406 | proteasome component | 100 | 452 | BCG_2117c | hypothetical protein | 96.9 | 452 | MAP1833c | hypothetical protein | 452 | 100 |
| MAP4_1996 | proteasome accessory factor B PafB | 351 | Rv2096c | Proteasome accessory factor B PafB | 85.29 | 332 | Mb2123c | hypothetical protein | 85.29 | 332 | MAV_2407 | hypothetical protein | 99.72 | 351 | BCG_2116c | hypothetical protein | 85.29 | 332 | MAP1832c | hypothetical protein | 351 | 100 |
| MAP4_1997 | proteasome accessory factor C PafC | 322 | Rv2095c | Proteasome accessory factor C PafC | 81.03 | 316 | Mb2122c | hypothetical protein | 81.35 | 316 | MAV_2408 | hypothetical protein | 99.38 | 322 | BCG_2115c | hypothetical protein | 81.03 | 316 | MAP1831c | hypothetical protein | 322 | 100 |
| MAP4_1998 | SEC-independent protein translocase membrane-boun | 93 | Rv2094c | Sec-independent protein translocase | 72.83 | 83 | Mb2121c | twin-arginine translocation pr | 72.83 | 83 | MAV_2409 | twin arginine translocase protein A | 100 | 93 | BCG_2114c | twin arginine translocase A | 72.83 | 83 | MAP1830c | twin arginine translocase protein A | 93 | 100 |
| MAP4_1999 | Sec-independent protein translocase transmembrane p | 318 | Rv2093c | Sec-independent protein translocase | 84.84 | 308 | Mb2120c | Sec-independent protein tran | 84.84 | 308 | MAV_2410 | twin arginine-targeting protein tran | 99.69 | 318 | BCG_2113c | Sec-independent protein transl | 84.84 | 308 | MAP1829c | hypothetical protein | 318 | 100 |
| MAP4_2002 | hypothetical protein | 263 | Rv2091c | Probable membrane protein | 65.41 | 244 | Mb2118c | hypothetical protein | 65.41 | 244 | MAV_2412 | hypothetical protein | 99.11 | 225 | BCG_2111c | hypothetical protein | 65.41 | 244 | MAP1826c | hypothetical protein | 263 | 100 |
| MAP4_2003 | putative 5'-3' exonuclease | 318 | Rv2090 | Probable 5'-3' exonuclease | 82.39 | 393 | Mb2117 | 5'-3' exonuclease | 82.08 | 374 | MAV_2413 | 5'-3' exonuclease | 98.4 | 313 | BCG_2110 | 5'-3' exonuclease | 82.39 | 355 | MAP1825 | hypothetical protein | 318 | 100 |
| MAP4_2004 | Transposase, IS30 family | 424 | Rv3191c | Probable transposase | 45.17 | 344 | Mb3213c | transposase | 45.17 | 344 | MAV_3355 | PPE family protein | 31.58 | 454 | BCG_3213c | transposase | 45.17 | 344 | MAP1824c | hypothetical protein | 424 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2005 | dipeptidase | 375 | Rv2089c | Dipeptidase PepE | 83.69 | 375 | Mb2116c | dipeptidase PepE | 83.69 | 375 | MAV_2414 | proline dipeptidase | 97.87 | 375 | BCG_2109c | dipeptidase PepE | 83.69 | 375 | MAP1823c | hypothetical protein | 375 | 100 |
| MAP4_2006 | hypothetical protein | 1020 | Rv3903c | Hypothetical alanine and proline ric | 47.53 | 846 | Mb3933c | hypothetical protein | 47.53 | 846 | MAV_2415 | hypothetical protein | 77.34 | 996 | BCG_3960c | hypothetical protein | 47.53 | 846 | MAP1822c | hypothetical protein | 1020 | 100 |
| MAP4_2007 | hypothetical protein | 178 | Rv3902c | Hypothetical protein | 38.86 | 176 | Mb3932c | hypothetical protein | 38.86 | 176 | MAV_2421 | hypothetical protein | 91.45 | 117 | BCG_3959c | hypothetical protein | 38.86 | 176 | MAP1821c | hypothetical protein | 178 | 100 |
| MAP4_2008 | hypothetical protein | 145 | Rv2074 | Possible pyridoxamine 5'-phosphate | 93.33 | 137 | Mb3015 | hypothetical protein | 21.85 | 163 | MAV_2422 | nitrilase/cyanide hydratase and apo | 100 | 136 | BCG_3012 | hypothetical protein | 21.85 | 163 | MAP1820 | hypothetical protein | 145 | 100 |
| MAP4_2011 | precorrin-6y methyltransferase cobL | 389 | Rv2072c | Precorrin-6Y C(5,15)-methyltransfer | 71.28 | 390 | Mb2098c | precorrin-6y methyltransfera | 71.33 | 294 | MAV_2424 | precorrin-6Y C5,15-methyltransfera | 95.37 | 389 | BCG_2091c | precorrin-6y methyltransferase | 71.33 | 294 | MAP1817c | CobL | 389 | 100 |
| MAP4_2012 | precorrin-4 C(11)-methyltransferase | 251 | Rv2071c | Precorrin-3 methylase CobM (preco | 83.27 | 251 | Mb2097c | precorrin-4 C(11)-methyltran | 83.67 | 251 | MAV_2425 | precorrin-4 C11-methyltransferase | 97.21 | 251 | BCG_2090c | precorrin-4 C11-methyltransfe | 83.67 | 251 | MAP1816c | hypothetical protein | 251 | 100 |
| MAP4_2013 | Cobalt-precorrin-6x reductase | 244 | Rv2070c | Precorrin-6X reductase CobK | 76.57 | 244 | Mb2096c | cobalt-precorrin-6x reductase | 75.45 | 231 | MAV_2427 | cobalt-precorrin-6x reductase | 97.95 | 244 | BCG_2089c | cobalt-precorrin-6x reductase | 75.45 | 231 | MAP1815c | cobalt-precorrin-6x reductase | 244 | 100 |
| MAP4_2014 | RNA polymerase sigma-70 factor, ECF subfamily | 459 | Rv2069 | RNA polymerase sigma factor, ECF s | 84.44 | 185 | Mb2095 | RNA polymerase sigma factor | 84.44 | 185 | MAV_2426 | RNA polymerase sigma factor SigC | 99 | 401 | BCG_2088 | RNA polymerase sigma factor S | 84.44 | 185 | MAP1814 | hypothetical protein | 459 | 100 |
| MAP4_2015 | PPE family protein | 550 | Rv0256c | PPE family protein PPE2 | 65.45 | 556 | Mb0262c | PPE family protein | 65.45 | 556 | MAV_2429 | PPE family protein | 98 | 550 | BCG_0294c | PPE family protein | 65.45 | 556 | MAP1813c | hypothetical protein | 550 | 100 |
| MAP4_2016 | bifunctional cobI-cobJ fusion protein | 496 | Rv2066 | Probable bifunctional protein, CobI- | 86.56 | 508 | Mb2092 | bifunctional S-adenosyl-L-me | 86.56 | 508 | MAV_2430 | cobalamin biosynthesis protein cob | 99.19 | 496 | BCG_2085 | bifunctional protein, CobI-CobJ | 86.56 | 508 | MAP1812 | CobI | 496 | 100 |
| MAP4_2017 | precorrin-8X methylmutase | 208 | Rv2065 | Precorrin-8X methylmutase CobH (a | 87.5 | 208 | Mb2091 | precorrin-8X methylmutase | 87.5 | 208 | MAV_2431 | precorrin-8X methylmutase | 98.27 | 173 | BCG_2084 | precorrin-8X methylmutase | 87.5 | 208 | MAP1811 | precorrin-8X methylmutase | 208 | 100 |
| MAP4_2018 | Cobalamin biosynthesis protein CobG | 366 | Rv2064 | Precorrin-3B synthase CobG | 74.32 | 363 | Mb2090 | cobalamin biosynthesis prote | 74.32 | 363 | MAV_1787 | sulfite reductase [ferredoxin] 2 | 23.19 | 569 | BCG_2083 | cobalamin biosynthesis protein | 74.32 | 363 | MAP1810 | CobG | 366 | 100 |
| MAP4_2019 | aliphatic sulfonates transmembrane ABC transporter p | 275 | Rv2835c | Probable Sn-glycerol-3-phosphate tr | 28.21 | 303 | Mb3782c | glycine betaine/carnitine/cho | 30.5 | 239 | MAV_2433 | aliphatic sulfonates ABC transporte | 99.64 | 275 | BCG_3815c | osmoprotectant (glycine betain | 30.5 | 239 | MAP1809c | hypothetical protein | 275 | 100 |
| MAP4_2020 | aliphatic sulfonates transmembrane ABC transporter p | 251 | Rv2397c | Sulfate-transport ATP-binding prote | 41.09 | 351 | Mb2419c | sulfate-transport ABC transpo | 41.09 | 351 | MAV_2434 | aliphatic sulfonates ABC transporte | 100 | 251 | BCG_2412c | sulfate-transport ATP-binding p | 41.09 | 351 | MAP1808c | hypothetical protein | 251 | 100 |
| MAP4_2021 | ABC transporter, substrate-binding protein,aliphatic su | 336 | Rv0411c | Probable glutamine-binding lipoprot | 38.04 | 328 | Mb0419c | glutamine-binding lipoprotein | 38.04 | 328 | MAV_2435 | sulfonate binding protein | 99.4 | 336 | BCG_0450c | glutamine-binding lipoprotein | 38.04 | 328 | MAP1807c | hypothetical protein | 336 | 100 |
| MAP4_2022 | hypothetical protein | 238 | Rv2284 | Probable esterase LipM | 37.84 | 431 | Mb2305 | esterase | 37.84 | 431 | MAV_2436 | hypothetical protein | 98.24 | 227 | BCG_2299 | esterase LipM | 37.84 | 431 | MAP1806c | hypothetical protein | 238 | 100 |
| MAP4_2023 | cobaltochelatase subunit CobN | 1191 | Rv2062c | Cobalamin biosynthesis protein Cob | 89.61 | 1194 | Mb2088c | cobaltochelatase subunit Cob | 89.53 | 1194 | MAV_2437 | cobaltochelatase subunit CobN | 98.99 | 1191 | BCG_2081c | cobaltochelatase subunit CobN | 89.45 | 1194 | MAP1805c | cobaltochelatase subunit CobN | 1191 | 100 |
| MAP4_2024 | hypothetical protein | 126 | Rv2061c | hypothetical protein | 79.84 | 134 | Mb2087c | hypothetical protein | 79.84 | 134 | MAV_2442 | pyridoxamine 5'-phosphate oxidase | 100 | 126 | BCG_2080c | hypothetical protein | 79.84 | 134 | MAP1804c | hypothetical protein | 126 | 100 |
| MAP4_2025 | Dienelactone hydrolase family protein | 233 | Rv2054 | hypothetical protein | 75.76 | 237 | Mb2080 | hypothetical protein | 75.76 | 237 | MAV_2443 | dienelactone hydrolase | 98.52 | 203 | BCG_2073 | hypothetical protein | 75.76 | 237 | MAP1803 | hypothetical protein | 233 | 100 |
| MAP4_2026 | putative transmembrane protein | 171 | Rv2053c | Probable transmembrane protein Fx | 52.94 | 175 | Mb2079c | FxsA protein | 52.94 | 175 | MAV_2444 | FxsA | 95.32 | 171 | BCG_2072c | FxsA protein | 52.94 | 175 | MAP1802c | FxsA | 171 | 100 |
| MAP4_2027 | Amidohydrolase family protein | 538 | Rv2052c | hypothetical protein | 78.11 | 534 | Mb2078c | hypothetical protein | 78.11 | 534 | MAV_2445 | amidohydrolase | 98.51 | 538 | BCG_2071c | hypothetical protein | 78.11 | 534 | MAP1801c | hypothetical protein | 538 | 100 |
| MAP4_2028 | Apolipoprotein N-acyltransferase | 627 | Rv2051c | Polyprenol-monophosphomannose | 69.19 | 874 | Mb2077c | polyprenol-monophosphoma | 69.19 | 874 | MAV_0791 | hypothetical protein | 28.57 | 565 | BCG_2070c | polyprenol-monophosphoman | 69.19 | 874 | MAP1800c | hypothetical protein | 627 | 100 |
| MAP4_2029 | putative glycosyl transferase | 267 | Rv2051c | Polyprenol-monophosphomannose | 86.26 | 874 | Mb2077c | polyprenol-monophosphoma | 86.26 | 874 | MAV_4605 | glycosyltransferase | 33.18 | 220 | BCG_2070c | polyprenol-monophosphoman | 86.26 | 874 | MAP1799c | hypothetical protein | 267 | 100 |
| MAP4_2030 | hypothetical protein | 111 | Rv2050 | hypothetical protein | 97.3 | 111 | Mb2076 | hypothetical protein | 97.3 | 111 | MAV_2447 | hypothetical protein | 98.98 | 98 | BCG_2069 | hypothetical protein | 97.3 | 111 | MAP1798 | hypothetical protein | 111 | 100 |
| MAP4_2031 | hypothetical protein | 116 | Rv2049c | hypothetical protein | 79.17 | 74 | Mb2075c | hypothetical protein | 79.17 | 74 | MAV_2448 | hypothetical protein | 100 | 95 | BCG_2068c | hypothetical protein | 79.17 | 74 | MAP1797c | hypothetical protein | 116 | 100 |
| MAP4_2032 | Polyketide synthase | 4170 | Rv2048c | Polyketide synthase Pks12 | 80.42 | 4151 | Mb2074c | polyketide synthase | 80.15 | 4151 | MAV_2450 | erythronolide synthase, modules 3 | 98.8 | 4171 | BCG_2067c | polyketide synthase | 80.23 | 4151 | MAP1796c | hypothetical protein | 4170 | 100 |
| MAP4_2033 | hypothetical protein | 868 | Rv2047c | hypothetical protein | 74.17 | 854 | Mb2073c | hypothetical protein | 74.17 | 854 | MAV_2451 | hypothetical protein | 98.85 | 868 | BCG_2066c | hypothetical protein | 74.17 | 854 | MAP1795c | hypothetical protein | 868 | 100 |
| MAP4_2034 | hypothetical protein | 144 | Rv3538 | Probable dehydrogenase Possible 2- | 29.79 | 286 | Mb3568 | dehydrogenase | 29.79 | 286 | MAV_2452 | hypothetical protein | 100 | 115 | BCG_3602 | dehydrogenase | 29.79 | 286 | MAP1794 | hypothetical protein | 144 | 100 |
| MAP4_2035 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_2036 | hypothetical protein | 238 | Rv0090 | Possible membrane protein | 29.27 | 256 | Mb0093 | hypothetical protein | 29.27 | 256 | MAV_2458 | hypothetical protein | 72.37 | 235 | BCG_0123 | hypothetical protein | 29.27 | 256 | MAP1792 | hypothetical protein | 180 | 100 |
| MAP4_2037 | hypothetical protein | 42 | Rv0996 | Probable conserved transmembrane | 34.21 | 358 | Mb1023 | transmembrane protein | 34.21 | 358 | MAV_2454 | hypothetical protein | 97.62 | 42 | BCG_1051 | hypothetical protein | 34.21 | 358 | MAP4173 | hypothetical protein | 313 | 50 |
| MAP4_2038 | nitric oxide reductase Q protein NorQ | 264 | Rv0370c | Possible oxidoreductase | 21.34 | 298 | Mb0377c | oxidoreductase | 21.34 | 298 | MAV_2455 | CbbQ/NirQ/NorQ/GpvN family pro | 99.24 | 264 | BCG_0408c | oxidoreductase | 21.34 | 298 | MAP1791 | NorQ | 264 | 100 |
| MAP4_2039 | nitric oxide reductase MorD | 512 | Rv0806c | Possible UDP-glucose-4-epimerase C | 29.55 | 532 | Mb0829c | UDP-glucose-4-epimerase Cp | 29.55 | 532 | MAV_2456 | MorD protein | 98.44 | 512 | BCG_0858c | udp-glucose-4-epimerase cpsY | 29.55 | 532 | MAP1790 | MorD | 512 | 100 |
| MAP4_2040 | hypothetical protein | 235 | Rv0481c | Hypothetical protein | 27.87 | 174 | Mb0491c | hypothetical protein | 27.87 | 174 | MAV_2458 | hypothetical protein | 99.15 | 235 | BCG_0522c | hypothetical protein | 27.87 | 174 | MAP1789 | hypothetical protein | 235 | 100 |
| MAP4_2041 | Transcriptional regulator, TetR family | 199 | Rv3574 | Transcriptional regulatory protein K | 35.38 | 199 | Mb3605 | transcriptional regulatory pro | 35.38 | 199 | MAV_2459 | TetR family transcriptional regulato | 99.49 | 197 | BCG_3639 | TetR family transcriptional regu | 35.38 | 199 | MAP1788 | hypothetical protein | 199 | 100 |
| MAP4_2044 | hypothetical protein | 360 | Rv0926c | hypothetical protein | 41.33 | 358 | Mb0949c | hypothetical protein | 41.33 | 358 | MAV_2461 | hypothetical protein | 99.44 | 360 | BCG_0978c | hypothetical protein | 41.33 | 358 | MAP1786c | hypothetical protein | 360 | 100 |
| MAP4_2045 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_2046 | hypothetical protein | 202 | Rv1048c | Hypothetical protein | 22.22 | 371 | Mb1077c | hypothetical protein | 22.22 | 371 | MAV_2462 | hypothetical protein | 97.52 | 202 | BCG_1106c | hypothetical protein | 20 | 371 | MAP1784c | hypothetical protein | 202 | 100 |
| MAP4_2047 | Transcriptional regulator, TetR family | 209 | Rv3055 | Possible transcriptional regulatory p | 48.39 | 204 | Mb3081 | TetR family transcriptional re | 48.39 | 204 | MAV_2463 | TetR family transcriptional regulato | 99.52 | 209 | BCG_3080 | TetR family transcriptional regu | 48.39 | 204 | MAP1783 | hypothetical protein | 209 | 100 |
| MAP4_2048 | putative cytochrome P450 hydroxylase | 407 | Rv3121 | Probable cytochrome P450 141 Cyp1 | 28.64 | 400 | Mb0801 | cytochrome P450 126 | 31.65 | 414 | MAV_2464 | cytochrome P450 family protein | 98.53 | 407 | BCG_2283 | cytochrome P450 124 CYP124 | 30.98 | 428 | MAP1782c | hypothetical protein | 412 | 100 |
| MAP4_2049 | putative lipoprotein lppI | 226 | Rv2046 | Probable lipoprotein LppI | 61.06 | 218 | Mb2072 | lipoprotein LppI | 61.06 | 218 | MAV_2465 | LppI protein | 99.1 | 221 | BCG_2065 | lipoprotein lppI | 61.06 | 218 | MAP1781 | hypothetical protein | 226 | 100 |
| MAP4_2050 | carboxylesterase LipT | 505 | Rv2045c | Carboxylesterase LipT | 83.93 | 511 | Mb2071c | carboxylesterase LipT | 83.93 | 511 | MAV_2466 | LppT protein | 99.41 | 505 | BCG_2064c | carboxylesterase LipT | 83.93 | 511 | MAP1780c | hypothetical protein | 519 | 100 |
| MAP4_2051 | hypothetical protein | 665 | Rv3761c | Possible acyl-CoA dehydrogenase Fa | 33.33 | 351 | Mb3787c | acyl-CoA dehydrogenase | 33.33 | 351 | MAV_2467 | phosphotransferase enzyme family | 99.4 | 665 | BCG_3820c | acyl-CoA dehydrogenase fadE3 | 33.33 | 351 | MAP1779c | hypothetical protein | 665 | 100 |
| MAP4_2052 | putative shikimate kinase | 164 | Rv2457c | Probable ATP-dependent CLP protea | 39.39 | 426 | Mb2484c | ATP-dependent protease ATP | 39.39 | 426 | MAV_2468 | shikimate kinase | 100 | 164 | BCG_2477c | ATP-dependent protease ATP- | 39.39 | 426 | MAP1778c | hypothetical protein | 164 | 100 |
| MAP4_2053 | hypothetical protein | 129 | Rv0367c | Hypothetical protein | 82.54 | 129 | Mb0374c | hypothetical protein | 82.54 | 129 | MAV_2469 | hypothetical protein | 98.45 | 140 | BCG_0405c | hypothetical protein | 82.54 | 129 | MAP1777c | hypothetical protein | 129 | 100 |
| MAP4_2054 | hypothetical protein | 192 | Rv0366c | hypothetical protein | 76.84 | 197 | Mb0373c | hypothetical protein | 76.84 | 197 | MAV_2470 | hypothetical protein | 100 | 192 | BCG_0404c | hypothetical protein | 76.84 | 197 | MAP1776c | hypothetical protein | 192 | 100 |
| MAP4_2055 | hypothetical protein | 355 | Rv2145c | Diviva family protein Wag31 | 35.59 | 260 | Mb2169c | hypothetical protein | 35.59 | 260 | MAV_2471 | DoxX subfamily protein, putative | 99.42 | 343 | BCG_2162c | hypothetical protein | 35.59 | 260 | MAP1775 | hypothetical protein | 355 | 100 |
| MAP4_2056 | pyrazinamidasenicotinamidas pncA | 186 | Rv2043c | Pyrazinamidase/nicotinamidase Pnc | 72.68 | 186 | Mb2069c | pyrazinamidase | 72.13 | 186 | MAV_2472 | isochorismatase | 97.85 | 186 | BCG_2062c | pyrazinamidase/nicotinamidas | 72.13 | 186 | MAP1774c | hypothetical protein | 187 | 99.46 |
| MAP4_2057 | hypothetical protein | 266 | Rv2042c | hypothetical protein | 67.55 | 265 | Mb2068c | hypothetical protein | 67.55 | 265 | MAV_2473 | steroid delta-isomerase | 99.25 | 266 | BCG_2061c | hypothetical protein | 67.55 | 265 | MAP1773c | hypothetical protein | 267 | 100 |
| MAP4_2058 | hypothetical protein | 138 | Rv1489 | hypothetical protein | 35.06 | 118 | Mb1525 | hypothetical protein | 35.06 | 118 | MAV_2474 | integral membrane protein | 99.14 | 116 | BCG_1551 | hypothetical protein | 35.06 | 118 | MAP1772 | hypothetical protein | 138 | 100 |
| MAP4_2059 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_2060 | putative sigma factor | 311 | Rv3328c | Probable alternative RNA polymeras | 40.68 | 312 | Mb3361c | RNA polymerase sigma factor | 41.03 | 312 | MAV_2475 | RNA polymerase sigma factor | 97.75 | 310 | BCG_3398c | RNA polymerase sigma factor S | 41.03 | 312 | MAP1770c | hypothetical protein | 311 | 100 |
| MAP4_2061 | putative sugar-binding lipoprotein | 442 | Rv2041c | Probable sugar-binding lipoprotein | 74.89 | 439 | Mb2067c | sugar-binding lipoprotein | 74.66 | 439 | MAV_2476 | sugar ABC transporter substrate-bi | 98.64 | 442 | BCG_2060c | sugar-binding lipoprotein | 74.89 | 439 | MAP1769c | hypothetical protein | 442 | 100 |
| MAP4_2062 | sugar-transport membrane protein ABC transporter | 314 | Rv2040c | Probable sugar-transport integral m | 81.47 | 300 | Mb2066c | sugar-transport integral mem | 81.47 | 300 | MAV_2477 | sugar ABC transporter permease | 99.68 | 314 | BCG_2059c | sugar-transport integral memb | 81.47 | 300 | MAP1768c | hypothetical protein | 314 | 100 |
| MAP4_2063 | sugar-transport membrane protein ABC transporter | 280 | Rv2039c | Probable sugar-transport integral m | 80.71 | 280 | Mb2065c | sugar-transport integral mem | 81.07 | 280 | MAV_2478 | sugar ABC transporter permease | 100 | 280 | BCG_2058c | sugar-transport integral memb | 81.07 | 280 | MAP1767c | hypothetical protein | 280 | 100 |
| MAP4_2064 | putative sugar-transport ATP-binding protein ABC trans | 356 | Rv2038c | Probable sugar-transport ATP-bindir | 83.38 | 357 | Mb2064c | sugar ABC transporter ATP-bi | 83.38 | 357 | MAV_2479 | glycerol-phosphate porter | 99.16 | 363 | BCG_2057c | sugar-transport ATP-binding pr | 83.38 | 357 | MAP1766c | hypothetical protein | 356 | 100 |
| MAP4_2065 | conserved membrane protein, patatin-likephospholipa | 322 | Rv2037c | Conserved transmembrane protein | 87.07 | 324 | Mb2063c | transmembrane protein | 87.38 | 324 | MAV_2480 | phospholipase, patatin family prote | 99.69 | 318 | BCG_2056c | hypothetical protein | 87.38 | 324 | MAP1765c | hypothetical protein | 322 | 100 |
| MAP4_2066 | hypothetical protein | 95 | Rv0543c | hypothetical protein | 47.13 | 100 | Mb0557c | hypothetical protein | 47.13 | 100 | MAV_2481 | hypothetical protein | 97.89 | 95 | BCG_0587c | hypothetical protein | 47.13 | 100 | MAP1764 | hypothetical protein | 95 | 100 |
| MAP4_2067 | hypothetical protein | 277 | Rv2033c | hypothetical protein | 84.12 | 280 | Mb2059c | hypothetical protein | 84.12 | 280 | MAV_2482 | hypothetical protein | 99.64 | 277 | BCG_2052c | hypothetical protein | 84.12 | 280 | MAP1763c | hypothetical protein | 277 | 100 |
| MAP4_2068 | iron permease FTR1 family protein | 536 | Rv0245 | Possible oxidoreductase | 27.84 | 162 | Mb0251 | oxidoreductase | 27.84 | 162 | MAV_2483 | iron permease FTR1 family protein | 99.81 | 536 | BCG_0283 | oxidoreductase | 27.84 | 162 | MAP1762c | hypothetical protein | 536 | 100 |
| MAP4_2069 | Peptidase M75, Imelysin family protein | 391 | Rv2608 | PPE family protein PPE42 | 32.47 | 580 | Mb2640 | PPE family protein | 32.47 | 580 | MAV_2484 | hypothetical protein | 99.23 | 391 | BCG_2633 | PPE family protein | 32.47 | 580 | MAP1761c | hypothetical protein | 417 | 100 |
| MAP4_2070 | heme peroxidase (Dyp-type peroxidase) family protein | 421 | Rv0799c | hypothetical protein | 24.79 | 335 | Mb0822c | hypothetical protein | 24.79 | 335 | MAV_2485 | Tat-translocated enzyme | 98.81 | 438 | BCG_0851c | hypothetical protein | 24.79 | 335 | MAP1760c | hypothetical protein | 421 | 100 |
| MAP4_2071 | hypothetical protein | 174 | Rv0320 | Possible conserved exported protein | 31.58 | 220 | Mb0328 | hypothetical protein | 31.58 | 220 | MAV_2486 | hypothetical protein | 99.43 | 174 | BCG_0360 | hypothetical protein | 31.58 | 220 | MAP1759c | hypothetical protein | 174 | 100 |
| MAP4_2072 | hypothetical protein | 355 | Rv1679 | Possible acyl-CoA dehydrogenase Fa | 24.49 | 373 | Mb1706 | acyl-CoA dehydrogenase | 24.49 | 373 | MAV_2487 | NtrC protein | 98.87 | 355 | BCG_1717 | acyl-CoA dehydrogenase fadE1 | 24.49 | 373 | MAP1758c | NrtC | 355 | 100 |
| MAP4_2073 | RNA polymerase sigma factor, sigma-70 family protein | 209 | Rv3414c | Probable alternative RNA polymeras | 36.76 | 212 | Mb3448c | RNA polymerase sigma factor | 36.76 | 212 | MAV_2488 | RNA polymerase sigma factor, sigm | 99.04 | 209 | BCG_3484c | RNA polymerase sigma factor S | 36.76 | 212 | MAP1757c | hypothetical protein | 209 | 100 |
| MAP4_2074 | hypothetical protein | 89 | Rv3570c | Possible oxidoreductase Possible 3-h | 36.96 | 394 | Mb3601c | oxidoreductase | 36.96 | 394 | MAV_2489 | hypothetical protein | 100 | 89 | BCG_3635c | oxidoreductase | 36.96 | 394 | MAP1756c | hypothetical protein | 89 | 100 |
| MAP4_2075 | Formatenitrite transporter family protein | 314 | Rv3481c | Probable integral membrane protein | 37.5 | 229 | Mb3511c | hypothetical protein | 37.5 | 229 | MAV_2490 | formate/nitrite transporter superfa | 98.73 | 314 | BCG_3545c | integral membrane protein | 37.5 | 229 | MAP1755c | hypothetical protein | 314 | 100 |
| MAP4_2076 | universal stress protein family protein | 294 | Rv2005c | Universal stress protein family prote | 58.7 | 295 | Mb2028c | hypothetical protein | 58.7 | 295 | MAV_2494 | universal stress protein family prot | 93.09 | 245 | BCG_2022c | hypothetical protein | 58.7 | 295 | MAP1754c | hypothetical protein | 294 | 100 |
| MAP4_2077 | hypothetical protein | 436 | Rv2643 | Probable arsenic-transport integral | 24.73 | 498 | Mb2676 | arsenic-transport integral me | 24.73 | 498 | MAV_2495 | hypothetical protein | 98.8 | 417 | BCG_2670 | arsenic-transport integral mem | 24.73 | 498 | MAP1753 | hypothetical protein | 436 | 100 |
| MAP4_2078 | aldoketo reductase | 323 | Rv2298 | hypothetical protein | 35.41 | 323 | Mb2320 | hypothetical protein | 35.41 | 323 | MAV_2496 | aldo/keto reductase | 98.76 | 323 | BCG_2314 | hypothetical protein | 35.41 | 323 | MAP1752c | hypothetical protein | 323 | 100 |
| MAP4_2079 | NAD dependent epimerasedehydratase family protein | 366 | Rv1511 | GDP-D-mannose dehydratase GmdA | 30.39 | 340 | Mb0116 | GDP-mannose 4,6-dehydrata | 27.57 | 318 | MAV_2497 | RmlD substrate binding domain-co | 100 | 366 | BCG_0145 | GDP-mannose 4,6-dehydratase | 27.57 | 318 | MAP1751 | hypothetical protein | 389 | 96.63 |
| MAP4_2080 | hypothetical protein | 172 | Rv0310c | hypothetical protein | 35.88 | 163 | Mb0318c | hypothetical protein | 35.88 | 163 | MAV_2498 | hypothetical protein | 99.42 | 172 | BCG_0350c | hypothetical protein | 35.88 | 163 | MAP1750 | hypothetical protein | 172 | 100 |
| MAP4_2081 | putative thioesterase-like superfamily protein | 268 | Rv2761c | Possible type I restriction/modificati | 29.17 | 364 | Mb2782c | type I restriction/modification | 29.17 | 364 | MAV_2499 | hypothetical protein | 98.88 | 268 | BCG_2777c | type I restriction/modification | 29.17 | 364 | MAP1749 | hypothetical protein | 268 | 100 |
| MAP4_2082 | putative acyl-CoA dehydrogenase | 415 | Rv3560c | Probable acyl-CoA dehydrogenase F | 34.02 | 385 | Mb3590c | acyl-CoA dehydrogenase | 34.02 | 385 | MAV_2500 | acyl-CoA dehydrogenase middle do | 99.76 | 415 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 34.02 | 385 | MAP1748c | hypothetical protein | 415 | 100 |
| MAP4_2083 | hypothetical protein | 288 | Rv3372 | Trehalose 6-phosphate phosphatase | 35.21 | 391 | Mb3407 | trehalose 6-phosphate phosp | 35.21 | 391 | MAV_2501 | hypothetical protein | 97.57 | 288 | BCG_3444 | trehalose 6-phosphate phosph | 35.21 | 391 | MAP1747c | hypothetical protein | 288 | 100 |
| MAP4_2084 | hypothetical protein | 332 | Rv3131 | hypothetical protein | 66.25 | 332 | Mb3155 | hypothetical protein | 66.25 | 332 | MAV_2502 | hypothetical protein | 99.1 | 332 | BCG_3154 | hypothetical protein | 66.25 | 332 | MAP1746c | hypothetical protein | 342 | 100 |
| MAP4_2085 | hypothetical protein | 125 | Rv2733c | Conserved hypothetical alanine, arg | 30 | 512 | Mb2752c | (dimethylallyl)adenosine tRN | 30 | 512 | MAV_2503 | hypothetical protein | 97.6 | 125 | BCG_2746c | (dimethylallyl)adenosine tRNA | 30 | 512 | MAP1745c | hypothetical protein | 125 | 100 |
| MAP4_2086 | hypothetical protein | 154 | Rv0996 | Probable conserved transmembrane | 39.66 | 358 | Mb1023 | transmembrane protein | 39.66 | 358 | MAV_2504 | hypothetical protein | 97.89 | 142 | BCG_1051 | hypothetical protein | 39.66 | 358 | MAP1744 | hypothetical protein | 154 | 100 |
| MAP4_2087 | hypothetical protein | 333 | Rv2032 | Conserved protein Acg | 52.81 | 331 | Mb2058 | hypothetical protein | 52.5 | 331 | MAV_2505 | hypothetical protein | 98.8 | 333 | BCG_2051 | hypothetical protein | 52.5 | 331 | MAP1743c | hypothetical protein | 333 | 100 |
| MAP4_2088 | Universal stress protein family protein | 293 | Rv2026c | Universal stress protein family prote | 69.37 | 294 | Mb2051c | hypothetical protein | 69.37 | 294 | MAV_2506 | universal stress protein family prot | 98.98 | 293 | BCG_2045c | hypothetical protein | 69.37 | 294 | MAP1742c | hypothetical protein | 293 | 100 |
| MAP4_2089 | Universal stress protein family protein | 294 | Rv2005c | Universal stress protein family prote | 65.42 | 295 | Mb2028c | hypothetical protein | 65.42 | 295 | MAV_2507 | universal stress protein family prot | 98.64 | 294 | BCG_2022c | hypothetical protein | 65.42 | 295 | MAP1741c | hypothetical protein | 294 | 100 |
| MAP4_2090 | putative two component sensor histidine kinase | 512 | Rv3132c | Two component sensor histidine kin | 54.82 | 578 | Mb3156c | two component sensor histid | 54.82 | 578 | MAV_2508 | PAS domain-containing protein | 98.51 | 470 | BCG_3155c | two component sensor histidin | 54.82 | 578 | MAP1740c | hypothetical protein | 512 | 100 |
| MAP4_2091 | 20-beta-hydroxysteroid dehydrogenase | 260 | Rv2002 | Possible 20-beta-hydroxysteroid deh | 83.46 | 260 | Mb2025 | 20-beta-hydroxysteroid dehy | 83.46 | 260 | MAV_2509 | 3-alpha-(or 20-beta)-hydroxysteroi | 99.62 | 260 | BCG_2019 | 20-beta-hydroxysteroid dehydr | 83.46 | 260 | MAP1739c | FabG3_1 | 260 | 100 |
| MAP4_2092 | transmembrane transport protein MmpL5 | 966 | Rv0676c | Probable conserved transmembrane | 72.78 | 964 | Mb0695c | transmembrane transport pro | 73 | 964 | MAV_2510 | MmpL4 protein | 99.9 | 966 | BCG_0725c | transmembrane transport prot | 73 | 964 | MAP1738 | hypothetical protein | 966 | 100 |
| MAP4_2093 | membrane protein, MmpS family | 138 | Rv0677c | Possible conserved membrane prote | 57.86 | 142 | Mb0696c | hypothetical protein | 57.86 | 142 | MAV_2511 | MmpS5 protein | 99.28 | 144 | BCG_0726c | membrane protein mmpS5 | 57.86 | 142 | MAP1737 | hypothetical protein | 138 | 100 |
| MAP4_2094 | Transcriptional regulator, TetR family | 202 | Rv0691c | Probable transcriptional regulatory | 26.04 | 198 | Mb0710c | transcriptional regulator | 26.04 | 198 | MAV_2512 | TetR family transcriptional regulato | 99.5 | 202 | BCG_0740c | transcriptional regulatory prote | 26.04 | 198 | MAP1736 | hypothetical protein | 202 | 100 |
| MAP4_2095 | alphabeta hydrolase domain-containing protein | 308 | Rv0217c | Possible esterase LipW | 51.36 | 302 | Mb0223c | esterase | 51.7 | 302 | MAV_2513 | alpha/beta hydrolase | 98.7 | 308 | BCG_0254c | esterase lipW | 51.7 | 302 | MAP1735 | hypothetical protein | 308 | 100 |
| MAP4_2098 | Transcriptional regulator, TetR family | 210 | Rv0302 | Probable transcriptional regulatory | 32.63 | 210 | Mb0310 | TetR/ACRR family transcriptio | 32.63 | 210 | MAV_1586 | TetR family transcriptional regulato | 29.09 | 262 | BCG_0342 | TetR family transcriptional regu | 32.63 | 210 | MAP1732c | hypothetical protein | 215 | 100 |
| MAP4_2099 | hypothetical protein | 89 | Rv3536c | Probable hydratase | 46.27 | 261 | Mb3566c | hydratase | 46.27 | 261 | MAV_0625 | 2-keto-4-pentenoate hydratase | 40.91 | 261 | BCG_3600c | hydratase | 46.27 | 261 | MAP1731c | hypothetical protein | 89 | 100 |
| MAP4_2100 | cobalamin synthesis protein | 340 | Rv2725c | Probable GTP-binding protein HflX | 45.71 | 495 | Mb2744c | GTP-binding protein HflX | 45.71 | 495 | MAV_3947 | NAD dependent epimerase/dehydr | 28.57 | 268 | BCG_2738c | GTP-binding protein hflX | 45.71 | 495 | MAP1730c | hypothetical protein | 340 | 100 |
| MAP4_2101 | putative thioesterase, thioesterase-like super family pr | 275 | Rv2605c | Probable acyl-CoA thioesterase II Te | 35.15 | 281 | Mb2637c | acyl-CoA thioesterase | 34.73 | 281 | MAV_2695 | acyl-CoA thioesterase | 88.43 | 268 | BCG_2630c | acyl-CoA thioesterase II tesB2 | 34.73 | 281 | MAP1729c | hypothetical protein | 275 | 100 |
| MAP4_2102 | hypothetical protein | 61 | Rv3872 | PE family-related protein PE35 | 30 | 99 | Mb3902 | PE family-like protein | 30 | 98 | MAV_2694 | hypothetical protein | 98.36 | 61 | BCG_1948c | ferric uptake regulation protein | 42.42 | 150 | MAP0843 | CtpE | 790 | 44.44 |
| MAP4_2103 | putative haloacid dehalogenase | 240 | Rv3376 | hypothetical protein | 23.08 | 217 | Mb3410 | hypothetical protein | 23.08 | 217 | MAV_2690 | haloacid dehalogenase, type II | 97.5 | 240 | BCG_3447 | hypothetical protein | 23.08 | 217 | MAP1728c | YfnB | 240 | 100 |
| MAP4_2104 | alphabeta hydrolase family protein | 301 | Rv2307c | hypothetical protein | 29.71 | 281 | Mb2330c | hypothetical protein | 29.71 | 281 | MAV_2688 | alpha/beta hydrolase | 97.01 | 67 | BCG_2324c | hypothetical protein | 29.71 | 281 | MAP1727 | hypothetical protein | 301 | 100 |
| MAP4_2105 | transcriptional regulator, TetR family | 200 | Rv0653c | Possible transcriptional regulatory p | 26.44 | 231 | Mb0672c | TetR family transcriptional re | 26.44 | 231 | MAV_3923 | TetR family transcriptional regulato | 31.91 | 204 | BCG_0702c | TetR family transcriptional regu | 26.44 | 231 | MAP1726c | hypothetical protein | 194 | 100 |
| MAP4_2106 | Catalase | 342 | Rv3107c | Possible alkyldihydroxyacetonephos | 28.17 | 527 | Mb3134c | alkyldihydroxyacetonephosph | 28.17 | 527 | MAV_3520 | catalase | 34.11 | 313 | BCG_3132c | alkyldihydroxyacetonephospha | 28.17 | 527 | MAP1725c | hypothetical protein | 342 | 100 |
| MAP4_2107 | Cytochrome B561 | 185 | Rv0051 | Probable conserved transmembrane | 32.31 | 560 | Mb0052 | transmembrane protein | 32.31 | 560 | MAV_3637 | CDP-diacylglycerol--glycerol-3-phos | 34.21 | 190 | BCG_0082 | hypothetical protein | 32.31 | 560 | MAP1724c | hypothetical protein | 185 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2108 | putative NADP oxidoreductase coenzymeF420-depend | 221 | Rv0886 | Probable NADPH:adrenodoxin oxido | 31.03 | 575 | Mb0910 | NADPH:adrenodoxin oxidored | 31.03 | 575 | MAV_2843 | LldD2 protein | 26.83 | 420 | BCG_0938 | NADPH:adrenodoxin oxidoredu | 31.03 | 575 | MAP1723 | hypothetical protein | 221 | 100 |
| MAP4_2109 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_2110 | Transcriptional regulator, TetR family | 223 | Rv3208 | Probable transcriptional regulatory | 29.13 | 228 | Mb3233 | TetR family transcriptional re | 29.13 | 228 | MAV_1611 | TetR family transcriptional regulato | 33.96 | 205 | BCG_3234 | TetR family transcriptional regu | 29.13 | 228 | MAP1721c | hypothetical protein | 223 | 100 |
| MAP4_2111 | hypothetical protein | 79 | Rv3425 | PPE family protein PPE57 | 54.55 | 176 | Mb1362c | glucanase GLGE | 40.91 | 701 | MAV_1547 | alpha-amylase | 40.91 | 694 | BCG_1389c | glucanase glgE | 40.91 | 701 | MAP2433 | hypothetical protein | 712 | 40.91 |
| MAP4_2112 | putative NAD-dependent epimerasedehydratase | 307 | Rv3784 | Possible dTDP-glucose 4,6-dehydrata | 43.59 | 326 | Mb3813 | dTDP-glucose 4,6-dehydratas | 43.59 | 326 | MAV_0588 | oxidoreductase | 51.68 | 293 | BCG_3846 | dTDP-glucose 4,6-dehydratase | 43.59 | 326 | MAP1720 | hypothetical protein | 339 | 99.67 |
| MAP4_2113 | Transcriptional regulator, TetR family | 204 | Rv0067c | Possible transcriptional regulatory p | 30.99 | 189 | Mb0068c | TetR family transcriptional re | 30.99 | 189 | MAV_4593 | TetR family transcriptional regulato | 45 | 179 | BCG_0098c | TetR family transcriptional regu | 30.99 | 189 | MAP1719c | hypothetical protein | 204 | 100 |
| MAP4_2114 | hypothetical protein | 151 | Rv1926c | Immunogenic protein Mpt63 (antige | 29.07 | 159 | Mb1961c | hypothetical protein | 29.07 | 159 | MAV_3737 | hypothetical protein | 37.74 | 190 | BCG_1965c | immunogenic protein mpt63 | 29.07 | 159 | MAP1718c | hypothetical protein | 151 | 100 |
| MAP4_2115 | hypothetical protein | 214 | Rv2721c | Possible conserved transmembrane | 30.25 | 699 | Mb2740c | hypothetical protein | 30.25 | 699 | MAV_2699 | hypothetical protein | 98.51 | 202 | BCG_2734c | transmembrane alanine and gl | 31.09 | 699 | MAP1717 | hypothetical protein | 214 | 100 |
| MAP4_2116 | short-chain dehydrogenase | 279 | Rv1865c | Probable short-chain type dehydrog | 51.87 | 286 | Mb1896c | short chain dehydrogenase | 51.87 | 286 | MAV_2700 | short chain dehydrogenase | 97.13 | 279 | BCG_1901c | short chain dehydrogenase | 51.87 | 286 | MAP1716 | short chain dehydrogenase | 279 | 100 |
| MAP4_2117 | fatty oxidation protein FadB | 710 | Rv0860 | Probable fatty oxidation protein Fad | 63.55 | 720 | Mb0883 | fatty oxidation protein FadB | 63.41 | 720 | MAV_2701 | acyl-CoA dehydrogenase | 95.21 | 710 | BCG_0912 | fatty oxidation protein fadB | 63.41 | 720 | MAP1715 | FadB_2 | 710 | 99.86 |
| MAP4_2118 | acyl-CoA thiolase fadA | 403 | Rv0859 | Possible acyl-CoA thiolase FadA | 73.82 | 403 | Mb0882 | acetyl-CoA acetyltransferase | 74.06 | 403 | MAV_2702 | acetyl-CoA acetyltransferase | 98.51 | 403 | BCG_0911 | acetyl-CoA acetyltransferase | 74.06 | 403 | MAP1714 | acetyl-CoA acetyltransferase | 403 | 100 |
| MAP4_2119 | acyl-CoA dehydrogenase | 387 | Rv2724c | Probable acyl-CoA dehydrogenase F | 50.67 | 386 | Mb2743c | acyl-CoA dehydrogenase | 50.4 | 386 | MAV_2703 | acyl-CoA dehydrogenase | 98.97 | 387 | BCG_2737c | acyl-CoA dehydrogenase fadE2 | 50.67 | 386 | MAP1713 | FadE20_1 | 387 | 100 |
| MAP4_2120 | CoA-transferase family III protein | 267 | Rv0855 | Probable fatty-acid-CoA racemase F | 33.07 | 359 | Mb0878 | fatty-acid-CoA racemase | 33.07 | 359 | MAV_2704 | L-carnitine dehydratase/bile acid-ir | 95.18 | 272 | BCG_0907 | fatty-acid-CoA racemase far | 33.07 | 359 | MAP1712 | hypothetical protein | 267 | 100 |
| MAP4_2121 | Transcriptional regulator, TetR family | 195 | Rv1219c | Probable transcriptional regulatory | 50 | 212 | Mb1251c | transcriptional regulator | 50 | 212 | MAV_2705 | TetR family transcriptional regulato | 99.49 | 197 | BCG_1279c | transcriptional regulatory prot | 50 | 212 | MAP1711c | hypothetical protein | 195 | 100 |
| MAP4_2122 | putative hydrolase | 294 | Rv3171c | Possible non-heme haloperoxidase H | 37.63 | 299 | Mb3196c | non-Heme haloperoxidase Hp | 37.63 | 299 | MAV_2706 | alpha/beta hydrolase | 98.93 | 281 | BCG_3195c | non-heme haloperoxidase hpx | 37.63 | 299 | MAP1710 | hypothetical protein | 294 | 100 |
| MAP4_2123 | fatty-acid--CoA ligase | 606 | Rv1550 | Probable fatty-acid-CoA ligase FadD | 51.1 | 571 | Mb1576 | fatty-acid--CoA ligase | 52.97 | 647 | MAV_3221 | acyl-CoA dehydrogenase | 53.05 | 606 | BCG_1602 | fatty-acid-CoA ligase FadD11 | 52.97 | 647 | MAP1709c | FadD11_2 | 606 | 100 |
| MAP4_2124 | hypothetical protein | 217 | Rv3835 | hypothetical protein | 43.9 | 449 | Mb3865 | hypothetical protein | 43.9 | 449 | MAV_2708 | metal-dependent phosphohydrolas | 99.08 | 217 | BCG_3898 | hypothetical protein | 43.9 | 452 | MAP1708 | hypothetical protein | 217 | 100 |
| MAP4_2125 | Short-chain dehdyrogenase | 236 | Rv1483 | 3-oxoacyl-[acyl-carrier protein] redu | 36.86 | 247 | Mb1519 | 3-oxoacyl-ACP reductase | 36.86 | 247 | MAV_2709 | short chain dehydrogenase | 98.73 | 236 | BCG_1545 | 3-oxoacyl-ACP reductase | 36.86 | 247 | MAP1707 | short chain dehydrogenase | 236 | 100 |
| MAP4_2126 | chitinase | 145 | Rv1987 | Possible chitinase | 73.79 | 142 | Mb2009 | chitinase | 73.79 | 142 | MAV_2710 | cellulose-binding domain-containin | 99.17 | 120 | BCG_0024c | chromosome partitioning prot | 41.03 | 347 | MAP1706 | hypothetical protein | 145 | 100 |
| MAP4_2127 | Transcriptional regulator, AraC family | 280 | Rv1931c | Probable transcriptional regulatory | 25.88 | 259 | Mb1966c | transcriptional regulator | 25.88 | 259 | MAV_2711 | AraC family transcriptional regulato | 98.57 | 280 | BCG_1970c | transcriptional regulatory prot | 25.88 | 259 | MAP1705c | hypothetical protein | 251 | 100 |
| MAP4_2128 | glyoxalase family protein | 133 | Rv0887c | hypothetical protein | 29.84 | 152 | Mb0911c | hypothetical protein | 29.84 | 152 | MAV_2712 | glyoxalase | 95.97 | 124 | BCG_0939c | hypothetical protein | 29.84 | 152 | MAP1704c | hypothetical protein | 133 | 100 |
| MAP4_2129 | hypothetical protein | 117 | Rv1291c | Conserved hypothetical secreted pr | 34.88 | 111 | Mb1323c | hypothetical protein | 34.88 | 111 | MAV_2713 | hypothetical protein | 99.03 | 103 | BCG_1351c | hypothetical protein | 34.88 | 111 | MAP1703c | hypothetical protein | 117 | 100 |
| MAP4_2130 | hypothetical protein | 106 | Rv0794c | Probable oxidoreductase | 28.57 | 499 | Mb1201c | hypothetical protein | 31.25 | 180 | MAV_1419 | hypothetical protein | 25.84 | 110 | BCG_1231c | PPE family protein | 31.25 | 180 | MAP2123 | hypothetical protein | 310 | 40.91 |
| MAP4_2131 | hypothetical protein | 151 | Rv1221 | Alternative RNA polymerase sigma f | 33.9 | 257 | Mb1253 | RNA polymerase sigma factor | 33.9 | 257 | MAV_1365 | RNA polymerase sigma-70 factor | 37.93 | 424 | BCG_1281 | RNA polymerase sigma factor S | 33.9 | 257 | MAP1702c | hypothetical protein | 245 | 100 |
| MAP4_2132 | carboxylase | 491 | Rv1722 | Possible carboxylase | 83.95 | 494 | Mb1751 | biotin carboxylase | 83.74 | 494 | MAV_2716 | biotin carboxylase-like protein | 99.58 | 480 | BCG_1761 | biotin carboxylase-like protein | 83.74 | 494 | MAP1701c | biotin carboxylase-like protein | 491 | 100 |
| MAP4_2133 | hydrolase | 391 | Rv1723 | Probable hydrolase | 78.09 | 415 | Mb1752 | hydrolase | 78.09 | 415 | MAV_2718 | beta-lactamase | 98.72 | 391 | BCG_1762 | hydrolase | 78.09 | 415 | MAP1700c | hypothetical protein | 391 | 100 |
| MAP4_2134 | thiamine biosynthesis protein thiI | 409 | Rv3917c | Probable chromosome partitioning | 34.21 | 344 | Mb3948c | chromosome partitioning pro | 34.21 | 344 | MAV_2717 | thiamine biosynthesis protein ThiI | 98.29 | 409 | BCG_0023c | chromosome partitioning prot | 34.21 | 344 | MAP1699 | thiamine biosynthesis protein ThiI | 409 | 100 |
| MAP4_2135 | 18 kDa heat shock protein Hsp18_2 | 146 | Rv2031c | Heat shock protein HspX (alpha-crys | 32.23 | 144 | Mb2057c | heat shock protein hspX | 32.23 | 144 | MAV_2719 | Hsp20/alpha crystallin family prote | 99.31 | 144 | BCG_2050c | heat shock protein hspX | 32.23 | 144 | MAP1698c | Hsp18_2 | 146 | 100 |
| MAP4_2136 | merR-family heat shock protein transcriptional repress | 126 | Rv0353 | Probable heat shock protein transcri | 40.78 | 126 | Mb0361 | HEAT shock protein transcrip | 40.78 | 126 | MAV_2720 | MerR family transcriptional regulat | 96.03 | 126 | BCG_0392 | heat shock protein transcriptio | 40.78 | 126 | MAP1697 | hypothetical protein | 126 | 99.21 |
| MAP4_2137 | 18 kDa antigen, heat shock protein | 142 | Rv2031c | Heat shock protein HspX (alpha-crys | 31.78 | 144 | Mb2057c | heat shock protein hspX | 31.78 | 144 | MAV_2721 | 18 kDa antigen 2 | 92.03 | 139 | BCG_2050c | heat shock protein hspX | 31.78 | 144 | MAP1696c | Hsp18_1 | 142 | 100 |
| MAP4_2138 | molecular chaperone, DnaJ domain-containing protein | 144 | Rv0352 | Probable chaperone protein DnaJ1 | 42.03 | 395 | Mb0360 | molecular chaperone DnaJ | 42.03 | 395 | MAV_2722 | DnaJ domain-containing protein | 98.11 | 106 | BCG_0391 | chaperone protein DnaJ | 42.03 | 395 | MAP1695c | hypothetical protein | 144 | 100 |
| MAP4_2139 | putative polyketide synthase associated protein PA PA | 505 | Rv3820c | Possible conserved polyketide synth | 54.9 | 468 | Mb3850c | polyketide synthase | 54.9 | 468 | MAV_2723 | PapA2 protein | 98.93 | 468 | BCG_3882c | polyketide synthase associated | 54.9 | 468 | MAP1694 | PapA2 | 505 | 100 |
| MAP4_2140 | peptidyl-prolyl cis-trans isomerase domain-containing | 188 | | | | | | | | | MAV_2725 | peptidyl-prolyl cis-trans isomerase | 97.84 | 185 | | | | | MAP1693c | hypothetical protein | 188 | 100 |
| MAP4_2141 | 3-oxoacyl-ACP reductasefabG2 | 253 | Rv1350 | Probable 3-oxoacyl-[acyl-carrier pro | 36.25 | 247 | Mb1385 | 3-ketoacyl-ACP reductase | 36.25 | 247 | MAV_2726 | acyl-CoA dehydrogenase | 99.6 | 253 | BCG_1412 | 3-ketoacyl-ACP reductase | 36.25 | 247 | MAP1692 | FabG2_1 | 253 | 100 |
| MAP4_2142 | hypothetical protein | 227 | | | | | Mb3492 | hypothetical protein | 36.21 | 285 | MAV_2727 | hypothetical protein | 100 | 227 | | | | | MAP1691c | hypothetical protein | 227 | 100 |
| MAP4_2143 | methyltransferasemethylase | 255 | Rv3342 | Possible methyltransferase (methyla | 38.31 | 243 | Mb3374 | methyltransferase | 38.31 | 243 | MAV_2728 | hypothetical protein | 99.61 | 255 | BCG_3412 | methyltransferase | 38.31 | 243 | MAP1690c | hypothetical protein | 255 | 100 |
| MAP4_2144 | hydrolase, peptidase M42 family protein | 411 | Rv2381c | Polyketide synthetase MbtD (polyke | 27.59 | 1004 | Mb2402c | polyketide synthase | 27.59 | 1004 | MAV_2729 | hydrolase, peptidase M42 family pr | 100 | 411 | BCG_2395c | polyketide synthase | 27.59 | 1004 | MAP1689 | hypothetical protein | 411 | 100 |
| MAP4_2145 | citrate (Pro-3S)-lyase beta subunit | 293 | Rv2498c | Probable citrate (pro-3S)-lyase (beta | 32.12 | 273 | Mb2526c | citrate (Pro-3S)-lyase subunit | 32.12 | 273 | MAV_2730 | citrate lyase beta chain (Citrase bet | 98.98 | 293 | BCG_2518c | citrate (pro-3s)-lyase subunit b | 32.12 | 273 | MAP1688 | hypothetical protein | 226 | 99.56 |
| MAP4_2146 | methyltransferase | 307 | Rv1729c | Possible S-adenosylmethionine-depe | 57.95 | 312 | Mb1758c | hypothetical protein | 57.95 | 312 | MAV_2732 | methyltransferase | 99.35 | 307 | BCG_1768c | hypothetical protein | 57.95 | 312 | MAP4190c | hypothetical protein | 306 | 61.33 |
| MAP4_2147 | glucose-6-phosphate 1-dehydrogenase | 518 | Rv1447c | Probable glucose-6-phosphate 1-deh | 40.06 | 514 | Mb1482c | glucose-6-phosphate 1-dehyd | 40.06 | 514 | MAV_2733 | glucose-6-phosphate 1-dehydroger | 99.72 | 505 | BCG_1508c | glucose-6-phosphate 1-dehydr | 40.06 | 514 | MAP1687 | hypothetical protein | 817 | 100 |
| MAP4_2148 | hypothetical protein | 60 | Rv0350 | Probable chaperone protein DnaK (h | 46.15 | 625 | Mb0358 | molecular chaperone DnaK | 46.15 | 625 | MAV_2734 | hypothetical protein | 100 | 60 | BCG_0389 | molecular chaperone DnaK | 46.15 | 625 | MAP3840 | molecular chaperone DnaK | 623 | 45.71 |
| MAP4_2149 | hypothetical protein | 323 | Rv1192 | hypothetical protein | 34.15 | 275 | Mb1224 | hypothetical protein | 34.15 | 275 | MAV_2735 | hypothetical protein | 99.69 | 325 | BCG_1252 | hypothetical protein | 34.15 | 275 | MAP1686 | hypothetical protein | 323 | 100 |
| MAP4_2150 | monooxygenase, FAD-binding domain-containing prote | 525 | Rv1751 | Probable oxidoreductase | 26.9 | 460 | Mb1780 | hypothetical protein | 26.9 | 460 | MAV_2736 | hypothetical protein | 98.41 | 503 | BCG_1790 | hypothetical protein | 26.9 | 460 | MAP1685 | hypothetical protein | 525 | 100 |
| MAP4_2151 | ATP-dependent helicase HrpA | 1314 | Rv3371 | Possible triacylglycerol synthase (dia | 31.37 | 446 | Mb3406 | hypothetical protein | 31.37 | 446 | MAV_2737 | ATP-dependent helicase HrpA | 99.32 | 1317 | BCG_3443 | hypothetical protein | 31.37 | 446 | MAP1684 | HrpA | 1314 | 100 |
| MAP4_2152 | putative diguanylate cyclase, GGDEF domain-containin | 365 | Rv1354c | hypothetical protein | 31.58 | 623 | Mb1389c | hypothetical protein | 31.58 | 623 | MAV_2738 | diguanylate cyclase | 98.47 | 327 | BCG_1416c | hypothetical protein | 31.58 | 623 | MAP1683c | hypothetical protein | 365 | 100 |
| MAP4_2153 | putative virulence factor, BrkB family protein | 340 | Rv3335c | Probable conserved integral membr | 30.47 | 289 | Mb3368c | hypothetical protein | 30.47 | 289 | MAV_2739 | hypothetical protein | 98.15 | 324 | BCG_3406c | integral membrane protein | 31.25 | 289 | MAP1682c | hypothetical protein | 340 | 100 |
| MAP4_2154 | Enoyl-CoA hydratase | 257 | Rv1070c | Probable enoyl-CoA hydratase EchA | 37.21 | 257 | Mb1099c | enoyl-CoA hydratase | 37.21 | 257 | MAV_2740 | enoyl-CoA hydratase/isomerase | 99.61 | 257 | BCG_1128c | enoyl-CoA hydratase | 37.21 | 257 | MAP1681c | hypothetical protein | 257 | 100 |
| MAP4_2155 | cutinase precursor cfp21 | 220 | Rv1984c | Probable cutinase precursor CFP21 | 74.88 | 217 | Mb2006c | cutinase CFP21 | 74.88 | 217 | MAV_2741 | serine esterase, cutinase | 98.47 | 196 | BCG_1798 | cutinase cut1 | 51.12 | 218 | MAP1680c | hypothetical protein | 220 | 100 |
| MAP4_2156 | hypothetical protein | 219 | Rv2677c | Probable protoporphyrinogen oxida | 30.68 | 452 | Mb2696c | protoporphyrinogen oxidase | 30.68 | 452 | MAV_2742 | hypothetical protein | 99.09 | 219 | BCG_2690c | protoporphyrinogen oxidase | 30.68 | 452 | MAP1679c | hypothetical protein | 219 | 100 |
| MAP4_2157 | hypothetical protein | 84 | Rv2674 | Probable peptide methionine sulfox | 26.42 | 136 | Mb2693 | hypothetical protein | 26.42 | 136 | MAV_2743 | hypothetical protein | 100 | 84 | BCG_2687 | hypothetical protein | 26.42 | 136 | MAP1222 | hypothetical protein | 480 | 52.17 |
| MAP4_2158 | hypothetical protein, MOSC domain-containing protein | 279 | Rv0595c | Possible toxin VapC4 | 36.17 | 130 | Mb0611c | hypothetical protein | 36.17 | 130 | MAV_2744 | mosc domain-containing protein | 99.64 | 280 | BCG_0641c | hypothetical protein | 36.17 | 130 | MAP1678 | hypothetical protein | 267 | 100 |
| MAP4_2159 | hypothetical protein | 275 | Rv1268c | Hypothetical protein | 41.41 | 232 | Mb1299c | hypothetical protein | 41.41 | 232 | MAV_2745 | hypothetical protein | 99.59 | 242 | BCG_1327c | hypothetical protein | 41.41 | 232 | MAP1677 | hypothetical protein | 275 | 100 |
| MAP4_2162 | glycosyltransferase | 390 | Rv1524 | Probable glycosyltransferase | 55.05 | 414 | Mb1551 | glycosyltransferase | 55.05 | 414 | MAV_2747 | rhamnosyltransferase RtfA | 97.69 | 390 | BCG_1576 | glycosyltransferase | 55.05 | 414 | MAP1674c | hypothetical protein | 390 | 100 |
| MAP4_2163 | hypothetical protein | 349 | Rv2423 | Hypothetical protein | 57.91 | 348 | Mb2446 | hypothetical protein | 57.91 | 348 | MAV_2748 | hypothetical protein | 98.85 | 349 | BCG_2439 | hypothetical protein | 57.91 | 348 | MAP1673c | hypothetical protein | 349 | 100 |
| MAP4_2164 | FAD dependent oxidoreductase | 506 | Rv0492c | Probable oxidoreductase GMC-type | 63.33 | 629 | Mb0502c | oxidoreductase GMC-type | 63.33 | 629 | MAV_2749 | FAD dependent oxidoreductase | 99.01 | 506 | BCG_0533c | oxidoreductase GMC-type | 63.33 | 629 | MAP1672 | hypothetical protein | 522 | 99.8 |
| MAP4_2165 | hypothetical protein | 264 | Rv0393 | Conserved 13E12 repeat family prot | 44.74 | 441 | Mb0399 | hypothetical protein | 44.74 | 441 | MAV_2750 | hypothetical protein | 93.18 | 259 | BCG_0430 | hypothetical protein | 44.74 | 441 | MAP1671 | hypothetical protein | 264 | 100 |
| MAP4_2166 | putative L,D-transpeptidase, catalytic domain protein | 427 | Rv2518c | Probable L,D-transpeptidase LdtB | 41.06 | 408 | Mb2547c | lipoprotein LppS | 41.06 | 408 | MAV_2751 | ErfK/YbiS/YcfS/YnhG family protein | 99.06 | 427 | BCG_2539c | lipoprotein lppS | 41.06 | 408 | MAP1670c | hypothetical protein | 427 | 100 |
| MAP4_2167 | ferric uptake regulation protein furA (fur) | 146 | Rv1909c | Ferric uptake regulation protein Fur | 79.86 | 147 | Mb1944c | ferric uptake regulation prote | 79.17 | 150 | MAV_2752 | Fur family transcriptional regulator | 99.25 | 134 | BCG_1948c | ferric uptake regulation protei | 78.47 | 150 | MAP1669c | FurA | 146 | 100 |
| MAP4_2168 | catalase-peroxidase-peroxynitritase T KATG | 748 | Rv1908c | Catalase-peroxidase-peroxynitritase | 70.7 | 740 | Mb1943c | catalase-peroxidase-peroxyni | 70.85 | 740 | MAV_2753 | catalase/peroxidase HPI | 99.6 | 748 | BCG_1947c | catalase-peroxidase-peroxynitr | 70.85 | 740 | MAP1668c | KatG | 748 | 100 |
| MAP4_2169 | hypothetical protein | 271 | Rv2525c | Conserved hypothetical protein Secr | 37.11 | 240 | Mb2554c | hypothetical protein | 37.11 | 240 | MAV_2754 | hypothetical protein | 99.26 | 271 | BCG_2546c | hypothetical protein | 37.11 | 240 | MAP1667 | hypothetical protein | 271 | 100 |
| MAP4_2170 | Glycosyltransferase | 416 | Rv0486 | Glycosyltransferase MshA | 29.35 | 480 | Mb0496 | mannosyltransferase | 29.35 | 480 | MAV_2755 | glycosyl transferase | 99.49 | 396 | BCG_0527 | mannosyltransferase | 29.35 | 480 | MAP1666c | hypothetical protein | 416 | 100 |
| MAP4_2171 | putative methyltransferase | 252 | Rv1405c | Putative methyltransferase | 33.93 | 274 | Mb1440c | methyltransferase | 33.93 | 274 | MAV_2756 | methyltransferase | 99.21 | 252 | BCG_1466c | methyltransferase | 33.93 | 274 | MAP1665c | hypothetical protein | 252 | 100 |
| MAP4_2172 | hypothetical protein | 356 | Rv3377c | Halimadienyl diphosphate synthase | 32.88 | 501 | Mb1667c | lysyl-tRNA synthetase | 34.92 | 1172 | MAV_2757 | hypothetical protein | 98.6 | 356 | BCG_1679c | lysyl-tRNA synthetase | 34.92 | 1172 | MAP1664c | hypothetical protein | 356 | 100 |
| MAP4_2173 | putative methyltransferase | 219 | Rv1703c | Probable catechol-O-methyltransfer | 25 | 196 | Mb1729c | catechol-o-methyltransferase | 25 | 196 | MAV_2758 | secreted protein | 99.54 | 219 | BCG_1741c | catechol-o-methyltransferase | 25.57 | 196 | MAP1663 | hypothetical protein | 219 | 100 |
| MAP4_2174 | cutinase | 218 | Rv2301 | Probable cutinase Cut2 | 72.91 | 230 | Mb2323 | cutinase | 72.91 | 230 | MAV_2759 | serine esterase, cutinase | 98.35 | 182 | BCG_2317 | cutinase cut2 | 72.91 | 230 | MAP1662c | hypothetical protein | 218 | 100 |
| MAP4_2175 | hypothetical protein | 78 | Rv1097c | Probable membrane glycine and pro | 34.15 | 293 | Mb1127c | hypothetical protein | 34.15 | 293 | MAV_2760 | hypothetical protein | 97.44 | 39 | BCG_1157c | membrane glycine and proline | 34.15 | 293 | MAP2966c | formate dehydrogenase accessory prot | 272 | 41.38 |
| MAP4_2176 | beta-1,3-glucanase precursor | 273 | Rv0315 | Possible beta-1,3-glucanase precurs | 60.5 | 294 | Mb0323 | beta-1,3-glucanase | 60.92 | 294 | MAV_2761 | glycosyl hydrolases family protein 1 | 99.63 | 273 | BCG_0355 | beta-1,3-glucanase | 60.92 | 294 | MAP1661c | hypothetical protein | 275 | 100 |
| MAP4_2177 | putative methyltransferase | 281 | Rv0893c | Possible S-adenosylmethionine-depe | 35.8 | 325 | Mb0917c | hypothetical protein | 35.8 | 325 | MAV_2762 | methyltransferase, putative, family | 97.86 | 281 | BCG_0945c | hypothetical protein | 35.8 | 325 | MAP1660 | hypothetical protein | 281 | 100 |
| MAP4_2178 | hypothetical protein | 223 | Rv3875 | 6 kDa early secretory antigenic targe | 42.31 | 95 | Mb3905 | hypothetical protein | 42.31 | 95 | MAV_2763 | hypothetical protein | 99.55 | 223 | BCG_1506c | 6-phosphogluconolactonase de | 35.29 | 247 | MAP1659 | hypothetical protein | 259 | 99.55 |
| MAP4_2179 | hypothetical protein | 84 | Rv3910 | Probable conserved transmembrane | 41.03 | 1184 | Mb3940 | transmembrane protein | 41.03 | 1184 | MAV_2764 | hypothetical protein | 98.81 | 84 | BCG_3967 | hypothetical protein | 41.03 | 1184 | MAP3365c | hypothetical protein | 505 | 35.14 |
| MAP4_2180 | Aldehyde dehydrogenase | 484 | Rv0223c | Probable aldehyde dehydrogenase | 39.83 | 487 | Mb2883c | aldehyde dehydrogenase | 37.83 | 455 | MAV_2765 | P-cumic aldehyde dehydrogenase | 99.79 | 484 | BCG_2880c | aldehyde dehydrogenase aldC | 37.83 | 455 | MAP1658 | hypothetical protein | 512 | 100 |
| MAP4_2181 | NAD dependent epimerasedehydratase family protein | 300 | Rv1512 | Probable nucleotide-sugar epimeras | 23.86 | 322 | Mb0116 | GDP-mannose 4,6-dehydratas | 24.02 | 318 | MAV_2766 | NAD dependent epimerase/dehydr | 99.67 | 307 | BCG_0145 | GDP-mannose 4,6-dehydratase | 24.02 | 318 | MAP1657 | hypothetical protein | 300 | 100 |
| MAP4_2182 | putative acyl-CoA dehydrogenase | 394 | Rv3094c | hypothetical protein | 31.14 | 376 | Mb3121c | hypothetical protein | 31.14 | 376 | MAV_2767 | acyl-CoA dehydrogenase domain-c | 99.49 | 394 | BCG_3119c | hypothetical protein | 31.14 | 376 | MAP1656 | hypothetical protein | 394 | 100 |
| MAP4_2183 | hypothetical protein | 126 | Rv1976c | hypothetical protein | 67.46 | 135 | Mb2289 | cytochrome P450 124 CYP124 | 36.84 | 428 | MAV_2768 | hypothetical protein | 100 | 119 | BCG_2283 | cytochrome P450 124 CYP124 | 36.84 | 428 | MAP1655c | hypothetical protein | 126 | 100 |
| MAP4_2184 | putative nitronate monooxygenase | 320 | Rv3553 | Possible oxidoreductase | 28.36 | 355 | Mb3583 | oxidoreductase | 28.36 | 355 | MAV_2769 | oxidoreductase, 2-nitropropane dio | 100 | 293 | BCG_3617 | oxidoreductase | 28.36 | 355 | MAP1654c | hypothetical protein | 320 | 100 |
| MAP4_2185 | thiol peroxidase tpx | 164 | Rv1932 | Probable thiol peroxidase Tpx | 84.15 | 165 | Mb1967 | thiol peroxidase | 84.15 | 165 | MAV_2770 | thiol peroxidase | 99.39 | 164 | BCG_1971 | thiol peroxidase | 84.15 | 165 | MAP1653 | thiol peroxidase | 164 | 100 |
| MAP4_2186 | Transcriptional regulator, AraC family | 320 | Rv1931c | Probable transcriptional regulatory | 84.71 | 259 | Mb1966c | transcriptional regulator | 84.71 | 259 | MAV_4981 | AraC family transcriptional regulato | 43.96 | 324 | BCG_1970c | transcriptional regulatory prot | 84.71 | 259 | MAP1652c | hypothetical protein | 320 | 100 |
| MAP4_2187 | putative amidotransferase | 247 | Rv1930c | hypothetical protein | 76.92 | 174 | Mb1965c | hypothetical protein | 76.92 | 174 | MAV_2773 | DJ-1/PfpI family protein | 99.19 | 247 | BCG_1969c | hypothetical protein | 76.92 | 174 | MAP1651c | hypothetical protein | 247 | 100 |
| MAP4_2188 | hypothetical protein | 158 | Rv0138 | hypothetical protein | 37.88 | 167 | Mb0143 | hypothetical protein | 37.88 | 167 | MAV_2774 | hypothetical protein | 99.37 | 161 | BCG_0174 | hypothetical protein | 37.88 | 167 | MAP1650 | hypothetical protein | 158 | 100 |
| MAP4_2189 | putative short-chain type dehydrogenase/reductase | 256 | Rv1928c | Probable short-chain type dehydrog | 75.78 | 255 | Mb1963c | short chain dehydrogenase | 75.78 | 255 | MAV_2775 | short chain dehydrogenase | 98.43 | 254 | BCG_1967c | short chain dehydrogenase | 75.78 | 255 | MAP1649c | short chain dehydrogenase | 256 | 100 |
| MAP4_2190 | hypothetical protein | 241 | Rv1748 | hypothetical protein | 61.51 | 243 | Mb1777 | hypothetical protein | 61.51 | 243 | MAV_2776 | hypothetical protein | 98.2 | 222 | BCG_1787 | hypothetical protein | 61.51 | 243 | MAP1648 | hypothetical protein | 241 | 100 |
| MAP4_2191 | acyl-CoA ligase fadD31 | 612 | Rv1925 | Probable acyl-CoA ligase FadD31 (ac | 74.6 | 620 | Mb1960 | fatty-acid--CoA ligase | 74.6 | 620 | MAV_2777 | fatty-acid--CoA ligase | 98.2 | 612 | BCG_1964 | fatty-acid--CoA ligase | 74.6 | 620 | MAP1647 | fatty-acid--CoA ligase | 612 | 100 |
| MAP4_2192 | hypothetical protein | 155 | Rv1919c | hypothetical protein | 78.15 | 154 | Mb1954c | hypothetical protein | 78.15 | 154 | MAV_2778 | hypothetical protein | 99.35 | 155 | BCG_1958c | hypothetical protein | 78.15 | 154 | MAP1646c | hypothetical protein | 155 | 100 |
| MAP4_2193 | monooxygenase | 387 | Rv3618 | Possible monooxygenase | 44.29 | 395 | Mb1971 | monooxygenase | 28.34 | 369 | MAV_2779 | limonene 1,2-monooxygenase | 99.22 | 387 | BCG_1975 | monooxygenase | 28.34 | 369 | MAP1645 | hypothetical protein | 387 | 100 |
| MAP4_2194 | hypothetical protein | 153 | Rv2874 | Possible integral membrane C-type | 38 | 695 | Mb2899 | integral membrane C-type cy | 38 | 695 | MAV_4188 | hypothetical protein | 55.56 | 380 | BCG_2896 | integral membrane C-type cyto | 38 | 695 | MAP1644 | hypothetical protein | 153 | 100 |
| MAP4_2195 | isocitrate lyase | 762 | Rv1916 | Probable isocitrate lyase AceAb [sec | 87.15 | 398 | Mb1950 | isocitrate lyase | 86.41 | 766 | MAV_2781 | isocitrate lyase | 99.87 | 762 | BCG_1954 | isocitrate lyase aceA | 86.41 | 766 | MAP1643 | isocitrate lyase | 762 | 100 |
| MAP4_2196 | metallo-beta-lactamase superfamily protein | 237 | Rv1913 | hypothetical protein | 75 | 250 | Mb1948 | hypothetical protein | 75 | 250 | MAV_2782 | metallo-beta-lactamase | 97.47 | 237 | BCG_1952 | hypothetical protein | 74.58 | 250 | MAP1642 | hypothetical protein | 237 | 100 |
| MAP4_2197 | Transcriptional regulator, ArsR family | 107 | Rv2034 | ArsR repressor protein | 39.05 | 107 | Mb2060 | ArsR family transcriptional re | 39.05 | 107 | MAV_2783 | ArsR family transcriptional regulato | 100 | 107 | BCG_2053 | ArsR family transcriptional regu | 39.05 | 107 | MAP1641c | hypothetical protein | 107 | 100 |
| MAP4_2198 | hypothetical protein | 135 | Rv1883c | hypothetical protein | 26.47 | 153 | Mb1915c | hypothetical protein | 27.4 | 158 | MAV_2784 | hypothetical protein | 98.52 | 135 | BCG_1920c | hypothetical protein | 27.4 | 158 | MAP1640c | hypothetical protein | 135 | 100 |
| MAP4_2199 | hypothetical protein | 149 | Rv0854 | hypothetical protein | 57.24 | 147 | Mb0877 | hypothetical protein | 57.24 | 147 | MAV_2785 | cyclase/dehydrase | 99.33 | 149 | BCG_0906 | hypothetical protein | 57.24 | 147 | MAP1639c | hypothetical protein | 149 | 100 |
| MAP4_2200 | phosphatidylethanolamine-binding protein | 202 | Rv1910c | Probable exported protein | 60.61 | 197 | Mb1945c | hypothetical protein | 60.61 | 197 | MAV_2786 | phosphatidylethanolamine-binding | 99.01 | 202 | BCG_1949c | hypothetical protein | 60.61 | 197 | MAP1638c | hypothetical protein | 206 | 95.15 |
| MAP4_2201 | 3-polyprenyl-4-hydroxybenzoate carboxy-lyase | 479 | Rv0333 | hypothetical protein | 29.03 | 124 | Mb0340 | hypothetical protein | 29.03 | 124 | MAV_3455 | metallophosphoesterase | 24.11 | 536 | BCG_0372 | hypothetical protein | 29.03 | 124 | MAP1637c | hypothetical protein | 479 | 100 |
| MAP4_2202 | hypothetical protein | 157 | Rv1527c | Probable polyketide synthase Pks5 | 42.86 | 2108 | Mb1554c | polyketide synthase | 42.86 | 2108 | MAV_4926 | catalase KatA | 25.84 | 484 | BCG_1579c | polyketide synthase pks5 | 42.86 | 2108 | MAP1636c | hypothetical protein | 157 | 100 |
| MAP4_2203 | putative flavoprotein | 207 | Rv0694 | Possible L-lactate dehydrogenase (cy | 25.26 | 396 | Mb0713 | L-lactate dehydrogenase (cyto | 25.26 | 396 | MAV_1508 | diaminopimelate decarboxylase | 40.62 | 472 | BCG_0743 | L-lactate dehydrogenase (cytoc | 25.26 | 396 | MAP1635c | hypothetical protein | 207 | 100 |
| MAP4_2204 | transcriptional regulator, LysR family | 305 | Rv0117 | Oxidative stress response regulatory | 29.2 | 314 | Mb0121 | oxidative stress response regu | 29.2 | 314 | MAV_2838 | hydrogen peroxide-inducible genes | 36.16 | 311 | BCG_0151 | oxidative stress response regul | 29.2 | 314 | MAP1634 | hypothetical protein | 305 | 100 |
| MAP4_2205 | hypothetical protein | 99 | Rv1833c | Possible haloalkane dehalogenase | 35.85 | 286 | Mb1864c | haloalkane dehalogenase | 35.85 | 286 | MAV_3056 | linear gramicidin synthetase subun | 38.71 | 10421 | BCG_1868c | haloalkane dehalogenase | 35.85 | 286 | MAP0109 | Mce1B | 359 | 36.11 |
| MAP4_2206 | hypothetical protein | 120 | Rv1489 | hypothetical protein | 36.47 | 118 | Mb1525 | hypothetical protein | 36.47 | 118 | MAV_2474 | integral membrane protein | 53.1 | 116 | BCG_1551 | hypothetical protein | 36.47 | 118 | MAP1633c | hypothetical protein | 117 | 99.15 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2207 | major facilitator superfamily (MFS) transporter | 455 | Rv2459 | Probable conserved integral membr | 33.18 | 508 | Mb2486 | integral membrane transport | 33.18 | 508 | MAV_1387 | drug transporter | 32.61 | 626 | BCG_2479 | integral membrane transport p | 33.18 | 508 | MAP1632c | hypothetical protein | 455 | 100 |
| MAP4_2208 | Transcriptional regulator, TetR family | 225 | Rv0196 | Possible transcriptional regulatory p | 26.02 | 194 | Mb0202 | transcriptional regulator | 26.02 | 194 | MAV_1931 | TetR family transcriptional regulato | 41.38 | 211 | BCG_0233 | transcriptional regulatory prote | 26.02 | 194 | MAP1631c | hypothetical protein | 225 | 100 |
| MAP4_2209 | hypothetical protein | 208 | Rv1906c | hypothetical protein | 53.71 | 156 | Mb1941c | hypothetical protein | 53.71 | 156 | MAV_2795 | hypothetical protein | 98.96 | 193 | BCG_1945c | hypothetical protein | 53.71 | 156 | MAP1630c | hypothetical protein | 208 | 100 |
| MAP4_2210 | D-amino-acid oxidase | 321 | Rv1905c | Probable D-amino acid oxidase Aao | 67.52 | 320 | Mb1940c | D-amino acid oxidase aao | 67.83 | 320 | MAV_2796 | FAD dependent oxidoreductase | 99.38 | 321 | BCG_1944c | D-amino acid oxidase aao | 67.83 | 320 | MAP1629c | Aao | 321 | 100 |
| MAP4_2211 | hypothetical protein | 129 | Rv1903 | Probable conserved membrane prot | 84 | 134 | Mb1938 | hypothetical protein | 84 | 134 | MAV_2797 | hypothetical protein | 100 | 129 | BCG_1942 | hypothetical protein | 84 | 134 | MAP1628 | hypothetical protein | 129 | 100 |
| MAP4_2212 | putative amidohydrolase | 355 | Rv2303c | Probable antibiotic-resistance prote | 27.17 | 307 | Mb2325c | antibiotic-resistance protein | 27.17 | 307 | MAV_2798 | amidohydrolase | 98.87 | 355 | BCG_2319c | antibiotic-resistance protein | 27.17 | 307 | MAP1627 | hypothetical protein | 355 | 100 |
| MAP4_2213 | sialic acid-transport membrane protein nanT | 424 | Rv1902c | Probable sialic acid-transport integra | 87.1 | 422 | Mb1937c | sialic acid-transport integral r | 87.1 | 422 | MAV_2799 | MFS transporter, sialate:H+ sympo | 98.82 | 450 | BCG_1941c | sialic acid-transport integral me | 87.1 | 422 | MAP1626c | NanT | 424 | 99.76 |
| MAP4_2214 | Competencedamage-inducible protein CinA | 434 | Rv1901 | Probable CinA-like protein CinA | 80.56 | 430 | Mb1936 | competence damage-inducibl | 80.56 | 430 | MAV_2800 | competence damage-inducible pro | 99.08 | 434 | BCG_1940 | competence damage-inducible | 80.56 | 430 | MAP1625 | competence damage-inducible protein | 434 | 100 |
| MAP4_2215 | hypothetical protein | 101 | Rv1898 | hypothetical protein | 87.76 | 102 | Mb1933 | hypothetical protein | 87.76 | 102 | MAV_2801 | hypothetical protein | 100 | 101 | BCG_1937 | hypothetical protein | 87.76 | 102 | MAP1624 | hypothetical protein | 101 | 100 |
| MAP4_2216 | D-tyrosyl-tRNA(Tyr) deacylase | 143 | Rv1897c | hypothetical protein | 80.28 | 143 | Mb1932c | D-tyrosyl-tRNA(Tyr) deacylase | 80.28 | 143 | MAV_2802 | D-tyrosyl-tRNA(Tyr) deacylase | 97.2 | 143 | BCG_1936c | D-tyrosyl-tRNA(Tyr) deacylase | 79.58 | 143 | MAP1623c | D-tyrosyl-tRNA(Tyr) deacylase | 143 | 100 |
| MAP4_2217 | methyltransferase, leucine carboxyl methyltransferase | 302 | Rv1896c | hypothetical protein | 74.83 | 303 | Mb1931c | hypothetical protein | 74.83 | 303 | MAV_2803 | methyltransferase, putative, family | 99.67 | 302 | BCG_1935c | hypothetical protein | 74.83 | 303 | MAP1622c | hypothetical protein | 302 | 100 |
| MAP4_2218 | dehydrogenase | 341 | Rv1895 | Possible dehydrogenase | 78.3 | 384 | Mb1929 | dehydrogenase | 83.26 | 234 | MAV_2804 | zinc-binding dehydrogenase | 99.71 | 341 | BCG_1934 | dehydrogenase | 83.26 | 234 | MAP1621 | hypothetical protein | 341 | 100 |
| MAP4_2219 | monooxygenase | 649 | Rv1393c | Probable monoxygenase | 36.71 | 492 | Mb1428c | monoxygenase | 36.71 | 492 | MAV_2805 | 4-hydroxyacetophenone monooxyg | 98.81 | 650 | BCG_1454c | monoxygenase | 36.71 | 492 | MAP1620 | hypothetical protein | 671 | 100 |
| MAP4_2220 | REP13E12 repeat protein | 469 | Rv1128c | hypothetical protein | 64.8 | 451 | Mb1159c | hypothetical protein | 64.8 | 451 | MAV_2806 | hypothetical protein | 96.59 | 469 | BCG_1189c | hypothetical protein | 64.8 | 451 | MAP1619 | hypothetical protein | 469 | 100 |
| MAP4_2221 | oxidoreductase, 2-nitropropane dioxygenase family pro | 376 | Rv1894c | hypothetical protein | 90.96 | 376 | Mb1927c | hypothetical protein | 90.96 | 376 | MAV_2807 | oxidoreductase, 2-nitropropane dic | 100 | 376 | BCG_1932c | hypothetical protein | 90.96 | 376 | MAP1618c | hypothetical protein | 376 | 100 |
| MAP4_2222 | hypothetical protein | 76 | Rv1893 | hypothetical protein | 82.61 | 72 | Mb1926 | hypothetical protein | 82.61 | 72 | MAV_2808 | hypothetical protein | 100 | 76 | BCG_1931 | hypothetical protein | 82.61 | 72 | MAP1617 | hypothetical protein | 76 | 100 |
| MAP4_2223 | hypothetical protein | 104 | Rv1892 | Probable membrane protein | 79.79 | 103 | Mb1925 | hypothetical protein | 79.79 | 103 | MAV_2809 | hypothetical protein | 98.08 | 109 | BCG_1930 | hypothetical protein | 79.79 | 103 | MAP1616 | hypothetical protein | 104 | 100 |
| MAP4_2224 | hypothetical protein | 132 | Rv1891 | hypothetical protein | 79.1 | 135 | Mb1924 | hypothetical protein | 79.1 | 135 | MAV_2810 | hypothetical protein | 100 | 132 | BCG_1929 | hypothetical protein | 79.1 | 135 | MAP1615 | hypothetical protein | 132 | 100 |
| MAP4_2225 | cytochrome P450 | 428 | Rv3545c | Probable cytochrome P450 125 Cyp | 74.41 | 433 | Mb3575c | cytochrome P450 125 | 74.41 | 433 | MAV_2811 | cytochrome P450 124 | 99.53 | 428 | BCG_3609c | cytochrome P450 125 cyp125 | 74.41 | 433 | MAP1614c | hypothetical protein | 428 | 100 |
| MAP4_2226 | Alcohol dehydrogenase | 337 | Rv3045 | Probable NADP-dependent alcohol d | 31.3 | 346 | Mb3071 | NADP-dependent alcohol deh | 31.3 | 346 | MAV_2812 | aldehyde dehydrogenase | 99.69 | 322 | BCG_3069 | NADP-dependent alcohol dehy | 31.3 | 346 | MAP1613c | AdhA_2 | 337 | 100 |
| MAP4_2227 | hypothetical protein | 188 | Rv1890c | Hypothetical protein | 70.17 | 203 | Mb1923c | hypothetical protein | 70.17 | 203 | MAV_2813 | hypothetical protein | 95.21 | 188 | BCG_1928c | hypothetical protein | 70.17 | 203 | MAP1612c | hypothetical protein | 188 | 100 |
| MAP4_2228 | hypothetical protein | 383 | Rv1887 | Hypothetical protein | 57.22 | 380 | Mb1919 | hypothetical protein | 57.22 | 380 | MAV_2814 | hypothetical protein | 98.67 | 375 | BCG_1924 | hypothetical protein | 56.96 | 380 | MAP1611 | hypothetical protein | 383 | 100 |
| MAP4_2229 | hypothetical protein | 194 | Rv0175 | Probable conserved Mce associated | 47.83 | 213 | Mb2199c | transposase | 50 | 221 | MAV_2396 | mercuric reductase | 27.47 | 456 | BCG_2192c | transposase | 50 | 221 | MAP1610 | hypothetical protein | 194 | 100 |
| MAP4_2230 | secreted fibronectin-binding protein antigen85-B fbpB | 330 | Rv1886c | Secreted antigen 85-B FbpB (85B) (a | 85.49 | 325 | Mb1918c | secreted antigen 85-B FbpB | 85.49 | 325 | MAV_2816 | antigen 85-B | 100 | 330 | BCG_1923c | hypothetical protein | 85.19 | 325 | MAP1609c | FbpB | 330 | 99.7 |
| MAP4_2231 | Periplasmic chorismate mutase I precursor | 187 | Rv1885c | Chorismate mutase | 60.98 | 199 | Mb1917c | chorismate mutase | 60.98 | 199 | MAV_2817 | chorismate mutase | 98.93 | 187 | BCG_1922c | chorismate mutase | 60.98 | 199 | MAP1608c | chorismate mutase | 168 | 99.4 |
| MAP4_2232 | resuscitation-promoting factor RpfC | 170 | Rv1884c | Probable resuscitation-promoting fa | 65.64 | 176 | Mb1916c | resuscitation-promoting facto | 65.64 | 176 | MAV_2818 | resuscitation-promoting factor Rpf | 99.08 | 109 | BCG_1921c | resuscitation-promoting factor | 65.64 | 176 | MAP1607c | hypothetical protein | 170 | 100 |
| MAP4_2233 | cyclasedehydrase superfamily protein | 159 | Rv1883c | hypothetical protein | 78.34 | 153 | Mb1915c | hypothetical protein | 80.89 | 158 | MAV_2819 | cyclase/dehydrase | 99.35 | 153 | BCG_1920c | hypothetical protein | 80.89 | 158 | MAP1606c | hypothetical protein | 159 | 100 |
| MAP4_2234 | short-chain type dehydrogenasereductase | 277 | Rv1882c | Probable short-chain type dehydrog | 80.87 | 277 | Mb1914c | short chain dehydrogenase | 80.87 | 277 | MAV_2820 | short chain dehydrogenase | 99.28 | 277 | BCG_1919c | short chain dehydrogenase | 80.87 | 277 | MAP1605c | short chain dehydrogenase | 277 | 100 |
| MAP4_2235 | lipoprotein LppE | 140 | Rv1881c | Possible conserved lipoprotein LppE | 65 | 140 | Mb1913c | lipoprotein LppE | 65 | 140 | MAV_2821 | LppE protein | 99.29 | 140 | BCG_1918c | lipoprotein lppE | 65 | 140 | MAP1604c | hypothetical protein | 140 | 100 |
| MAP4_2236 | Putative cytochrome P450 cyp140 | 450 | Rv1880c | Probable cytochrome P450 140 Cyp | 77.8 | 438 | Mb1912c | cytochrome p450 140 CYP140 | 77.8 | 438 | MAV_2822 | P450 heme-thiolate protein | 99.78 | 450 | BCG_1917c | cytochrome p450 140 CYP140 | 77.8 | 438 | MAP1603c | hypothetical protein | 450 | 100 |
| MAP4_2237 | hypothetical protein | 152 | Rv2740 | Epoxide hydrolase | 24.64 | 149 | Mb2760 | hypothetical protein | 24.64 | 149 | MAV_2823 | limonene-1,2-epoxide hydrolase ca | 97.28 | 147 | BCG_2754 | epoxide hydrolase | 24.64 | 149 | MAP1602c | hypothetical protein | 152 | 100 |
| MAP4_2238 | hypothetical protein | 426 | Rv0229c | Possible conserved membrane prote | 44 | 226 | Mb0234c | hypothetical protein | 44 | 226 | MAV_2824 | hypothetical protein | 98.72 | 392 | BCG_0266c | hypothetical protein | 44 | 226 | MAP1601 | hypothetical protein | 426 | 100 |
| MAP4_2239 | putative amidohydrolase | 372 | Rv1879 | hypothetical protein | 75.75 | 378 | Mb1911 | hypothetical protein | 75.75 | 378 | MAV_2828 | amidohydrolase | 97.58 | 372 | BCG_1916 | hypothetical protein | 75.75 | 378 | MAP1600 | hypothetical protein | 372 | 100 |
| MAP4_2240 | Glutamine synthetase | 450 | Rv1878 | Probable glutamine synthetase GlnA | 80.89 | 450 | Mb1910 | glutamine synthetase | 80.67 | 450 | MAV_2829 | glutamine synthetase catalytic dom | 99.56 | 450 | BCG_1915 | glutamine synthetase glnA3 | 80.89 | 450 | MAP1599 | GlnA3 | 450 | 100 |
| MAP4_2241 | oxidoreductase | 293 | Rv0940c | Possible oxidoreductase | 35.43 | 288 | Mb0965c | oxidoreductase | 35.43 | 288 | MAV_2830 | hypothetical protein | 97.95 | 293 | BCG_0994c | oxidoreductase | 35.43 | 288 | MAP1598 | hypothetical protein | 293 | 100 |
| MAP4_2242 | hypothetical protein | 164 | Rv2159c | hypothetical protein | 40.48 | 344 | Mb2183c | hypothetical protein | 40.48 | 344 | MAV_2831 | hypothetical protein | 100 | 164 | BCG_2176c | hypothetical protein | 40.48 | 344 | MAP1597 | hypothetical protein | 164 | 100 |
| MAP4_2243 | hypothetical protein | 689 | Rv1877 | Probable conserved integral membr | 62.93 | 687 | Mb1909 | hypothetical protein | 61.58 | 404 | MAV_2832 | drug transporter | 99.12 | 682 | BCG_1914 | integral membrane protein | 61.58 | 404 | MAP1596 | hypothetical protein | 689 | 100 |
| MAP4_2244 | Bacterioferritin (BFR) | 159 | Rv1876 | Probable bacterioferritin BfrA | 88.05 | 159 | Mb1907 | bacterioferritin | 88.05 | 159 | MAV_2833 | bacterioferritin | 100 | 159 | BCG_1912 | bacterioferritin bfrA | 88.05 | 159 | MAP1595 | BfrA | 159 | 100 |
| MAP4_2245 | hypothetical protein | 61 | Rv3370c | Probable DNA polymerase III (alpha | 33.33 | 1079 | Mb3405c | error-prone DNA polymerase | 33.33 | 1091 | MAV_2834 | hypothetical protein | 100 | 61 | BCG_3442c | error-prone DNA polymerase | 33.33 | 1079 | MAP1594c | hypothetical protein | 61 | 100 |
| MAP4_2246 | Enoyl-CoA hydratase | 249 | Rv1070c | Probable enoyl-CoA hydratase EchA | 30.12 | 257 | Mb1099c | enoyl-CoA hydratase | 30.12 | 257 | MAV_2835 | enoyl-CoA hydratase/isomerase | 100 | 249 | BCG_1128c | enoyl-CoA hydratase | 30.12 | 257 | MAP1593 | hypothetical protein | 249 | 100 |
| MAP4_2247 | hypothetical protein | 147 | Rv1875 | hypothetical protein | 82.99 | 147 | Mb1906 | hypothetical protein | 82.99 | 147 | MAV_2836 | pyridoxamine 5'-phosphate oxidase | 98.64 | 147 | BCG_1911 | hypothetical protein | 82.99 | 147 | MAP1592 | hypothetical protein | 147 | 100 |
| MAP4_2248 | hypothetical protein | 233 | Rv1874 | hypothetical protein | 76.55 | 228 | Mb1905 | hypothetical protein | 76.55 | 228 | MAV_2837 | hypothetical protein | 99.14 | 233 | BCG_1910 | hypothetical protein | 76.55 | 228 | MAP1591 | hypothetical protein | 233 | 100 |
| MAP4_2249 | Hydrogen peroxide-inducible genes activator | 306 | Rv2282c | Probable transcription regulator (Ly | 30.23 | 312 | Mb2303c | LysR family transcriptional re | 30.23 | 312 | MAV_2838 | hydrogen peroxide-inducible genes | 96.14 | 311 | BCG_2297c | LysR family transcriptional regu | 30.23 | 312 | MAP1590 | OxyR | 325 | 100 |
| MAP4_2250 | alkyl hydroperoxide reductase C protein AhpC | 195 | Rv2428 | Alkyl hydroperoxide reductase C pro | 89.74 | 195 | Mb2454 | alkyl hydroperoxide reductas | 89.74 | 195 | MAV_2839 | alkylhydroperoxide reductase | 99.49 | 195 | BCG_2447 | alkyl hydroperoxide reductase | 89.74 | 195 | MAP1589c | hypothetical protein | 195 | 100 |
| MAP4_2251 | alkyl hydroperoxide reductase D protein ahpD | 178 | Rv2429 | Alkyl hydroperoxide reductase D pro | 73.45 | 177 | Mb2455 | alkyl hydroperoxide reductas | 73.45 | 177 | MAV_2840 | alkylhydroperoxidase, AhpD family | 99.44 | 178 | BCG_2448 | alkyl hydroperoxide reductase | 73.45 | 177 | MAP1588c | AhpD | 178 | 100 |
| MAP4_2252 | putative alpha amylase | 444 | Rv0126 | Trehalose synthase TreS | 31.34 | 601 | Mb0131 | trehalose synthase TRES | 31.34 | 601 | MAV_2842 | alpha-amylase 3 | 98.64 | 440 | BCG_0160 | trehalose synthase treS | 31.34 | 601 | MAP1587c | hypothetical protein | 444 | 100 |
| MAP4_2253 | hypothetical protein | 151 | Rv1873 | hypothetical protein | 74.13 | 145 | Mb1904 | hypothetical protein | 73.43 | 145 | MAV_2841 | hypothetical protein | 97.24 | 145 | BCG_1909 | hypothetical protein | 74.13 | 145 | MAP1586 | hypothetical protein | 151 | 100 |
| MAP4_2254 | L-lactate dehydrogenase | 420 | Rv1872c | Possible L-lactate dehydrogenase (c | 85.61 | 414 | Mb1903c | L-lactate dehydrogenase (cyt | 86.1 | 414 | MAV_2843 | LldD2 protein | 99.05 | 420 | BCG_1908c | L-lactate dehydrogenase (cyto | 86.1 | 414 | MAP1585c | LldD2 | 420 | 100 |
| MAP4_2255 | ATP-dependent protease La | 773 | Rv2897c | hypothetical protein | 30.87 | 503 | Mb2921c | hypothetical protein | 30.87 | 503 | MAV_3751 | Mg-chelatase subunits D/I family p | 30.14 | 503 | BCG_2918c | hypothetical protein | 30.87 | 503 | MAP1584c | hypothetical protein | 773 | 100 |
| MAP4_2256 | hypothetical protein | 132 | Rv1871c | hypothetical protein | 81.4 | 129 | Mb1902c | hypothetical protein | 81.4 | 129 | MAV_2845 | hypothetical protein | 98.4 | 125 | BCG_1907c | hypothetical protein | 81.4 | 129 | MAP1583c | hypothetical protein | 132 | 100 |
| MAP4_2257 | hypothetical protein | 110 | Rv2940c | Probable multifunctional mycoceros | 56.52 | 2111 | Mb1197 | GTP-binding translation elong | 42.5 | 628 | MAV_2846 | hypothetical protein | 99.09 | 110 | BCG_1227 | GTP-binding translation elonga | 42.5 | 628 | MAP1582c | hypothetical protein | 110 | 100 |
| MAP4_2258 | hypothetical protein | 222 | Rv1870c | hypothetical protein | 72.04 | 211 | Mb1901c | hypothetical protein | 71.17 | 222 | MAV_2847 | hypothetical protein | 98.58 | 211 | BCG_1906c | hypothetical protein | 71.17 | 222 | MAP1581c | hypothetical protein | 222 | 100 |
| MAP4_2259 | hypothetical protein | 241 | Rv2924c | Probable formamidopyrimidine-DNA | 27.66 | 289 | Mb2949c | formamidopyrimidine-DNA gl | 27.66 | 289 | MAV_2848 | hypothetical protein | 99.17 | 241 | BCG_2946c | formamidopyrimidine-DNA gly | 27.66 | 289 | MAP1580c | hypothetical protein | 241 | 100 |
| MAP4_2260 | anthranilate dioxygenase reductase | 410 | Rv1869c | Probable reductase | 76.72 | 411 | Mb1900c | reductase | 76.72 | 411 | MAV_2849 | anthranilate dioxygenase reductase | 98.54 | 410 | BCG_1905c | reductase | 76.72 | 411 | MAP1579c | hypothetical protein | 410 | 100 |
| MAP4_2261 | hypothetical protein | 707 | Rv1868 | hypothetical protein | 70.16 | 699 | Mb1899 | hypothetical protein | 70.16 | 699 | MAV_2850 | hypothetical protein | 98.17 | 709 | BCG_1904 | hypothetical protein | 70.01 | 699 | MAP1578 | hypothetical protein | 707 | 100 |
| MAP4_2262 | putative acetyl-CoA acetyltransferase | 494 | Rv1867 | hypothetical protein | 78.34 | 494 | Mb1898 | acetyl-CoA acetyltransferase | 78.34 | 494 | MAV_2851 | acetyl-CoA acetyltransferase | 99.39 | 494 | BCG_1903 | acetyl-CoA acetyltransferase | 78.34 | 494 | MAP1577 | acetyl-CoA acetyltransferase | 494 | 100 |
| MAP4_2263 | CoA-transferase family III protein | 814 | Rv1866 | hypothetical protein | 78.22 | 778 | Mb1897 | hypothetical protein | 78.09 | 778 | MAV_2852 | caib/baif family protein | 99.26 | 814 | BCG_1902 | hypothetical protein | 78.09 | 778 | MAP1576 | hypothetical protein | 814 | 100 |
| MAP4_2264 | membrane protein, bacitracin resistance protein BacA | 305 | Rv2136c | Possible conserved transmembrane | 33.66 | 276 | Mb2160c | undecaprenyl pyrophosphate | 33.66 | 276 | MAV_2853 | undecaprenyl pyrophosphate phos | 99.34 | 305 | BCG_2153c | UDP pyrophosphate phosphata | 33.66 | 276 | MAP1575c | UDP pyrophosphate phosphatase | 305 | 100 |
| MAP4_2265 | short-chain dehydrogenase | 282 | Rv1865c | Probable short-chain type dehydrog | 77.27 | 286 | Mb1896c | short chain dehydrogenase | 77.27 | 286 | MAV_2854 | short chain dehydrogenase | 99.65 | 282 | BCG_1901c | short chain dehydrogenase | 77.27 | 286 | MAP1574c | short chain dehydrogenase | 282 | 100 |
| MAP4_2266 | putative phosphoketolase | 804 | Rv0853c | Probable pyruvate or indole-3-pyruv | 38.78 | 560 | Mb0876c | pyruvate or indole-3-pyruvate | 38.78 | 560 | MAV_2855 | phosphoketolase | 99.63 | 804 | BCG_0905c | pyruvate or indole-3-pyruvate | 38.78 | 560 | MAP1573c | phosphoketolase | 804 | 100 |
| MAP4_2267 | hypothetical protein | 251 | Rv1863c | Probable conserved integral membr | 83.76 | 256 | Mb1894c | hypothetical protein | 83.76 | 256 | MAV_2856 | caax amino protease | 99.2 | 251 | BCG_1899c | integral membrane protein | 83.76 | 256 | MAP1572c | hypothetical protein | 251 | 100 |
| MAP4_2268 | Alcohol dehydrogenase | 343 | Rv1862 | Probable alcohol dehydrogenase Ad | 84.97 | 346 | Mb1893 | alcohol dehydrogenase | 84.97 | 346 | MAV_2857 | zinc-binding alcohol dehydrogenase | 99.11 | 338 | BCG_1898 | alcohol dehydrogenase adhA | 84.97 | 346 | MAP1571 | AdhA_1 | 343 | 100 |
| MAP4_2269 | hypothetical protein | 99 | Rv1861 | Probable conserved transmembrane | 57.43 | 101 | Mb1892 | transmembrane protein | 57.43 | 101 | MAV_2858 | integral membrane protein | 100 | 116 | BCG_1897 | hypothetical protein | 57.43 | 101 | MAP1570 | hypothetical protein | 99 | 100 |
| MAP4_2270 | alanine and proline rich secreted protein apa | 368 | Rv1860 | Alanine and proline rich secreted pr | 74.74 | 325 | Mb1891 | hypothetical protein | 75.26 | 325 | MAV_2859 | ModD protein | 100 | 385 | BCG_1896 | hypothetical protein | 75.26 | 325 | MAP1569 | ModD | 368 | 100 |
| MAP4_2271 | molybdenum ABC transport ATP-binding protein ModC | 371 | Rv1859 | Probable molybdenum-transport AT | 77.53 | 369 | Mb1890 | molybdenum ABC transporte | 77.53 | 369 | MAV_2860 | molybdenum import ATP-binding p | 98.92 | 371 | BCG_1895 | molybdenum-transport ATP-bi | 77.53 | 369 | MAP1568 | hypothetical protein | 371 | 100 |
| MAP4_2272 | molbdenum-transport integral membrane protein ABC | 258 | Rv1858 | Probable molybdenum-transport int | 85.27 | 264 | Mb1889 | molbdenum-transport integra | 85.27 | 264 | MAV_2861 | molybdate ABC transporter permea | 98.03 | 254 | BCG_1894 | molbdenum-transport integral | 85.27 | 264 | MAP1567 | ModB | 258 | 100 |
| MAP4_2273 | hypothetical protein | 357 | Rv1645c | hypothetical protein | 34.88 | 351 | Mb1672c | hypothetical protein | 34.88 | 351 | MAV_2862 | hypothetical protein | 100 | 369 | BCG_1684c | hypothetical protein | 34.88 | 351 | MAP1566 | hypothetical protein | 357 | 100 |
| MAP4_2274 | molybdate-binding lipoprotein ModA1 | 255 | Rv1857 | Probable molybdate-binding lipopro | 65.9 | 261 | Mb1888 | molybdate-binding lipoprotei | 65.9 | 261 | MAV_2863 | molybdate ABC transporter peripla | 99.61 | 255 | BCG_1893 | molybdate-binding lipoprotein | 65.9 | 261 | MAP1565 | hypothetical protein | 255 | 100 |
| MAP4_2275 | oxidoreductase, short-chaindehydrogenase/reductase | 225 | Rv1856c | Possible oxidoreductase | 80.36 | 225 | Mb1887c | short chain dehydrogenase | 79.91 | 225 | MAV_2864 | short chain dehydrogenase | 99.1 | 223 | BCG_1892c | short chain dehydrogenase | 79.91 | 225 | MAP1564c | short chain dehydrogenase | 225 | 100 |
| MAP4_2276 | oxidoreductase | 305 | Rv1855c | Possible oxidoreductase | 71.9 | 307 | Mb1886c | oxidoreductase | 71.9 | 307 | MAV_2865 | hypothetical protein | 98.69 | 305 | BCG_1891c | oxidoreductase | 71.9 | 307 | MAP1563c | hypothetical protein | 305 | 100 |
| MAP4_2277 | hypothetical protein | 127 | Rv1813c | hypothetical protein | 35.82 | 143 | Mb1843c | hypothetical protein | 35.82 | 143 | MAV_2866 | hypothetical protein | 100 | 127 | BCG_1847c | hypothetical protein | 35.82 | 143 | MAP1562c | hypothetical protein | 127 | 100 |
| MAP4_2278 | NADH dehydrogenase | 324 | Rv1854c | Probable NADH dehydrogenase Ndh | 88.44 | 463 | Mb1885c | NADH dehydrogenase | 88.44 | 463 | MAV_2867 | DoxD family protein/pyridine nucle | 100 | 461 | BCG_1890c | NADH dehydrogenase ndh | 88.12 | 463 | MAP1561c | hypothetical protein | 461 | 100 |
| MAP4_2279 | Thioesterase superfamily protein | 140 | Rv1847 | hypothetical protein | 70.5 | 140 | Mb1878 | hypothetical protein | 71.22 | 140 | MAV_2868 | hypothetical protein | 100 | 140 | BCG_1883 | hypothetical protein | 71.22 | 140 | MAP1560 | hypothetical protein | 140 | 100 |
| MAP4_2280 | Transcriptional regulator, MecI family | 139 | Rv1846c | Transcriptional repressor BlaI | 89.86 | 138 | Mb1877c | transcriptional regulator | 89.13 | 138 | MAV_2869 | CopY family transcriptional regulat | 99.28 | 139 | BCG_1882c | transcriptional regulatory prot | 89.13 | 138 | MAP1559c | hypothetical protein | 139 | 100 |
| MAP4_2281 | hypothetical protein | 316 | Rv1845c | Possible sensor-transducer protein | 88.22 | 316 | Mb1876c | hypothetical protein | 88.22 | 316 | MAV_2870 | integral membrane protein | 100 | 316 | BCG_1881c | hypothetical protein | 87.9 | 316 | MAP1558c | hypothetical protein | 316 | 100 |
| MAP4_2282 | 6-phosphogluconate dehydrogenase | 489 | Rv1844c | Probable 6-phosphogluconate dehy | 85.31 | 485 | Mb1875c | 6-phosphogluconate dehydro | 87.73 | 685 | MAV_2871 | 6-phosphogluconate dehydrogenas | 99.59 | 494 | BCG_1880c | 6-phosphogluconate dehydrog | 87.73 | 685 | MAP1557c | 6-phosphogluconate dehydrogenase | 489 | 100 |
| MAP4_2283 | Inosine-5'-monophosphate dehydrogenase | 478 | Rv1843c | Probable inosine-5'-monophosphate | 86.19 | 479 | Mb1874c | inosine 5-monophosphate de | 86.19 | 479 | MAV_2872 | inosine 5-monophosphate dehydro | 99.58 | 478 | BCG_1879c | inosine 5-monophosphate deh | 86.19 | 479 | MAP1556c | inosine 5-monophosphate dehydrogena | 478 | 100 |
| MAP4_2284 | acyl carrier protein | 89 | Rv1344 | Acyl carrier protein (ACP) MbtL | 81.94 | 106 | Mb1379 | acyl carrier protein | 81.94 | 106 | MAV_2873 | acyl carrier protein | 100 | 101 | BCG_1406 | acyl carrier protein | 81.94 | 106 | MAP1555c | acyl carrier protein | 89 | 100 |
| MAP4_2285 | Long-chain-fatty-acid--CoA ligase | 521 | Rv1345 | Probable fatty acyl-AMP ligase Mbt | 69.96 | 521 | Mb1380 | long-chain-fatty-acid--CoA lig | 69.96 | 521 | MAV_2874 | long-chain-fatty-acid--[acyl-carrier- | 99.23 | 521 | BCG_1407 | long-chain-fatty-acid--ACP ligas | 69.96 | 521 | MAP1554c | long-chain-fatty-acid--ACP ligase | 521 | 100 |
| MAP4_2286 | acyl-CoA dehydrogenase FadE14 | 391 | Rv1346 | Acyl-CoA dehydrogenase MbtN | 81.94 | 386 | Mb1381 | acyl-CoA dehydrogenase | 81.94 | 386 | MAV_2876 | acyl-CoA dehydrogenase | 99.49 | 391 | BCG_1408 | acyl-CoA dehydrogenase fadE1 | 81.94 | 386 | MAP1553c | FadE14 | 388 | 99.74 |
| MAP4_2288 | hypothetical protein | 454 | Rv1842c | hypothetical protein | 79.03 | 455 | Mb1873c | hypothetical protein | 79.03 | 455 | MAV_2878 | CBS domain-containing protein | 100 | 454 | BCG_1878c | hypothetical protein | 79.03 | 455 | MAP1551c | hypothetical protein | 454 | 100 |
| MAP4_2289 | hypothetical protein | 346 | Rv1841c | hypothetical protein | 75.68 | 345 | Mb1872c | hypothetical protein | 76.58 | 349 | MAV_2879 | CBS domain-containing protein | 99.42 | 346 | BCG_1877c | hypothetical protein | 76.58 | 349 | MAP1550c | hypothetical protein | 346 | 100 |
| MAP4_2290 | Malate synthase G | 734 | Rv1837c | Malate synthase G GlcB | 84.29 | 741 | Mb1868c | malate synthase G | 84.29 | 741 | MAV_2880 | malate synthase G | 99.73 | 734 | BCG_1872c | malate synthase G | 84.29 | 741 | MAP1549c | malate synthase G | 734 | 100 |
| MAP4_2291 | hypothetical protein | 683 | Rv1836c | hypothetical protein | 68.69 | 677 | Mb1867c | hypothetical protein | 68.69 | 677 | MAV_2881 | hypothetical protein | 98.98 | 683 | BCG_1871c | hypothetical protein | 68.69 | 677 | MAP1548c | hypothetical protein | 683 | 100 |
| MAP4_2292 | hypothetical protein | 325 | Rv0826 | hypothetical protein | 23.64 | 351 | Mb0849 | hypothetical protein | 23.48 | 351 | MAV_2882 | hypothetical protein | 99.69 | 325 | BCG_0879 | hypothetical protein | 23.48 | 351 | MAP1547c | hypothetical protein | 295 | 99.66 |
| MAP4_2293 | Transcriptional regulator, TetR family | 229 | Rv2506 | Probable transcriptional regulatory | 29.69 | 215 | Mb2534 | TetR family transcriptional re | 29.69 | 215 | MAV_2883 | TetR family transcriptional regulato | 99.04 | 209 | BCG_2526 | TetR family transcriptional regu | 29.69 | 215 | MAP1546c | hypothetical protein | 229 | 100 |
| MAP4_2294 | Glycine dehydrogenase | 941 | Rv1832 | Probable glycine dehydrogenase Gc | 88.2 | 941 | Mb1863 | glycine dehydrogenase | 88.1 | 941 | MAV_2884 | glycine dehydrogenase | 99.47 | 941 | BCG_1867 | glycine dehydrogenase | 88.1 | 941 | MAP1545 | glycine dehydrogenase | 941 | 100 |
| MAP4_2295 | hypothetical protein | 81 | Rv1831 | Hypothetical protein | 55.7 | 85 | Mb1862 | hypothetical protein | 55.7 | 85 | MAV_4046 | TetR family transcriptional regulato | 37.04 | 230 | BCG_1866 | hypothetical protein | 55.7 | 85 | MAP1544 | hypothetical protein | 81 | 100 |
| MAP4_2296 | MerR family transcriptional regulator | 225 | Rv1830 | hypothetical protein | 88.84 | 225 | Mb1861 | hypothetical protein | 88.84 | 225 | MAV_2885 | MerR family transcriptional regulat | 99.52 | 209 | BCG_1865 | hypothetical protein | 88.84 | 225 | MAP1543 | hypothetical protein | 225 | 100 |
| MAP4_2297 | hypothetical protein | 164 | Rv1829 | hypothetical protein | 96.34 | 164 | Mb1860 | hypothetical protein | 95.73 | 164 | MAV_2886 | hypothetical protein | 99.32 | 146 | BCG_1864 | hypothetical protein | 96.34 | 164 | MAP1542 | hypothetical protein | 164 | 100 |
| MAP4_2298 | MerR family transcriptional regulator | 250 | Rv1828 | hypothetical protein | 85.2 | 247 | Mb1859 | hypothetical protein | 85.2 | 247 | MAV_2887 | MerR family transcriptional regulat | 99.2 | 250 | BCG_1863 | hypothetical protein | 85.2 | 247 | MAP1541 | hypothetical protein | 250 | 100 |
| MAP4_2299 | conserved hypothetical protein,FHA-domain-containing | 159 | Rv1827 | Conserved protein with FHA domain | 91.25 | 162 | Mb1858 | hypothetical protein | 91.25 | 162 | MAV_2888 | forkhead-associated protein | 100 | 159 | BCG_1862 | hypothetical protein | 91.25 | 162 | MAP1540 | hypothetical protein | 159 | 100 |
| MAP4_2300 | Glycine cleavage system H protein | 132 | Rv1826 | Probable glycine cleavage system H | 83.58 | 134 | Mb1857 | glycine cleavage system prote | 84.33 | 134 | MAV_2889 | glycine cleavage system protein H | 100 | 132 | BCG_1861 | glycine cleavage system protei | 84.33 | 134 | MAP1539 | glycine cleavage system protein H | 132 | 100 |
| MAP4_2301 | hypothetical protein | 279 | Rv1825 | hypothetical protein | 81.78 | 292 | Mb1856 | hypothetical protein | 81.78 | 292 | MAV_2890 | hypothetical protein | 99.28 | 279 | BCG_1860 | hypothetical protein | 81.78 | 292 | MAP1538 | hypothetical protein | 279 | 100 |
| MAP4_2302 | hypothetical protein | 110 | Rv1824 | hypothetical protein | 94.55 | 121 | Mb1855 | hypothetical protein | 94.55 | 121 | MAV_2891 | integral membrane protein | 100 | 110 | BCG_1859 | hypothetical protein | 94.55 | 121 | MAP1537 | hypothetical protein | 110 | 100 |
| MAP4_2303 | hypothetical protein | 308 | Rv1823 | hypothetical protein | 75.9 | 307 | Mb1854 | hypothetical protein | 75.9 | 307 | MAV_2892 | hypothetical protein | 100 | 308 | BCG_1858 | hypothetical protein | 75.9 | 307 | MAP1536 | hypothetical protein | 308 | 100 |
| MAP4_2304 | CDP-diacylglycerol--glycerol-3-phosphate3- phosphatid | 209 | Rv1822 | Probable CDP-diacylglycerol--glycero | 77.61 | 209 | Mb1853 | CDP-diacylglycerol--glycerol-3 | 77.61 | 209 | MAV_2893 | CDP-alcohol phosphatidyltransfera | 97.61 | 209 | BCG_1857 | CDP-diacylglycerol--glycerol-3- | 77.61 | 209 | MAP1535 | hypothetical protein | 213 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2305 | preprotein translocase ATPase secA2 | 777 | Rv1821 | Possible preprotein translocase ATP | 90.65 | 808 | Mb1852 | preprotein translocase subun | 90.65 | 808 | MAV_2894 | preprotein translocase subunit Sec | 99.74 | 777 | BCG_1856 | preprotein translocase subunit | 90.65 | 808 | MAP1534 | preprotein translocase subunit SecA | 777 | 100 |
| MAP4_2308 | drugs-transport transmembrane ATP-binding protein A | 639 | Rv1819c | Probable drug-transport transmemb | 76.21 | 639 | Mb1850c | drugs-transport transmembra | 76.37 | 639 | MAV_2896 | SbmA protein | 100 | 639 | BCG_1854c | drugs-transport transmembran | 76.37 | 639 | MAP1531c | hypothetical protein | 639 | 100 |
| MAP4_2309 | succinate dehydrogenasefumarate reductase,flavoprot | 497 | Rv1817 | Possible flavoprotein | 76.14 | 487 | Mb1848 | hypothetical protein | 76.14 | 487 | MAV_2897 | hypothetical protein | 99.8 | 497 | BCG_1852 | hypothetical protein | 76.14 | 487 | MAP1530 | hypothetical protein | 497 | 100 |
| MAP4_2310 | hypothetical protein | 166 | Rv1101c | hypothetical protein | 34.83 | 385 | Mb1131c | hypothetical protein | 34.83 | 342 | MAV_2898 | hypothetical protein | 98.77 | 162 | BCG_1161c | hypothetical protein | 34.83 | 342 | MAP1529 | hypothetical protein | 127 | 99.21 |
| MAP4_2311 | Transcriptional regulator, TetR family | 233 | Rv1816 | Possible transcriptional regulatory p | 80.34 | 234 | Mb1846 | transcriptional regulator | 80.34 | 234 | MAV_2899 | TetR family transcriptional regulato | 99.56 | 227 | BCG_1850 | transcriptional regulatory prote | 80.34 | 234 | MAP1528 | hypothetical protein | 233 | 100 |
| MAP4_2312 | hypothetical protein | 148 | Rv1598c | hypothetical protein | 28.89 | 136 | Mb1624c | hypothetical protein | 28.89 | 136 | MAV_2900 | hypothetical protein | 98.65 | 148 | BCG_1636c | hypothetical protein | 28.89 | 136 | MAP1527c | hypothetical protein | 172 | 100 |
| MAP4_2313 | hypothetical protein | 225 | Rv1815 | hypothetical protein | 71.89 | 221 | Mb1845 | hypothetical protein | 72.35 | 221 | MAV_2901 | hypothetical protein | 99.55 | 224 | BCG_1849 | hypothetical protein | 72.35 | 221 | MAP1526 | hypothetical protein | 225 | 100 |
| MAP4_2314 | membrane-bound C-5 sterol desaturase erg3 | 308 | Rv1814 | Membrane-bound C-5 sterol desatu | 80.6 | 300 | Mb1844 | membrane-bound C-5 sterol | 80.6 | 300 | MAV_2902 | C-5 sterol desaturase | 97.73 | 308 | BCG_1848 | membrane-bound C-5 sterol de | 80.6 | 300 | MAP1525 | hypothetical protein | 294 | 99.66 |
| MAP4_2315 | Mg(2+) transport ATPase protein C | 239 | Rv1811 | Possible Mg2+ transport P-type ATP | 77.45 | 234 | Mb1841 | Mg2+ transport P-type ATPas | 77.45 | 234 | MAV_2903 | Mg2+ transporter-C (MgtC) family | 99.58 | 239 | BCG_1845 | Mg2+ transporter | 77.45 | 234 | MAP1524 | MgtC | 239 | 100 |
| MAP4_2316 | hypothetical protein | 106 | Rv1810 | hypothetical protein | 59.41 | 118 | Mb1840 | hypothetical protein | 59.41 | 118 | MAV_2904 | hypothetical protein | 97.09 | 103 | BCG_1844 | hypothetical protein | 59.41 | 118 | MAP1523 | hypothetical protein | 106 | 100 |
| MAP4_2317 | PPE family protein | 461 | Rv1809 | PPE family protein PPE33 | 61.99 | 468 | Mb1830 | PPE family protein | 48.84 | 463 | MAV_2905 | PPE family protein | 98.92 | 461 | BCG_1834 | PPE family protein | 48.84 | 463 | MAP1522 | hypothetical protein | 461 | 100 |
| MAP4_2318 | PPE family protein | 414 | Rv1808 | PPE family protein PPE32 | 60.14 | 409 | Mb1837 | PPE family protein | 60.14 | 409 | MAV_2906 | PPE family protein | 98.79 | 414 | BCG_1841 | PPE family protein | 60.14 | 409 | MAP1521 | hypothetical protein | 414 | 100 |
| MAP4_2319 | hypothetical protein | 102 | Rv1810 | hypothetical protein | 48.54 | 118 | Mb1840 | hypothetical protein | 48.54 | 118 | MAV_2907 | hypothetical protein | 100 | 102 | BCG_1844 | hypothetical protein | 48.54 | 118 | MAP1523 | hypothetical protein | 106 | 50 |
| MAP4_2320 | hypothetical protein | 112 | Rv1804c | hypothetical protein | 49.46 | 108 | Mb1833c | hypothetical protein | 49.46 | 108 | MAV_2908 | hypothetical protein | 100 | 112 | BCG_1837c | hypothetical protein | 49.46 | 108 | MAP1520 | hypothetical protein | 112 | 100 |
| MAP4_2321 | PPE family protein | 467 | Rv1802 | PPE family protein PPE30 | 49.06 | 463 | Mb1830 | PPE family protein | 49.06 | 463 | MAV_2909 | PPE family protein | 99.14 | 467 | BCG_1834 | PPE family protein | 49.06 | 463 | MAP1519 | hypothetical protein | 467 | 100 |
| MAP4_2322 | PPE family protein | 419 | Rv1808 | PPE family protein PPE32 | 55.71 | 409 | Mb1837 | PPE family protein | 56.09 | 409 | MAV_2910 | PPE family protein | 98.81 | 419 | BCG_1841 | PPE family protein | 56.09 | 409 | MAP1518 | hypothetical protein | 419 | 100 |
| MAP4_2323 | hypothetical protein | 118 | Rv1810 | hypothetical protein | 48.18 | 118 | Mb1840 | hypothetical protein | 48.18 | 118 | MAV_2912 | hypothetical protein | 99.1 | 111 | BCG_1844 | hypothetical protein | 48.18 | 118 | MAP1517 | hypothetical protein | 118 | 100 |
| MAP4_2324 | PPE family protein | 404 | Rv1807 | PPE family protein PPE31 | 45.97 | 399 | Mb1836 | PPE family protein | 46.21 | 399 | MAV_2913 | PPE family protein | 98.76 | 404 | BCG_1840 | PPE family protein | 46.21 | 399 | MAP1516 | hypothetical protein | 404 | 100 |
| MAP4_2325 | PPE family protein | 376 | Rv1807 | PPE family protein PPE31 | 46.38 | 399 | Mb1836 | PPE family protein | 46.27 | 399 | MAV_2914 | PPE family protein | 98.14 | 376 | BCG_1840 | PPE family protein | 46.27 | 399 | MAP1515 | hypothetical protein | 376 | 100 |
| MAP4_2326 | PE family protein | 99 | Rv1788 | PE family protein PE18 | 68.89 | 99 | Mb1816 | PE family protein | 68.89 | 99 | MAV_2915 | PE family protein | 97.98 | 99 | BCG_1820 | PE family protein | 68.89 | 99 | MAP1514 | hypothetical protein | 99 | 100 |
| MAP4_2327 | ESX-5 type VII secretion system protein | 610 | Rv1798 | ESX conserved component EccA5 ES | 89.16 | 610 | Mb1826 | hypothetical protein | 89.16 | 610 | MAV_2916 | ATPase AAA | 99.33 | 596 | BCG_1830 | hypothetical protein | 89.16 | 610 | MAP1513 | hypothetical protein | 610 | 100 |
| MAP4_2328 | ESX-5 type VII secretion system protein,probable mem | 402 | Rv1797 | ESX conserved component EccE5 ES | 65.77 | 406 | Mb1825 | hypothetical protein | 65.77 | 406 | MAV_2917 | hypothetical protein | 99.5 | 402 | BCG_1829 | hypothetical protein | 65.77 | 406 | MAP1512 | hypothetical protein | 402 | 100 |
| MAP4_2329 | proline rich membrane-anchored mycosin MycP5(serin | 608 | Rv1796 | Probable proline rich membrane-an | 73.44 | 585 | Mb1824 | Pro-rich protease | 73.44 | 585 | MAV_2918 | subtilase | 98.69 | 609 | BCG_1828 | protease | 73.44 | 585 | MAP1511 | hypothetical protein | 608 | 100 |
| MAP4_2330 | ESX-5 type VII secretion system protein,probable mem | 503 | Rv1795 | ESX conserved component EccD5 ES | 79.13 | 503 | Mb1823 | hypothetical protein | 79.32 | 503 | MAV_2919 | secretion protein Snm4 | 99.8 | 503 | BCG_1827 | hypothetical protein | 79.13 | 503 | MAP1510 | hypothetical protein | 503 | 100 |
| MAP4_2331 | hypothetical protein | 300 | Rv1794 | hypothetical protein | 94 | 300 | Mb1822 | hypothetical protein | 94 | 300 | MAV_2920 | hypothetical protein | 100 | 300 | BCG_1826 | hypothetical protein | 94 | 300 | MAP1509 | hypothetical protein | 300 | 100 |
| MAP4_2332 | Esat-6 like protein EsxO | 94 | Rv1793 | Putative ESAT-6 like protein EsxN (E | 93.62 | 94 | Mb1821 | ESAT-6 like protein 5 | 93.62 | 94 | MAV_1177 | hypothetical protein | 100 | 94 | BCG_1825 | ESAT-6 like protein 5 | 93.62 | 94 | MAP3217c | hypothetical protein | 383 | 38.1 |
| MAP4_2333 | ESAT-6 like protein EsxP | 98 | Rv2347c | Putative ESAT-6 like protein EsxP (E | 87.76 | 98 | Mb1820 | hypothetical protein | 87.76 | 98 | MAV_1178 | hypothetical protein | 100 | 98 | BCG_1824 | hypothetical protein | 87.76 | 98 | MAP1508 | hypothetical protein | 98 | 100 |
| MAP4_2334 | PE family protein | 99 | Rv1788 | PE family protein PE18 | 86.21 | 99 | Mb1816 | PE family protein | 86.21 | 99 | MAV_1346 | PE family protein | 65.96 | 278 | BCG_1820 | PE family protein | 86.21 | 99 | MAP1507 | hypothetical protein | 99 | 100 |
| MAP4_2335 | PPE family protein | 407 | Rv1705c | PPE family protein PPE22 | 49.88 | 385 | Mb1731c | PPE family protein | 50.12 | 385 | MAV_2926 | PPE family protein | 95.09 | 407 | BCG_1821 | PPE family protein | 55.31 | 393 | MAP1506 | hypothetical protein | 407 | 100 |
| MAP4_2336 | PPE family protein | 421 | Rv1787 | PPE family protein PPE25 | 52.26 | 365 | Mb1815 | PPE family protein | 52.02 | 364 | MAV_2928 | PPE family protein | 98.1 | 421 | BCG_1819 | PPE family protein | 52.02 | 364 | MAP1505 | hypothetical protein | 421 | 99.76 |
| MAP4_2337 | ferredoxin | 64 | Rv1786 | Probable ferredoxin | 84.38 | 67 | Mb1814 | ferredoxin | 84.38 | 67 | MAV_1876 | hypothetical protein | 87.5 | 64 | BCG_1818 | ferredoxin | 84.38 | 67 | MAP1504 | hypothetical protein | 64 | 100 |
| MAP4_2338 | putative cytochrome P450 hydroxylase | 387 | Rv1785c | Probable cytochrome P450 143 Cyp | 73.39 | 393 | Mb1813c | cytochrome P450 143 | 73.39 | 393 | MAV_2931 | P450 heme-thiolate protein | 100 | 387 | BCG_1817c | cytochrome P450 143 cyp143 | 73.39 | 393 | MAP1503c | hypothetical protein | 438 | 97.61 |
| MAP4_2339 | ESX-5 type VII secretion system protein EccC5 | 1389 | Rv1783 | ESX conserved component EccC5 ES | 90.16 | 1391 | Mb1812 | hypothetical protein | 90.23 | 1391 | MAV_2932 | ftsk/SpoIIIE family protein | 99.93 | 1375 | BCG_1816 | hypothetical protein | 90.16 | 1391 | MAP1502 | hypothetical protein | 1389 | 100 |
| MAP4_2340 | ESX-5 type VII secretion system protein EccB5,probable | 505 | Rv1782 | ESX conserved component EccB5 ES | 82.41 | 506 | Mb1811 | hypothetical protein | 82.21 | 506 | MAV_2933 | hypothetical protein | 99.8 | 505 | BCG_1815 | hypothetical protein | 82.21 | 506 | MAP1501 | hypothetical protein | 505 | 100 |
| MAP4_2341 | 4-alpha-glucanotransferase (amylomaltase) | 713 | Rv1781c | Probable 4-alpha-glucanotransferase | 81.42 | 724 | Mb1810c | 4-alpha-glucanotransferase | 81.42 | 724 | MAV_2934 | 4-alpha-glucanotransferase | 99.58 | 723 | BCG_1814c | 4-alpha-glucanotransferase ma | 81.28 | 724 | MAP1500c | hypothetical protein | 713 | 100 |
| MAP4_2342 | putative monooxygenase, Luciferase family protein | 292 | Rv3079c | hypothetical protein | 35.53 | 275 | Mb3106c | hypothetical protein | 35.53 | 275 | MAV_2935 | hypothetical protein | 99.66 | 292 | BCG_3104c | hypothetical protein | 35.53 | 275 | MAP1499c | hypothetical protein | 292 | 100 |
| MAP4_2343 | hypothetical protein | 156 | Rv2910c | hypothetical protein | 26.03 | 147 | Mb2934c | hypothetical protein | 26.03 | 147 | MAV_2936 | hypothetical protein | 97.44 | 156 | BCG_2931c | hypothetical protein | 26.03 | 147 | MAP1498c | hypothetical protein | 169 | 99.36 |
| MAP4_2344 | oxidoreductase, molybdopterin binding subunit | 661 | Rv0218 | Probable conserved transmembrane | 30.66 | 442 | Mb0224 | transmembrane protein | 30.66 | 442 | MAV_2937 | oxidoreductase molybdopterin bin | 99.83 | 580 | BCG_0255 | hypothetical protein | 30.66 | 442 | MAP1497c | hypothetical protein | 661 | 100 |
| MAP4_2345 | hypothetical protein | 96 | Rv3288c | Putative protein UsfY | 32.61 | 137 | Mb3316c | hypothetical protein | 32.61 | 137 | MAV_2939 | hypothetical protein | 96.7 | 91 | BCG_3317c | protein usfY | 32.61 | 137 | MAP1496c | hypothetical protein | 96 | 100 |
| MAP4_2346 | hypothetical protein | 151 | Rv0910 | hypothetical protein | 40.43 | 144 | Mb0934 | hypothetical protein | 40.43 | 144 | MAV_2938 | hypothetical protein | 98.63 | 146 | BCG_0962 | hypothetical protein | 40.43 | 144 | MAP1495 | hypothetical protein | 151 | 100 |
| MAP4_2347 | hypothetical protein | 186 | Rv1780 | hypothetical protein | 88.71 | 187 | Mb1809 | hypothetical protein | 88.71 | 187 | MAV_2940 | hypothetical protein | 100 | 186 | BCG_1813 | hypothetical protein | 88.71 | 187 | MAP1494 | hypothetical protein | 186 | 100 |
| MAP4_2348 | hypothetical protein | 616 | Rv1779c | Possible integral membrane protein | 56.54 | 597 | Mb1808c | hypothetical protein | 56.54 | 597 | MAV_2942 | hypothetical protein | 97 | 598 | BCG_1812c | hypothetical protein | 56.54 | 597 | MAP1493c | hypothetical protein | 616 | 99.84 |
| MAP4_2349 | hypothetical protein | 95 | Rv1772 | Hypothetical protein | 69.15 | 103 | Mb1801 | hypothetical protein | 69.15 | 103 | MAV_2944 | ANTAR domain-containing protein | 100 | 95 | BCG_3174 | NADH dehydrogenase subunit | 56.25 | 806 | MAP1492 | hypothetical protein | 95 | 100 |
| MAP4_2352 | putative dehydrogenase | 290 | Rv2750 | Probable dehydrogenase | 44.4 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 44.4 | 272 | MAV_2946 | carveol dehydrogenase | 98.97 | 290 | BCG_2766 | 3-ketoacyl-ACP reductase | 44.4 | 272 | MAP1489c | hypothetical protein | 290 | 100 |
| MAP4_2353 | pyruvate dehydrogenase E1 component alpha subunit | 330 | Rv2497c | Probable branched-chain keto acid | 36.65 | 367 | Mb2525c | pyruvate dehydrogenase E1 | 36.65 | 367 | MAV_2947 | dehydrogenase E1 component sup | 99.09 | 330 | BCG_2517c | pyruvate dehydrogenase E1 co | 36.65 | 367 | MAP1488c | hypothetical protein | 330 | 100 |
| MAP4_2354 | pyruvate dehydrogenase E1 component beta-subunit | 336 | Rv2496c | Probable branched-chain keto acid | 41.69 | 348 | Mb2524c | pyruvate dehydrogenase E1 | 41.69 | 348 | MAV_2948 | acetoin:2,6-dichlorophenolindophe | 99.11 | 336 | BCG_2516c | pyruvate dehydrogenase E1 co | 41.69 | 348 | MAP1487c | hypothetical protein | 336 | 100 |
| MAP4_2355 | dihydrolipoamide acetyltransferase | 78 | Rv2215 | DlaT, dihydrolipoamide acyltransfer | 31.08 | 553 | Mb2238 | dihydrolipoamide acetyltrans | 31.08 | 553 | MAV_2949 | dihydrolipoamide acetyltransferase | 100 | 78 | BCG_2231 | dihydrolipoamide acetyltransfe | 31.08 | 553 | MAP1956 | dihydrolipoamide acetyltransferase | 590 | 31.08 |
| MAP4_2356 | Enoyl-CoA hydrataseisomerase | 290 | Rv0456c | enoyl-CoA hydratase EchA2 (enoyl h | 31.46 | 304 | Mb0464c | enoyl-CoA hydratase | 31.46 | 304 | MAV_2950 | enoyl-CoA hydratase/isomerase | 100 | 290 | BCG_0495c | enoyl-CoA hydratase | 31.46 | 304 | MAP1486c | hypothetical protein | 290 | 100 |
| MAP4_2358 | rieske (2Fe-2S) domain-containing protein | 461 | Rv3161c | Possible dioxygenase | 33 | 382 | Mb3186c | dioxygenase | 33 | 382 | MAV_2952 | Rieske (2Fe-2S) domain-containing | 99.33 | 450 | BCG_3185c | dioxygenase | 33 | 382 | MAP1484c | hypothetical protein | 461 | 100 |
| MAP4_2359 | 3-ketosteroid-delta-1-dehydrogenase | 581 | Rv3537 | Probable dehydrogenase | 38.49 | 563 | Mb3567 | 3-ketosteroid-delta-1-dehydr | 38.49 | 563 | MAV_2953 | 3-ketosteroid-delta-1-dehydrogena | 98.79 | 579 | BCG_3601 | 3-ketosteroid-delta-1-dehydro | 38.49 | 563 | MAP1483c | 3-ketosteroid-delta-1-dehydrogenase | 581 | 99.83 |
| MAP4_2360 | Enoyl-CoA hydratase | 301 | Rv0456c | enoyl-CoA hydratase EchA2 (enoyl h | 29.62 | 304 | Mb0464c | enoyl-CoA hydratase | 29.62 | 304 | MAV_2954 | enoyl-CoA hydratase/isomerase | 99.67 | 301 | BCG_0495c | enoyl-CoA hydratase | 29.62 | 304 | MAP1482 | hypothetical protein | 301 | 100 |
| MAP4_2361 | ATP-dependent RNA helicase | 497 | Rv3211 | Probable ATP-dependent RNA helica | 39.69 | 527 | Mb3237 | ATP-dependent RNA helicase | 39.47 | 527 | MAV_2956 | ATP-dependent RNA helicase | 98.68 | 455 | BCG_3238 | ATP-dependent RNA helicase r | 39.69 | 527 | MAP1481c | hypothetical protein | 497 | 100 |
| MAP4_2362 | methyltransferase | 193 | Rv1377c | Putative transferase | 31.3 | 212 | Mb0333 | hypothetical protein | 33.78 | 229 | MAV_2957 | thiopurine S-methyltransferase | 98.95 | 191 | BCG_0365 | hypothetical protein | 33.78 | 229 | MAP1480 | hypothetical protein | 193 | 100 |
| MAP4_2363 | TetR family transcriptional regulator | 198 | Rv0767c | hypothetical protein | 49.21 | 213 | Mb0790c | hypothetical protein | 49.21 | 213 | MAV_2958 | TetR family transcriptional regulato | 100 | 201 | BCG_0819c | hypothetical protein | 49.21 | 213 | MAP1479c | hypothetical protein | 198 | 100 |
| MAP4_2364 | D-amino acid aminohydrolase | 597 | Rv2913c | Possible D-amino acid aminohydrola | 55.97 | 611 | Mb2937c | D-amino acid aminohydrolase | 55.97 | 611 | MAV_2959 | N-acyl-D-glutamate amidohydrolas | 99.15 | 588 | BCG_2934c | D-amino acid aminohydrolase | 55.97 | 611 | MAP1478 | hypothetical protein | 597 | 100 |
| MAP4_2365 | Transcriptional regulator, TetR family | 224 | Rv3249c | Possible transcriptional regulatory p | 28.33 | 211 | Mb3277c | TetR family transcriptional re | 28.33 | 211 | MAV_2960 | TetR family transcriptional regulato | 99.55 | 224 | BCG_3278c | TetR family transcriptional regu | 28.33 | 211 | MAP1477c | hypothetical protein | 224 | 100 |
| MAP4_2366 | cutinase | 234 | Rv1758 | Probable cutinase Cut1 | 62.21 | 174 | Mb1788 | cutinase | 62.62 | 218 | MAV_2961 | cutinase Cut3 | 98.6 | 215 | BCG_1798 | cutinase cut1 | 62.62 | 218 | MAP1476c | hypothetical protein | 234 | 100 |
| MAP4_2367 | Short-chain dehydrogenasereductase SDR | 299 | Rv3548c | Probable short-chain type dehydrog | 35.51 | 304 | Mb3578c | short chain dehydrogenase | 35.51 | 304 | MAV_2962 | oxidoreductase, short chain dehydr | 99 | 299 | BCG_3612c | short chain dehydrogenase | 35.51 | 304 | MAP1475 | hypothetical protein | 299 | 100 |
| MAP4_2368 | RNA polymerase sigma factor SigF | 269 | Rv3286c | Alternative RNA polymerase sigma f | 54.96 | 261 | Mb3314c | RNA polymerase sigma factor | 54.96 | 261 | MAV_2963 | RNA polymerase sigma factor SigF | 99.63 | 269 | BCG_3315c | RNA polymerase sigma factor S | 54.96 | 261 | MAP1474c | RNA polymerase sigma factor SigF | 269 | 100 |
| MAP4_2369 | hypothetical protein | 205 | Rv1677 | Probable conserved lipoprotein Dsb | 42.86 | 182 | Mb1704 | lipoprotein DsbF | 42.86 | 182 | MAV_2964 | hypothetical protein | 99.51 | 205 | BCG_1715 | lipoprotein dsbF | 42.86 | 182 | MAP1473c | hypothetical protein | 201 | 99.5 |
| MAP4_2370 | hypothetical protein | 163 | Rv3089 | Probable chain-fatty-acid-CoA ligase | 34.67 | 503 | Mb3116 | chain-fatty-acid-CoA ligase | 34.67 | 503 | MAV_2965 | hypothetical protein | 99.39 | 163 | BCG_3114 | chain-fatty-acid-CoA ligase fad | 34.67 | 503 | MAP1472c | hypothetical protein | 163 | 100 |
| MAP4_2371 | hypothetical protein | 158 | Rv3547 | Deazaflavin-dependent nitroreducta | 28.12 | 151 | Mb3577 | hypothetical protein | 28.12 | 151 | MAV_2966 | hypothetical protein | 98.73 | 158 | BCG_3611 | hypothetical protein | 28.12 | 151 | MAP1471 | hypothetical protein | 141 | 100 |
| MAP4_2372 | Transcriptional regulator, TetR family | 239 | Rv1685c | hypothetical protein | 38.2 | 207 | Mb1711c | hypothetical protein | 38.2 | 207 | MAV_2967 | TetR family transcriptional regulato | 98.74 | 244 | BCG_1723c | hypothetical protein | 38.2 | 207 | MAP1470c | hypothetical protein | 239 | 100 |
| MAP4_2373 | cytochrome P450 | 409 | Rv3121 | Probable cytochrome P450 141 Cyp | 29.03 | 400 | Mb2289 | cytochrome P450 124 CYP124 | 32.62 | 428 | MAV_2968 | cytochrome P450-SU2 | 99.76 | 409 | BCG_2283 | cytochrome P450 124 CYP124 | 32.62 | 428 | MAP1469c | hypothetical protein | 409 | 100 |
| MAP4_2374 | short chain dehydrogenase | 315 | Rv2263 | Possible oxidoreductase | 62.38 | 317 | Mb2286 | short chain dehydrogenase | 62.38 | 317 | MAV_2969 | short chain dehydrogenase | 98.73 | 314 | BCG_2280 | short chain dehydrogenase | 62.38 | 317 | MAP1468c | short chain dehydrogenase | 315 | 100 |
| MAP4_2375 | peptidase, M24 family protein | 409 | Rv2089c | Dipeptidase PepE | 29.18 | 375 | Mb2116c | dipeptidase PepE | 29.18 | 375 | MAV_2970 | peptidase, M24 family protein | 98.04 | 409 | BCG_2109c | dipeptidase PepE | 29.18 | 375 | MAP1467c | hypothetical protein | 389 | 100 |
| MAP4_2376 | peptidase, M24 family protein | 376 | Rv2861c | Methionine aminopeptidase MapB ( | 25.2 | 285 | Mb2886c | methionine aminopeptidase | 25.2 | 285 | MAV_2971 | peptidase, M24 family protein | 97.61 | 376 | BCG_2883c | methionine aminopeptidase | 25.2 | 285 | MAP1466c | hypothetical protein | 376 | 100 |
| MAP4_2377 | REP13E12 repeat protein | 484 | Rv1702c | hypothetical protein | 63.81 | 454 | Mb1728c | hypothetical protein | 63.81 | 454 | MAV_3043 | hypothetical protein | 87.61 | 447 | BCG_1740c | hypothetical protein | 63.81 | 454 | MAP1465c | hypothetical protein | 484 | 99.79 |
| MAP4_2378 | fatty-acid-CoA ligase fadD1 | 539 | Rv1750c | Possible fatty-acid-CoA ligase FadD1 | 64.37 | 532 | Mb1779c | acyl-CoA synthetase | 64.37 | 532 | MAV_3000 | acyl-CoA synthetase | 98.89 | 539 | BCG_1789c | acyl-CoA synthetase | 64.37 | 532 | MAP1464 | acyl-CoA synthetase | 539 | 100 |
| MAP4_2379 | putative monooxygenase | 552 | Rv1393c | Probable monoxygenase | 33.53 | 492 | Mb1428c | monoxygenase | 33.53 | 492 | MAV_3001 | steroid monooxygenase | 99.06 | 531 | BCG_1454c | monoxygenase | 33.53 | 492 | MAP1463 | hypothetical protein | 552 | 100 |
| MAP4_2380 | hypothetical protein | 133 | Rv3542c | hypothetical protein | 27.19 | 311 | Mb3572c | hypothetical protein | 27.19 | 311 | MAV_3003 | acyl dehydratase | 100 | 133 | BCG_3606c | hypothetical protein | 27.19 | 311 | MAP4301c | hypothetical protein | 137 | 64.12 |
| MAP4_2381 | lipid-transfer protein | 400 | Rv3540c | Probable lipid transfer protein or ke | 30.26 | 386 | Mb3570c | lipid-transfer protein | 30.26 | 386 | MAV_3004 | nonspecific lipid-transfer protein | 99.5 | 400 | BCG_3604c | lipid-transfer protein | 30.26 | 386 | MAP1462 | hypothetical protein | 400 | 100 |
| MAP4_2382 | dehydratase, MaoC like domain-containing protein | 145 | Rv3541c | hypothetical protein | 27.82 | 129 | Mb3571c | hypothetical protein | 27.82 | 129 | MAV_3005 | MaoC like domain-containing prote | 97.93 | 145 | BCG_3605c | hypothetical protein | 27.82 | 129 | MAP1461 | hypothetical protein | 145 | 100 |
| MAP4_2383 | putative dehydratase, MaoC like (N-term) domain-cont | 161 | Rv3542c | hypothetical protein | 40.35 | 311 | Mb3572c | hypothetical protein | 40.35 | 311 | MAV_3006 | hypothetical protein | 99.38 | 161 | BCG_3606c | hypothetical protein | 40.35 | 311 | MAP1460 | hypothetical protein | 161 | 100 |
| MAP4_2384 | acyl-CoA dehydrogenase | 378 | Rv1933c | Probable acyl-CoA dehydrogenase F | 31.51 | 363 | Mb1968c | acyl-CoA dehydrogenase | 31.51 | 363 | MAV_3007 | acyl-CoA dehydrogenase domain-c | 97.35 | 378 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 31.51 | 363 | MAP1459 | hypothetical protein | 378 | 100 |
| MAP4_2385 | acyl-CoA dehydrogenase | 392 | Rv3504 | Probable acyl-CoA dehydrogenase F | 39.79 | 400 | Mb3534 | acyl-CoA dehydrogenase | 39.79 | 400 | MAV_3008 | acyl-CoA dehydrogenase | 99.49 | 392 | BCG_3568 | acyl-CoA dehydrogenase fadE2 | 39.79 | 400 | MAP1458 | hypothetical protein | 392 | 100 |
| MAP4_2386 | hypothetical protein | 54 | Rv1701 | Probable integrase/recombinase | 40 | 311 | Mb1727 | site-specific tyrosine recombi | 40 | 311 | MAV_3009 | hypothetical protein | 100 | 54 | BCG_1739 | site-specific tyrosine recombin | 40 | 311 | MAP3545 | hypothetical protein | 364 | 35 |
| MAP4_2387 | conserved transmembrane ABC transporter ATP-bindin | 854 | Rv1747 | Probable conserved transmembrane | 80 | 865 | Mb1776 | ABC transporter ATP-binding | 80 | 865 | MAV_3010 | ABC transporter ATP-binding prote | 98.69 | 862 | BCG_1786 | transmembrane ABC transport | 80 | 865 | MAP1457 | hypothetical protein | 854 | 100 |
| MAP4_2388 | putative esteraselipase | 351 | Rv1076 | Possible lipase LipU | 38.46 | 297 | Mb1105 | lipase LIPU | 38.46 | 297 | MAV_3011 | alpha/beta hydrolase | 99.7 | 333 | BCG_1134 | lipase lipU | 38.46 | 297 | MAP1456 | hypothetical protein | 364 | 100 |
| MAP4_2389 | short-chain dehydrogenase | 281 | Rv1350 | Probable 3-oxoacyl-[acyl-carrier pro | 34.66 | 247 | Mb1385 | 3-ketoacyl-ACP reductase | 34.66 | 247 | MAV_3012 | short chain dehydrogenase/reduct | 98.93 | 281 | BCG_1412 | 3-ketoacyl-ACP reductase | 34.66 | 247 | MAP1455c | hypothetical protein | 198 | 99.49 |
| MAP4_2390 | hypothetical protein | 298 | Rv0883c | hypothetical protein | 31.68 | 253 | Mb0907c | hypothetical protein | 31.68 | 253 | MAV_3013 | hypothetical protein | 100 | 77 | BCG_0935c | hypothetical protein | 31.68 | 253 | MAP1454 | hypothetical protein | 298 | 100 |
| MAP4_2391 | putative triacylglycerol synthase | 513 | Rv1760 | Possible triacylglycerol synthase (dia | 64.85 | 502 | Mb1791 | hypothetical protein | 64.32 | 509 | MAV_3015 | acyltransferase, ws/dgat/mgat sub | 98.01 | 453 | BCG_1801 | hypothetical protein | 64.32 | 509 | MAP1453c | hypothetical protein | 513 | 100 |
| MAP4_2392 | possible2-hydroxy-6-oxo-6-phenylhexa-2, 4-dienoate h | 300 | Rv3569c | 4,9-DHSA hydrolase | 38.63 | 291 | Mb3600c | 2-hydroxy-6-oxo-6-phenylhex | 38.63 | 291 | MAV_3016 | 2-hydroxy-6-oxo-6-phenylhexa-2,4- | 98.32 | 297 | BCG_3634c | 2-hydroxy-6-oxo-6-phenylhexa | 38.63 | 291 | MAP1452c | hypothetical protein | 300 | 99.67 |
| MAP4_2393 | putative dehydrogenase | 282 | Rv2750 | Probable dehydrogenase | 48.75 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 48.75 | 272 | MAV_3017 | carveol dehydrogenase | 99.25 | 267 | BCG_2766 | 3-ketoacyl-ACP reductase | 48.75 | 272 | MAP1451 | hypothetical protein | 282 | 100 |
| MAP4_2394 | putative oxidoreductase, Pyridinenucleotide-disulfide | 541 | Rv1393c | Probable monoxygenase | 33.73 | 492 | Mb1428c | monoxygenase | 33.73 | 492 | MAV_3018 | steroid monooxygenase | 99.26 | 541 | BCG_1454c | monoxygenase | 33.73 | 492 | MAP1450c | hypothetical protein | 541 | 100 |
| MAP4_2395 | putative dehydrogenase | 268 | Rv2750 | Probable dehydrogenase | 42.65 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 42.65 | 272 | MAV_3019 | carveol dehydrogenase | 98.88 | 268 | BCG_2766 | 3-ketoacyl-ACP reductase | 42.65 | 272 | MAP1449c | hypothetical protein | 268 | 100 |
| MAP4_2396 | putative oxidoreductase | 394 | Rv3570c | Possible oxidoreductase Possible 3-h | 40.82 | 394 | Mb3601c | oxidoreductase | 40.82 | 394 | MAV_3020 | pigment production hydroxylase | 99.49 | 394 | BCG_3635c | oxidoreductase | 40.82 | 394 | MAP1448c | hypothetical protein | 394 | 100 |
| MAP4_2397 | fumarate reductasesuccinate dehydrogenase flavoprot | 502 | Rv1817 | Possible flavoprotein | 39.79 | 487 | Mb1848 | hypothetical protein | 39.79 | 487 | MAV_3022 | hypothetical protein | 98.98 | 491 | BCG_1852 | hypothetical protein | 39.79 | 487 | MAP1447c | hypothetical protein | 502 | 100 |
| MAP4_2398 | Transcriptional regulator, IclR family | 278 | Rv1719 | Probable transcriptional regulatory | 33.65 | 259 | Mb1748 | transcriptional regulator | 33.65 | 259 | MAV_3024 | IclR family transcriptional regulator | 99.64 | 278 | BCG_1758 | transcriptional regulatory prot | 33.65 | 259 | MAP1446c | hypothetical protein | 278 | 100 |
| MAP4_2399 | Esteraselipase | 307 | Rv2970c | Probable lipase/esterase LipN | 43.62 | 376 | Mb2994c | lipase/esterase | 43.62 | 376 | MAV_3025 | esterase | 98.69 | 307 | BCG_2991c | lipase/esterase lipN | 43.62 | 376 | MAP1445c | hypothetical protein | 307 | 100 |
| MAP4_2400 | hypothetical protein | 132 | Rv3124 | Transcriptional regulatory protein M | 38.24 | 289 | Mb3147 | transcriptional regulator | 38.24 | 289 | MAV_3026 | hypothetical protein | 95.76 | 118 | BCG_3145 | transcriptional regulatory prot | 38.24 | 289 | MAP1444c | hypothetical protein | 132 | 100 |
| MAP4_2401 | stress responsive AB barrel domain-containing protein | 208 | Rv2508c | Probable conserved integral membr | 40.62 | 445 | Mb2536c | hypothetical protein | 40.62 | 445 | MAV_3028 | stress responsive A/B barrel domai | 95.67 | 208 | BCG_2528c | integral membrane leucine and | 40.62 | 445 | MAP1443c | hypothetical protein | 191 | 100 |
| MAP4_2402 | short-chain dehydrogenase | 295 | Rv3224 | Possible iron-regulated short-chain | 27.89 | 282 | Mb3251 | short chain dehydrogenase | 27.89 | 282 | MAV_3027 | short chain dehydrogenase/reduct | 99.32 | 295 | BCG_3252 | short chain dehydrogenase | 27.89 | 282 | MAP1442 | hypothetical protein | 295 | 100 |
| MAP4_2403 | FAD dependent oxidoreductase | 646 | Rv3049c | Probable monooxygenase | 34.3 | 524 | Mb3075c | monooxygenase | 34.3 | 524 | MAV_3029 | hypothetical protein | 98.75 | 642 | BCG_3073c | monooxygenase | 34.3 | 524 | MAP1441 | hypothetical protein | 646 | 99.85 |
| MAP4_2404 | hypothetical protein | 171 | Rv3073c | hypothetical protein | 40.43 | 118 | Mb3100c | hypothetical protein | 40.43 | 118 | MAV_3030 | hypothetical protein | 97.48 | 159 | BCG_3098c | hypothetical protein | 40.43 | 118 | MAP1440c | hypothetical protein | 171 | 100 |
| MAP4_2405 | putative short-chain dehydrogenasereductase | 289 | Rv2214c | Possible short-chain dehydrogenase | 34.16 | 592 | Mb2237c | short chain dehydrogenase | 34.16 | 592 | MAV_3031 | oxidoreductase, short chain dehydr | 97.46 | 277 | BCG_2230c | short chain dehydrogenase | 34.16 | 592 | MAP1439c | hypothetical protein | 256 | 100 |
| MAP4_2406 | lipase LipH | 327 | Rv1399c | Probable non lipolytic carboxylester | 42.28 | 319 | Mb1434c | lipase LipH | 42.28 | 319 | MAV_3032 | alpha/beta hydrolase | 99.39 | 327 | BCG_1460c | lipase lipH | 41.81 | 319 | MAP1438c | hypothetical protein | 327 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2407 | hypothetical protein | 328 | Rv1319c | Possible adenylate cyclase (ATP pyro | 40 | 535 | Mb1353c | adenylate cyclase | 40 | 535 | MAV_3033 | hypothetical protein | 98.78 | 358 | BCG_1380c | adenylate cyclase | 40 | 535 | MAP1437c | hypothetical protein | 328 | 100 |
| MAP4_2408 | short chain dehydrogenase | 260 | Rv2857c | Probable short-chain type dehydrog | 35.66 | 258 | Mb2882c | short chain dehydrogenase | 35.66 | 258 | MAV_3034 | oxidoreductase | 99.23 | 260 | BCG_2879c | short chain dehydrogenase | 35.66 | 258 | MAP1436c | hypothetical protein | 260 | 100 |
| MAP4_2409 | short chain dehydrogenasereductase SDR family protei | 262 | Rv1928c | Probable short-chain type dehydrog | 26.18 | 255 | Mb1963c | short chain dehydrogenase | 26.18 | 255 | MAV_3035 | short chain dehydrogenase/reducta | 99.62 | 262 | BCG_1967c | short chain dehydrogenase | 26.18 | 255 | MAP1435 | hypothetical protein | 237 | 99.58 |
| MAP4_2410 | hypothetical protein | 94 | Rv3527 | Hypothetical protein | 32.93 | 149 | Mb3557 | hypothetical protein | 32.93 | 149 | MAV_3036 | hypothetical protein | 98.85 | 89 | BCG_3591 | hypothetical protein | 32.93 | 149 | MAP0538c | hypothetical protein | 145 | 36.36 |
| MAP4_2411 | oxidoreductase | 372 | Rv3526 | Oxygenase component of 3-ketoster | 61.2 | 386 | Mb3556 | oxidoreductase | 61.2 | 386 | MAV_3037 | oxygenase KshA | 99.19 | 370 | BCG_3590 | oxidoreductase | 61.2 | 386 | MAP1434 | hypothetical protein | 372 | 100 |
| MAP4_2412 | 3-ketosteroid 1-dehydrogenase | 581 | Rv3537 | Probable dehydrogenase | 43.6 | 563 | Mb3567 | 3-ketosteroid-delta-1-dehydr | 43.6 | 563 | MAV_3039 | 3-ketosteroid-delta-1-dehydrogena | 99.48 | 581 | BCG_3601 | 3-ketosteroid-delta-1-dehydro | 43.6 | 563 | MAP1433c | 3-ketosteroid-delta-1-dehydrogenase | 581 | 100 |
| MAP4_2413 | REP13E12 repeat protein | 476 | Rv1128c | hypothetical protein | 63.64 | 451 | Mb1159c | hypothetical protein | 63.85 | 451 | MAV_3043 | hypothetical protein | 91.43 | 447 | BCG_1189c | hypothetical protein | 63.85 | 451 | MAP1432 | hypothetical protein | 496 | 99.16 |
| MAP4_2414 | Transcriptional regulator, PadR family | 226 | Rv1176c | hypothetical protein | 27.85 | 189 | Mb1209c | hypothetical protein | 27.85 | 189 | MAV_3044 | PadR family transcriptional regulat | 99.12 | 226 | BCG_1239c | hypothetical protein | 27.85 | 189 | MAP1431 | hypothetical protein | 226 | 100 |
| MAP4_2415 | monooxygenase, luciferase-like monooxygenase doma | 306 | Rv3079c | hypothetical protein | 33.51 | 275 | Mb3106c | hypothetical protein | 33.51 | 275 | MAV_3045 | hypothetical protein | 98.69 | 306 | BCG_3104c | hypothetical protein | 33.51 | 275 | MAP1430c | hypothetical protein | 296 | 100 |
| MAP4_2416 | hypothetical protein | 292 | Rv1062 | hypothetical protein | 24.18 | 285 | Mb1091 | hypothetical protein | 24.18 | 285 | MAV_3046 | hypothetical protein | 98.63 | 291 | BCG_1120 | hypothetical protein | 24.18 | 285 | MAP1429 | hypothetical protein | 292 | 100 |
| MAP4_2417 | putative pyridine nucleotide-disulfideoxido reductase | 383 | Rv0392c | Probable membrane NADH dehydro | 24.62 | 470 | Mb1885c | NADH dehydrogenase | 24.04 | 463 | MAV_3047 | pyridine nucleotide-disulphide oxid | 99.48 | 383 | BCG_0429c | membrane NADH dehydrogena | 24.32 | 470 | MAP1428c | hypothetical protein | 383 | 100 |
| MAP4_2418 | putative multicopper oxidase | 481 | Rv0846c | Probable oxidase | 28.65 | 504 | Mb0869c | oxidase | 28.65 | 504 | MAV_3048 | multicopper oxidase | 99.17 | 482 | BCG_0898c | oxidase | 28.65 | 504 | MAP1427 | hypothetical protein | 481 | 100 |
| MAP4_2419 | oxidoreductase | 211 | Rv3007c | Possible oxidoreductase | 54.01 | 204 | Mb3032c | oxidoreductase | 54.01 | 204 | MAV_3049 | oxidoreductase | 98.79 | 165 | BCG_3029c | oxidoreductase | 54.01 | 204 | MAP1426c | hypothetical protein | 211 | 100 |
| MAP4_2420 | putative riboflavin biosynthesis protein | 227 | Rv2671 | Possible bifunctional enzyme ribofla | 38.1 | 258 | Mb2690 | hypothetical protein | 38.1 | 258 | MAV_3050 | hypothetical protein | 99.56 | 236 | BCG_2684 | hypothetical protein | 38.1 | 258 | MAP1425c | hypothetical protein | 227 | 100 |
| MAP4_2421 | hypothetical protein | 152 | Rv1442 | Probable biotin sulfoxide reductase | 36.96 | 766 | Mb1477 | biotin sulfoxide reductase | 36.96 | 766 | MAV_3051 | hypothetical protein | 99.34 | 155 | BCG_1503 | biotin sulfoxide reductase bisC | 36.96 | 766 | MAP1424c | hypothetical protein | 152 | 100 |
| MAP4_2422 | sugar transporter | 496 | Rv1902c | Probable sialic acid-transport integra | 27.44 | 422 | Mb1937c | sialic acid-transport integral r | 27.44 | 422 | MAV_3053 | sugar ABC transporter | 99.8 | 496 | BCG_1941c | sialic acid-transport integral me | 27.44 | 422 | MAP1423 | hypothetical protein | 466 | 99.79 |
| MAP4_2423 | acetyltransferase, GNAT family ATP-grasp domain prot | 597 | Rv2981c | Probable D-alanine--D-alanine ligase | 32.52 | 373 | Mb3005c | D-alanyl-alanine synthetase A | 32.52 | 370 | MAV_3054 | GNAT family acetyltransferase | 99.83 | 597 | BCG_3002c | D-alanyl-alanine synthetase A | 32.52 | 373 | MAP1422 | hypothetical protein | 595 | 100 |
| MAP4_2424 | Asparagine synthetase | 601 | Rv2201 | Probable asparagine synthetase Asn | 31.68 | 652 | Mb2224 | asparagine synthetase AsnB | 31.68 | 652 | MAV_3055 | asparagine synthase (glutamine-hy | 99.48 | 579 | BCG_2217 | asparagine synthetase AsnB | 31.68 | 652 | MAP1421 | AsnB_1 | 601 | 100 |
| MAP4_2425 | peptide synthetase | 6384 | Rv0101 | Probable peptide synthetase Nrp (pe | 51.12 | 2512 | Mb0104 | peptide synthetase | 51.12 | 2512 | MAV_3239 | syringomycin synthetase | 61.09 | 6212 | BCG_0134 | peptide synthetase nrp | 51.07 | 2512 | MAP1242 | hypothetical protein | 4027 | 58.53 |
| MAP4_2426 | MbtH-like protein | 72 | Rv2377c | Putative conserved protein MbtH | 70.59 | 71 | Mb2398c | protein MbtH | 69.57 | 71 | MAV_3057 | hypothetical protein | 100 | 72 | BCG_2391c | protein mbtH | 69.57 | 71 | MAP1419 | hypothetical protein | 72 | 100 |
| MAP4_2427 | hypothetical protein | 261 | Rv1517 | hypothetical protein | 33.46 | 254 | Mb1544 | hypothetical protein | 33.33 | 254 | MAV_3059 | hypothetical protein | 99.23 | 261 | BCG_1569 | hypothetical protein | 33.33 | 254 | MAP1418c | hypothetical protein | 261 | 100 |
| MAP4_2428 | hypothetical protein | 144 | Rv0166 | Probable fatty-acid-CoA ligase FadD | 33.85 | 554 | Mb0172 | long-chain-fatty-acid--CoA lig | 33.85 | 554 | MAV_3060 | hypothetical protein | 98.61 | 144 | BCG_0203 | long-chain-fatty-acid--CoA ligas | 33.85 | 554 | MAP1417c | hypothetical protein | 144 | 100 |
| MAP4_2429 | hypothetical protein | 221 | Rv3437 | Possible conserved transmembrane | 52.94 | 158 | Mb3467 | transmembrane protein | 52.94 | 158 | MAV_3061 | hypothetical protein | 100 | 221 | BCG_3503 | hypothetical protein | 52.94 | 158 | MAP1416c | hypothetical protein | 221 | 100 |
| MAP4_2430 | GTP-binding protein EngA | 466 | Rv1713 | Probable GTP-binding protein EngA | 87.55 | 463 | Mb1740 | GTP-binding protein EngA | 87.55 | 463 | MAV_3063 | GTP-binding protein EngA | 99.57 | 466 | BCG_1752 | GTP-binding protein EngA | 87.55 | 463 | MAP1415 | GTP-binding protein EngA | 466 | 100 |
| MAP4_2431 | Cytidylate kinase | 228 | Rv1712 | Cytidylate kinase Cmk (CMP kinase) | 78.76 | 230 | Mb1739 | cytidylate kinase | 78.76 | 230 | MAV_3064 | cytidylate kinase | 98.25 | 228 | BCG_1751 | cytidylate kinase | 78.76 | 230 | MAP1414 | cytidylate kinase | 228 | 100 |
| MAP4_2432 | ribosomal large subunit pseudouridine synthase B | 247 | Rv1711 | hypothetical protein | 87.76 | 254 | Mb1738 | hypothetical protein | 87.76 | 254 | MAV_3065 | ribosomal large subunit pseudouri | 99.6 | 248 | BCG_1750 | hypothetical protein | 87.76 | 254 | MAP1413 | hypothetical protein | 247 | 100 |
| MAP4_2433 | Segregation and condensation protein B | 235 | Rv1710 | Possible segregation and condensati | 79.57 | 231 | Mb1737 | hypothetical protein | 79.57 | 231 | MAV_3066 | segregation and condensation prot | 99.15 | 235 | BCG_1749 | hypothetical protein | 79.57 | 231 | MAP1412 | hypothetical protein | 235 | 100 |
| MAP4_2434 | Segregation and condensation protein A | 272 | Rv1709 | Possible segregation and condensati | 81.61 | 278 | Mb1736 | hypothetical protein | 81.61 | 278 | MAV_3067 | segregation and condensation prot | 100 | 272 | BCG_1748 | hypothetical protein | 81.61 | 278 | MAP1411 | hypothetical protein | 272 | 100 |
| MAP4_2435 | putative initiation inhibitor protein | 313 | Rv1708 | Putative initiation inhibitor protein | 84.86 | 318 | Mb1735 | initiation inhibitor protein | 84.86 | 318 | MAV_3068 | SpoOJ regulator protein | 99.65 | 287 | BCG_1747 | initiation inhibitor protein | 84.86 | 318 | MAP1410 | hypothetical protein | 313 | 100 |
| MAP4_2436 | catechol-o-methyltransferase | 234 | Rv1703c | Probable catechol-O-methyltransfer | 80.71 | 196 | Mb1729c | catechol-o-methyltransferase | 80.71 | 196 | MAV_3069 | catechol-O-methyltransferase | 99.57 | 250 | BCG_1741c | catechol-o-methyltransferase | 80.2 | 196 | MAP1409c | hypothetical protein | 234 | 100 |
| MAP4_2437 | integraserecombinase | 313 | Rv1701 | Probable integrase/recombinase | 89.78 | 311 | Mb1727 | site-specific tyrosine recombi | 89.78 | 311 | MAV_3070 | site-specific tyrosine recombinase X | 99.36 | 313 | BCG_1739 | site-specific tyrosine recombin | 89.78 | 311 | MAP1408 | site-specific tyrosine recombinase XerD | 313 | 100 |
| MAP4_2438 | NUDIX hydrolase | 207 | Rv1700 | NUDIX hydrolase | 78.26 | 207 | Mb1726 | hypothetical protein | 77.29 | 207 | MAV_3071 | MutT/nudix family protein | 100 | 207 | BCG_1738 | hypothetical protein | 78.26 | 207 | MAP1407 | hypothetical protein | 207 | 100 |
| MAP4_2439 | CTP synthase | 583 | Rv1699 | Probable CTP synthase PyrG | 91.3 | 586 | Mb1725 | CTP synthetase | 91.3 | 586 | MAV_3072 | CTP synthetase | 99.83 | 583 | BCG_1737 | CTP synthetase | 91.3 | 586 | MAP1406 | CTP synthetase | 583 | 99.83 |
| MAP4_2440 | outer membrane protein | 317 | Rv1698 | Outer membrane protein MctB | 74.76 | 314 | Mb1724 | hypothetical protein | 74.76 | 314 | MAV_3073 | hypothetical protein | 99.05 | 317 | BCG_1736 | hypothetical protein | 74.76 | 314 | MAP1405 | hypothetical protein | 317 | 100 |
| MAP4_2441 | hypothetical protein | 393 | Rv1697 | hypothetical protein | 89.82 | 393 | Mb1723 | hypothetical protein | 89.82 | 393 | MAV_3074 | hypothetical protein | 100 | 393 | BCG_1735 | hypothetical protein | 89.82 | 393 | MAP1404 | hypothetical protein | 393 | 100 |
| MAP4_2442 | DNA repair protein RecN | 589 | Rv1696 | Probable DNA repair protein RecN (r | 76.78 | 587 | Mb1722 | DNA repair protein recN (rec | 76.78 | 587 | MAV_3075 | DNA repair protein RecN | 99.83 | 589 | BCG_1734 | DNA repair protein recN | 76.78 | 587 | MAP1403 | hypothetical protein | 589 | 100 |
| MAP4_2443 | inorganic polyphosphateATP-NAD kinase | 308 | Rv1695 | Inorganic polyphosphate/ATP-NAD k | 90.82 | 307 | Mb1721 | inorganic polyphosphate/ATP | 90.82 | 307 | MAV_3076 | inorganic polyphosphate/ATP-NAD | 99.68 | 308 | BCG_1733 | inorganic polyphosphate/ATP- | 90.82 | 307 | MAP1402 | inorganic polyphosphate/ATP-NAD kina | 308 | 100 |
| MAP4_2444 | cytotoxinhemolysin TlyA | 269 | Rv1694 | 2'-O-methyltransferase TlyA | 80.22 | 268 | Mb1720 | cytotoxin | 80.22 | 268 | MAV_3077 | hemolysin A | 99.63 | 269 | BCG_1732 | cytotoxin/hemolysin TlyA | 80.22 | 268 | MAP1401 | TlyA | 269 | 100 |
| MAP4_2445 | hypothetical protein | 61 | Rv1693 | hypothetical protein | 78.69 | 58 | Mb1719 | hypothetical protein | 78.69 | 58 | MAV_3078 | hypothetical protein | 100 | 61 | BCG_1731 | hypothetical protein | 78.69 | 58 | MAP1400 | hypothetical protein | 61 | 100 |
| MAP4_2446 | phosphatase | 337 | Rv1692 | Probable phosphatase | 74.71 | 353 | Mb1718 | phosphatase | 74.71 | 353 | MAV_3079 | HAD-superfamily protein hydrolase | 99.41 | 340 | BCG_1730 | phosphatase | 74.71 | 353 | MAP1399 | hypothetical protein | 337 | 100 |
| MAP4_2447 | hypothetical protein | 264 | Rv1691 | hypothetical protein | 87.61 | 250 | Mb1717 | hypothetical protein | 87.61 | 250 | MAV_3080 | TPR repeat-containing protein | 99.53 | 211 | BCG_1729 | hypothetical protein | 87.61 | 250 | MAP1398 | hypothetical protein | 264 | 100 |
| MAP4_2448 | lipoprotein LprJ | 122 | Rv1690 | Probable lipoprotein LprJ | 58.41 | 127 | Mb1716 | lipoprotein LprJ | 58.41 | 139 | MAV_3081 | LprJ protein | 98.36 | 122 | BCG_1728 | lipoprotein lprJ | 58.41 | 127 | MAP1397 | hypothetical protein | 122 | 100 |
| MAP4_2449 | tyrosyl-tRNA synthetase | 421 | Rv1689 | Probable tyrosyl-tRNA synthase TyrS | 86.76 | 424 | Mb1715 | tyrosyl-tRNA synthetase | 86.76 | 424 | MAV_3082 | tyrosyl-tRNA synthetase | 99.52 | 421 | BCG_1727 | tyrosyl-tRNA synthetase | 86.76 | 424 | MAP1396 | tyrosyl-tRNA synthetase | 421 | 100 |
| MAP4_2450 | 3-methyladenine DNA glycosylase | 205 | Rv1688 | Possible 3-methyladenine DNA glyco | 79.1 | 203 | Mb1714 | 3-methyladenine DNA glycosy | 79.1 | 203 | MAV_3083 | 3-methyladenine DNA glycosylase | 99.51 | 212 | BCG_1726 | 3-methyladenine DNA glycosyl | 79.1 | 203 | MAP1395 | 3-methyladenine DNA glycosylase | 205 | 100 |
| MAP4_2451 | putative ammonium transporter | 425 | Rv2920c | Probable ammonium-transport inte | 47.76 | 477 | Mb2944c | ammonium transporter | 47.76 | 477 | MAV_3084 | ammonium transporter | 99.06 | 425 | BCG_2941c | ammonium-transport integral | 47.76 | 477 | MAP1394c | Amt_1 | 425 | 100 |
| MAP4_2452 | ABC transporter ATP-binding protein | 253 | Rv1687c | Probable conserved ATP-binding pro | 75.5 | 255 | Mb1713c | ABC transporter ATP-binding | 75.5 | 255 | MAV_3085 | ABC transporter ATP-binding prote | 99.21 | 253 | BCG_1725c | ABC transporter ATP-binding p | 75.5 | 255 | MAP1393c | hypothetical protein | 253 | 100 |
| MAP4_2453 | hypothetical protein | 226 | Rv1686c | Probable conserved integral membr | 88.44 | 226 | Mb1712c | integral membrane protein A | 88.44 | 226 | MAV_3086 | efflux ABC transporter | 98.67 | 228 | BCG_1724c | integral membrane protein AB | 88.44 | 226 | MAP1392c | hypothetical protein | 226 | 100 |
| MAP4_2454 | Transcriptional regulator, TetR family | 207 | Rv1685c | hypothetical protein | 71.01 | 207 | Mb1711c | hypothetical protein | 71.01 | 207 | MAV_3088 | TetR family transcriptional regulat | 99.52 | 207 | BCG_1723c | hypothetical protein | 71.01 | 207 | MAP1391c | hypothetical protein | 207 | 100 |
| MAP4_2455 | hypothetical protein | 71 | Rv1684 | hypothetical protein | 77.03 | 74 | Mb1710A | hypothetical protein | 77.03 | 74 | MAV_3087 | hypothetical protein | 95.77 | 71 | BCG_1722 | hypothetical protein | 77.03 | 74 | MAP1390 | hypothetical protein | 71 | 100 |
| MAP4_2456 | long-chain acyl-CoA synthetase and lipase | 968 | Rv1683 | Possible bifunctional enzyme; long-c | 84.25 | 999 | Mb1710 | acyl-CoA synthetase | 84.25 | 999 | MAV_3089 | acyl-CoA synthetase | 99.69 | 998 | BCG_1721 | acyl-CoA synthetase | 84.25 | 999 | MAP1389 | acyl-CoA synthetase | 968 | 100 |
| MAP4_2457 | hypothetical protein | 131 | Rv3312A | Secreted protein antigen | 35.71 | 103 | Mb3341c | hypothetical protein | 35.71 | 103 | MAV_3090 | hypothetical protein | 98.92 | 93 | BCG_3378c | hypothetical protein | 35.71 | 103 | MAP1388 | hypothetical protein | 131 | 99.24 |
| MAP4_2458 | hypothetical protein | 244 | Rv2161c | hypothetical protein | 30.14 | 288 | Mb2185c | hypothetical protein | 30.14 | 288 | MAV_3091 | hypothetical protein | 99.4 | 166 | BCG_2178c | hypothetical protein | 30.14 | 288 | MAP1387c | hypothetical protein | 244 | 100 |
| MAP4_2459 | hypothetical protein | 248 | Rv3394c | hypothetical protein | 34.09 | 527 | Mb3426c | hypothetical protein | 34.09 | 527 | MAV_3092 | hypothetical protein | 98.39 | 248 | BCG_3463c | hypothetical protein | 34.09 | 527 | MAP1386c | hypothetical protein | 248 | 100 |
| MAP4_2460 | Glucose-methanol-choline (GMC) oxidoreductase | 565 | Rv0492c | Probable oxidoreductase GMC-type | 27.92 | 629 | Mb0502c | oxidoreductase GMC-type | 27.74 | 629 | MAV_3093 | glucose-methanol-choline oxidored | 98.89 | 540 | BCG_0533c | oxidoreductase GMC-type | 27.74 | 629 | MAP1385c | hypothetical protein | 566 | 100 |
| MAP4_2461 | glycosyl hydrolase, family 15 protein | 598 | Rv2402 | hypothetical protein | 28.18 | 642 | Mb2425 | hypothetical protein | 28.18 | 642 | MAV_3094 | glycosyl hydrolase, family protein 1 | 99.16 | 598 | BCG_2418 | hypothetical protein | 28.18 | 642 | MAP1384c | hypothetical protein | 598 | 100 |
| MAP4_2462 | short-chain dehydrogenase | 340 | Rv1050 | Probable oxidoreductase | 34.93 | 301 | Mb1079 | oxidoreductase | 34.93 | 301 | MAV_3095 | short chain dehydrogenase | 99.71 | 340 | BCG_1108 | oxidoreductase | 34.93 | 301 | MAP1383c | short chain dehydrogenase | 340 | 100 |
| MAP4_2463 | mandelate racemasemuconate lactonizing enzyme | 368 | Rv0553 | Probable muconate cycloisomerase | 26.98 | 326 | Mb0568 | O-succinylbenzoate synthase | 26.98 | 326 | MAV_3096 | mandelate racemase/muconate lac | 98.91 | 368 | BCG_0598 | O-succinylbenzoate synthase | 26.98 | 326 | MAP1382c | hypothetical protein | 368 | 100 |
| MAP4_2464 | putative dehydrogenasereductase | 256 | Rv0769 | Probable dehydrogenase/reductase | 34.92 | 248 | Mb0792 | short chain dehydrogenase | 34.52 | 248 | MAV_3097 | NAD dependent epimerase/dehydr | 98.83 | 256 | BCG_0821 | short chain dehydrogenase | 34.52 | 248 | MAP1381 | hypothetical protein | 256 | 100 |
| MAP4_2465 | short-chain dehydrogenasereductase | 270 | Rv0687 | Probable short-chain type dehydrog | 42.48 | 275 | Mb0706 | 3-ketoacyl-ACP reductase | 42.48 | 275 | MAV_3098 | carveol dehydrogenase | 96.3 | 270 | BCG_0736 | 3-ketoacyl-ACP reductase | 42.48 | 275 | MAP1380 | hypothetical protein | 270 | 100 |
| MAP4_2466 | hypothetical protein | 354 | Rv2159c | hypothetical protein | 32.89 | 344 | Mb2183c | hypothetical protein | 32.89 | 344 | MAV_3099 | hypothetical protein | 98.46 | 325 | BCG_2176c | hypothetical protein | 32.89 | 344 | MAP1379 | hypothetical protein | 354 | 100 |
| MAP4_2468 | oxidoreductase, short chaindehydrogenase/reductase | 292 | Rv1350 | Probable 3-oxoacyl-[acyl-carrier pro | 32.44 | 247 | Mb1385 | 3-ketoacyl-ACP reductase | 32.44 | 247 | MAV_3101 | oxidoreductase, short chain dehydr | 98.57 | 280 | BCG_1412 | 3-ketoacyl-ACP reductase | 32.44 | 247 | MAP1377 | hypothetical protein | 262 | 99.62 |
| MAP4_2469 | transcriptional regulator, LysR family | 317 | Rv2282c | Probable transcription regulator (Ly | 31.96 | 312 | Mb2303c | LysR family transcriptional re | 31.96 | 312 | MAV_3102 | LysR family transcriptional regulato | 99.68 | 317 | BCG_2297c | LysR family transcriptional regu | 31.96 | 312 | MAP1376c | hypothetical protein | 317 | 100 |
| MAP4_2471 | macrolide-transport ATP-binding protein ABC transpor | 591 | Rv1668c | Probable first part of macrolide-tran | 85.59 | 372 | Mb1695c | macrolide ABC transporter AT | 81.99 | 591 | MAV_3104 | macrolide ABC transporter ATP-bin | 98.95 | 574 | BCG_1706c | macrolide ABC transporter ATP | 81.99 | 591 | MAP1374c | hypothetical protein | 591 | 100 |
| MAP4_2472 | Cytochrome P450 | 427 | Rv1666c | Probable cytochrome P450 139 Cyp | 75.35 | 430 | Mb1694c | cytochrome P450 139 CYP13 | 75.35 | 430 | MAV_3106 | P450 heme-thiolate protein | 96.96 | 427 | BCG_1705c | cytochrome P450 139 CYP139 | 75.35 | 430 | MAP1373c | hypothetical protein | 427 | 100 |
| MAP4_2473 | Chalcone synthase | 353 | Rv1665 | Chalcone synthase Pks11 | 75.64 | 353 | Mb1693 | chalcone synthase | 75.64 | 353 | MAV_3105 | Pks11 protein | 99.15 | 353 | BCG_1704 | chalcone synthase pks11 | 75.64 | 353 | MAP1372 | hypothetical protein | 353 | 100 |
| MAP4_2474 | Polyketide synthase | 1095 | Rv1662 | Probable polyketide synthase Pks8 | 72.38 | 1602 | Mb1690 | polyketide synthase | 72.38 | 1602 | MAV_3108 | erythronolide synthase, modules 3 | 92.88 | 2128 | BCG_1701 | polyketide synthase | 72.38 | 1601 | MAP1371 | hypothetical protein | 1095 | 99.91 |
| MAP4_2475 | putative polyketide synthase pks7 | 2018 | Rv1661 | Probable polyketide synthase Pks7 | 70.14 | 2126 | Mb1689 | polyketide synthase | 70.09 | 2126 | MAV_3109 | RifB protein | 98.84 | 2124 | BCG_1700 | polyketide synthase pks7 | 70.09 | 2126 | MAP1370 | hypothetical protein | 2018 | 100 |
| MAP4_2476 | putative chalcone synthase pks10 | 353 | Rv1660 | Chalcone synthase Pks10 | 82.72 | 353 | Mb1688 | chalcone synthase | 82.72 | 353 | MAV_3110 | Pks10 protein | 99.72 | 353 | BCG_1699 | chalcone synthase pks10 | 82.72 | 353 | MAP1369 | hypothetical protein | 353 | 100 |
| MAP4_2477 | argininosuccinate lyase | 472 | Rv1659 | Probable argininosuccinate lyase Ar | 89.32 | 470 | Mb1687 | argininosuccinate lyase | 89.32 | 470 | MAV_3111 | argininosuccinate lyase | 99.79 | 472 | BCG_1698 | argininosuccinate lyase | 89.32 | 470 | MAP1368 | argininosuccinate lyase | 472 | 100 |
| MAP4_2478 | Argininosuccinate synthase | 398 | Rv1658 | Probable argininosuccinate synthase | 93.72 | 398 | Mb1686 | argininosuccinate synthase | 93.72 | 398 | MAV_3112 | argininosuccinate synthase | 99.5 | 398 | BCG_1697 | argininosuccinate synthase | 93.72 | 398 | MAP1367 | argininosuccinate synthase | 398 | 100 |
| MAP4_2479 | arginine repressor ArgR | 164 | Rv1657 | Probable arginine repressor ArgR (A | 76.92 | 170 | Mb1685 | arginine repressor ArgR | 76.92 | 170 | MAV_3113 | arginine repressor | 98.78 | 164 | BCG_1696 | arginine repressor | 76.92 | 170 | MAP1366 | arginine repressor | 164 | 100 |
| MAP4_2480 | Ornithine carbamoyltransferase | 309 | Rv1656 | Probable ornithine carbamoyltransfe | 81.25 | 307 | Mb1684 | ornithine carbamoyltransfera | 81.25 | 307 | MAV_3114 | ornithine carbamoyltransferase | 98.71 | 309 | BCG_1695 | ornithine carbamoyltransferase | 81.25 | 307 | MAP1365 | ornithine carbamoyltransferase | 309 | 100 |
| MAP4_2481 | acetylornithine aminotransferase | 409 | Rv1655 | Probable acetylornithine aminotrans | 83.21 | 400 | Mb1683 | acetylornithine aminotransfe | 83.21 | 400 | MAV_3115 | acetylornithine aminotransferase | 99.27 | 409 | BCG_1694 | acetylornithine aminotransfera | 83.21 | 400 | MAP1364 | acetylornithine aminotransferase | 409 | 100 |
| MAP4_2482 | acetylglutamate kinase | 295 | Rv1654 | Probable acetylglutamate kinase Arg | 90.62 | 294 | Mb1682 | acetylglutamate kinase | 90.62 | 294 | MAV_3116 | acetylglutamate kinase | 99.66 | 295 | BCG_1693 | acetylglutamate kinase | 90.62 | 294 | MAP1363 | acetylglutamate kinase | 295 | 100 |
| MAP4_2483 | glutamate N-acetyltransferase argJ | 404 | Rv1653 | Probable glutamate N-acetyltransfe | 83.91 | 404 | Mb1681 | bifunctional ornithine acetylt | 83.91 | 404 | MAV_3117 | bifunctional ornithine acetyltransfe | 99.26 | 404 | BCG_1692 | bifunctional ornithine acetyltra | 83.91 | 404 | MAP1362 | bifunctional ornithine acetyltransferase | 404 | 100 |
| MAP4_2484 | N-acetyl-gamma-glutamyl-phosphate reductase | 347 | Rv1652 | Probable N-acetyl-gamma-glutamyl- | 86.17 | 352 | Mb1680 | N-acetyl-gamma-glutamyl-ph | 86.17 | 352 | MAV_3118 | N-acetyl-gamma-glutamyl-phospha | 98.85 | 347 | BCG_1691 | N-acetyl-gamma-glutamyl-pho | 86.17 | 352 | MAP1361 | N-acetyl-gamma-glutamyl-phosphate re | 347 | 100 |
| MAP4_2485 | Phenylalanyl-tRNA synthetase beta chain | 828 | Rv1650 | Probable phenylalanyl-tRNA synthet | 83.61 | 831 | Mb1677 | phenylalanyl-tRNA synthetase | 83.49 | 831 | MAV_3119 | phenylalanyl-tRNA synthetase subu | 98.91 | 828 | BCG_1689 | phenylalanyl-tRNA synthetase | 83.49 | 831 | MAP1360 | phenylalanyl-tRNA synthetase subunit b | 828 | 100 |
| MAP4_2486 | Phenylalanyl-tRNA synthetase alpha chain | 347 | Rv1649 | Probable phenylalanyl-tRNA synthet | 86.76 | 341 | Mb1676 | phenylalanyl-tRNA synthetase | 86.76 | 341 | MAV_3120 | phenylalanyl-tRNA synthetase subu | 98.25 | 342 | BCG_1688 | phenylalanyl-tRNA synthetase | 86.76 | 341 | MAP1359 | phenylalanyl-tRNA synthetase subunit a | 347 | 100 |
| MAP4_2487 | putative transmembrane protein | 272 | Rv1648 | Probable transmembrane protein | 58.3 | 268 | Mb1675 | transmembrane protein | 58.3 | 268 | MAV_3121 | hypothetical protein | 99.25 | 267 | BCG_1687 | hypothetical protein | 58.3 | 268 | MAP1358 | hypothetical protein | 272 | 100 |
| MAP4_2488 | putative adenylate cyclase | 322 | Rv1647 | Adenylate cyclase (ATP pyrophospha | 79.25 | 316 | Mb1674 | hypothetical protein | 79.25 | 316 | MAV_3122 | adenylate and guanylate cyclase ca | 99.14 | 306 | BCG_1686 | hypothetical protein | 79.25 | 316 | MAP1357 | hypothetical protein | 322 | 100 |
| MAP4_2489 | hypothetical protein | 355 | Rv1645c | hypothetical protein | 82.54 | 351 | Mb1672c | hypothetical protein | 82.54 | 351 | MAV_3124 | hypothetical protein | 99.72 | 355 | BCG_1684c | hypothetical protein | 82.54 | 351 | MAP1356c | hypothetical protein | 355 | 100 |
| MAP4_2490 | 23S rRNA methyltransferase | 263 | Rv1644 | Possible 23S rRNA methyltransferase | 76.26 | 260 | Mb1671 | 23S rRNA methyltransferase | 76.65 | 260 | MAV_3123 | TsnR protein | 97.34 | 263 | BCG_1683 | 23S rRNA methyltransferase ts | 76.65 | 260 | MAP1355 | TsnR | 263 | 100 |
| MAP4_2491 | 50S ribosomal protein L20 | 131 | Rv1643 | 50S ribosomal protein L20 RplT | 95.42 | 129 | Mb1670 | 50S ribosomal protein L20 | 95.42 | 129 | MAV_3125 | 50S ribosomal protein L20 | 99.22 | 128 | BCG_1682 | 50S ribosomal protein L20 | 95.42 | 129 | MAP1354 | 50S ribosomal protein L20 | 131 | 100 |
| MAP4_2492 | 50S ribosomal protein L35 | 64 | Rv1642 | 50S ribosomal protein L35 RpmI | 90.62 | 64 | Mb1669 | 50S ribosomal protein L35 | 90.62 | 64 | MAV_3126 | 50S ribosomal protein L35 | 100 | 64 | BCG_1681 | 50S ribosomal protein L35 | 90.62 | 64 | MAP1353 | 50S ribosomal protein L35 | 64 | 100 |
| MAP4_2493 | translation initiation factor IF-3 infC | 184 | Rv1641 | Probable initiation factor if-3 InfC | 88.59 | 201 | Mb1668 | translation initiation factor IF | 88.59 | 201 | MAV_3127 | translation initiation factor IF-3 | 98.84 | 173 | BCG_1680 | translation initiation factor IF-3 | 88.04 | 201 | MAP1352 | translation initiation factor IF-3 | 184 | 100 |
| MAP4_2494 | lysyl-tRNA synthetase | 1177 | Rv1640c | Lysyl-tRNA synthetase 2 LysX | 79.68 | 1172 | Mb1667c | lysyl-tRNA synthetase | 79.6 | 1172 | MAV_3128 | lysyl-tRNA synthetase | 99.91 | 1075 | BCG_1679c | lysyl-tRNA synthetase | 79.51 | 1172 | MAP1351c | lysyl-tRNA synthetase | 1177 | 100 |
| MAP4_2495 | hypothetical protein | 494 | Rv1639c | hypothetical protein | 71.78 | 489 | Mb1666c | hypothetical protein | 71.78 | 489 | MAV_3129 | esterase | 99.36 | 467 | BCG_1678c | hypothetical protein | 71.78 | 489 | MAP1350c | hypothetical protein | 494 | 100 |
| MAP4_2496 | hypothetical protein | 139 | Rv1063c | hypothetical protein | 36.17 | 360 | Mb1092c | hypothetical protein | 36.17 | 360 | MAV_5256 | hypothetical protein | 26.67 | 216 | BCG_1121c | hypothetical protein | 36.17 | 360 | MAP4295c | hypothetical protein | 216 | 32.69 |
| MAP4_2497 | Transcriptional regulator, TetR family | 219 | Rv1219c | Probable transcriptional regulatory | 33.09 | 212 | Mb1251c | transcriptional regulator | 33.09 | 212 | MAV_3130 | TetR family transcriptional regulat | 71.75 | 189 | BCG_1279c | transcriptional regulatory prot | 31.85 | 212 | MAP1349c | hypothetical protein | 219 | 100 |
| MAP4_2498 | putative molybdopterin biosynthesis protein MoeY | 709 | Rv1355c | Possible molybdopterin biosynthesis | 59.12 | 715 | Mb1390c | hypothetical protein | 59.27 | 715 | MAV_3131 | hypothetical protein | 77.35 | 703 | BCG_1417c | hypothetical protein | 59.27 | 715 | MAP1348c | hypothetical protein | 709 | 100 |
| MAP4_2501 | putative methyltransferase | 199 | Rv1377c | Putative transferase | 38.68 | 212 | Mb1412c | transferase | 38.68 | 212 | MAV_0982 | methyltransferase type 12 | 71.5 | 200 | BCG_1438c | transferase | 38.68 | 212 | MAP1345 | hypothetical protein | 199 | 100 |
| MAP4_2502 | putative cytochrome P450 | 456 | Rv3685c | Probable cytochrome P450 137 Cyp | 31.1 | 476 | Mb3710c | cytochrome P450 137 | 30.81 | 476 | MAV_3106 | P450 heme-thiolate protein | 30.16 | 427 | BCG_3744c | cytochrome P450 137 cyp137 | 30.81 | 476 | MAP1344 | hypothetical protein | 456 | 100 |
| MAP4_2503 | hypothetical protein | 243 | Rv1356c | Hypothetical protein | 58.57 | 263 | Mb1391c | hypothetical protein | 58.57 | 263 | MAV_3133 | hypothetical protein | 98.74 | 239 | BCG_1418c | hypothetical protein | 58.57 | 263 | MAP1343 | hypothetical protein | 243 | 100 |
| MAP4_2504 | hypothetical protein | 78 | Rv1638A | hypothetical protein | 60.98 | 85 | Mb1665c | hypothetical protein | 60.98 | 85 | MAV_3134 | hypothetical protein | 97.44 | 78 | BCG_1677c | hypothetical protein | 60.98 | 85 | MAP1342c | hypothetical protein | 78 | 100 |
| MAP4_2505 | excinuclease ABC subunit A | 971 | Rv1638 | Probable excinuclease ABC (subunit | 93.02 | 972 | Mb1664 | excinuclease ABC subunit A | 93.02 | 972 | MAV_3135 | excinuclease ABC subunit A | 99.9 | 971 | BCG_1676 | excinuclease ABC subunit A | 93.02 | 972 | MAP1341 | excinuclease ABC subunit A | 971 | 100 |
| MAP4_2506 | metallo-beta-lactamase superfamily protein | 259 | Rv1637c | hypothetical protein | 75.38 | 264 | Mb1663c | hypothetical protein | 75.38 | 264 | MAV_3136 | hydrolase | 98.27 | 231 | BCG_1675c | hypothetical protein | 75.38 | 264 | MAP1340c | hypothetical protein | 259 | 100 |
| MAP4_2507 | iron-regulated conserved hypothetical protein | 147 | Rv1636 | Iron-regulated universal stress prote | 87.67 | 146 | Mb1662 | hypothetical protein | 87.67 | 146 | MAV_3137 | universal stress protein family prot | 99.23 | 130 | BCG_1674 | hypothetical protein | 87.67 | 146 | MAP1339 | hypothetical protein | 147 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2508 | hypothetical protein | 525 | Rv1635c | Probable mannosyltransferase Prob | 68.45 | 556 | Mb1661c | hypothetical protein | 68.45 | 556 | MAV_3138 | hypothetical protein | 99 | 498 | BCG_1673c | hypothetical protein | 68.45 | 556 | MAP1338c | hypothetical protein | 616 | 100 |
| MAP4_2509 | Mg2+ transport ATPase C mgtC | 240 | Rv1811 | Possible Mg2+ transport P-type ATP | 39.23 | 234 | Mb1841 | Mg2+ transport P-type ATPas | 39.23 | 234 | MAV_3139 | Mg2+ transporter-C (MgtC) family | 100 | 240 | BCG_1845 | Mg2+ transporter | 39.23 | 234 | MAP1337c | hypothetical protein | 240 | 100 |
| MAP4_2510 | drug efflux membrane protein | 356 | Rv1634 | Possible drug efflux membrane prot | 67.99 | 471 | Mb1660 | drug efflux membrane protei | 68.84 | 471 | MAV_3140 | drug efflux membrane protein | 99.44 | 472 | BCG_1672 | drug efflux membrane protein | 68.84 | 471 | MAP1336 | hypothetical protein | 356 | 100 |
| MAP4_2511 | excinuclease ABC subunit B | 722 | Rv1633 | Probable excinuclease ABC (subunit | 94.84 | 698 | Mb1659 | excinuclease ABC subunit B | 94.84 | 698 | MAV_3141 | excinuclease ABC subunit B | 99.86 | 722 | BCG_1671 | excinuclease ABC subunit B | 94.7 | 698 | MAP1335 | excinuclease ABC subunit B | 722 | 100 |
| MAP4_2512 | Hypothetical Protein | 168 | Rv3082c | Virulence-regulating transcriptional | 42.31 | 340 | Mb3109c | virulence-regulating transcrip | 42.31 | 340 | MAV_3142 | hypothetical protein | 99.4 | 168 | BCG_3107c | virulence-regulating transcripti | 42.31 | 340 | MAP1334 | hypothetical protein | 115 | 100 |
| MAP4_2513 | hypothetical protein | 261 | Rv2077c | Possible conserved transmembrane | 47.5 | 323 | Mb2102c | transmembrane protein | 47.5 | 323 | MAV_3143 | hypothetical protein | 97.03 | 353 | BCG_2095c | hypothetical protein | 47.5 | 323 | MAP1333 | hypothetical protein | 261 | 100 |
| MAP4_2514 | hypothetical protein | 102 | Rv2541 | Hypothetical alanine rich protein | 41.49 | 135 | Mb2570 | hypothetical protein | 41.49 | 135 | MAV_3144 | hypothetical protein | 93.26 | 89 | BCG_2563 | hypothetical protein | 41.49 | 135 | MAP1218c | hypothetical protein | 97 | 39.58 |
| MAP4_2515 | anchored-membrane serinethreonine-protein kinase P | 691 | Rv1746 | Anchored-membrane serine/threon | 63.7 | 476 | Mb1775 | anchored-membrane serine/t | 63.7 | 476 | MAV_3145 | PknF protein | 98.41 | 691 | BCG_1785 | anchored-membrane serine/th | 63.7 | 476 | MAP1332 | hypothetical protein | 620 | 99.84 |
| MAP4_2516 | transmembrane ABC transporter, ATP-binding protein | 866 | Rv1747 | Probable conserved transmembrane | 62.2 | 865 | Mb1776 | ABC transporter ATP-binding | 62.2 | 865 | MAV_3146 | ABC transporter ATP-binding prote | 98.93 | 840 | BCG_1786 | transmembrane ABC transport | 62.2 | 865 | MAP1331c | hypothetical protein | 866 | 100 |
| MAP4_2517 | hypothetical protein | 154 | Rv1632c | Hypothetical protein | 83.33 | 147 | Mb1658c | hypothetical protein | 83.33 | 147 | MAV_3147 | hypothetical protein | 99.35 | 154 | BCG_1670c | hypothetical protein | 83.33 | 147 | MAP1330c | hypothetical protein | 154 | 100 |
| MAP4_2518 | ATP-dependent DNA ligase | 332 | Rv0938 | ATP dependent DNA ligase LigD (AT | 35.46 | 759 | Mb0963 | ATP-dependent DNA ligase | 35.46 | 759 | MAV_3148 | DNA polymerase LigD ligase subuni | 99.4 | 332 | BCG_0992 | ATP-dependent DNA ligase | 35.46 | 759 | MAP1329c | hypothetical protein | 354 | 99.7 |
| MAP4_2519 | formamidopyrimidine-DNA glycosylase | 262 | Rv2924c | Probable formamidopyrimidine-DN | 34.36 | 289 | Mb2949c | formamidopyrimidine-DNA gl | 34.36 | 289 | MAV_3149 | formamidopyrimidine DNA-glyxosy | 98.85 | 262 | BCG_2946c | formamidopyrimidine-DNA gly | 34.36 | 289 | MAP1328c | hypothetical protein | 262 | 100 |
| MAP4_2520 | hypothetical protein | 137 | Rv3709c | Aspartokinase Ask (aspartate kinase | 28.57 | 421 | Mb3736c | aspartate kinase | 28.57 | 421 | MAV_3150 | hypothetical protein | 100 | 137 | BCG_3769c | aspartate kinase | 28.57 | 421 | MAP1327c | hypothetical protein | 137 | 100 |
| MAP4_2521 | dephospho-CoA kinase CoaE | 407 | Rv1631 | Probable dephospho-CoA kinase Co | 77.4 | 407 | Mb1657 | dephospho-CoA kinase/prote | 77.4 | 407 | MAV_3151 | dephospho-CoA kinase/protein fol | 99.51 | 407 | BCG_1669 | dephospho-CoA kinase/protei | 77.4 | 407 | MAP1326 | dephospho-CoA kinase/protein folding | 407 | 100 |
| MAP4_2522 | 30S ribosomal protein S1 | 480 | Rv1630 | 30S ribosomal protein S1 RpsA | 96.67 | 481 | Mb1656 | 30S ribosomal protein S1 | 96.47 | 481 | MAV_3152 | 30S ribosomal protein S1 | 100 | 480 | BCG_1668 | 30S ribosomal protein S1 | 96.47 | 481 | MAP1325 | 30S ribosomal protein S1 | 480 | 100 |
| MAP4_2523 | dioxygenase | 508 | Rv0913c | Possible dioxygenase | 27.22 | 502 | Mb0937c | dioxygenase | 27.22 | 502 | MAV_3153 | retinal pigment epithelial membra | 99.01 | 503 | BCG_0965c | dioxygenase | 27.22 | 502 | MAP1324 | hypothetical protein | 508 | 100 |
| MAP4_2524 | Transcriptional regulator, TetR family | 209 | Rv3208 | Probable transcriptional regulatory | 25.48 | 228 | Mb3233 | TetR family transcriptional re | 25.48 | 228 | MAV_3154 | TetR family transcriptional regulat | 99.04 | 209 | BCG_3234 | TetR family transcriptional regu | 25.48 | 228 | MAP1323 | hypothetical protein | 209 | 100 |
| MAP4_2525 | DNA polymerase I | 919 | Rv1629 | Probable DNA polymerase I PolA | 87.14 | 904 | Mb1655 | DNA polymerase I | 87.14 | 904 | MAV_3155 | DNA polymerase I | 99.56 | 913 | BCG_1667 | DNA polymerase I | 87.14 | 904 | MAP1322 | DNA polymerase I | 919 | 100 |
| MAP4_2526 | hypothetical protein | 146 | Rv1628c | hypothetical protein | 81.25 | 163 | Mb1654c | hypothetical protein | 81.25 | 163 | MAV_3156 | hypothetical protein | 100 | 146 | BCG_1666c | hypothetical protein | 80.56 | 163 | MAP1321c | hypothetical protein | 146 | 100 |
| MAP4_2527 | nonspecific lipid-transfer protein | 404 | Rv1627c | Probable nonspecific lipid-transfer | 91.44 | 402 | Mb1653c | lipid-transfer protein | 91.44 | 402 | MAV_3157 | lipid-transfer protein | 100 | 404 | BCG_1665c | lipid-transfer protein | 91.44 | 402 | MAP1320c | lipid-transfer protein | 404 | 100 |
| MAP4_2528 | two-component system transcriptional regulator | 207 | Rv1626 | Probable two-component system tr | 93.14 | 205 | Mb1652 | two-component system trans | 93.14 | 205 | MAV_3158 | response regulator | 99.52 | 207 | BCG_1664 | two-component system transc | 93.14 | 205 | MAP1319 | hypothetical protein | 207 | 100 |
| MAP4_2529 | Adenylate cyclase | 443 | Rv1625c | Membrane-anchored adenylyl cycla | 71.78 | 443 | Mb1651c | adenylate cyclase | 72.66 | 418 | MAV_3162 | adenylate cyclase | 99.1 | 443 | BCG_1663c | membrane-anchored adenylyl | 72.66 | 418 | MAP1318c | hypothetical protein | 443 | 100 |
| MAP4_2530 | hypothetical protein | 197 | Rv1624c | Probable conserved membrane prot | 80.1 | 195 | Mb1650c | hypothetical protein | 80.1 | 195 | MAV_3163 | integral membrane protein | 99.44 | 180 | BCG_1662c | hypothetical protein | 80.1 | 195 | MAP1317c | hypothetical protein | 197 | 100 |
| MAP4_2531 | membrane cytochrome D ubiquinol oxidase subunit I c | 490 | Rv1623c | Probable integral membrane cytoch | 79.59 | 485 | Mb1649c | integral membrane cytochro | 79.59 | 485 | MAV_3164 | cytochrome D ubiquinol oxidase su | 99.18 | 490 | BCG_1661c | integral membrane cytochrom | 79.59 | 485 | MAP1316c | AppC | 490 | 100 |
| MAP4_2532 | membrane cytochrome D ubiquinol oxidase subunit II | 346 | Rv1622c | Probable integral membrane cytoch | 82.85 | 346 | Mb1648c | integral membrane cytochro | 82.85 | 346 | MAV_3165 | cytochrome D ubiquinol oxidase, su | 99.71 | 346 | BCG_1660c | integral membrane cytochrom | 82.85 | 346 | MAP1315c | CydB | 346 | 100 |
| MAP4_2533 | transmembrane ATP-binding protein ABC transporter | 532 | Rv1621c | Probable 'component linked with th | 77.38 | 527 | Mb1647c | cytochrome assembly ABC tr | 77.38 | 527 | MAV_3166 | cysteine ABC transporter ATP-bind | 98.12 | 540 | BCG_1659c | cytochrome assembly ABC tra | 77.38 | 527 | MAP1314c | CydD | 532 | 100 |
| MAP4_2534 | transmembrane ATP-binding protein ABC transporter | 561 | Rv1620c | Probable 'component linked with th | 73.74 | 576 | Mb1646c | cytochrome assembly ABC tr | 73.74 | 576 | MAV_3167 | ABC transporter ATP-binding prote | 97.49 | 560 | BCG_1658c | cytochrome assembly ABC tra | 73.74 | 576 | MAP1313c | CydC | 565 | 99.82 |
| MAP4_2537 | Acyl-CoA thioesterase II | 300 | Rv1618 | Probable acyl-CoA thioesterase II Te | 83.45 | 300 | Mb1644 | acyl-CoA thioesterase | 83.8 | 300 | MAV_3169 | Acyl-CoA thioesterase | 98.33 | 300 | BCG_1656 | acyl-CoA thioesterase II tesB1 | 83.8 | 300 | MAP1311 | TesB1 | 300 | 100 |
| MAP4_2538 | Pyruvate kinase | 472 | Rv1617 | Probable pyruvate kinase PykA | 91.53 | 472 | Mb1643 | pyruvate kinase | 91.31 | 472 | MAV_3170 | pyruvate kinase | 99.78 | 451 | BCG_1655 | pyruvate kinase | 91.53 | 472 | MAP1310 | pyruvate kinase | 472 | 100 |
| MAP4_2539 | hypothetical protein | 139 | Rv1616 | hypothetical protein | 64.84 | 132 | Mb1642 | hypothetical protein | 64.84 | 132 | MAV_3171 | hypothetical protein | 96.58 | 117 | BCG_1654 | hypothetical protein | 64.84 | 132 | MAP1309 | hypothetical protein | 139 | 100 |
| MAP4_2540 | Prolipoprotein diacylglyceryl transferase | 427 | Rv1614 | Possible prolipoprotein diacylglycer | 59.17 | 468 | Mb1640 | prolipoprotein diacylglyceryl | 59.17 | 468 | MAV_3172 | prolipoprotein diacylglyceryl transf | 84.77 | 440 | BCG_1652 | prolipoprotein diacylglyceryl tr | 59.17 | 468 | MAP1308 | prolipoprotein diacylglyceryl transfera | 427 | 100 |
| MAP4_2541 | Tryptophan synthase alpha chain | 271 | Rv1613 | Probable tryptophan synthase, alph | 85.66 | 270 | Mb1639 | tryptophan synthase subunit | 85.66 | 270 | MAV_3173 | tryptophan synthase subunit alpha | 99.26 | 271 | BCG_1651 | tryptophan synthase subunit a | 85.66 | 270 | MAP1307 | tryptophan synthase subunit alpha | 271 | 100 |
| MAP4_2542 | Tryptophan synthase beta chain | 421 | Rv1612 | Tryptophan synthase, beta subunit | 87.01 | 410 | Mb1638 | tryptophan synthase subunit | 87.01 | 410 | MAV_3174 | tryptophan synthase subunit beta | 99.29 | 423 | BCG_1650 | tryptophan synthase subunit b | 87.01 | 410 | MAP1306 | tryptophan synthase subunit beta | 421 | 100 |
| MAP4_2543 | Indole-3-glycerol phosphate synthase | 272 | Rv1611 | Probable indole-3-glycerol phosphat | 93.38 | 272 | Mb1637 | indole-3-glycerol phosphate | 93.38 | 272 | MAV_3175 | indole-3-glycerol-phosphate synth | 100 | 272 | BCG_1649 | indole-3-glycerol-phosphate sy | 93.38 | 272 | MAP1305 | indole-3-glycerol-phosphate synthase | 272 | 100 |
| MAP4_2544 | hypothetical protein | 143 | Rv1610 | Possible conserved membrane prot | 74.4 | 235 | Mb1636 | hypothetical protein | 74.4 | 235 | MAV_3176 | hypothetical protein | 97.83 | 226 | BCG_1648 | hypothetical protein | 74.4 | 235 | MAP1304 | hypothetical protein | 143 | 100 |
| MAP4_2545 | anthranilate synthase component I | 510 | Rv1609 | Anthranilate synthase component I | 88.5 | 516 | Mb1635 | anthranilate synthase compo | 88.5 | 516 | MAV_3177 | anthranilate synthase component I | 99.8 | 510 | BCG_1647 | anthranilate synthase compon | 88.5 | 516 | MAP1303 | anthranilate synthase component I | 510 | 100 |
| MAP4_2546 | peroxidoxin BcpB | 155 | Rv1608c | Probable peroxidoxin BcpB | 84.67 | 154 | Mb1634c | peroxidoxin bcpB | 84.67 | 154 | MAV_3178 | antioxidant, AhpC/TSA family prote | 99.34 | 152 | BCG_1646c | peroxidoxin bcpB | 84.67 | 154 | MAP1302c | BcpB | 185 | 99.35 |
| MAP4_2547 | ionic transporter integral membrane protein chaA | 368 | Rv1607 | Probable ionic transporter integral | 78.43 | 360 | Mb1633 | ionic transporter integral me | 78.43 | 360 | MAV_3179 | calcium/proton exchanger | 100 | 368 | BCG_1645 | ionic transporter integral mem | 78.43 | 360 | MAP1301 | ChaA | 368 | 100 |
| MAP4_2548 | Phosphoribosyl-AMP cyclohydrolase | 115 | Rv1606 | Probable phosphoribosyl-AMP 1,6 c | 88.7 | 115 | Mb1632 | phosphoribosyl-AMP cyclohy | 88.7 | 115 | MAV_3180 | phosphoribosyl-AMP cyclohydrola | 98.26 | 115 | BCG_1644 | phosphoribosyl-AMP cyclohyd | 88.7 | 115 | MAP1300 | phosphoribosyl-AMP cyclohydrolase | 115 | 100 |
| MAP4_2549 | cyclase | 265 | Rv1605 | Probable cyclase HisF | 89.62 | 267 | Mb1631 | imidazole glycerol phosphate | 89.23 | 267 | MAV_3181 | imidazole glycerol phosphate synth | 99.62 | 265 | BCG_1643 | imidazole glycerol phosphate s | 89.23 | 267 | MAP1299 | imidazole glycerol phosphate synthase | 265 | 100 |
| MAP4_2550 | inositol-monophosphatase | 266 | Rv1604 | Probable inositol-monophosphatase | 77.78 | 270 | Mb1630 | inositol-monophosphatase | 77.41 | 270 | MAV_3182 | inositol monophosphatase | 99.25 | 266 | BCG_1642 | inositol-monophosphatase imp | 77.41 | 270 | MAP1298 | ImpA | 266 | 100 |
| MAP4_2551 | phosphoribosylformimino-5- aminoimidazolecarboxam | 243 | Rv1603 | Probable phosphoribosylformimino- | 91.67 | 245 | Mb1629 | phosphoribosyl isomerase A | 91.67 | 245 | MAV_3183 | phosphoribosyl isomerase A | 99.18 | 243 | BCG_1641 | phosphoribosyl isomerase A | 91.67 | 245 | MAP1297 | phosphoribosyl isomerase A | 243 | 100 |
| MAP4_2552 | amidotransferase HisH | 206 | Rv1602 | Probable amidotransferase HisH | 79.13 | 206 | Mb1628 | imidazole glycerol phosphate | 79.61 | 206 | MAV_3184 | imidazole glycerol phosphate synth | 99.51 | 206 | BCG_1640 | imidazole glycerol phosphate s | 79.61 | 206 | MAP1296 | imidazole glycerol phosphate synthase | 206 | 100 |
| MAP4_2553 | imidazole glycerol-phosphate dehydratase HisB | 207 | Rv1601 | Probable imidazole glycerol-phosph | 88.1 | 210 | Mb1627 | imidazoleglycerol-phosphate | 88.1 | 210 | MAV_3185 | imidazoleglycerol-phosphate dehy | 100 | 207 | BCG_1639 | imidazoleglycerol-phosphate d | 88.1 | 210 | MAP1295 | imidazoleglycerol-phosphate dehydrata | 207 | 100 |
| MAP4_2554 | Histidinol-phosphate aminotransferase | 398 | Rv1600 | Probable histidinol-phosphate amin | 86.61 | 380 | Mb1626 | histidinol-phosphate aminotr | 86.61 | 380 | MAV_3186 | histidinol-phosphate aminotransfe | 99.5 | 398 | BCG_1638 | histidinol-phosphate aminotra | 86.61 | 380 | MAP1294 | histidinol-phosphate aminotransferase | 398 | 100 |
| MAP4_2555 | Histidinol dehydrogenase | 467 | Rv1599 | Probable histidinol dehydrogenase H | 84.55 | 438 | Mb1625 | histidinol dehydrogenase | 84.55 | 438 | MAV_3187 | histidinol dehydrogenase | 99.57 | 467 | BCG_1637 | histidinol dehydrogenase | 84.55 | 438 | MAP1293 | histidinol dehydrogenase | 480 | 100 |
| MAP4_2556 | hypothetical protein | 137 | Rv1598c | hypothetical protein | 75.91 | 136 | Mb1624c | hypothetical protein | 75.91 | 136 | MAV_3188 | hypothetical protein | 99.27 | 137 | BCG_1636c | hypothetical protein | 75.91 | 136 | MAP1292c | hypothetical protein | 137 | 100 |
| MAP4_2557 | nicotinate-nucleotide pyrophosphorylase NadC | 284 | Rv1596 | Probable nicotinate-nucleotide pyro | 80.92 | 285 | Mb1622 | nicotinate-nucleotide pyroph | 81.27 | 285 | MAV_3189 | nicotinate-nucleotide pyrophosph | 100 | 284 | BCG_1634 | nicotinate-nucleotide pyropho | 81.27 | 285 | MAP1291 | nicotinate-nucleotide pyrophosphoryla | 284 | 100 |
| MAP4_2558 | L-aspartate oxidase | 530 | Rv1595 | Probable L-aspartate oxidase NadB | 77.26 | 527 | Mb1621 | L-aspartate oxidase | 77.26 | 527 | MAV_3190 | L-aspartate oxidase | 99.43 | 530 | BCG_1633 | L-aspartate oxidase | 77.26 | 527 | MAP1290 | L-aspartate oxidase | 530 | 100 |
| MAP4_2559 | Quinolinate synthetase | 349 | Rv1594 | Probable quinolinate synthetase Na | 89.4 | 349 | Mb1620 | quinolinate synthetase | 89.4 | 349 | MAV_3191 | quinolinate synthetase | 99.43 | 349 | BCG_1632 | quinolinate synthetase | 89.4 | 349 | MAP1289 | quinolinate synthetase | 349 | 100 |
| MAP4_2560 | putative NUDIX hydrolase | 241 | Rv1593c | hypothetical protein | 86.55 | 236 | Mb1619c | hypothetical protein | 86.55 | 236 | MAV_3192 | hydrolase, NUDIX family protein | 99.12 | 228 | BCG_1631c | hypothetical protein | 86.55 | 236 | MAP1288c | hypothetical protein | 241 | 100 |
| MAP4_2561 | transposase, IS1601_B family | 407 | Rv2014 | Transposase | 31.65 | 196 | Mb2037 | transposase | 31.65 | 196 | MAV_0496 | transposase IS116/IS110/IS902 | 46.4 | 404 | BCG_2031 | transposase | 31.65 | 196 | MAP0832c | IS1601_B_1 transposase | 407 | 100 |
| MAP4_2562 | putative secretory lipase | 446 | Rv1592c | hypothetical protein | 79.37 | 446 | Mb1618c | hypothetical protein | 79.6 | 446 | MAV_3194 | secretory lipase | 100 | 446 | BCG_1630c | hypothetical protein | 79.6 | 446 | MAP1286c | hypothetical protein | 446 | 100 |
| MAP4_2563 | putative transmembrane protein | 225 | Rv1591 | Probable transmembrane protein | 61.19 | 221 | Mb1617 | hypothetical protein | 61.19 | 221 | MAV_3193 | hypothetical protein | 96 | 225 | BCG_1629 | hypothetical protein | 61.19 | 221 | MAP1285 | hypothetical protein | 196 | 99.49 |
| MAP4_2564 | hypothetical protein | 78 | Rv1590 | hypothetical protein | 82.09 | 79 | Mb1616 | hypothetical protein | 82.09 | 79 | MAV_3195 | hypothetical protein | 98.72 | 78 | BCG_1628 | hypothetical protein | 82.09 | 79 | MAP1284 | hypothetical protein | 78 | 100 |
| MAP4_2565 | biotin synthase | 344 | Rv1589 | Probable biotin synthetase BioB | 89.11 | 349 | Mb1615 | biotin synthase | 89.11 | 349 | MAV_3196 | biotin synthase | 99.13 | 345 | BCG_1627 | biotin synthase | 89.11 | 349 | MAP1283 | biotin synthase | 344 | 100 |
| MAP4_2566 | hypothetical protein | 63 | Rv3842c | Probable glycerophosphoryl diester | 68.75 | 274 | Mb3872c | glycerophosphoryl diester ph | 68.75 | 274 | MAV_3197 | hypothetical protein | 96.83 | 63 | BCG_3905c | glycerophosphoryl diester pho | 68.75 | 274 | MAP0190 | GlpQ1 | 272 | 68.75 |
| MAP4_2567 | hypothetical protein | 615 | Rv3157 | Probable NADH dehydrogenase I (ch | 38.78 | 553 | Mb3181 | NADH dehydrogenase subuni | 38.78 | 553 | MAV_3198 | hypothetical protein | 99.51 | 610 | BCG_3180 | NADH dehydrogenase subunit | 38.78 | 553 | MAP1282c | hypothetical protein | 615 | 100 |
| MAP4_2568 | hypothetical protein | 120 | Rv2712c | Hypothetical protein | 33.33 | 352 | Mb2731c | hypothetical protein | 33.33 | 352 | MAV_3199 | hypothetical protein | 100 | 120 | BCG_2725c | hypothetical protein | 33.33 | 352 | MAP1281c | hypothetical protein | 120 | 100 |
| MAP4_2569 | hypothetical protein | 454 | Rv1430 | PE family protein PE16 | 35 | 528 | Mb1465 | PE family protein | 35 | 528 | MAV_3200 | hypothetical protein | 99.34 | 454 | BCG_1491 | PE family protein | 35 | 528 | MAP1280c | hypothetical protein | 454 | 100 |
| MAP4_2570 | cyclase | 730 | Rv2435c | Probable cyclase (adenylyl-or guany | 65.87 | 730 | Mb2461c | cyclase | 65.87 | 730 | MAV_1745 | adenylate and guanylate cyclase ca | 63.38 | 731 | BCG_2454c | cyclase | 65.87 | 730 | MAP1279c | hypothetical protein | 730 | 99.86 |
| MAP4_2572 | hypothetical protein | 169 | Rv1571 | hypothetical protein | 74.56 | 169 | Mb1598 | hypothetical protein | 74.56 | 169 | MAV_3203 | hypothetical protein | 99.41 | 169 | BCG_1624 | hypothetical protein | 74.56 | 169 | MAP1277 | hypothetical protein | 169 | 100 |
| MAP4_2573 | Dethiobiotin synthetase | 226 | Rv1570 | Dethiobiotin synthetase BioD | 72.08 | 226 | Mb1597 | dithiobiotin synthetase | 72.08 | 226 | MAV_3204 | dithiobiotin synthetase | 99.12 | 226 | BCG_1623 | dithiobiotin synthetase | 71.57 | 226 | MAP1276 | dithiobiotin synthetase | 235 | 99.56 |
| MAP4_2574 | 8-amino-7-oxononanoate synthase | 381 | Rv1569 | Probable 8-amino-7-oxononanoate | 82.23 | 386 | Mb1596 | 8-amino-7-oxononanoate sy | 82.23 | 386 | MAV_3205 | 8-amino-7-oxononanoate synthase | 98.43 | 381 | BCG_1622 | 8-amino-7-oxononanoate synt | 82.23 | 386 | MAP1275 | 8-amino-7-oxononanoate synthase | 381 | 100 |
| MAP4_2575 | Adenosylmethionine-8-amino-7-oxononanoate aminot | 438 | Rv1568 | Adenosylmethionine-8-amino-7-oxo | 81.84 | 437 | Mb1595 | adenosylmethionine-8-amino | 81.84 | 437 | MAV_3206 | adenosylmethionine--8-amino-7-o | 99.09 | 438 | BCG_1621 | adenosylmethionine-8-amino- | 81.84 | 437 | MAP1274 | adenosylmethionine--8-amino-7-oxono | 438 | 100 |
| MAP4_2576 | hypothetical protein | 155 | Rv1567c | Probable hypothetical membrane pr | 59.14 | 94 | Mb1594c | hypothetical protein | 59.14 | 94 | MAV_3207 | hypothetical protein | 99.35 | 155 | BCG_1620c | hypothetical protein | 59.14 | 94 | MAP1273c | hypothetical protein | 95 | 98.95 |
| MAP4_2577 | invasion-associated protein | 316 | Rv1566c | Possible Inv protein | 77.21 | 230 | Mb1593c | inv protein | 77.21 | 230 | MAV_3208 | NlpC/P60 family protein | 94.12 | 289 | BCG_1619c | inv protein | 77.21 | 230 | MAP1272c | hypothetical protein | 316 | 100 |
| MAP4_2578 | hypothetical protein | 721 | Rv1565c | hypothetical protein | 74.03 | 729 | Mb1592c | hypothetical protein | 74.03 | 729 | MAV_3209 | acyltransferase domain-containing | 99.45 | 720 | BCG_1618c | hypothetical protein | 74.03 | 729 | MAP1271c | hypothetical protein | 721 | 100 |
| MAP4_2579 | malto-oligosyltrehalose synthase | 732 | Rv1564c | Probable maltooligosyltrehalose sy | 83.27 | 721 | Mb1591c | malto-oligosyltrehalose synth | 83.27 | 721 | MAV_3210 | glycogen debranching enzyme Glg | 99.86 | 732 | BCG_1617c | maltooligosyltrehalose synthas | 83.27 | 721 | MAP1270c | GlgX_1 | 732 | 100 |
| MAP4_2580 | Malto-oligosyltrehalose synthase | 766 | Rv1563c | Maltooligosyltrehalose synthase Tre | 75.49 | 765 | Mb1589c | malto-oligosyltrehalose synth | 73.33 | 244 | MAV_3211 | malto-oligosyltrehalose synthase | 98.3 | 766 | BCG_1616c | maltooligosyltrehalose synthas | 75.49 | 765 | MAP1269c | GlgY | 766 | 100 |
| MAP4_2581 | Malto-oligosyltrehalose trehalohydrolase | 590 | Rv1562c | Maltooligosyltrehalose trehalohydr | 79.93 | 580 | Mb1588c | malto-oligosyltrehalose treha | 79.76 | 580 | MAV_3212 | malto-oligosyltrehalose trehalohyd | 98.98 | 590 | BCG_1615c | maltooligosyltrehalose trehalo | 82.06 | 394 | MAP1268c | GlgZ | 590 | 100 |
| MAP4_2582 | hypothetical protein | 53 | Rv2200c | Probable transmembrane cytochron | 50 | 363 | Mb2223c | transmembrane cytochrome | 50 | 363 | MAV_3213 | hypothetical protein | 98.11 | 53 | BCG_2216c | transmembrane cytochrome C | 50 | 363 | MAP1844c | mercuric reductase | 456 | 28.89 |
| MAP4_2583 | GntR family transcriptional regulator | 442 | Rv1152 | Probable transcriptional regulatory | 46.77 | 121 | Mb1183 | transcriptional regulator | 46.77 | 121 | MAV_3214 | GntR-family protein transcriptional | 98.64 | 442 | BCG_1213 | transcriptional regulatory prot | 46.77 | 121 | MAP1267 | hypothetical protein | 442 | 100 |
| MAP4_2584 | putative flavin-nucleotide-binding protein | 221 | Rv2705c | hypothetical protein | 35.71 | 129 | Mb2724c | hypothetical protein | 35.71 | 129 | MAV_3215 | flavin-nucleotide-binding protein | 98.19 | 221 | BCG_2718c | hypothetical protein | 35.71 | 129 | MAP1266c | hypothetical protein | 264 | 100 |
| MAP4_2587 | Threonine dehydratase | 427 | Rv1559 | Probable threonine dehydratase IlvA | 91.46 | 429 | Mb1585 | threonine dehydratase | 91.46 | 429 | MAV_3217 | threonine dehydratase | 100 | 427 | BCG_1611 | threonine dehydratase | 91.46 | 429 | MAP1264 | threonine dehydratase | 427 | 100 |
| MAP4_2588 | hypothetical protein | 145 | Rv1558 | hypothetical protein | 83.33 | 148 | Mb1584 | hypothetical protein | 83.33 | 148 | MAV_3218 | hypothetical protein | 99.31 | 145 | BCG_1610 | hypothetical protein | 83.33 | 148 | MAP1263 | hypothetical protein | 145 | 100 |
| MAP4_2589 | hypothetical protein | 262 | Rv0861c | DNA helicase Ercc3 | 26.76 | 542 | Mb0884c | DNA helicase | 26.76 | 542 | MAV_3219 | hypothetical protein | 99.24 | 262 | BCG_0913c | DNA helicase | 26.76 | 542 | MAP1262 | hypothetical protein | 262 | 100 |
| MAP4_2590 | acyltransferase PlsB1 | 633 | Rv1551 | Possible acyltransferase PlsB1 | 84.94 | 621 | Mb1577 | glycerol-3-phosphate acyltra | 84.94 | 621 | MAV_3220 | glycerol-3-phosphate acyltransfera | 99.53 | 633 | BCG_1603 | glycerol-3-phosphate acyltrans | 84.94 | 621 | MAP1261 | glycerol-3-phosphate acyltransferase | 633 | 100 |
| MAP4_2591 | fatty-acid--CoA ligase | 606 | Rv1550 | Probable fatty-acid-CoA ligase FadD | 80.47 | 571 | Mb1576 | fatty-acid--CoA ligase | 80.72 | 647 | MAV_3221 | acyl-CoA dehydrogenase | 99.17 | 606 | BCG_1602 | fatty-acid-CoA ligase FadD11 | 80.72 | 647 | MAP1260 | FadD11_1 | 606 | 100 |
| MAP4_2592 | Transcriptional regulator, MerR family | 138 | Rv3334 | Probable transcriptional regulatory | 33.67 | 146 | Mb3367 | MerR family transcriptional r | 33.67 | 146 | MAV_3222 | MerR family transcriptional regula | 97.83 | 138 | BCG_3405 | MerR family transcriptional reg | 33.67 | 146 | MAP1259 | hypothetical protein | 158 | 100 |
| MAP4_2593 | hypothetical protein | 148 | Rv2061c | hypothetical protein | 30 | 134 | Mb2087c | hypothetical protein | 30 | 134 | MAV_3223 | pyridoxamine 5'-phosphate oxidas | 99.32 | 148 | BCG_2080c | hypothetical protein | 30 | 134 | MAP1258c | hypothetical protein | 148 | 100 |
| MAP4_2594 | DNA polymerase III alpha subunit | 1177 | Rv1547 | Probable DNA polymerase III (alpha | 91.5 | 1184 | Mb1574 | DNA polymerase III subunit a | 91.5 | 1184 | MAV_3224 | DNA polymerase III subunit alpha | 99.66 | 1177 | BCG_1600 | DNA polymerase III subunit alp | 91.5 | 1184 | MAP1257 | DNA polymerase III subunit alpha | 1177 | 100 |
| MAP4_2595 | hypothetical protein | 143 | Rv1546 | hypothetical protein | 76.92 | 143 | Mb1573 | hypothetical protein | 76.92 | 143 | MAV_3225 | hypothetical protein | 100 | 143 | BCG_1599 | hypothetical protein | 76.92 | 143 | MAP1256 | hypothetical protein | 143 | 100 |
| MAP4_2596 | ketoacyl reductase | 267 | Rv1544 | Possible ketoacyl reductase | 82.77 | 267 | Mb1571 | ketoacyl reductase | 82.77 | 267 | MAV_3226 | ketoacyl reductase | 100 | 267 | BCG_1597 | ketoacyl reductase | 82.25 | 231 | MAP1255 | hypothetical protein | 267 | 100 |
| MAP4_2598 | hemoglobin-like protein | 136 | Rv1542c | Hemoglobin GlbN | 81.68 | 136 | Mb1569c | hemoglobin glbN | 81.68 | 136 | MAV_3228 | globin | 97.79 | 137 | BCG_1594c | hemoglobin glbN | 81.68 | 136 | MAP1253c | GlbN | 136 | 100 |
| MAP4_2599 | hypothetical protein | 252 | Rv1597 | Hypothetical protein | 68.13 | 252 | Mb1623 | hypothetical protein | 68.53 | 252 | MAV_3229 | hypothetical protein | 93.25 | 252 | BCG_1635 | hypothetical protein | 68.13 | 252 | MAP1252c | hypothetical protein | 252 | 99.6 |
| MAP4_2600 | Ribosomal large subunit pseudouridine synthase D | 308 | Rv1540 | Conserved hypothetical protein me | 89.94 | 308 | Mb1567 | hypothetical protein | 89.94 | 308 | MAV_3230 | ribosomal large subunit pseudouri | 100 | 294 | BCG_1592 | hypothetical protein | 89.94 | 308 | MAP1251 | hypothetical protein | 308 | 100 |
| MAP4_2601 | Lipoprotein signal peptidase | 184 | Rv1539 | Probable lipoprotein signal peptidas | 82.54 | 202 | Mb1566 | lipoprotein signal peptidase | 82.54 | 202 | MAV_3231 | lipoprotein signal peptidase | 98.35 | 182 | BCG_1591 | lipoprotein signal peptidase | 82.54 | 202 | MAP1250 | lipoprotein signal peptidase | 184 | 100 |
| MAP4_2602 | L-asparaginase | 319 | Rv1538c | Probable L-aparaginase AnsA | 72.05 | 326 | Mb1565c | L-aparaginase ansA | 72.05 | 326 | MAV_3233 | L-asparaginase | 99.04 | 312 | BCG_1590c | L-aparaginase ansA | 72.05 | 326 | MAP1249c | AnsA | 319 | 100 |
| MAP4_2603 | DNA polymerase IV | 463 | Rv1537 | Probable DNA polymerase IV DinX ( | 79.53 | 463 | Mb1564 | DNA polymerase IV | 79.96 | 468 | MAV_3232 | DNA polymerase IV | 99.34 | 458 | BCG_1589 | DNA polymerase IV | 79.53 | 463 | MAP1248 | DNA polymerase IV | 463 | 100 |
| MAP4_2604 | hypothetical protein | 286 | Rv3555c | hypothetical protein | 55.76 | 289 | Mb3585c | hypothetical protein | 56.12 | 289 | MAV_3234 | hypothetical protein | 98.57 | 279 | BCG_3619c | hypothetical protein | 56.12 | 289 | MAP1247 | hypothetical protein | 286 | 100 |
| MAP4_2605 | isoleucyl-tRNA synthetase | 1053 | Rv1536 | Isoleucyl-tRNA synthetase IleS | 87.85 | 1041 | Mb1563 | isoleucyl-tRNA synthetase | 87.75 | 1041 | MAV_3235 | isoleucyl-tRNA synthetase | 99.34 | 1053 | BCG_1588 | isoleucyl-tRNA synthetase | 87.75 | 1041 | MAP1246 | isoleucyl-tRNA synthetase | 1053 | 100 |
| MAP4_2606 | hypothetical protein | 78 | Rv1535 | hypothetical protein | 67.95 | 78 | Mb1562 | hypothetical protein | 67.95 | 78 | MAV_3236 | hypothetical protein | 98.72 | 78 | BCG_1587 | hypothetical protein | 67.95 | 78 | MAP1245 | hypothetical protein | 78 | 100 |
| MAP4_2607 | hypothetical protein | 372 | Rv1533 | hypothetical protein | 84.8 | 375 | Mb1560 | hypothetical protein | 84.8 | 375 | MAV_3237 | 2-nitropropane dioxygenase, NPD | 99.19 | 372 | BCG_1585 | hypothetical protein | 84.8 | 375 | MAP1244 | hypothetical protein | 372 | 100 |
| MAP4_2608 | hypothetical protein | 189 | Rv1531 | hypothetical protein | 80.21 | 188 | Mb1558 | hypothetical protein | 80.21 | 188 | MAV_3238 | hypothetical protein | 97.88 | 189 | BCG_1583 | hypothetical protein | 80.21 | 188 | MAP1243 | hypothetical protein | 189 | 100 |
| MAP4_2609 | peptide synthetase | 4027 | Rv0101 | Probable peptide synthetase Nrp (p | 55.35 | 2512 | Mb0104 | peptide synthetase | 55.35 | 2512 | MAV_3239 | syringomycin synthetase | 82.12 | 6212 | BCG_0134 | peptide synthetase nrp | 55.3 | 2512 | MAP1242 | hypothetical protein | 4027 | 100 |
| MAP4_2610 | putative MbtH like protein | 76 | Rv2377c | Putative conserved protein MbtH | 78.26 | 71 | Mb2398c | protein MbtH | 79.71 | 71 | MAV_3245 | hypothetical protein | 98.68 | 76 | BCG_2391c | protein mbtH | 79.71 | 71 | MAP1872c | hypothetical protein | 77 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2611 | membrane protein, MmpS family | 139 | Rv0451c | Probable conserved membrane prot | 59.42 | 140 | Mb0459c | hypothetical protein | 59.42 | 140 | MAV_3247 | MmpS4 protein | 100 | 139 | BCG_0490c | membrane protein mmpS4 | 59.42 | 140 | MAP1241c | hypothetical protein | 139 | 100 |
| MAP4_2612 | transmembrane transport protein MmpL4 | 963 | Rv0450c | Probable conserved transmembrane | 61.75 | 967 | Mb0458c | transmembrane transport pr | 61.64 | 967 | MAV_3248 | Mmp14A protein | 98.44 | 963 | BCG_0489c | transmembrane transport prot | 61.75 | 967 | MAP1240c | hypothetical protein | 963 | 100 |
| MAP4_2613 | transmembrane transport protein MmpL4 | 972 | Rv0450c | Probable conserved transmembrane | 65.67 | 967 | Mb0458c | transmembrane transport pr | 65.56 | 967 | MAV_3249 | Mmp14A protein | 98.63 | 952 | BCG_0489c | transmembrane transport prot | 65.67 | 967 | MAP1239c | hypothetical protein | 972 | 100 |
| MAP4_2614 | daunorubicin-DIM-transport ATP-binding protein ABC t | 315 | Rv2936 | Daunorubicin-dim-transport ATP-bir | 54.37 | 331 | Mb2961 | daunorubicin-DIM-transport | 54.37 | 331 | MAV_3250 | daunorubicin resistance ATP-bindir | 95.86 | 315 | BCG_2958 | daunorubicin-DIM-transport A | 54.37 | 331 | MAP1238c | DrrA | 315 | 100 |
| MAP4_2615 | daunorubicin-dim-transport membrane protein ABC tra | 246 | Rv2937 | Daunorubicin-dim-transport integral | 33 | 289 | Mb2962 | daunorubicin-DIM-transport i | 33 | 289 | MAV_3251 | ABC transporter efflux protein, Drr | 83.33 | 246 | BCG_2959 | daunorubicin-DIM-transport in | 33 | 289 | MAP1237c | DrrB | 246 | 100 |
| MAP4_2616 | daunorubicin-dim-transport membrane protein ABC tra | 263 | Rv2938 | Probable daunorubicin-dim-transpo | 33.06 | 276 | Mb2963 | daunorubicin-DIM-transport i | 33.06 | 276 | MAV_3252 | daunorubicin resistance protein C | 83.27 | 264 | BCG_2960 | daunorubicin-DIM-transport in | 33.06 | 276 | MAP1236c | DrrC | 263 | 100 |
| MAP4_2617 | putative acyltransferase | 444 | Rv0111 | Possible transmembrane acyltransfe | 35.71 | 685 | Mb0115 | transmembrane acyltransfera | 35.71 | 685 | MAV_3274 | acyltransferase | 56.43 | 387 | BCG_0144 | acyltransferase | 35.71 | 685 | MAP1235 | hypothetical protein | 444 | 100 |
| MAP4_2618 | putative glycosyltransferase | 266 | Rv2957 | Possible glycosyl transferase | 68.78 | 275 | Mb2981 | glycosyl transferase family pr | 68.78 | 275 | MAV_3253 | hypothetical protein | 75 | 223 | BCG_2978 | glycosyl transferase family prot | 68.78 | 275 | MAP1234 | hypothetical protein | 266 | 100 |
| MAP4_2619 | hypothetical protein | 240 | Rv2956 | hypothetical protein | 66.67 | 243 | Mb2980 | hypothetical protein | 66.26 | 243 | MAV_1133 | methyltransferase FkbM | 28.39 | 264 | BCG_2977 | hypothetical protein | 66.26 | 243 | MAP1233 | hypothetical protein | 240 | 100 |
| MAP4_2620 | nucleotide-sugar epimerase epiA | 320 | Rv1512 | Probable nucleotide-sugar epimeras | 84.28 | 322 | Mb3658c | UDP-glucose 4-epimerase | 28.08 | 314 | MAV_0524 | nucleoside-diphosphate-sugar epim | 27.36 | 313 | BCG_3692c | UDP-glucose 4-epimerase | 28.08 | 314 | MAP1232 | EpiA | 320 | 100 |
| MAP4_2621 | GDP-D-mannose dehydratase gmdA | 343 | Rv1511 | GDP-D-mannose dehydratase GmdA | 89.05 | 340 | Mb0116 | GDP-mannose 4,6-dehydrata | 27.59 | 318 | MAV_4406 | dTDP-glucose 4,6-dehydratase | 29.08 | 331 | BCG_0145 | GDP-mannose 4,6-dehydratase | 27.59 | 318 | MAP1231 | GmdA | 343 | 100 |
| MAP4_2622 | hypothetical protein | 406 | Rv1075c | Conserved exported protein | 28.04 | 314 | Mb1104c | hypothetical protein | 28.04 | 314 | MAV_3273 | hypothetical protein | 96.56 | 309 | BCG_1133c | hypothetical protein | 28.04 | 314 | MAP1230 | hypothetical protein | 406 | 100 |
| MAP4_2625 | Esterase | 428 | Rv1497 | Probable esterase LipL | 77.16 | 429 | Mb1534 | esterase | 77.16 | 429 | MAV_3275 | beta-lactamase | 99.53 | 426 | BCG_1560 | esterase lipL | 77.16 | 429 | MAP1228 | hypothetical protein | 428 | 100 |
| MAP4_2626 | arginineornithine transport system ATPase | 326 | Rv1496 | Possible transport system kinase | 82.55 | 334 | Mb1533 | arginine/ornithine transport | 82.55 | 334 | MAV_3276 | arginine/ornithine transport system | 99.39 | 326 | BCG_1559 | arginine/ornithine transport sy | 82.55 | 334 | MAP1227 | arginine/ornithine transport system AT | 326 | 100 |
| MAP4_2627 | methylmalonyl-CoA mutase large subunit mutB | 750 | Rv1493 | Probable methylmalonyl-CoA mutas | 90.79 | 750 | Mb1530 | methylmalonyl-CoA mutase | 90.79 | 750 | MAV_3277 | methylmalonyl-CoA mutase | 100 | 750 | BCG_1556 | methylmalonyl-CoA mutase | 90.79 | 750 | MAP1226 | methylmalonyl-CoA mutase | 750 | 100 |
| MAP4_2628 | methylmalonyl-CoA mutase small subunit mutA | 625 | Rv1492 | Probable methylmalonyl-CoA mutas | 74.88 | 615 | Mb1529 | methylmalonyl-CoA mutase s | 74.88 | 615 | MAV_3278 | methylmalonyl-CoA mutase, small | 98.88 | 625 | BCG_1555 | methylmalonyl-CoA mutase sm | 74.88 | 615 | MAP1225 | MutA | 625 | 100 |
| MAP4_2629 | hypothetical protein | 258 | Rv1491c | hypothetical protein | 64.17 | 252 | Mb1528c | hypothetical protein | 64.17 | 252 | MAV_3279 | hypothetical protein | 99.22 | 255 | BCG_1554c | hypothetical protein | 64.17 | 252 | MAP1224c | hypothetical protein | 258 | 100 |
| MAP4_2630 | hypothetical protein | 329 | Rv1815 | hypothetical protein | 28.47 | 221 | Mb1845 | hypothetical protein | 28.47 | 221 | MAV_3280 | hypothetical protein | 98.48 | 329 | BCG_1849 | hypothetical protein | 28.47 | 221 | MAP1223c | hypothetical protein | 270 | 99.63 |
| MAP4_2631 | two component system sensor kinase phoR | 480 | Rv0758 | Possible two component system res | 35.07 | 485 | Mb0781 | two component system respo | 35.07 | 485 | MAV_3282 | hypothetical protein | 96.9 | 484 | BCG_0810 | two component system respon | 35.07 | 485 | MAP1222 | hypothetical protein | 480 | 100 |
| MAP4_2632 | two component response transcriptional regulatory pr | 240 | Rv0981 | Mycobacterial persistence regulator | 41.7 | 228 | Mb1007 | two component response tra | 41.7 | 230 | MAV_3283 | two component system response r | 99.58 | 239 | BCG_1036 | two component response trans | 41.7 | 230 | MAP1221 | hypothetical protein | 219 | 99.54 |
| MAP4_2633 | hypothetical protein | 111 | Rv2537c | 3-dehydroquinate dehydratase AroD | 46.67 | 147 | Mb2566c | 3-dehydroquinate dehydrata | 46.67 | 147 | MAV_3284 | hypothetical protein | 99.1 | 111 | BCG_2559c | 3-dehydroquinate dehydratase | 46.67 | 147 | MAP1220c | hypothetical protein | 111 | 100 |
| MAP4_2634 | hypothetical protein | 172 | Rv1261c | hypothetical protein | 29.8 | 149 | Mb1292c | hypothetical protein | 29.8 | 149 | MAV_3285 | hypothetical protein | 96.82 | 175 | BCG_1320c | hypothetical protein | 29.8 | 149 | MAP1219c | hypothetical protein | 156 | 99.36 |
| MAP4_2635 | hypothetical protein | 97 | Rv3898c | hypothetical protein | 33.33 | 110 | Mb1986c | hypothetical protein | 29.73 | 98 | MAV_3286 | hypothetical protein | 95.24 | 63 | BCG_1990c | hypothetical protein | 29.73 | 98 | MAP1218c | hypothetical protein | 97 | 100 |
| MAP4_2636 | hypothetical protein | 259 | Rv2077c | Possible conserved transmembrane | 43.29 | 323 | Mb2102c | transmembrane protein | 43.29 | 323 | MAV_3287 | hypothetical protein | 99.57 | 232 | BCG_2095c | hypothetical protein | 43.29 | 323 | MAP1217c | hypothetical protein | 259 | 100 |
| MAP4_2637 | lipoprotein LpqQ | 206 | Rv0835 | Possible lipoprotein LpqQ | 38.62 | 214 | Mb0858 | lipoprotein LpqQ | 38.62 | 214 | MAV_3288 | LpqQ protein | 97.98 | 99 | BCG_0887 | lipoprotein lpqQ | 38.62 | 214 | MAP1216c | hypothetical protein | 99 | 98.99 |
| MAP4_2638 | hypothetical protein | 118 | Rv1489 | hypothetical protein | 72.03 | 118 | Mb1525 | hypothetical protein | 72.03 | 118 | MAV_3289 | hypothetical protein | 100 | 118 | BCG_1551 | hypothetical protein | 72.03 | 118 | MAP1215 | hypothetical protein | 118 | 100 |
| MAP4_2639 | putative exported conserved protein | 377 | Rv1488 | Possible exported conserved protein | 93.05 | 381 | Mb1524 | hypothetical protein | 93.05 | 381 | MAV_3290 | secreted protein | 99.73 | 377 | BCG_1550 | hypothetical protein | 93.05 | 381 | MAP1214 | hypothetical protein | 377 | 100 |
| MAP4_2640 | hypothetical protein | 147 | Rv1487 | hypothetical protein | 75.32 | 144 | Mb1523 | hypothetical protein | 75.32 | 144 | MAV_3291 | nodulation efficiency protein D (Nf | 98.61 | 145 | BCG_1549 | hypothetical protein | 75.32 | 144 | MAP1213 | hypothetical protein | 147 | 100 |
| MAP4_2641 | hypothetical protein | 322 | Rv1486c | hypothetical protein | 77.99 | 288 | Mb1522c | hypothetical protein | 77.99 | 288 | MAV_3292 | hypothetical protein | 99.35 | 308 | BCG_1548c | hypothetical protein | 77.32 | 323 | MAP1212c | hypothetical protein | 322 | 100 |
| MAP4_2642 | ferrochelatase HemZ | 336 | Rv1485 | Ferrochelatase HemZ (protoheme fe | 81.49 | 344 | Mb1521 | ferrochelatase | 81.49 | 344 | MAV_3293 | ferrochelatase | 98.51 | 336 | BCG_1547 | ferrochelatase | 81.49 | 344 | MAP1211 | ferrochelatase | 336 | 100 |
| MAP4_2643 | NADH-dependent enoyl-ACP reductase inhA | 269 | Rv1484 | NADH-dependent enoyl-[acyl-carrie | 89.22 | 269 | Mb1520 | enoyl-ACP reductase | 89.22 | 269 | MAV_3294 | enoyl-(acyl carrier protein) reducta | 99.63 | 269 | BCG_1546 | enoyl-ACP reductase | 89.22 | 269 | MAP1210 | enoyl-ACP reductase | 269 | 100 |
| MAP4_2644 | 3-oxoacyl-ACP reductase | 255 | Rv1483 | 3-oxoacyl-[acyl-carrier protein] redu | 83.92 | 247 | Mb1519 | 3-oxoacyl-ACP reductase | 83.92 | 247 | MAV_3295 | 3-oxoacyl-(acyl-carrier-protein) red | 99.61 | 255 | BCG_1545 | 3-oxoacyl-ACP reductase | 83.92 | 247 | MAP1209 | FabG1 | 255 | 100 |
| MAP4_2645 | hypothetical protein | 275 | Rv0456A | Possible toxin MazF1 | 42.86 | 93 | Mb0465c | hypothetical protein | 42.86 | 93 | MAV_3989 | phospholipase D family protein | 25.47 | 486 | BCG_0496c | hypothetical protein | 42.86 | 93 | MAP1208 | hypothetical protein | 275 | 100 |
| MAP4_2646 | hypothetical protein | 335 | Rv1481 | Probable membrane protein | 91.64 | 335 | Mb1517 | hypothetical protein | 91.64 | 335 | MAV_3297 | hypothetical protein | 100 | 335 | BCG_1543 | hypothetical protein | 91.34 | 335 | MAP1207 | hypothetical protein | 335 | 100 |
| MAP4_2647 | hypothetical protein | 316 | Rv1480 | hypothetical protein | 88.64 | 317 | Mb1516 | hypothetical protein | 88.64 | 317 | MAV_3298 | hypothetical protein | 99.68 | 316 | BCG_1542 | hypothetical protein | 88.64 | 317 | MAP1206 | hypothetical protein | 316 | 100 |
| MAP4_2648 | transcriptional regulatory protein moxR1 | 380 | Rv1479 | Probable transcriptional regulatory | 90.19 | 377 | Mb1515 | transcriptional regulator Mox | 90.19 | 377 | MAV_3299 | MoxR protein | 100 | 380 | BCG_1541 | transcriptional regulatory prot | 90.19 | 377 | MAP1205 | MoxR | 380 | 100 |
| MAP4_2649 | invasion-associated protein, NlpCP60 family | 244 | Rv1478 | Possible invasion protein | 77.87 | 241 | Mb1514 | invasion protein | 77.87 | 241 | MAV_3300 | invasin 1 | 100 | 244 | BCG_1540 | invasion protein | 77.87 | 241 | MAP1204 | hypothetical protein | 244 | 100 |
| MAP4_2650 | invasion-associated protein, NlpCP60 family | 470 | Rv1477 | Peptidoglycan hydrolase | 78.57 | 472 | Mb1513 | invasion protein | 78.57 | 472 | MAV_3301 | invasion protein | 99.33 | 450 | BCG_1539 | invasion protein | 78.57 | 472 | MAP1203 | hypothetical protein | 470 | 100 |
| MAP4_2651 | hypothetical protein | 208 | Rv1476 | Possible membrane protein | 79.63 | 186 | Mb1512 | hypothetical protein | 79.63 | 186 | MAV_3302 | hypothetical protein | 99.45 | 181 | BCG_1538 | hypothetical protein | 79.63 | 186 | MAP1202 | hypothetical protein | 208 | 100 |
| MAP4_2652 | iron-regulated aconitate hydratase acn | 937 | Rv1475c | Probable iron-regulated aconitate h | 88.54 | 943 | Mb1511c | aconitate hydratase | 88.54 | 943 | MAV_3303 | aconitate hydratase | 99.79 | 937 | BCG_1537c | aconitate hydratase | 88.54 | 943 | MAP1201c | aconitate hydratase | 937 | 100 |
| MAP4_2653 | Transcriptional regulator, TetR family | 192 | Rv1474c | Probable transcriptional regulatory | 91.44 | 187 | Mb1510c | transcriptional regulator | 91.44 | 187 | MAV_3305 | HTH-type transcriptional repressor | 100 | 192 | BCG_1536c | transcriptional regulatory prot | 91.44 | 187 | MAP1200c | hypothetical protein | 192 | 100 |
| MAP4_2654 | putative transcriptional regulatory protein | 65 | Rv1473A | Possible transcriptional regulatory p | 75.41 | 63 | Mb1509 | transcriptional regulator | 79.31 | 63 | MAV_3304 | hypothetical protein | 100 | 65 | BCG_1535 | transcriptional regulatory prot | 79.31 | 63 | MAP1199 | hypothetical protein | 65 | 100 |
| MAP4_2655 | macrolide ABC transporter ATP-binding protein | 545 | Rv1473 | Probable macrolide-transport ATP-b | 90.83 | 542 | Mb1508 | macrolide ABC transporter A | 90.83 | 542 | MAV_3306 | ABC transporter ATP-binding prote | 99.82 | 545 | BCG_1534 | macrolide-transport ATP-bindi | 90.83 | 542 | MAP1198 | hypothetical protein | 545 | 100 |
| MAP4_2656 | Enoyl-CoA hydratase EchA12 | 269 | Rv1472 | Possible enoyl-CoA hydratase EchA1 | 89.93 | 285 | Mb1507 | enoyl-CoA hydratase | 90.3 | 285 | MAV_3307 | enoyl-CoA hydratase | 99.63 | 269 | BCG_1533 | enoyl-CoA hydratase | 90.3 | 285 | MAP1197 | enoyl-CoA hydratase | 269 | 100 |
| MAP4_2657 | thioredoxin | 117 | Rv1471 | Probable thioredoxin TrxB1 | 78.18 | 123 | Mb1506 | thioredoxin | 78.18 | 123 | MAV_3308 | thioredoxin | 100 | 117 | BCG_1532 | thioredoxin trxB1 | 78.18 | 123 | MAP1196 | hypothetical protein | 117 | 100 |
| MAP4_2658 | Acyl-CoA dehydrogenase FadE15 | 609 | Rv1467c | Probable acyl-CoA dehydrogenase F | 84.4 | 609 | Mb1502c | acyl-CoA dehydrogenase | 84.4 | 609 | MAV_3309 | acyl-CoA dehydrogenase | 99.67 | 609 | BCG_1528c | acyl-CoA dehydrogenase fadE1 | 84.4 | 609 | MAP1195c | FadE15 | 609 | 100 |
| MAP4_2659 | hypothetical protein | 258 | Rv2946c | Probable polyketide synthase Pks1 | 35.71 | 1616 | | | | | MAV_3310 | 27 kDa lipoprotein antigen | 99.61 | 258 | | | | | MAP1194c | hypothetical protein | 258 | 100 |
| MAP4_2660 | hypothetical protein | 244 | Rv2999 | Probable conserved lipoprotein LppY | 37.93 | 321 | Mb3024 | lipoprotein LppY | 41.38 | 321 | MAV_3312 | hypothetical protein | 98.2 | 222 | BCG_3021 | lipoprotein lppY | 41.38 | 321 | MAP1193c | hypothetical protein | 244 | 100 |
| MAP4_2661 | hypothetical protein | 115 | Rv1466 | hypothetical protein | 91.3 | 115 | Mb1501 | hypothetical protein | 91.3 | 115 | MAV_3313 | hypothetical protein | 100 | 115 | BCG_1527 | hypothetical protein | 91.3 | 115 | MAP1192 | hypothetical protein | 115 | 100 |
| MAP4_2662 | nitrogen fixation related protein | 159 | Rv1465 | Possible nitrogen fixation related pr | 81.25 | 162 | Mb1500 | nitrogen fixation-like protein | 81.25 | 162 | MAV_3314 | SUF system FeS assembly protein, | 100 | 159 | BCG_1526 | nitrogen fixation-like protein | 81.25 | 162 | MAP1191 | hypothetical protein | 159 | 100 |
| MAP4_2663 | Cysteine desulfurase, SufS subfamily | 415 | Rv1464 | Probable cysteine desulfurase Csd | 86.51 | 417 | Mb1499 | cysteine desulfurase | 86.51 | 417 | MAV_3315 | cysteine desulfurase | 98.77 | 408 | BCG_1525 | cysteine desulfurase csd | 86.51 | 417 | MAP1190 | hypothetical protein | 415 | 100 |
| MAP4_2664 | putative iron-sulfur cluster assembly ATPase protein Su | 260 | Rv1463 | Probable conserved ATP-binding pro | 89.84 | 266 | Mb1498 | ABC transporter ATP-binding | 89.84 | 266 | MAV_3316 | FeS assembly ATPase SufC | 100 | 260 | BCG_1524 | ABC transporter ATP-binding p | 89.84 | 266 | MAP1189 | hypothetical protein | 260 | 100 |
| MAP4_2665 | putative iron-sulfur cluster assembly protein SufD | 396 | Rv1462 | hypothetical protein | 84.79 | 397 | Mb1497 | hypothetical protein | 85.05 | 397 | MAV_3317 | FeS assembly protein SufD | 99.49 | 396 | BCG_1523 | hypothetical protein | 85.05 | 397 | MAP1188 | hypothetical protein | 396 | 100 |
| MAP4_2666 | putative Iron-sulfur cluster assembly protein SufB | 482 | Rv1461 | hypothetical protein | 92.89 | 846 | Mb1496 | hypothetical protein | 92.89 | 846 | MAV_3318 | FeS assembly protein SufB | 99.59 | 482 | BCG_1522 | hypothetical protein | 92.89 | 846 | MAP1187 | hypothetical protein | 482 | 100 |
| MAP4_2667 | transcriptional regulator | 281 | Rv1460 | Probable transcriptional regulatory | 80.97 | 268 | Mb1495 | transcriptional regulator | 80.97 | 268 | MAV_3319 | DNA-binding protein | 99.17 | 241 | BCG_1521 | transcriptional regulatory prot | 80.57 | 268 | MAP1186 | hypothetical protein | 281 | 100 |
| MAP4_2668 | hypothetical protein | 567 | Rv1459c | Possible conserved integral membra | 79.9 | 591 | Mb1494c | hypothetical protein | 79.9 | 591 | MAV_3320 | hypothetical protein | 99.47 | 567 | BCG_1520c | hypothetical protein | 79.9 | 591 | MAP1185c | hypothetical protein | 567 | 100 |
| MAP4_2669 | putative antibiotic-transport ATP-binding protein ABC t | 311 | Rv1458c | Probable unidentified antibiotic-tra | 90.26 | 313 | Mb1493c | unidentified antibiotic-transp | 90.26 | 313 | MAV_3321 | ABC transporter ATP-binding subu | 99.67 | 302 | BCG_1519c | unidentified antibiotic-transpo | 90.26 | 313 | MAP1184c | hypothetical protein | 311 | 100 |
| MAP4_2670 | putative antibiotic-transport membrane ABC transport | 259 | Rv1457c | Probable unidentified antibiotic-tra | 83.72 | 261 | Mb1492c | unidentified antibiotic-transp | 83.72 | 261 | MAV_3322 | ABC transporter efflux protein, Drr | 99.61 | 259 | BCG_1518c | unidentified antibiotic-transpo | 83.72 | 261 | MAP1183c | hypothetical protein | 259 | 100 |
| MAP4_2671 | putative antibiotic-transport membrane ABC transport | 317 | Rv1456c | Probable unidentified antibiotic-tra | 81.64 | 310 | Mb1491c | unidentified antibiotic-transp | 81.64 | 310 | MAV_3324 | cytochrome aa3 controlling protein | 99.68 | 317 | BCG_1517c | unidentified antibiotic-transpo | 81.64 | 310 | MAP1182c | hypothetical protein | 311 | 99.68 |
| MAP4_2672 | hypothetical protein | 212 | Rv1455 | hypothetical protein | 46.34 | 287 | Mb1490 | hypothetical protein | 46.34 | 287 | MAV_3323 | hypothetical protein | 97.64 | 219 | BCG_1516 | hypothetical protein | 46.34 | 287 | MAP1181 | hypothetical protein | 219 | 100 |
| MAP4_2673 | Quinone oxidoreductase Qor | 331 | Rv1454c | Probable quinone reductase Qor (N | 76.52 | 328 | Mb1489c | quinone reductase | 76.52 | 328 | MAV_3325 | quinone oxidoreductase | 98.77 | 324 | BCG_1515c | quinone reductase qor | 76.52 | 328 | MAP1180c | Qor | 331 | 100 |
| MAP4_2674 | cytochrome C oxidase assembly factor ctaB | 308 | Rv1451 | Probable cytochrome C oxidase asse | 82.41 | 308 | Mb1486 | protoheme IX farnesyltransfe | 82.41 | 308 | MAV_3326 | protoheme IX farnesyltransferase | 98.96 | 289 | BCG_1512 | protoheme IX farnesyltransfera | 82.41 | 308 | MAP1179 | protoheme IX farnesyltransferase | 308 | 100 |
| MAP4_2675 | Transketolase Tkt | 699 | Rv1449c | Transketolase Tkt (TK) | 86.86 | 700 | Mb1484c | transketolase | 87 | 700 | MAV_3327 | transketolase | 99.71 | 699 | BCG_1510c | transketolase | 87 | 700 | MAP1178c | transketolase | 699 | 100 |
| MAP4_2676 | transaldolase Tal | 373 | Rv1448c | Probable transaldolase Tal | 83.65 | 373 | Mb1483c | transaldolase | 83.91 | 373 | MAV_3328 | transaldolase | 99.72 | 356 | BCG_1509c | transaldolase | 83.91 | 373 | MAP1177c | transaldolase | 373 | 100 |
| MAP4_2677 | glucose-6-phosphate 1-dehydrogenase Zwf2 | 514 | Rv1447c | Probable glucose-6-phosphate 1-de | 90.66 | 514 | Mb1482c | glucose-6-phosphate 1-dehy | 90.66 | 514 | MAV_3329 | glucose-6-phosphate 1-dehydroge | 100 | 518 | BCG_1508c | glucose-6-phosphate 1-dehyd | 90.66 | 514 | MAP1176c | glucose-6-phosphate 1-dehydrogenase | 514 | 100 |
| MAP4_2678 | OXPP cycle protein OPCA | 303 | Rv1446c | Putative OXPP cycle protein OpcA | 83.11 | 303 | Mb1481c | OXPP cycle protein OPCA | 83.44 | 303 | MAV_3330 | OpcA protein | 98.68 | 306 | BCG_1507c | OXPP cycle protein opcA | 83.44 | 303 | MAP1175c | OpcA | 303 | 100 |
| MAP4_2679 | 6-phosphogluconolactonase | 251 | Rv1445c | Probable 6-phosphogluconolactona | 79.27 | 247 | Mb1480c | 6-phosphogluconolactonase | 79.27 | 247 | MAV_3331 | 6-phosphogluconolactonase | 99.6 | 251 | BCG_1506c | 6-phosphogluconolactonase de | 79.27 | 247 | MAP1174c | 6-phosphogluconolactonase | 251 | 100 |
| MAP4_2680 | hypothetical protein | 132 | Rv1444c | hypothetical protein | 76.52 | 136 | Mb1479c | hypothetical protein | 76.52 | 136 | MAV_3332 | hypothetical protein | 100 | 129 | BCG_1505c | hypothetical protein | 76.52 | 136 | MAP1173c | hypothetical protein | 132 | 100 |
| MAP4_2681 | histone deacetylase superfamily protein | 309 | Rv2001 | hypothetical protein | 50 | 250 | Mb2024 | hypothetical protein | 50 | 250 | MAV_3333 | histone deacetylase | 98.38 | 309 | BCG_2018 | hypothetical protein | 50 | 250 | MAP1172c | hypothetical protein | 309 | 100 |
| MAP4_2682 | aldoketo reductase family protein | 328 | Rv2298 | hypothetical protein | 34.78 | 323 | Mb2320 | hypothetical protein | 34.78 | 323 | MAV_3334 | general stress protein 69 | 99.39 | 328 | BCG_2314 | hypothetical protein | 34.78 | 323 | MAP1171 | hypothetical protein | 328 | 100 |
| MAP4_2683 | hypothetical protein | 259 | Rv3542c | hypothetical protein | 35.48 | 311 | Mb3572c | hypothetical protein | 35.48 | 311 | MAV_3335 | hypothetical protein | 99.23 | 259 | BCG_3606c | hypothetical protein | 35.48 | 311 | MAP1170 | hypothetical protein | 259 | 100 |
| MAP4_2684 | phosphoenolpyruvate carboxylase | 935 | Rv0035 | Probable fatty-acid-CoA ligase FadD | 26.98 | 562 | Mb0036 | fatty-acid--CoA ligase | 26.98 | 562 | MAV_3336 | phosphoenolpyruvate carboxylase | 99.14 | 935 | BCG_0066 | fatty-acid-CoA ligase | 26.98 | 562 | MAP1169 | phosphoenolpyruvate carboxylase | 935 | 100 |
| MAP4_2685 | putative monooxygenase | 305 | Rv1360 | Probable oxidoreductase | 27.16 | 340 | Mb1395 | oxidoreductase | 27.16 | 340 | MAV_3337 | monooxygenase | 99.34 | 305 | BCG_1422 | oxidoreductase | 27.16 | 340 | MAP1168c | hypothetical protein | 305 | 100 |
| MAP4_2686 | protein-export membrane protein translocase subunit | 77 | Rv1440 | Probable protein-export membrane | 92.21 | 77 | Mb1475 | preprotein translocase subun | 92.21 | 77 | MAV_3338 | preprotein translocase subunit Sec | 100 | 77 | BCG_1501 | preprotein translocase subunit | 92.21 | 77 | MAP1167 | preprotein translocase subunit SecG | 77 | 100 |
| MAP4_2687 | triosephosphate isomerase | 261 | Rv1438 | Probable triosephosphate isomerase | 89.66 | 261 | Mb1473 | triosephosphate isomerase | 89.66 | 261 | MAV_3339 | triosephosphate isomerase | 99.62 | 261 | BCG_1499 | triosephosphate isomerase | 89.27 | 261 | MAP1166 | triosephosphate isomerase | 261 | 100 |
| MAP4_2688 | phosphoglycerate kinase | 415 | Rv1437 | Probable phosphoglycerate kinase P | 82.08 | 412 | Mb1472 | phosphoglycerate kinase | 82.08 | 412 | MAV_3340 | phosphoglycerate kinase | 100 | 415 | BCG_1498 | phosphoglycerate kinase | 82.08 | 412 | MAP1165 | phosphoglycerate kinase | 415 | 100 |
| MAP4_2689 | glyceraldehyde 3-phosphate dehydrogenase Gap | 339 | Rv1436 | Probable glyceraldehyde 3-phospha | 94.1 | 339 | Mb1471 | glyceraldehyde-3-phosphate | 94.1 | 339 | MAV_3341 | glyceraldehyde-3-phosphate dehyd | 100 | 339 | BCG_1497 | glyceraldehyde 3-phosphate de | 94.1 | 339 | MAP1164 | glyceraldehyde-3-phosphate dehydroge | 339 | 100 |
| MAP4_2690 | dehydrogenase | 474 | Rv1432 | Probable dehydrogenase | 79.24 | 473 | Mb1467 | dehydrogenase | 79.24 | 473 | MAV_3342 | dehydrogenase | 98.51 | 470 | BCG_1493 | dehydrogenase | 79.24 | 473 | MAP1163 | hypothetical protein | 474 | 100 |
| MAP4_2691 | hypothetical protein | 581 | Rv1431 | hypothetical protein | 74.96 | 589 | Mb1466 | hypothetical protein | 74.96 | 589 | MAV_3343 | hypothetical protein | 99.48 | 581 | BCG_1492 | hypothetical protein | 74.96 | 589 | MAP1162 | hypothetical protein | 581 | 100 |
| MAP4_2692 | hypothetical protein | 124 | Rv3909 | hypothetical protein | 36.23 | 802 | Mb3939 | hypothetical protein | 36.23 | 802 | MAV_3344 | hypothetical protein | 94.68 | 95 | BCG_3966 | hypothetical protein | 36.23 | 802 | MAP1161 | hypothetical protein | 124 | 100 |
| MAP4_2693 | acyltransferase family protein | 269 | Rv1428c | hypothetical protein | 82.77 | 275 | Mb1463c | hypothetical protein | 82.77 | 275 | MAV_3346 | acyltransferase domain-containing | 100 | 269 | BCG_1489c | hypothetical protein | 82.77 | 275 | MAP1160c | hypothetical protein | 269 | 100 |
| MAP4_2694 | long-chain fatty-acid-CoA ligase fadD12 | 539 | Rv1427c | Possible long-chain-fatty-acid--CoA l | 80.71 | 535 | Mb1462c | acyl-CoA synthetase | 80.71 | 535 | MAV_3349 | acyl-CoA synthetase | 98.88 | 447 | BCG_1488c | acyl-CoA synthetase | 80.71 | 535 | MAP1159c | acyl-CoA synthetase | 539 | 100 |
| MAP4_2695 | esterase LipO | 423 | Rv1426c | Probable esterase LipO | 79.38 | 420 | Mb1461c | esterase | 79.38 | 420 | MAV_3350 | alpha/beta hydrolase | 99.53 | 423 | BCG_1487c | esterase lipO | 79.38 | 420 | MAP1158c | hypothetical protein | 420 | 100 |
| MAP4_2696 | hypothetical protein | 234 | Rv1482c | hypothetical protein | 56.42 | 280 | Mb1518c | hypothetical protein | 56.42 | 280 | MAV_3351 | hypothetical protein | 99.1 | 283 | BCG_1544c | hypothetical protein | 56.42 | 280 | MAP1157c | hypothetical protein | 234 | 100 |
| MAP4_2697 | putative acyltransferase, wsdgatmgat subfamily protei | 464 | Rv1425 | Possible triacylglycerol synthase (dia | 85.93 | 459 | Mb1460 | hypothetical protein | 86.15 | 459 | MAV_3352 | acyltransferase, ws/dgat/mgat sub | 99.14 | 468 | BCG_1486 | hypothetical protein | 86.15 | 459 | MAP1156 | hypothetical protein | 464 | 100 |
| MAP4_2698 | PPE family protein | 320 | Rv1808 | PPE family protein PPE32 | 48.02 | 409 | Mb1837 | PPE family protein | 48.02 | 409 | MAV_3353 | PPE family protein | 97.81 | 321 | BCG_1841 | PPE family protein | 48.02 | 409 | MAP1155 | hypothetical protein | 320 | 100 |
| MAP4_2699 | hypothetical protein | 117 | Rv1810 | hypothetical protein | 49.54 | 118 | Mb1840 | hypothetical protein | 49.54 | 118 | MAV_3354 | hypothetical protein | 98.29 | 117 | BCG_1844 | hypothetical protein | 49.54 | 118 | MAP1154 | hypothetical protein | 117 | 100 |
| MAP4_2700 | PPE family protein | 454 | Rv1809 | PPE family protein PPE33 | 47.77 | 468 | Mb1830 | PPE family protein | 45.94 | 463 | MAV_3355 | PPE family protein | 98.68 | 454 | BCG_1834 | PPE family protein | 45.94 | 463 | MAP1153 | hypothetical protein | 454 | 100 |
| MAP4_2701 | PPE family protein | 416 | Rv1808 | PPE family protein PPE32 | 50.48 | 409 | Mb1837 | PPE family protein | 50.48 | 409 | MAV_3356 | PPE family protein | 98.32 | 417 | BCG_1841 | PPE family protein | 50.48 | 409 | MAP1152 | hypothetical protein | 416 | 100 |
| MAP4_2702 | hypothetical protein | 98 | Rv0862c | hypothetical protein | 32.14 | 756 | Mb0885c | hypothetical protein | 32.14 | 756 | MAV_4861 | hypothetical protein | 36.96 | 399 | BCG_0914c | hypothetical protein | 32.14 | 756 | MAP1151c | hypothetical protein | 98 | 100 |
| MAP4_2703 | transposase, IS1311 | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 99.76 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0028c | hypothetical protein | 411 | 100 |
| MAP4_2704 | transcriptional regulatory protein WHIA | 325 | Rv1423 | Probable transcriptional regulatory | 95.38 | 325 | Mb1458 | transcriptional regulator Whi | 95.38 | 325 | MAV_3357 | hypothetical protein | 100 | 327 | BCG_1484 | transcriptional regulatory prot | 95.38 | 325 | MAP1149 | hypothetical protein | 325 | 100 |
| MAP4_2705 | hypothetical protein | 358 | Rv1422 | hypothetical protein | 87.85 | 342 | Mb1457 | hypothetical protein | 87.57 | 342 | MAV_3358 | hypothetical protein | 99.16 | 358 | BCG_1483 | hypothetical protein | 87.85 | 342 | MAP1148 | hypothetical protein | 358 | 100 |
| MAP4_2706 | putative ATP-binding protein, P-loop ATPase protein fa | 310 | Rv1421 | hypothetical protein | 88.01 | 301 | Mb1456 | hypothetical protein | 88.01 | 301 | MAV_3359 | hypothetical protein | 98.99 | 298 | BCG_1482 | hypothetical protein | 88.01 | 301 | MAP1147 | hypothetical protein | 310 | 100 |
| MAP4_2707 | excinuclease ABC subunit C | 647 | Rv1420 | Probable excinuclease ABC (subunit | 90.87 | 646 | Mb1455 | excinuclease ABC subunit C | 90.87 | 646 | MAV_3360 | excinuclease ABC subunit C | 99.84 | 628 | BCG_1481 | excinuclease ABC subunit C | 90.87 | 646 | MAP1146 | excinuclease ABC subunit C | 647 | 100 |
| MAP4_2708 | putative cupin superfamily protein | 393 | Rv2626c | Hypoxic response protein 1 Hrp1 | 34.07 | 143 | Mb2659c | hypothetical protein | 34.07 | 143 | MAV_3361 | cupin superfamily protein | 98.8 | 361 | BCG_2653c | hypothetical protein | 34.07 | 143 | MAP1145c | hypothetical protein | 393 | 100 |
| MAP4_2709 | PPE family protein | 488 | Rv0453 | PPE family protein PPE11 | 39.37 | 518 | Mb0461 | PPE family protein | 39.37 | 518 | MAV_4872 | PPE family protein | 54.85 | 488 | BCG_0492 | PPE family protein | 39.37 | 518 | MAP1144c | hypothetical protein | 488 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2710 | hypothetical protein | 111 | Rv1174c | Low molecular weight T-cell antigen | 37.84 | 110 | Mb1207c | hypothetical protein | 37.84 | 110 | MAV_3362 | hypothetical protein | 99.1 | 112 | BCG_1237c | hypothetical protein | 37.84 | 110 | MAP1143c | hypothetical protein | 111 | 100 |
| MAP4_2711 | hypothetical protein | 154 | Rv1417 | Possible conserved membrane prote | 78.23 | 154 | Mb1452 | hypothetical protein | 78.23 | 154 | MAV_3363 | hypothetical protein | 99.35 | 154 | BCG_1478 | hypothetical protein | 78.23 | 154 | MAP1142 | hypothetical protein | 154 | 100 |
| MAP4_2712 | riboflavin synthase beta chain ribH | 160 | Rv1416 | Probable riboflavin synthase beta ch | 81.88 | 160 | Mb1451 | 6,7-dimethyl-8-ribityllumazin | 82.47 | 154 | MAV_3364 | 6,7-dimethyl-8-ribityllumazine synt | 98.12 | 160 | BCG_1477 | 6,7-dimethyl-8-ribityllumazine | 82.47 | 154 | MAP1141 | 6,7-dimethyl-8-ribityllumazine synthase | 160 | 100 |
| MAP4_2713 | riboflavin biosynthesis protein ribA2 | 425 | Rv1415 | Probable riboflavin biosynthesis pro | 96.71 | 425 | Mb1450 | bifunctional 3,4-dihydroxy-2- | 96.71 | 425 | MAV_3365 | bifunctional 3,4-dihydroxy-2-butan | 99.53 | 425 | BCG_1476 | bifunctional 3,4-dihydroxy-2-bu | 96.71 | 425 | MAP1140 | bifunctional 3,4-dihydroxy-2-butanone | 425 | 100 |
| MAP4_2714 | Riboflavin synthase alpha chain | 199 | Rv1412 | Probable riboflavin synthase alpha c | 84.77 | 201 | Mb1447 | riboflavin synthase subunit al | 84.77 | 201 | MAV_3366 | riboflavin synthase subunit alpha | 100 | 199 | BCG_1473 | riboflavin synthase subunit alp | 84.77 | 201 | MAP1139 | riboflavin synthase subunit alpha | 199 | 100 |
| MAP4_2715 | lipoprotein lprG | 238 | Rv1411c | Conserved lipoprotein LprG | 67.93 | 236 | Mb1446c | lipoprotein LprG | 67.93 | 236 | MAV_3367 | LprG protein | 100 | 235 | BCG_1472c | lipoprotein lprG | 67.93 | 236 | MAP1138c | hypothetical protein | 238 | 100 |
| MAP4_2716 | aminoglycosidestetracycline-transport membrane prot | 518 | Rv1410c | Aminoglycosides/tetracycline-transp | 80.83 | 518 | Mb1445c | aminoglycosides/tetracycline | 80.83 | 518 | MAV_3369 | aminoglycosides/tetracycline-trans | 100 | 518 | BCG_1471c | aminoglycosides/tetracycline-t | 80.83 | 518 | MAP1137c | hypothetical protein | 532 | 99.81 |
| MAP4_2717 | riboflavin biosynthesis protein ribG | 341 | Rv1409 | Probable bifunctional riboflavin bios | 77.95 | 339 | Mb1444 | bifunctional diaminohydroxyp | 77.95 | 339 | MAV_3368 | riboflavin biosynthesis protein RibD | 98.53 | 341 | BCG_1470 | bifunctional riboflavin biosynth | 77.95 | 339 | MAP1136 | RibG | 341 | 100 |
| MAP4_2718 | Ribulose-phosphate 3-epimerase | 232 | Rv1408 | Probable ribulose-phosphate 3-epim | 86.52 | 232 | Mb1443 | ribulose-phosphate 3-epimer | 86.52 | 232 | MAV_3370 | ribulose-phosphate 3-epimerase | 100 | 232 | BCG_1469 | ribulose-phosphate 3-epimeras | 86.52 | 232 | MAP1135 | ribulose-phosphate 3-epimerase | 232 | 99.57 |
| MAP4_2719 | putative Fmu protein (SUN protein), ribosomal RNA me | 464 | Rv1407 | Probable Fmu protein (sun protein) | 87.25 | 457 | Mb1442 | Fmu protein (SUN protein) | 87.25 | 457 | MAV_3371 | Fmu protein | 98.41 | 439 | BCG_1468 | fmu protein | 87.25 | 457 | MAP1134 | Fmu | 464 | 100 |
| MAP4_2720 | Methionyl-tRNA formyltransferase | 315 | Rv1406 | Probable methionyl-tRNA formyltra | 82.22 | 312 | Mb1441 | methionyl-tRNA formyltransf | 82.22 | 312 | MAV_3372 | methionyl-tRNA formyltransferase | 97.78 | 317 | BCG_1467 | methionyl-tRNA formyltransfer | 82.22 | 312 | MAP1133 | methionyl-tRNA formyltransferase | 315 | 100 |
| MAP4_2721 | putative methyltransferase | 274 | Rv1405c | Putative methyltransferase | 75.18 | 274 | Mb1440c | methyltransferase | 75.18 | 274 | MAV_3373 | methyltransferase, UbiE/COQ5 fam | 98.91 | 275 | BCG_1466c | methyltransferase | 75.18 | 274 | MAP1132c | hypothetical protein | 274 | 100 |
| MAP4_2722 | Transcriptional regulator, MarR family | 161 | Rv1404 | Probable transcriptional regulatory | 81.58 | 160 | Mb1439 | transcriptional regulator | 81.58 | 160 | MAV_3374 | MarR family transcriptional regulat | 100 | 161 | BCG_1465 | transcriptional regulatory prote | 81.58 | 160 | MAP1131 | hypothetical protein | 161 | 100 |
| MAP4_2723 | primosome assembly protein PriA | 655 | Rv1402 | Putative primosomal protein N' PriA | 82.22 | 655 | Mb1437 | primosome assembly protein | 82.22 | 655 | MAV_3375 | primosome assembly protein PriA | 99.08 | 674 | BCG_1463 | primosome assembly protein P | 82.22 | 655 | MAP1130 | primosome assembly protein PriA | 655 | 100 |
| MAP4_2724 | membrane protein | 263 | Rv1401 | Possible membrane protein | 71.78 | 200 | Mb1436 | hypothetical protein | 71.78 | 200 | MAV_3376 | hypothetical protein | 98.86 | 263 | BCG_1462 | hypothetical protein | 71.78 | 200 | MAP1129 | hypothetical protein | 263 | 100 |
| MAP4_2725 | lipase | 320 | Rv1400c | Probable lipase LipH | 76.88 | 320 | Mb1435c | lipase LipH | 76.88 | 320 | MAV_3377 | alpha/beta hydrolase | 98.75 | 320 | BCG_1461c | lipase lipH | 76.88 | 320 | MAP1128c | hypothetical protein | 320 | 100 |
| MAP4_2726 | monooxygenase | 496 | Rv1393c | Probable monoxygenase | 83.1 | 492 | Mb1428c | monoxygenase | 83.1 | 492 | MAV_3378 | lipolytic enzyme | 93.95 | 496 | BCG_1454c | monoxygenase | 83.1 | 492 | MAP1127c | hypothetical protein | 496 | 99.8 |
| MAP4_2727 | S-adenosylmethionine synthetase | 403 | Rv1392 | Probable S-adenosylmethionine syn | 91.81 | 403 | Mb1427 | S-adenosylmethionine synthe | 91.56 | 403 | MAV_3382 | S-adenosylmethionine synthetase | 97.77 | 403 | BCG_1453 | S-adenosylmethionine synthet | 91.56 | 403 | MAP1126 | S-adenosylmethionine synthetase | 403 | 100 |
| MAP4_2728 | DNApantothenate metabolism flavoprotein dfp | 420 | Rv1391 | Probable DNA/pantothenate metab | 87.8 | 418 | Mb1426 | bifunctional phosphopantoth | 87.8 | 418 | MAV_3383 | bifunctional phosphopantothenoyl | 94.1 | 424 | BCG_1452 | bifunctional phosphopantothe | 87.8 | 418 | MAP1125 | bifunctional phosphopantothenoylcyste | 420 | 100 |
| MAP4_2729 | DNA-directed RNA polymerase omega subunit | 108 | Rv1390 | Probable DNA-directed RNA polyme | 89.09 | 110 | Mb1425 | DNA-directed RNA polymeras | 89.09 | 110 | MAV_3384 | DNA-directed RNA polymerase sub | 99.07 | 108 | BCG_1451 | DNA-directed RNA polymerase | 89.09 | 110 | MAP1124 | DNA-directed RNA polymerase subunit | 108 | 100 |
| MAP4_2730 | Guanylate kinase | 223 | Rv1389 | Probable guanylate kinase Gmk | 80.98 | 208 | Mb1424 | guanylate kinase | 80.98 | 208 | MAV_3385 | guanylate kinase | 99 | 201 | BCG_1450 | guanylate kinase | 80.98 | 208 | MAP1123 | guanylate kinase | 223 | 100 |
| MAP4_2731 | integration host factor | 111 | Rv1388 | Putative integration host factor Mih | 96.36 | 190 | Mb1423 | integration host factor MIHF | 96.36 | 190 | MAV_3386 | MihF protein | 99.04 | 104 | BCG_1449 | integration host factor mihF | 96.36 | 190 | MAP1122 | MIHF | 111 | 100 |
| MAP4_2732 | DNA binding domain-containing protein | 140 | Rv2085 | hypothetical protein | 38.46 | 101 | Mb2112 | hypothetical protein | 38.46 | 101 | MAV_3387 | TobE protein | 100 | 140 | BCG_2105 | hypothetical protein | 38.46 | 101 | MAP1121c | hypothetical protein | 165 | 99.29 |
| MAP4_2733 | Orotidine 5'-phosphate decarboxylase | 274 | Rv1385 | Probable orotidine 5'-phosphate de | 82.12 | 274 | Mb1420 | orotidine 5'-phosphate decar | 82.12 | 274 | MAV_3388 | orotidine 5'-phosphate decarboxyla | 99.63 | 274 | BCG_1446 | orotidine 5'-phosphate decarb | 82.12 | 274 | MAP1120 | orotidine 5'-phosphate decarboxylase | 274 | 100 |
| MAP4_2734 | Carbamoyl-phosphate synthase large chain | 1117 | Rv1384 | Probable carbamoyl-phosphate synt | 92.43 | 1115 | Mb1419 | carbamoyl phosphate syntha | 92.52 | 1115 | MAV_3389 | carbamoyl phosphate synthase larg | 99.73 | 1117 | BCG_1445 | carbamoyl phosphate synthase | 92.52 | 1115 | MAP1119 | carbamoyl phosphate synthase large su | 1117 | 100 |
| MAP4_2735 | Carbamoyl-phosphate synthase small chain | 373 | Rv1383 | Probable carbamoyl-phosphate synt | 88.17 | 376 | Mb1418 | carbamoyl phosphate syntha | 87.9 | 376 | MAV_3390 | carbamoyl phosphate synthase sma | 99.46 | 373 | BCG_1444 | carbamoyl phosphate synthase | 87.9 | 376 | MAP1118 | carbamoyl phosphate synthase small su | 373 | 100 |
| MAP4_2736 | hypothetical protein | 170 | Rv1382 | Probable export or membrane prote | 71.6 | 165 | Mb1417 | export or membrane protein | 71.6 | 165 | MAV_3391 | hypothetical protein | 99.41 | 170 | BCG_1443 | export or membrane protein | 71.6 | 165 | MAP1117 | hypothetical protein | 170 | 100 |
| MAP4_2737 | Dihydroorotase | 430 | Rv1381 | Probable dihydroorotase PyrC (DHO | 90.7 | 430 | Mb1416 | dihydroorotase | 90.47 | 430 | MAV_3392 | dihydroorotase | 99.77 | 430 | BCG_1442 | dihydroorotase | 90.47 | 430 | MAP1116 | dihydroorotase | 430 | 100 |
| MAP4_2738 | Aspartate carbamoyltransferase | 318 | Rv1380 | Probable aspartate carbamoyltransf | 91.05 | 319 | Mb1415 | aspartate carbamoyltransfera | 91.05 | 319 | MAV_3393 | aspartate carbamoyltransferase cat | 100 | 318 | BCG_1441 | aspartate carbamoyltransferas | 91.05 | 319 | MAP1115 | aspartate carbamoyltransferase catalyt | 318 | 100 |
| MAP4_2739 | pyrimidine operon regulatory protein pyrR | 190 | Rv1379 | Probable pyrimidine operon regulat | 88.08 | 193 | Mb1414 | bifunctional pyrimidine regul | 88.08 | 193 | MAV_3394 | bifunctional pyrimidine regulatory | 98.95 | 190 | BCG_1440 | bifunctional pyrimidine regulat | 88.08 | 193 | MAP1114 | bifunctional pyrimidine regulatory prot | 190 | 100 |
| MAP4_2740 | putative beta-lactamase | 401 | Rv1367c | hypothetical protein | 82.23 | 377 | Mb1402c | hypothetical protein | 82.49 | 377 | MAV_3395 | beta-lactamase | 99.5 | 401 | BCG_1429c | hypothetical protein | 82.49 | 377 | MAP1113c | hypothetical protein | 377 | 100 |
| MAP4_2741 | acetyltransferase, GNAT domain-containing protein | 179 | Rv2669 | GCN5-related N-acetyltransferase | 29.67 | 156 | Mb2688 | hypothetical protein | 29.67 | 156 | MAV_3396 | acetyltransferase, gnat family prote | 100 | 184 | BCG_2682 | hypothetical protein | 29.67 | 156 | MAP1112c | hypothetical protein | 179 | 100 |
| MAP4_2742 | oxidoreductaseHEAT repeat-containing protein | 906 | Rv0248c | Probable succinate dehydrogenase [ | 25.97 | 646 | Mb0254c | succinate dehydrogenase flav | 25.97 | 646 | MAV_3397 | oxidoreductase/HEAT repeat-conta | 99.45 | 906 | BCG_0286c | succinate dehydrogenase flavo | 25.97 | 646 | MAP1111 | oxidoreductase/HEAT repeat-containing | 906 | 100 |
| MAP4_2743 | sugar-transport ATP-binding protein ABC transporter S | 245 | Rv2397c | Sulfate-transport ATP-binding prote | 40.61 | 351 | Mb2419c | sulfate-transport ABC transpo | 40.61 | 351 | MAV_3398 | ABC transporter ATP-binding prote | 100 | 245 | BCG_2412c | sulfate-transport ATP-binding | 40.61 | 351 | MAP1110 | hypothetical protein | 245 | 100 |
| MAP4_2744 | ABC transporter permease | 286 | Rv3757c | Possible osmoprotectant (glycine be | 27.98 | 229 | Mb3783c | glycine betaine/carnitine/cho | 27.98 | 229 | MAV_3399 | ABC transporter permease | 100 | 286 | BCG_3816c | osmoprotectant (glycine betair | 27.98 | 229 | MAP1109 | hypothetical protein | 286 | 100 |
| MAP4_2747 | putative ferredoxin | 76 | Rv3153 | Probable NADH dehydrogenase I (ch | 32.84 | 211 | Mb3177 | NADH dehydrogenase subuni | 32.84 | 211 | MAV_3401 | hypothetical protein | 98.68 | 76 | BCG_3176 | NADH dehydrogenase subunit | 32.84 | 211 | MAP1106 | hypothetical protein | 76 | 100 |
| MAP4_2748 | Transcriptional regulator, GntR family | 253 | Rv0792c | Probable transcriptional regulatory | 28.09 | 269 | Mb0816c | GntR family transcriptional re | 28.09 | 269 | MAV_3402 | GntR-family protein transcriptional | 98.8 | 250 | BCG_0845c | GntR family transcriptional reg | 28.09 | 269 | MAP1105 | hypothetical protein | 314 | 99.6 |
| MAP4_2749 | hypothetical protein | 268 | Rv3779 | Probable conserved transmembrane | 43.18 | 666 | Mb3808 | transmembrane protein alani | 43.18 | 666 | MAV_3403 | hypothetical protein | 99.25 | 268 | BCG_3841 | transmembrane protein alanin | 43.18 | 666 | MAP1104c | hypothetical protein | 268 | 100 |
| MAP4_2750 | hypothetical protein | 108 | Rv2274c | Possible toxin MazF8 | 28.57 | 105 | Mb2297c | hypothetical protein | 28.57 | 105 | MAV_3404 | hypothetical protein | 97.14 | 105 | BCG_2291c | hypothetical protein | 28.57 | 105 | MAP1103c | hypothetical protein | 108 | 100 |
| MAP4_2751 | two component DNA binding transcriptional regulatory | 222 | Rv0602c | Two component DNA binding transc | 50.45 | 253 | Mb0618c | two component DNA binding | 50 | 253 | MAV_3406 | TcrA protein | 99.1 | 222 | BCG_0648c | two component DNA binding t | 50 | 253 | MAP1102c | TcrA | 222 | 100 |
| MAP4_2752 | putative histidine kinase | 467 | Rv0758 | Possible two component system res | 31.25 | 485 | Mb0781 | two component system respo | 31.05 | 485 | MAV_3405 | hypothetical protein | 99.36 | 467 | BCG_0810 | two component system respon | 31.05 | 485 | MAP1101 | hypothetical protein | 467 | 100 |
| MAP4_2753 | hypothetical protein | 80 | Rv0151c | PE family protein PE1 | 37.74 | 588 | Mb0156c | PE family protein | 37.74 | 588 | MAV_3407 | hypothetical protein | 98.75 | 80 | BCG_0187c | PE family protein | 37.74 | 588 | MAP2083c | hypothetical protein | 304 | 32.2 |
| MAP4_2754 | amino acid decarboxylase | 950 | Rv2531c | Probable amino acid decarboxylase | 86.02 | 947 | Mb2560c | amino acid decarboxylase | 86.02 | 947 | MAV_3408 | Orn/Lys/Arg decarboxylase | 99.89 | 950 | BCG_2553c | amino acid decarboxylase | 86.02 | 947 | MAP1100 | Adi | 950 | 100 |
| MAP4_2755 | hypothetical protein | 129 | Rv2532c | Hypothetical protein | 75.19 | 133 | Mb2561c | hypothetical protein | 75.19 | 133 | MAV_3409 | N utilization substance protein B | 99.22 | 129 | BCG_2554c | hypothetical protein | 75.19 | 133 | MAP1099 | hypothetical protein | 129 | 100 |
| MAP4_2756 | N utilization substance protein B nusB | 156 | Rv2533c | N utilization substance protein NusB | 82.67 | 156 | Mb2562c | transcription antitermination | 83.33 | 156 | MAV_3410 | transcription antitermination prote | 100 | 156 | BCG_2555c | transcription antitermination p | 83.33 | 156 | MAP1098 | transcription antitermination protein N | 156 | 100 |
| MAP4_2757 | translation elongation factor P | 187 | Rv2534c | Probable elongation factor P Efp | 92.51 | 187 | Mb2563c | elongation factor P | 92.51 | 187 | MAV_3411 | elongation factor P | 100 | 187 | BCG_2556c | elongation factor P | 92.51 | 187 | MAP1097 | elongation factor P | 187 | 100 |
| MAP4_2758 | cytoplasmic peptidase PepQ | 369 | Rv2535c | Probable cytoplasmic peptidase Pep | 80.75 | 372 | Mb2564c | peptidase PepQ | 80.75 | 372 | MAV_3412 | peptidase, M24 family protein | 100 | 369 | BCG_2557c | cytoplasmic peptidase pepQ | 80.75 | 372 | MAP1096 | PepQ | 369 | 100 |
| MAP4_2759 | hypothetical protein | 223 | Rv2536 | Probable conserved transmembrane | 67.38 | 230 | Mb2565 | transmembrane protein | 67.38 | 230 | MAV_3414 | hypothetical protein | 100 | 219 | BCG_2558 | hypothetical protein | 67.38 | 230 | MAP1095c | hypothetical protein | 223 | 100 |
| MAP4_2760 | 3-dehydroquinate dehydratase II | 143 | Rv2537c | 3-dehydroquinate dehydratase AroD | 88.49 | 147 | Mb2566c | 3-dehydroquinate dehydratas | 88.49 | 147 | MAV_3413 | 3-dehydroquinate dehydratase | 99.3 | 143 | BCG_2559c | 3-dehydroquinate dehydratase | 88.49 | 147 | MAP1094 | 3-dehydroquinate dehydratase | 143 | 100 |
| MAP4_2761 | 3-dehydroquinate synthase | 365 | Rv2538c | 3-dehydroquinate synthase AroB | 88.14 | 362 | Mb2567c | 3-dehydroquinate synthase | 88.14 | 362 | MAV_3415 | 3-dehydroquinate synthase | 99.72 | 358 | BCG_2560c | 3-dehydroquinate synthase | 88.14 | 362 | MAP1093 | 3-dehydroquinate synthase | 365 | 100 |
| MAP4_2762 | Shikimate kinase I | 176 | Rv2539c | Shikimate kinase AroK (SK) | 85.8 | 176 | Mb2568c | shikimate kinase | 85.8 | 176 | MAV_3416 | shikimate kinase | 100 | 176 | BCG_2561c | shikimate kinase | 85.8 | 176 | MAP1092 | shikimate kinase | 176 | 100 |
| MAP4_2763 | chorismate synthase | 404 | Rv2540c | Probable chorismate synthase AroF | 89.95 | 401 | Mb2569c | chorismate synthase | 89.95 | 401 | MAV_3417 | chorismate synthase | 99.5 | 401 | BCG_2562c | chorismate synthase | 89.95 | 401 | MAP1091 | chorismate synthase | 404 | 100 |
| MAP4_2764 | dipeptide ABC transport ATP-binding protein DppD | 535 | Rv3663c | Probable dipeptide-transport ATP-bi | 49.26 | 548 | Mb3687c | peptide ABC transporter ATP- | 49.26 | 548 | MAV_3418 | ABC transporter ATP-binding prote | 99.44 | 535 | BCG_3721c | dipeptide-transport ATP-bindir | 49.26 | 548 | MAP1090 | DppD_2 | 535 | 100 |
| MAP4_2765 | dipeptide-transport membrane protein ABC transporte | 268 | Rv3664c | Probable dipeptide-transport integr | 38.24 | 266 | Mb3688c | peptide ABC transporter | 38.24 | 266 | MAV_3419 | ABC transporter permease | 99.25 | 268 | BCG_3722c | dipeptide-transport integral m | 38.24 | 266 | MAP1089 | hypothetical protein | 268 | 100 |
| MAP4_2768 | ABC-type dipeptide transport system, periplasmic com | 530 | Rv1280c | Probable periplasmic oligopeptide-b | 24.24 | 591 | Mb1311c | periplasmic oligopeptide-bind | 24.24 | 591 | MAV_3421 | extracellular solute-binding protein | 99.43 | 530 | BCG_1339c | periplasmic oligopeptide-bindi | 24.24 | 591 | MAP1086 | hypothetical protein | 530 | 99.81 |
| MAP4_2769 | putative acyl-CoA dehydrogenase | 403 | Rv1679 | Possible acyl-CoA dehydrogenase Fa | 28.93 | 373 | Mb1706 | acyl-CoA dehydrogenase | 28.93 | 373 | MAV_3422 | acyl-CoA dehydrogenase domain-c | 99.75 | 403 | BCG_1717 | acyl-CoA dehydrogenase fadE1 | 28.93 | 373 | MAP1085 | hypothetical protein | 406 | 100 |
| MAP4_2770 | hypothetical protein | 320 | Rv3618 | Possible monooxygenase | 40.43 | 395 | Mb0978c | oxidoreductase | 33.33 | 282 | MAV_3424 | hypothetical protein | 97.62 | 126 | BCG_1007c | oxidoreductase | 33.33 | 282 | MAP1084c | hypothetical protein | 320 | 100 |
| MAP4_2771 | putative nitrilotriacetate monooxygenase component A | 413 | Rv1936 | Possible monooxygenase | 25.11 | 369 | Mb1971 | monooxygenase | 25.11 | 369 | MAV_3425 | nitrilotriacetate monooxygenase co | 98.79 | 426 | BCG_1975 | monooxygenase | 25.11 | 369 | MAP1083c | hypothetical protein | 413 | 100 |
| MAP4_2772 | putative alkanesulfonate monooxygenase | 361 | Rv0132c | Putative F420-dependent glucose-6- | 30.09 | 360 | Mb0137c | F420-dependent glucose-6-ph | 30.09 | 360 | MAV_3426 | alkanesulfonate monooxygenase | 99.17 | 361 | BCG_0166c | F420-dependent glucose-6-pho | 30.09 | 360 | MAP1082c | hypothetical protein | 361 | 100 |
| MAP4_2773 | putative peptidase, type IV leader peptidase family pro | 142 | Rv2551c | hypothetical protein | 63.57 | 139 | Mb2581c | hypothetical protein | 63.57 | 139 | MAV_3427 | peptidase, A24 (type IV prepilin pe | 98.59 | 142 | BCG_2574c | hypothetical protein | 63.57 | 139 | MAP1081 | hypothetical protein | 142 | 100 |
| MAP4_2774 | shikimate 5-dehydrogenase | 276 | Rv2552c | Probable shikimate 5-dehydrogenas | 82.46 | 269 | Mb2582c | shikimate 5-dehydrogenase | 80.8 | 275 | MAV_3428 | shikimate 5-dehydrogenase | 93.2 | 294 | BCG_2575c | shikimate 5-dehydrogenase | 80.8 | 275 | MAP1080 | shikimate 5-dehydrogenase | 276 | 100 |
| MAP4_2775 | hypothetical protein | 415 | Rv2553c | Probable conserved membrane prot | 74.94 | 417 | Mb2583c | hypothetical protein | 74.94 | 417 | MAV_3429 | hypothetical protein | 99.76 | 415 | BCG_2576c | hypothetical protein | 74.94 | 417 | MAP1079 | hypothetical protein | 415 | 100 |
| MAP4_2776 | hypothetical protein | 167 | Rv2554c | hypothetical protein | 81.66 | 170 | Mb2584c | Holliday junction resolvase-lik | 81.66 | 170 | MAV_3430 | Holliday junction resolvase-like pro | 98.18 | 165 | BCG_2577c | Holliday junction resolvase-like | 81.66 | 170 | MAP1078 | Holliday junction resolvase-like protein | 167 | 100 |
| MAP4_2777 | alanyl-tRNA synthetase | 900 | Rv2555c | Probable alanyl-tRNA synthetase Ala | 89.05 | 904 | Mb2585c | alanyl-tRNA synthetase | 88.94 | 904 | MAV_3431 | alanyl-tRNA synthetase | 100 | 900 | BCG_2578c | alanyl-tRNA synthetase | 88.94 | 904 | MAP1077 | alanyl-tRNA synthetase | 900 | 100 |
| MAP4_2778 | hypothetical protein | 133 | Rv2556c | hypothetical protein | 83.72 | 129 | Mb2586c | hypothetical protein | 83.72 | 129 | MAV_3432 | hypothetical protein | 99.25 | 133 | BCG_2579c | hypothetical protein | 83.72 | 129 | MAP1076 | hypothetical protein | 133 | 100 |
| MAP4_2781 | hypothetical protein | 111 | Rv2280 | Probable dehydrogenase | 34.85 | 459 | Mb2301 | dehydrogenase | 34.85 | 459 | MAV_3434 | hypothetical protein | 98.2 | 111 | BCG_2295 | dehydrogenase | 34.85 | 459 | MAP1073 | hypothetical protein | 111 | 100 |
| MAP4_2782 | putative ATPase, conservedalanine-leucine-valine rich | 450 | Rv2559c | Conserved hypothetical alanine leuc | 88.5 | 452 | Mb2589c | recombination factor protein | 88.72 | 452 | MAV_3435 | recombination factor protein RarA | 99.33 | 446 | BCG_2582c | recombination factor protein R | 88.72 | 452 | MAP1072 | recombination factor protein RarA | 450 | 100 |
| MAP4_2783 | proline and glycine rich membrane protein | 319 | Rv2560 | Probable proline and glycine rich tra | 42.4 | 325 | Mb2590 | hypothetical protein | 42.8 | 325 | MAV_3436 | hypothetical protein | 92.64 | 325 | BCG_2583 | proline and glycine rich transm | 42.8 | 325 | MAP1071c | hypothetical protein | 319 | 100 |
| MAP4_2784 | conserved alanine and leucine rich protein | 887 | Rv2567 | Conserved hypothetical alanine and | 80.27 | 884 | Mb2597 | hypothetical protein | 80.39 | 884 | MAV_3438 | hypothetical protein | 99.32 | 887 | BCG_2590 | hypothetical protein | 80.39 | 884 | MAP1070c | hypothetical protein | 887 | 100 |
| MAP4_2785 | hypothetical protein | 340 | Rv2568c | hypothetical protein | 81.9 | 341 | Mb2598c | hypothetical protein | 81.9 | 341 | MAV_3437 | hypothetical protein | 99.41 | 340 | BCG_2591c | hypothetical protein | 81.9 | 341 | MAP1069 | hypothetical protein | 340 | 100 |
| MAP4_2786 | transglutaminase-like superfamily protein | 311 | Rv2569c | hypothetical protein | 86.99 | 314 | Mb2599c | hypothetical protein | 86.99 | 314 | MAV_3439 | transglutaminase | 99.02 | 307 | BCG_2592c | hypothetical protein | 86.99 | 314 | MAP1068 | hypothetical protein | 311 | 100 |
| MAP4_2787 | hypothetical protein | 129 | Rv2570 | hypothetical protein | 75 | 129 | Mb2600 | hypothetical protein | 75 | 129 | MAV_3440 | hypothetical protein | 98.45 | 129 | BCG_2593 | hypothetical protein | 75 | 129 | MAP1067c | hypothetical protein | 129 | 100 |
| MAP4_2788 | transmembrane alanine and valine and leucinerich pro | 352 | Rv2571c | Probable transmembrane alanine ar | 51.3 | 355 | Mb2601c | transmembrane alanine and | 51.3 | 355 | MAV_3441 | hypothetical protein | 99.15 | 352 | BCG_2594c | transmembrane alanine and va | 51.01 | 355 | MAP1066 | hypothetical protein | 352 | 100 |
| MAP4_2789 | hypothetical protein | 143 | Rv3547 | Deazaflavin-dependent nitroreducta | 41.53 | 151 | Mb3577 | hypothetical protein | 41.53 | 151 | MAV_3442 | hypothetical protein | 99.3 | 143 | BCG_3611 | hypothetical protein | 41.53 | 151 | MAP1065 | hypothetical protein | 143 | 100 |
| MAP4_2790 | hypothetical protein | 240 | Rv2916c | Probable signal recognition particle | 36.36 | 525 | Mb2940c | signal recognition particle pro | 36.36 | 525 | MAV_3443 | hypothetical protein | 98.33 | 240 | BCG_2937c | signal recognition particle prot | 36.36 | 525 | MAP1796c | hypothetical protein | 4170 | 28.41 |
| MAP4_2791 | hypothetical protein | 188 | Rv3286c | Alternative RNA polymerase sigma f | 41.03 | 261 | Mb3314c | RNA polymerase sigma factor | 41.03 | 261 | MAV_3444 | hypothetical protein | 98.94 | 188 | BCG_3315c | RNA polymerase sigma factor S | 41.03 | 261 | MAP3665c | hypothetical protein | 565 | 37.1 |
| MAP4_2792 | hypothetical protein | 154 | Rv2079 | hypothetical protein | 71.91 | 656 | Mb2105 | hypothetical protein | 73.03 | 656 | MAV_0331 | hypothetical protein | 78.65 | 545 | BCG_2098 | hypothetical protein | 73.03 | 656 | MAP1064 | hypothetical protein | 154 | 100 |
| MAP4_2793 | aspartyl-tRNA synthetase | 591 | Rv2572c | Probable aspartyl-tRNA synthetase A | 87.78 | 596 | Mb2602c | aspartyl-tRNA synthetase | 87.04 | 611 | MAV_3447 | aspartyl-tRNA synthetase | 98.98 | 591 | BCG_2595c | aspartyl-tRNA synthetase | 87.04 | 611 | MAP1063 | aspartyl-tRNA synthetase | 591 | 99.83 |
| MAP4_2794 | 2-dehydropantoate 2-reductase | 268 | Rv2573 | hypothetical protein | 76.83 | 246 | Mb2603 | 2-dehydropantoate 2-reducta | 76.4 | 275 | MAV_3448 | 2-dehydropantoate 2-reductase | 98.13 | 267 | BCG_2596 | 2-dehydropantoate 2-reductas | 76.83 | 246 | MAP1062c | 2-dehydropantoate 2-reductase | 268 | 100 |
| MAP4_2795 | hypothetical protein | 165 | Rv2574 | hypothetical protein | 80.5 | 167 | Mb2604 | hypothetical protein | 80.5 | 167 | MAV_3449 | hypothetical protein | 100 | 165 | BCG_2597 | hypothetical protein | 80.5 | 167 | MAP1061c | hypothetical protein | 165 | 100 |
| MAP4_2796 | putative metallopeptidase, zinc binding protein | 292 | Rv2575 | Possible conserved membrane glyci | 77.47 | 293 | Mb2605 | hypothetical protein | 77.47 | 293 | MAV_3451 | metallopeptidase, zinc binding | 100 | 292 | BCG_2598 | membrane glycine rich protein | 77.47 | 293 | MAP1060c | hypothetical protein | 292 | 100 |
| MAP4_2797 | dihydrodipicolinate synthase | 291 | Rv2753c | Probable dihydrodipicolinate syntha | 30.65 | 300 | Mb2774c | dihydrodipicolinate synthase | 30.65 | 300 | MAV_3450 | dihydrodipicolinate synthetase | 97.94 | 291 | BCG_2769c | dihydrodipicolinate synthase | 30.65 | 300 | MAP1059 | DapA_1 | 291 | 100 |
| MAP4_2798 | class II aldolaseadducin domain-containing protein | 265 | Rv0727c | Possible L-fuculose phosphate aldol | 27.42 | 218 | Mb0748c | L-fuculose phosphate aldolas | 27.42 | 218 | MAV_3452 | class II aldolase/adducin domain pr | 99.62 | 265 | BCG_0777c | L-fuculose phosphate aldolase | 27.42 | 218 | MAP1058 | class II aldolase/adducin domain protei | 268 | 100 |
| MAP4_2799 | Transcriptional regulator | 178 | Rv3471c | hypothetical protein | 37.25 | 177 | Mb3500c | hypothetical protein | 37.25 | 177 | MAV_3453 | transcriptional regulator | 99.44 | 178 | BCG_3536c | hypothetical protein | 37.25 | 177 | MAP1057c | hypothetical protein | 178 | 100 |
| MAP4_2800 | putative conserved membrane protein | 162 | Rv2576c | Possible conserved membrane prote | 54.19 | 154 | Mb2606c | hypothetical protein | 54.19 | 154 | MAV_3454 | hypothetical protein | 98.43 | 127 | BCG_2599c | hypothetical protein | 54.19 | 154 | MAP1056 | hypothetical protein | 162 | 100 |
| MAP4_2801 | hypothetical protein | 536 | Rv2577 | hypothetical protein | 76.57 | 529 | Mb2608 | hypothetical protein | 81.06 | 434 | MAV_3455 | metallophosphoesterase | 97.01 | 536 | BCG_2600 | hypothetical protein | 76.57 | 529 | MAP1055c | hypothetical protein | 536 | 100 |
| MAP4_2802 | hypothetical protein | 342 | Rv2578c | hypothetical protein | 86.55 | 340 | Mb2609c | hypothetical protein | 86.55 | 340 | MAV_3456 | radical SAM domain-containing pro | 99.42 | 342 | BCG_2601c | hypothetical protein | 86.55 | 340 | MAP1054 | hypothetical protein | 342 | 100 |
| MAP4_2803 | REP13E12 repeat family protein | 419 | Rv0336 | Conserved 13E12 repeat family prot | 57.55 | 503 | Mb0343 | hypothetical protein | 57.55 | 503 | MAV_3457 | hypothetical protein | 99.76 | 489 | BCG_0375 | hypothetical protein | 57.55 | 503 | MAP1053 | hypothetical protein | 419 | 100 |
| MAP4_2804 | Histidyl-tRNA synthetase | 420 | Rv2580c | Probable histidyl-tRNA synthetase H | 90.36 | 423 | Mb2611c | histidyl-tRNA synthetase | 90.36 | 423 | MAV_3460 | histidyl-tRNA synthetase | 99.52 | 420 | BCG_2603c | histidyl-tRNA synthetase | 90.36 | 423 | MAP1052 | histidyl-tRNA synthetase | 420 | 100 |
| MAP4_2805 | glyoxalase II | 218 | Rv2581c | Possible glyoxalase II (hydroxyacylgl | 82.88 | 224 | Mb2612c | glyoxalase II | 82.88 | 224 | MAV_3461 | metallo-beta-lactamase | 98.62 | 218 | BCG_2604c | glyoxalase II | 82.88 | 224 | MAP1051 | hypothetical protein | 218 | 100 |
| MAP4_2806 | Peptidyl-prolyl cis-trans isomerase B | 313 | Rv2582 | Probable peptidyl-prolyl cis-trans isc | 76.77 | 308 | Mb2613 | peptidyl-prolyl cis-trans isom | 76.43 | 308 | MAV_3462 | peptidyl-prolyl cis-trans isomerase, | 98.98 | 295 | BCG_2605 | peptidyl-prolyl cis-trans isomer | 76.43 | 308 | MAP1050c | PpiB | 313 | 100 |
| MAP4_2807 | transmembrane serinethreonine-protein kinase | 550 | Rv1266c | Probable transmembrane serine/thr | 53.18 | 626 | Mb1297c | Ser/Thr protein kinase | 53.18 | 596 | MAV_3463 | protein kinase/peptidyl-prolyl cis-tr | 98.73 | 550 | BCG_1325c | transmembrane serine/threoni | 53.18 | 596 | MAP1049c | hypothetical protein | 550 | 100 |
| MAP4_2808 | transposase | 329 | Rv2812 | Probable transposase | 32.65 | 469 | Mb2836 | transposase | 32.29 | 265 | MAV_2002 | transposase | 83.28 | 345 | BCG_2830 | transposase | 32.65 | 469 | MAP2608 | hypothetical protein | 329 | 100 |
| MAP4_2809 | GTP pyrophosphokinase | 788 | Rv2583c | Probable GTP pyrophosphokinase Re | 93.16 | 790 | Mb2614c | GTP pyrophosphokinase | 93.16 | 790 | MAV_3464 | GTP pyrophosphokinase | 99.62 | 791 | BCG_2606c | GTP pyrophosphokinase relA | 93.16 | 790 | MAP1047 | RelA | 788 | 100 |
| MAP4_2810 | Adenine phosphoribosyltransferase | 180 | Rv2584c | Adenine phosphoribosyltransferase | 69.19 | 223 | Mb2615c | adenine phosphoribosyltrans | 69.77 | 223 | MAV_3465 | adenine phosphoribosyltransferase | 98.89 | 180 | BCG_2607c | adenine phosphoribosyltransfe | 69.77 | 223 | MAP1046 | adenine phosphoribosyltransferase | 180 | 100 |
| MAP4_2811 | conserved lipoprotein | 557 | Rv2585c | Possible conserved lipoprotein | 76.38 | 557 | Mb2616c | lipoprotein | 76.57 | 557 | MAV_3466 | extracellular solute-binding protein | 98.92 | 557 | BCG_2608c | lipoprotein | 76.57 | 557 | MAP1045 | hypothetical protein | 557 | 100 |
| MAP4_2812 | Protein-export membrane protein SecF | 435 | Rv2586c | Probable protein-export membrane | 74.22 | 442 | Mb2617c | preprotein translocase subun | 73.77 | 442 | MAV_3467 | preprotein translocase subunit Sec | 99.08 | 435 | BCG_2609c | preprotein translocase subunit | 73.77 | 442 | MAP1044 | preprotein translocase subunit SecF | 435 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2813 | Protein-export membrane protein SecD | 607 | Rv2587c | Probable protein-export membrane | 79.08 | 573 | Mb2618c | preprotein translocase subun | 78.91 | 573 | MAV_3468 | preprotein translocase subunit Sec | 100 | 608 | BCG_2610c | preprotein translocase subunit | 79.08 | 573 | MAP1043 | preprotein translocase subunit SecD | 607 | 100 |
| MAP4_2814 | membrane protein secretion factor yajC | 108 | Rv2588c | Probable conserved membrane prot | 74.78 | 115 | Mb2619c | preprotein translocase subun | 74.78 | 115 | MAV_3469 | preprotein translocase subunit Yaj | 100 | 110 | BCG_2611c | preprotein translocase subunit | 74.78 | 115 | MAP1042 | preprotein translocase subunit YajC | 108 | 100 |
| MAP4_2815 | 4-aminobutyrate aminotransferase | 449 | Rv2589 | 4-aminobutyrate aminotransferase | 84.86 | 449 | Mb2620 | 4-aminobutyrate aminotrans | 84.86 | 449 | MAV_3470 | 4-aminobutyrate aminotransferase | 99.33 | 449 | BCG_2612 | 4-aminobutyrate aminotransfe | 84.86 | 449 | MAP1041c | 4-aminobutyrate aminotransferase | 449 | 100 |
| MAP4_2816 | fatty-acid--CoA ligase | 1173 | Rv2590 | Probable fatty-acid-CoA ligase FadD | 69.84 | 1168 | Mb2621 | fatty-acid--CoA ligase | 69.75 | 1168 | MAV_3471 | acyl-CoA dehydrogenase | 99.32 | 1173 | BCG_2613 | fatty-acid-CoA ligase fadD9 | 69.75 | 1168 | MAP1040c | FadD9 | 1173 | 100 |
| MAP4_2817 | hypothetical protein | 314 | Rv3340 | Probable O-acetylhomoserine sulfhy | 32.93 | 449 | Mb3372 | O-acetylhomoserine aminoca | 32.93 | 449 | MAV_3472 | hypothetical protein | 100 | 225 | BCG_1809c | transcriptional regulatory prote | 27.42 | 186 | MAP1039 | hypothetical protein | 314 | 100 |
| MAP4_2818 | holliday junction DNA helicase RuvB | 351 | Rv2592c | Probable holliday junction DNA heli | 94.2 | 344 | Mb2623c | Holliday junction DNA helicas | 94.2 | 344 | MAV_3473 | Holliday junction DNA helicase Ruv | 100 | 351 | BCG_2615c | Holliday junction DNA helicase | 94.2 | 344 | MAP1038 | Holliday junction DNA helicase RuvB | 351 | 100 |
| MAP4_2819 | holliday junction DNA helicase RuvA | 199 | Rv2593c | Probable holliday junction DNA heli | 83.92 | 196 | Mb2624c | Holliday junction DNA helicas | 83.92 | 196 | MAV_3474 | Holliday junction DNA helicase Ruv | 100 | 199 | BCG_2616c | Holliday junction DNA helicase | 83.92 | 196 | MAP1037 | Holliday junction DNA helicase RuvA | 199 | 100 |
| MAP4_2820 | crossover junction endodeoxyribonuclease RuvC | 188 | Rv2594c | Probable crossover junction endode | 84.41 | 188 | Mb2625c | Holliday junction resolvase | 84.41 | 188 | MAV_3475 | Holliday junction resolvase | 100 | 188 | BCG_2617c | Holliday junction resolvase | 84.41 | 188 | MAP1036 | Holliday junction resolvase | 188 | 100 |
| MAP4_2821 | membrane protein | 203 | Rv2597 | Probable membrane protein | 72.33 | 206 | Mb2628 | hypothetical protein | 72.33 | 206 | MAV_3476 | hypothetical protein | 99.51 | 203 | BCG_2620 | hypothetical protein | 72.33 | 206 | MAP1035c | hypothetical protein | 203 | 100 |
| MAP4_2822 | hypothetical protein | 167 | Rv2598 | hypothetical protein | 67.66 | 164 | Mb2629 | hypothetical protein | 67.66 | 164 | MAV_3477 | hypothetical protein | 98.2 | 183 | BCG_2621 | hypothetical protein | 67.66 | 164 | MAP1034c | hypothetical protein | 167 | 100 |
| MAP4_2823 | putative conserved membrane protein | 143 | Rv2599 | Probable conserved membrane prot | 69.11 | 143 | Mb2630 | hypothetical protein | 69.11 | 143 | MAV_3478 | hypothetical protein | 98.6 | 143 | BCG_2622 | hypothetical protein | 69.11 | 143 | MAP0128c | hypothetical protein | 285 | 38.89 |
| MAP4_2824 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_2825 | hypothetical protein | 151 | Rv2600 | Probable conserved integral membr | 62.88 | 133 | Mb2631 | hypothetical protein | 62.88 | 133 | MAV_3479 | hypothetical protein | 98.01 | 151 | BCG_2623 | integral membrane protein | 65.15 | 68 | MAP1032c | hypothetical protein | 151 | 100 |
| MAP4_2826 | spermidine synthase | 523 | Rv2601 | Probable spermidine synthase SpeE | 80.71 | 523 | Mb2632 | spermidine synthase | 80.71 | 523 | MAV_3480 | spermidine synthase | 98.66 | 523 | BCG_2625 | spermidine synthase | 80.71 | 523 | MAP1031c | spermidine synthase | 523 | 99.81 |
| MAP4_2827 | hypothetical protein | 250 | Rv2603c | Highly conserved protein | 87.6 | 251 | Mb2635c | hypothetical protein | 87.6 | 251 | MAV_3481 | hypothetical protein | 99.2 | 250 | BCG_2628c | hypothetical protein | 87.6 | 251 | MAP1030 | hypothetical protein | 250 | 100 |
| MAP4_2828 | Mycothiol S-conjugate amidase Mca | 296 | Rv1082 | Mycothiol conjugate amidase Mca ( | 83.8 | 288 | Mb1111 | mycothiol conjugate amidase | 83.8 | 288 | MAV_1206 | mycothiol conjugate amidase Mca | 99.65 | 290 | BCG_1140 | Mycothiol conjugate amidase | 83.8 | 288 | MAP1029 | hypothetical protein | 296 | 100 |
| MAP4_2829 | hypothetical protein | 141 | Rv1081c | Probable conserved membrane prot | 69.72 | 144 | Mb1110c | hypothetical protein | 69.72 | 144 | MAV_1205 | hypothetical protein | 97.87 | 141 | BCG_1139c | hypothetical protein | 69.72 | 144 | MAP1028c | hypothetical protein | 141 | 100 |
| MAP4_2830 | Transcription elongation factor GreA | 164 | Rv1080c | Probable transcription elongation fa | 96.95 | 164 | Mb1109c | transcription elongation facto | 96.95 | 164 | MAV_1204 | transcription elongation factor Gre | 99.37 | 159 | BCG_1138c | transcription elongation factor | 96.95 | 164 | MAP1027c | transcription elongation factor GreA | 164 | 100 |
| MAP4_2831 | cystathionine gamma-lyase | 388 | Rv1079 | Cystathionine gamma-synthase Met | 85.01 | 388 | Mb1108 | cystathionine gamma-syntha | 85.01 | 388 | MAV_1203 | cystathionine gamma-synthase | 100 | 388 | BCG_1137 | cystathionine gamma-synthase | 85.01 | 388 | MAP1026 | cystathionine gamma-synthase | 388 | 100 |
| MAP4_2832 | proline-rich antigen pra | 239 | Rv0176 | Probable conserved Mce associated | 43.08 | 322 | Mb1107 | hypothetical protein | 68.94 | 240 | MAV_1202 | Pra protein | 99.16 | 239 | BCG_1136 | hypothetical protein | 68.94 | 240 | MAP1025 | Pra | 241 | 100 |
| MAP4_2833 | Cystathionine beta-synthase | 468 | Rv1077 | Probable cystathionine beta-synthas | 91.45 | 464 | Mb1106 | cystathionine beta-synthase | 91.45 | 464 | MAV_1201 | cystathionine beta-synthase | 100 | 468 | BCG_1135 | cystathionine beta-synthase | 91.45 | 464 | MAP1024 | CysM2 | 468 | 100 |
| MAP4_2834 | lipase LipU | 354 | Rv1076 | Possible lipase LipU | 80.13 | 297 | Mb1105 | lipase LIPU | 80.13 | 297 | MAV_1200 | alpha/beta hydrolase | 99.15 | 354 | BCG_1134 | lipase lipU | 80.13 | 297 | MAP1023 | hypothetical protein | 357 | 100 |
| MAP4_2835 | conserved exported protein | 324 | Rv1075c | Conserved exported protein | 76.92 | 314 | Mb1104c | hypothetical protein | 76.92 | 314 | MAV_1199 | hypothetical protein | 99.69 | 324 | BCG_1133c | hypothetical protein | 76.92 | 314 | MAP1022c | hypothetical protein | 324 | 100 |
| MAP4_2838 | hypothetical protein | 283 | Rv1072 | Probable conserved transmembrane | 86.22 | 278 | Mb1101 | transmembrane protein | 86.22 | 278 | MAV_1197 | permease of the major facilitator s | 100 | 255 | BCG_1130 | hypothetical protein | 86.22 | 278 | MAP1019 | hypothetical protein | 283 | 100 |
| MAP4_2839 | enoyl-CoA hydratase echA9 | 345 | Rv1071c | Possible enoyl-CoA hydratase EchA9 | 80.29 | 345 | Mb1100c | 3-hydroxyisobutyryl-CoA hyd | 80.29 | 345 | MAV_1196 | 3-hydroxyisobutyryl-CoA hydrolase | 99.42 | 345 | BCG_1129c | 3-hydroxyisobutyryl-CoA hydro | 80.29 | 345 | MAP1018c | 3-hydroxyisobutyryl-CoA hydrolase | 350 | 99.71 |
| MAP4_2840 | enoyl-CoA hydratase echA8 | 263 | Rv1070c | Probable enoyl-CoA hydratase EchA | 89.06 | 257 | Mb1099c | enoyl-CoA hydratase | 89.06 | 257 | MAV_1195 | enoyl-CoA hydratase | 98.86 | 263 | BCG_1128c | enoyl-CoA hydratase | 89.06 | 257 | MAP1017c | enoyl-CoA hydratase | 263 | 100 |
| MAP4_2841 | putative hydrolase | 594 | Rv1069c | hypothetical protein | 77.4 | 587 | Mb1098c | hypothetical protein | 77.4 | 587 | MAV_1193 | hypothetical protein | 99.33 | 594 | BCG_1127c | hypothetical protein | 77.23 | 587 | MAP1016c | hypothetical protein | 594 | 100 |
| MAP4_2842 | hypothetical protein | 145 | Rv1066 | hypothetical protein | 81.68 | 131 | Mb1095 | hypothetical protein | 81.68 | 131 | MAV_1194 | hypothetical protein | 99.31 | 145 | BCG_1124 | hypothetical protein | 81.68 | 131 | MAP1015 | hypothetical protein | 146 | 100 |
| MAP4_2843 | hypothetical protein | 195 | Rv1065 | hypothetical protein | 82.35 | 188 | Mb1094 | hypothetical protein | 82.35 | 188 | MAV_1192 | cysteine dioxygenase type I superfa | 99.49 | 197 | BCG_1123 | hypothetical protein | 82.35 | 188 | MAP1014 | hypothetical protein | 195 | 100 |
| MAP4_2844 | putative lipoprotein LpqV | 151 | Rv1064c | Possible lipoprotein LpqV | 61.54 | 139 | Mb1093c | lipoprotein LPQV | 61.54 | 139 | MAV_1191 | LpqV protein | 94.81 | 135 | BCG_1122c | lipoprotein lpqV | 61.54 | 139 | MAP1013c | hypothetical protein | 151 | 100 |
| MAP4_2845 | putative phospholipase, patatin-like phospholipase fam | 356 | Rv1063c | hypothetical protein | 76.29 | 360 | Mb1092c | hypothetical protein | 76.29 | 360 | MAV_1190 | patatin | 98.84 | 345 | BCG_1121c | hypothetical protein | 76.29 | 360 | MAP1012c | hypothetical protein | 356 | 100 |
| MAP4_2846 | putative phospholipase, patatin-like phospholipase fam | 289 | Rv1062 | hypothetical protein | 74.39 | 285 | Mb1091 | hypothetical protein | 74.39 | 285 | MAV_1189 | phospholipase, patatin family prote | 98.62 | 289 | BCG_1120 | hypothetical protein | 74.39 | 285 | MAP1011 | hypothetical protein | 289 | 100 |
| MAP4_2847 | putative glutamine amidotransferase, class-II family pr | 295 | Rv1061 | hypothetical protein | 74.83 | 287 | Mb1090 | hypothetical protein | 74.83 | 287 | MAV_1188 | glutamine amidotransferase, class- | 97.63 | 295 | BCG_1119 | hypothetical protein | 74.83 | 287 | MAP1010 | hypothetical protein | 295 | 100 |
| MAP4_2848 | hypothetical protein | 157 | Rv1060 | hypothetical protein | 57.42 | 157 | Mb1089 | hypothetical protein | 57.42 | 157 | MAV_1187 | hypothetical protein | 98.73 | 157 | BCG_1118 | hypothetical protein | 57.42 | 157 | MAP1009 | hypothetical protein | 157 | 100 |
| MAP4_2849 | medium chain fatty-acid-CoA ligase fadD14 | 543 | Rv1058 | Probable medium chain fatty-acid-C | 83.33 | 543 | Mb1087 | long-chain-fatty-acid--CoA lig | 83.33 | 543 | MAV_1186 | long-chain-fatty-acid--CoA ligase | 98.53 | 543 | BCG_1116 | long-chain-fatty-acid--CoA ligas | 83.33 | 543 | MAP1008 | long-chain-fatty-acid--CoA ligase | 549 | 99.63 |
| MAP4_2850 | hypothetical protein | 395 | Rv1057 | hypothetical protein | 51.74 | 393 | Mb1086 | hypothetical protein | 51.74 | 393 | MAV_1185 | hypothetical protein | 98.99 | 395 | BCG_1115 | hypothetical protein | 51.74 | 393 | MAP1007 | hypothetical protein | 395 | 100 |
| MAP4_2851 | hypothetical protein | 256 | Rv1056 | hypothetical protein | 83.67 | 254 | Mb1085 | hypothetical protein | 83.67 | 254 | MAV_1184 | hypothetical protein | 98.83 | 256 | BCG_1114 | hypothetical protein | 83.67 | 254 | MAP1006 | hypothetical protein | 256 | 100 |
| MAP4_2852 | hypothetical protein | 263 | Rv0987 | Probable adhesion component trans | 30 | 855 | Mb1013 | adhesion component transpo | 30 | 423 | MAV_1182 | hypothetical protein | 99.62 | 265 | BCG_1042 | adhesion component transport | 30 | 855 | MAP1005 | hypothetical protein | 263 | 100 |
| MAP4_2853 | hypothetical protein | 403 | Rv2067c | hypothetical protein | 62.72 | 407 | Mb2093c | hypothetical protein | 62.72 | 407 | MAV_1181 | hypothetical protein | 98.76 | 403 | BCG_2086c | hypothetical protein | 62.72 | 407 | MAP1004 | hypothetical protein | 403 | 100 |
| MAP4_2854 | PPE family protein | 696 | Rv2768c | PPE family protein PPE43 | 50.5 | 394 | Mb1068c | PPE family protein | 51.52 | 391 | MAV_1347 | PPE family protein | 44.67 | 383 | BCG_1097c | PPE family protein | 51.26 | 391 | MAP1003c | hypothetical protein | 696 | 100 |
| MAP4_2855 | putative ESAT-6 like protein EsxP (ESAT-6 like protein 7 | 98 | Rv2347c | Putative ESAT-6 like protein EsxP (E | 87.76 | 98 | Mb1820 | hypothetical protein | 87.76 | 98 | MAV_1178 | hypothetical protein | 100 | 98 | BCG_1824 | hypothetical protein | 87.76 | 98 | MAP1508 | hypothetical protein | 98 | 100 |
| MAP4_2856 | putative ESAT-6 like protein ESXO (ESAT-6 like protein | 94 | Rv1793 | Putative ESAT-6 like protein EsxN (E | 93.62 | 94 | Mb1821 | ESAT-6 like protein 5 | 93.62 | 94 | MAV_1177 | hypothetical protein | 100 | 94 | BCG_1825 | ESAT-6 like protein 5 | 93.62 | 94 | MAP3217c | hypothetical protein | 383 | 38.1 |
| MAP4_2857 | two-component transcriptional regulator TrcR | 257 | Rv1033c | Two component transcriptional regu | 85.21 | 257 | Mb1062c | two component transcription | 85.21 | 257 | MAV_1176 | TrcR family transcriptional regulato | 100 | 254 | BCG_1091c | two component transcriptional | 85.21 | 257 | MAP1002c | hypothetical protein | 257 | 100 |
| MAP4_2858 | two component sensor histidine kinase TrcS | 512 | Rv1032c | Two component sensor histidine kin | 73.85 | 509 | Mb1061c | two component sensor histid | 73.85 | 509 | MAV_1175 | two component sensor histidine ki | 99.22 | 512 | BCG_1090c | two component sensor histidin | 73.85 | 509 | MAP1001c | hypothetical protein | 512 | 100 |
| MAP4_2859 | potassium-transporting ATPase A chain | 556 | Rv1029 | Probable potassium-transporting AT | 52.23 | 571 | Mb1058 | potassium-transporting ATPa | 52.23 | 571 | MAV_1173 | potassium-transporting ATPase sub | 99.28 | 556 | BCG_1087 | potassium-transporting ATPase | 52.23 | 571 | MAP1000c | potassium-transporting ATPase subunit | 556 | 100 |
| MAP4_2862 | Potassium-transporting ATPase C chain | 291 | Rv1031 | Probable potassium-transporting AT | 46.09 | 189 | Mb1060 | potassium-transporting ATPa | 46.09 | 189 | MAV_1171 | K+-transporting ATPase, C subunit | 99.66 | 291 | BCG_1089 | potassium-transporting ATPase | 46.09 | 189 | MAP0997c | hypothetical protein | 291 | 100 |
| MAP4_2863 | sensor protein KdpD | 858 | Rv1028c | Probable sensor protein KdpD | 80 | 860 | Mb1056c | sensor protein KDPD | 80 | 860 | MAV_1170 | sensor protein KdpD | 99.65 | 854 | BCG_1085c | sensor protein kdpD | 79.76 | 860 | MAP0996c | hypothetical protein | 858 | 100 |
| MAP4_2864 | transcriptional regulatory protein KdpE | 226 | Rv1027c | Probable transcriptional regulatory | 91.15 | 226 | Mb1055c | transcriptional regulator Kdp | 91.15 | 226 | MAV_1169 | KDP operon transcriptional regulat | 100 | 226 | BCG_1084c | transcriptional regulatory prot | 91.15 | 226 | MAP0995c | KdpE | 226 | 100 |
| MAP4_2865 | hypothetical protein | 108 | Rv0405 | Probable membrane bound polyketi | 39.29 | 1402 | Mb0413 | polyketide synthase | 39.29 | 946 | MAV_1168 | hypothetical protein | 100 | 108 | BCG_0444 | membrane bound polyketide s | 39.29 | 946 | MAP0994 | hypothetical protein | 108 | 100 |
| MAP4_2866 | putative exopolyphosphatase, PpxGppA phosphatase f | 316 | Rv1026 | hypothetical protein | 78.12 | 319 | Mb1054 | hypothetical protein | 78.12 | 319 | MAV_1167 | exopolyphosphatase | 99.37 | 315 | BCG_1083 | hypothetical protein | 78.12 | 319 | MAP0993 | hypothetical protein | 316 | 100 |
| MAP4_2867 | hypothetical protein | 162 | Rv1025 | hypothetical protein | 85.62 | 155 | Mb1053 | hypothetical protein | 85.62 | 155 | MAV_1166 | hypothetical protein | 99.3 | 142 | BCG_1082 | hypothetical protein | 85.62 | 155 | MAP0992 | hypothetical protein | 162 | 100 |
| MAP4_2868 | putative conserved membrane protein | 225 | Rv1024 | Possible conserved membrane prot | 68.42 | 228 | Mb1052 | hypothetical protein | 68.42 | 228 | MAV_1165 | septum formation initiator subfami | 98.67 | 225 | BCG_1081 | hypothetical protein | 68.42 | 228 | MAP0991 | hypothetical protein | 225 | 100 |
| MAP4_2869 | enolase Eno | 429 | Rv1023 | Probable enolase Eno | 93.47 | 429 | Mb1051 | phosphopyruvate hydratase | 93.71 | 429 | MAV_1164 | phosphopyruvate hydratase | 100 | 429 | BCG_1080 | phosphopyruvate hydratase | 93.71 | 429 | MAP0990 | phosphopyruvate hydratase | 429 | 100 |
| MAP4_2870 | putative conserved lipoprotein LpqU | 264 | Rv1022 | Probable conserved lipoprotein Lpq | 83.95 | 243 | Mb1050 | lipoprotein LpqU | 84.36 | 243 | MAV_1163 | LpqU protein | 99.17 | 242 | BCG_1079 | lipoprotein lpqU | 84.36 | 243 | MAP0989 | hypothetical protein | 264 | 100 |
| MAP4_2871 | putative nucleoside triphosphate pyrophosphohydrola | 333 | Rv1021 | hypothetical protein | 74.05 | 325 | Mb1049 | nucleoside triphosphate pyro | 74.05 | 325 | MAV_1162 | nucleoside triphosphate pyrophos | 99.4 | 334 | BCG_1078 | nucleoside triphosphate pyrop | 74.05 | 325 | MAP0988 | nucleoside triphosphate pyrophosphoh | 333 | 100 |
| MAP4_2872 | Transcription-repair coupling factor | 1220 | Rv1020 | Probable transcription-repair coupli | 85.98 | 1234 | Mb1048 | transcription-repair coupling | 85.98 | 1234 | MAV_3818 | ATP-dependent DNA helicase RecG | 34.23 | 738 | BCG_1077 | transcription-repair coupling fa | 85.98 | 1234 | MAP0987 | hypothetical protein | 1221 | 99.92 |
| MAP4_2873 | Diaminopimelate decarboxylase | 444 | Rv1293 | Diaminopimelate decarboxylase Lys | 45.98 | 447 | Mb1325 | diaminopimelate decarboxyla | 45.98 | 447 | MAV_1160 | diaminopimelate decarboxylase | 99.1 | 444 | BCG_1353 | diaminopimelate decarboxylas | 45.98 | 447 | MAP0986c | LysA_1 | 444 | 100 |
| MAP4_2874 | Transcriptional regulator, TetR family | 204 | Rv1019 | Probable transcriptional regulatory | 96.45 | 197 | Mb1047 | TetR family transcriptional re | 96.45 | 197 | MAV_1159 | TetR family transcriptional regulato | 99.51 | 219 | BCG_1076 | TetR family transcriptional regu | 96.45 | 197 | MAP0985 | hypothetical protein | 204 | 100 |
| MAP4_2875 | UDP-N-acetylglucosamine pyrophosphorylase glmU | 490 | Rv1018c | Probable UDP-N-acetylglucosamine | 84.54 | 495 | Mb1046c | bifunctional N-acetylglucosan | 84.54 | 495 | MAV_1157 | bifunctional N-acetylglucosamine-1 | 99.8 | 490 | BCG_1075c | bifunctional N-acetylglucosami | 84.54 | 495 | MAP0984c | bifunctional N-acetylglucosamine-1-ph | 490 | 100 |
| MAP4_2876 | ribose-phosphate pyrophosphokinase prsA | 326 | Rv1017c | Probable ribose-phosphate pyropho | 96.01 | 326 | Mb1045c | ribose-phosphate pyrophosp | 96.01 | 326 | MAV_1156 | ribose-phosphate pyrophosphokina | 100 | 326 | BCG_1074c | ribose-phosphate pyrophosph | 96.01 | 326 | MAP0983c | ribose-phosphate pyrophosphokinase | 326 | 100 |
| MAP4_2877 | arsenate reductase | 115 | Rv1674c | Probable transcriptional regulatory | 50 | 218 | Mb1701c | transcriptional regulator | 50 | 218 | MAV_1155 | arsenate reductase | 99.13 | 115 | BCG_1712c | transcriptional regulatory prot | 50 | 218 | MAP0982c | ArsC | 115 | 100 |
| MAP4_2878 | putativelipoprotein LpqT | 219 | Rv1016c | Probable conserved lipoprotein Lpq | 62.84 | 226 | Mb1044c | lipoprotein LpqT | 63.03 | 252 | MAV_1154 | LpqT protein | 100 | 219 | BCG_1073c | lipoprotein lpqT | 63.03 | 252 | MAP0981c | hypothetical protein | 219 | 100 |
| MAP4_2879 | putative oxidoreductase | 289 | Rv0068 | Probable oxidoreductase | 47.06 | 303 | Mb0069 | short chain dehydrogenase | 47.39 | 303 | MAV_1153 | retinol dehydrogenase | 99.31 | 289 | BCG_0099 | short chain dehydrogenase | 47.39 | 303 | MAP0980c | hypothetical protein | 289 | 100 |
| MAP4_2880 | 50S ribosomal protein L25 | 219 | Rv1015c | 50S ribosomal protein L25 RplY | 85.11 | 215 | Mb1043c | 50S ribosomal protein L25 | 85.11 | 215 | MAV_1152 | 50S ribosomal protein L25 | 100 | 219 | BCG_1072c | 50S ribosomal protein L25 | 85.11 | 215 | MAP0979c | 50S ribosomal protein L25/general stre | 219 | 100 |
| MAP4_2881 | Peptidyl-tRNA hydrolase | 191 | Rv1014c | Probable peptidyl-tRNA hydrolase P | 87.43 | 191 | Mb1042c | peptidyl-tRNA hydrolase | 87.43 | 191 | MAV_1151 | peptidyl-tRNA hydrolase | 99.48 | 191 | BCG_1071c | peptidyl-tRNA hydrolase | 87.43 | 191 | MAP0978c | peptidyl-tRNA hydrolase | 191 | 100 |
| MAP4_2882 | Putative polyketide synthase pks16 | 544 | Rv1013 | Putative polyketide synthase Pks16 | 93.57 | 544 | Mb1041 | long-chain-fatty-acid--CoA lig | 93.57 | 544 | MAV_1150 | long-chain-fatty-acid--CoA ligase | 99.82 | 544 | BCG_1070 | long-chain-fatty-acid--CoA ligas | 93.57 | 544 | MAP0977 | long-chain-fatty-acid--CoA ligase | 544 | 100 |
| MAP4_2883 | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase ispE | 316 | Rv1011 | Probable 4-diphosphocytidyl-2-C-me | 88.56 | 306 | Mb1038 | 4-diphosphocytidyl-2-C-meth | 88.56 | 306 | MAV_1149 | 4-diphosphocytidyl-2-C-methyl-D-e | 99.37 | 316 | BCG_1068 | 4-diphosphocytidyl-2-C-methyl | 88.56 | 306 | MAP0976 | 4-diphosphocytidyl-2-C-methyl-D-eryth | 316 | 100 |
| MAP4_2884 | dimethyladenosine transferase KsgA | 318 | Rv1010 | Probable dimethyladenosine transfe | 83.44 | 317 | Mb1037 | dimethyladenosine transfera | 83.44 | 317 | MAV_1148 | dimethyladenosine transferase | 99.05 | 318 | BCG_1067 | dimethyladenosine transferase | 83.44 | 317 | MAP0975 | dimethyladenosine transferase | 318 | 100 |
| MAP4_2885 | resuscitation-promoting factor rpfB | 372 | Rv1009 | Probable resuscitation-promoting fa | 85.63 | 362 | Mb1036 | resuscitation-promoting fact | 85.34 | 362 | MAV_1147 | resuscitation-promoting factor Rpf | 99.12 | 340 | BCG_1066 | resuscitation-promoting factor | 85.34 | 362 | MAP0974 | hypothetical protein | 372 | 100 |
| MAP4_2886 | deoxyribonuclease tatD | 284 | Rv1008 | Probable deoxyribonuclease TatD (Y | 82.13 | 264 | Mb1035 | deoxyribonuclease TatD (YjjV | 82.51 | 264 | MAV_1146 | hydrolase, TatD family protein | 98.94 | 284 | BCG_1065 | deoxyribonuclease TatD (YjjV p | 82.51 | 264 | MAP0973 | hypothetical protein | 284 | 100 |
| MAP4_2887 | methionyl-tRNA synthetase MetS | 519 | Rv1007c | Methionyl-tRNA synthetase MetS (M | 82.81 | 519 | Mb1034c | methionyl-tRNA synthetase | 83.01 | 519 | MAV_1145 | methionyl-tRNA synthetase | 99.61 | 519 | BCG_1064c | methionyl-tRNA synthetase | 83.01 | 519 | MAP0972c | methionyl-tRNA synthetase | 519 | 100 |
| MAP4_2888 | hypothetical protein | 115 | Rv1894c | hypothetical protein | 32.99 | 376 | Mb1927c | hypothetical protein | 32.99 | 376 | MAV_1143 | two-component sensor histidine ki | 99.13 | 120 | BCG_1932c | hypothetical protein | 32.99 | 376 | MAP1740c | hypothetical protein | 512 | 26.05 |
| MAP4_2889 | polysaccharide deacetylase | 338 | Rv3045 | Probable NADP-dependent alcohol | 38.33 | 346 | Mb3071 | NADP-dependent alcohol deh | 38.33 | 346 | MAV_1144 | polysaccharide deacetylase | 96.75 | 338 | BCG_3069 | NADP-dependent alcohol dehy | 38.33 | 346 | MAP0971 | hypothetical protein | 338 | 100 |
| MAP4_2890 | hypothetical protein | 670 | Rv3375 | Probable amidase AmiD (acylamidas | 23.59 | 475 | Mb3409 | amidase | 23.59 | 475 | MAV_4056 | oxidoreductase, short chain dehyd | 29.49 | 461 | BCG_3446 | amidase amiD | 23.59 | 475 | MAP0970 | hypothetical protein | 697 | 99.85 |
| MAP4_2891 | Transcriptional regulator, TetR family | 231 | Rv1474c | Probable transcriptional regulatory | 26.86 | 187 | Mb1510c | transcriptional regulator | 26.86 | 187 | MAV_1141 | TetR family transcriptional regulato | 99.13 | 231 | BCG_1536c | transcriptional regulatory prot | 26.86 | 187 | MAP0969 | CprA | 231 | 100 |
| MAP4_2892 | Transcriptional regulator, TetR family | 225 | Rv2506 | Probable transcriptional regulatory | 32.52 | 215 | Mb2534 | TetR family transcriptional re | 32.52 | 215 | MAV_1140 | TetR family transcriptional regulato | 99.56 | 225 | BCG_2526 | TetR family transcriptional regu | 32.52 | 215 | MAP0968 | hypothetical protein | 240 | 100 |
| MAP4_2893 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_2894 | PPE family protein | 398 | Rv1808 | PPE family protein PPE32 | 45.03 | 409 | Mb3160 | PPE family protein | 44.72 | 380 | MAV_2928 | PPE family protein | 44.24 | 421 | BCG_3159 | PPE family protein | 44.72 | 380 | MAP0966c | hypothetical protein | 422 | 99.75 |
| MAP4_2895 | dTDP-4-dehydrorhamnose 3,5-epimerase | 190 | Rv3465 | dTDP-4-dehydrorhamnose 3,5-epim | 32.4 | 202 | Mb3494 | dTDP-4-dehydrorhamnose 3, | 32.4 | 202 | MAV_4407 | dTDP-4-dehydrorhamnose 3,5-epin | 32.24 | 201 | BCG_3530 | dTDP-4-dehydrorhamnose 3,5- | 32.4 | 202 | MAP0965c | hypothetical protein | 190 | 100 |
| MAP4_2896 | putative bacterial sugar transferase | 513 | Rv1640c | Lysyl-tRNA synthetase 2 LysX | 37.5 | 1172 | Mb1667c | lysyl-tRNA synthetase | 37.5 | 1172 | MAV_4706 | hypothetical protein | 37.66 | 293 | BCG_1679c | lysyl-tRNA synthetase | 37.5 | 1172 | MAP0964c | hypothetical protein | 513 | 100 |
| MAP4_2897 | putative polysaccharide biosynthesis protein | 491 | Rv0191 | Probable conserved integral membr | 29.63 | 413 | Mb0197 | hypothetical protein | 29.63 | 413 | MAV_1168 | hypothetical protein | 32.26 | 108 | BCG_0228 | integral membrane protein | 29.63 | 413 | MAP0963c | hypothetical protein | 491 | 100 |
| MAP4_2898 | putative glycosyl transferase | 600 | Rv0486 | Glycosyltransferase MshA | 42.19 | 480 | Mb0496 | mannosyltransferase | 42.19 | 480 | MAV_2755 | glycosyl transferase | 35.79 | 396 | BCG_0527 | mannosyltransferase | 42.19 | 480 | MAP0962c | hypothetical protein | 600 | 100 |
| MAP4_2899 | hypothetical protein | 352 | Rv0557 | Mannosyltransferase MgtA | 26.75 | 378 | Mb0572 | mannosyltransferase | 26.75 | 378 | MAV_1632 | hypothetical protein | 40 | 283 | BCG_0602 | mannosyltransferase | 26.75 | 378 | MAP0961c | hypothetical protein | 352 | 100 |
| MAP4_2900 | hypothetical protein | 161 | Rv1664 | Probable polyketide synthase Pks9 | 37.1 | 1017 | Mb1692 | polyketide synthase | 37.1 | 1017 | MAV_2450 | erythronolide synthase, modules 3 | 42.86 | 4171 | BCG_1703 | polyketide synthase pks9 | 37.1 | 1017 | MAP0960 | hypothetical protein | 161 | 100 |
| MAP4_2901 | oligosaccharide biosynthesis protein | 151 | Rv1668c | Probable first part of macrolide-tran | 47.37 | 372 | Mb1695c | macrolide ABC transporter A | 47.37 | 591 | MAV_4542 | exodeoxyribonuclease V, gamma s | 33.33 | 1096 | BCG_1706c | macrolide ABC transporter ATP | 47.37 | 591 | MAP0959 | hypothetical protein | 151 | 100 |
| MAP4_2902 | putative oxidoreductase | 385 | Rv2524c | Probable fatty acid synthase Fas (fat | 35 | 3069 | Mb2553c | fatty acid synthase | 35 | 3069 | MAV_2987 | NAD binding oxidoreductase | 27.34 | 336 | BCG_2545c | fatty acid synthase fas | 35 | 3069 | MAP0958c | hypothetical protein | 387 | 100 |
| MAP4_2903 | hypothetical protein | 295 | Rv0574c | hypothetical protein | 30.34 | 380 | Mb0589c | hypothetical protein | 30.34 | 380 | MAV_1005 | hypothetical protein | 36 | 567 | BCG_0619c | hypothetical protein | 30.34 | 380 | MAP0957c | hypothetical protein | 295 | 100 |
| MAP4_2904 | putative oxidoreductase | 560 | Rv1279 | Probable dehydrogenase FAD flavop | 40.68 | 528 | Mb1310 | dehydrogenase FAD flavopro | 40.68 | 528 | MAV_1139 | hypothetical protein | 100 | 266 | BCG_1338 | dehydrogenase FAD flavoprote | 40.68 | 528 | MAP0956 | hypothetical protein | 560 | 100 |
| MAP4_2905 | putative oxidoreductase, aldoketo reductase family | 317 | Rv2298 | hypothetical protein | 51.35 | 323 | Mb2320 | hypothetical protein | 51.35 | 323 | MAV_3334 | general stress protein 69 | 29.01 | 328 | BCG_2314 | hypothetical protein | 51.35 | 323 | MAP0955 | hypothetical protein | 317 | 100 |
| MAP4_2906 | putative glycosyl transferase | 337 | Rv1212c | Putative glycosyl transferase GlgA | 25.82 | 387 | Mb1244c | glycosyl transferase family pr | 25.82 | 387 | MAV_1137 | glycosyl transferase, group 1 family | 99.11 | 337 | BCG_1272c | glycosyl transferase family pro | 25.41 | 387 | MAP0954 | hypothetical protein | 337 | 100 |
| MAP4_2907 | O-antigen polymerase family protein | 496 | Rv2939 | Possible conserved polyketide synth | 28.92 | 422 | Mb2964 | acyltransferase | 28.92 | 422 | MAV_1136 | O-antigen polymerase | 99.19 | 496 | BCG_2961 | acyltransferase | 28.92 | 422 | MAP0953 | hypothetical protein | 496 | 100 |
| MAP4_2908 | hypothetical protein | 487 | Rv3918c | Probable chromosome partitioning | 25.5 | 347 | Mb3949c | chromosome partitioning pro | 25.5 | 347 | MAV_1135 | chain length determinant protein | 99.59 | 487 | BCG_0024c | chromosome partitioning prot | 25.5 | 347 | MAP0952 | hypothetical protein | 487 | 100 |
| MAP4_2909 | hypothetical protein | 541 | Rv1006 | hypothetical protein | 69.51 | 567 | Mb1033 | hypothetical protein | 69.33 | 567 | MAV_1134 | hypothetical protein | 99.26 | 586 | BCG_1063 | hypothetical protein | 69.33 | 567 | MAP0951 | hypothetical protein | 541 | 100 |
| MAP4_2910 | putative methyltransferase, FkbM family protein | 264 | Rv2955c | hypothetical protein | 33.95 | 321 | Mb2979c | hypothetical protein | 33.95 | 321 | MAV_1133 | methyltransferase FkbM | 99.24 | 264 | BCG_2976c | hypothetical protein | 33.95 | 321 | MAP0950c | hypothetical protein | 264 | 100 |
| MAP4_2911 | cyclic diguanylate phosphodiesterase domain-containi | 617 | Rv1354c | hypothetical protein | 57.71 | 623 | Mb1389c | hypothetical protein | 57.71 | 623 | MAV_1132 | cyclic diguanylate phosphodiestera | 99.51 | 617 | BCG_1416c | hypothetical protein | 57.71 | 623 | MAP0949 | hypothetical protein | 617 | 100 |
| MAP4_2912 | hypothetical protein | 569 | Rv1006 | hypothetical protein | 68.38 | 567 | Mb1033 | hypothetical protein | 68.38 | 567 | MAV_1131 | hypothetical protein | 99.11 | 562 | BCG_1063 | hypothetical protein | 68.21 | 567 | MAP0948 | hypothetical protein | 569 | 100 |
| MAP4_2913 | putative dehydrogenase | 390 | Rv1812c | Probable dehydrogenase | 30.77 | 400 | Mb1842c | dehydrogenase | 30.77 | 400 | MAV_1130 | dehydrogenase | 99.49 | 390 | BCG_1846c | dehydrogenase | 30.77 | 400 | MAP0947c | hypothetical protein | 415 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_2914 | putative sigma factor | 307 | Rv3328c | Probable alternative RNA polymeras | 39.39 | 312 | Mb3361c | RNA polymerase sigma factor | 39.39 | 312 | MAV_1129 | sigma factor | 99.02 | 308 | BCG_3398c | RNA polymerase sigma factor S | 39.39 | 312 | MAP0946c | hypothetical protein | 307 | 100 |
| MAP4_2915 | para-aminobenzoate synthase component I | 430 | Rv1005c | Probable para-aminobenzoate synth | 78.4 | 458 | Mb1032c | aminodeoxychorismate synth | 78.4 | 478 | MAV_1127 | aminodeoxychorismate synthase co | 98.8 | 416 | BCG_1062c | aminodeoxychorismate syntha | 78.4 | 478 | MAP0945c | aminodeoxychorismate synthase comp | 430 | 100 |
| MAP4_2916 | putative methylase, tetrapyrrole methylase domain-co | 278 | Rv1003 | hypothetical protein | 78.06 | 285 | Mb1030 | hypothetical protein | 78.06 | 285 | MAV_1128 | hypothetical protein | 100 | 278 | BCG_1060 | hypothetical protein | 78.06 | 285 | MAP0944 | hypothetical protein | 278 | 100 |
| MAP4_2917 | hypothetical protein | 528 | Rv1002c | hypothetical protein | 85.07 | 503 | Mb1029c | hypothetical protein | 84.87 | 503 | MAV_1126 | dolichyl-phosphate-mannose-prote | 99.42 | 519 | BCG_1059c | hypothetical protein | 84.87 | 503 | MAP0943c | hypothetical protein | 508 | 99.8 |
| MAP4_2918 | Arginine deiminase | 400 | Rv1001 | Probable arginine deiminase ArcA (a | 89.5 | 402 | Mb1028 | arginine deiminase | 89.5 | 402 | MAV_1125 | arginine deiminase | 99.5 | 402 | BCG_1058 | arginine deiminase | 89.5 | 402 | MAP0942 | arginine deiminase | 400 | 100 |
| MAP4_2919 | Alkylated DNA repair protein | 198 | Rv1000c | hypothetical protein | 83.84 | 205 | Mb1027c | hypothetical protein | 83.84 | 205 | MAV_1124 | alkylated DNA repair protein | 99.49 | 198 | BCG_1057c | hypothetical protein | 83.84 | 205 | MAP1371 | hypothetical protein | 1095 | 45.71 |
| MAP4_2920 | hypothetical protein | 223 | Rv0999 | hypothetical protein | 68.75 | 252 | Mb1026 | hypothetical protein | 68.75 | 252 | MAV_1123 | hypothetical protein | 99.54 | 217 | BCG_1056 | hypothetical protein | 68.75 | 252 | MAP0940 | hypothetical protein | 223 | 100 |
| MAP4_2921 | hypothetical protein | 259 | Rv0999 | hypothetical protein | 29.08 | 252 | Mb1026 | hypothetical protein | 29.08 | 252 | MAV_1122 | hypothetical protein | 97.73 | 220 | BCG_1056 | hypothetical protein | 29.08 | 252 | MAP0939 | hypothetical protein | 259 | 100 |
| MAP4_2922 | cyclic nucleotide-binding protein | 330 | Rv0998 | hypothetical protein | 76.67 | 333 | Mb1025 | hypothetical protein | 76.67 | 333 | MAV_1121 | cyclic nucleotide-binding protein | 100 | 330 | BCG_1055 | hypothetical protein | 76.67 | 333 | MAP0938 | hypothetical protein | 330 | 100 |
| MAP4_2923 | putative phosphatase | 188 | Rv0114 | Possible D-alpha,beta-D-heptose-1,7 | 37.88 | 190 | Mb0118 | dehydratase | 37.88 | 190 | MAV_1120 | hypothetical protein | 98.4 | 188 | BCG_0147 | dehydratase | 37.88 | 190 | MAP0937 | hypothetical protein | 188 | 100 |
| MAP4_2924 | Phosphoheptose isomerase 1 | 202 | Rv0113 | Probable sedoheptulose-7-phosphat | 48.94 | 196 | Mb0117 | phosphoheptose isomerase | 48.94 | 196 | MAV_1119 | phosphoheptose isomerase | 99.5 | 205 | BCG_0146 | phosphoheptose isomerase | 48.94 | 196 | MAP0936 | hypothetical protein | 202 | 100 |
| MAP4_2925 | D-alpha-D-heptose-7-phosphate kinase | 338 | Rv0115 | Possible D-alpha-D-heptose-7-phosp | 39.53 | 386 | Mb0119 | sugar kinase | 40.74 | 305 | MAV_1118 | D-glycero-D-manno-heptose 7-pho | 100 | 338 | BCG_0149 | sugar kinase | 39.53 | 355 | MAP0935 | hypothetical protein | 338 | 100 |
| MAP4_2926 | M42 glutamyl aminopeptidase superfamily protein | 377 | Rv2141c | hypothetical protein | 32.14 | 448 | Mb2165c | hypothetical protein | 32.14 | 448 | MAV_1117 | M42 glutamyl aminopeptidase | 98.67 | 377 | BCG_2158c | hypothetical protein | 32.14 | 448 | MAP0934 | hypothetical protein | 377 | 100 |
| MAP4_2927 | putative dioxygenase, Rieske (2Fe-2S)iron-sulfur domai | 389 | Rv3161c | Possible dioxygenase | 27.63 | 382 | Mb3186c | dioxygenase | 28.02 | 382 | MAV_1116 | Rieske (2Fe-2S) domain-containing | 98.97 | 389 | BCG_3185c | dioxygenase | 28.02 | 382 | MAP0933 | hypothetical protein | 409 | 99.74 |
| MAP4_2928 | Transcriptional regulator, TetR family | 207 | Rv1255c | Probable transcriptional regulatory | 26.32 | 202 | Mb3076c | AsnC family transcriptional re | 27.34 | 246 | MAV_1115 | TetR family transcriptional regulato | 98.51 | 201 | BCG_3074c | AsnC family transcriptional reg | 27.34 | 246 | MAP0932c | hypothetical protein | 207 | 100 |
| MAP4_2929 | hypothetical protein | 164 | Rv2048c | Polyketide synthase Pks12 | 36.59 | 4151 | Mb2074c | polyketide synthase | 36.59 | 4151 | MAV_1114 | hypothetical protein | 98.78 | 164 | BCG_2067c | polyketide synthase | 36.59 | 4151 | MAP0931 | hypothetical protein | 164 | 100 |
| MAP4_2930 | Transcriptional regulator, TetR family | 217 | Rv0302 | Probable transcriptional regulatory | 28.81 | 210 | Mb0310 | TetR/ACRR family transcriptio | 28.81 | 210 | MAV_1113 | TetR family transcriptional regulato | 99.08 | 217 | BCG_0342 | TetR family transcriptional regu | 28.81 | 210 | MAP0930 | hypothetical protein | 208 | 99.52 |
| MAP4_2931 | hypothetical protein | 56 | Rv2529 | Hypothetical protein | 43.33 | 463 | Mb2558 | hypothetical protein | 43.33 | 463 | MAV_1112 | hypothetical protein | 97.87 | 47 | BCG_2550 | hypothetical protein | 43.33 | 463 | MAP0929 | hypothetical protein | 56 | 100 |
| MAP4_2932 | hypothetical protein | 50 | Rv2448c | Probable valyl-tRNA synthase protei | 32.69 | 876 | Mb2475c | valyl-tRNA synthetase | 32.69 | 876 | MAV_1111 | hypothetical protein | 97.37 | 38 | BCG_2468c | valyl-tRNA synthetase | 32.69 | 876 | MAP0928 | hypothetical protein | 50 | 100 |
| MAP4_2933 | hypothetical protein | 362 | Rv0996 | Probable conserved transmembrane | 65.04 | 358 | Mb1023 | transmembrane protein | 63.2 | 358 | MAV_1105 | hypothetical protein | 98.21 | 335 | BCG_1051 | hypothetical protein | 64.5 | 358 | MAP0927 | hypothetical protein | 373 | 100 |
| MAP4_2934 | ribosomal-protein-alanine acetyltransferase rimJ | 217 | Rv0995 | Ribosomal-protein-alanine acetyltra | 88.61 | 203 | Mb1022 | ribosomal-protein-alanine ac | 88.61 | 203 | MAV_1104 | acetyltransferase, GNAT family pro | 99.54 | 217 | BCG_1050 | ribosomal-protein-alanine acet | 88.61 | 203 | MAP0926 | RimJ | 217 | 100 |
| MAP4_2935 | molybdopterin biosynthesis protein MoeA1 | 428 | Rv0994 | Probable molybdopterin biosynthesi | 87.85 | 426 | Mb1021 | molybdopterin biosynthesis p | 88.08 | 426 | MAV_1103 | molybdopterin biosynthesis protei | 100 | 428 | BCG_1049 | molybdopterin biosynthesis pr | 88.08 | 426 | MAP0925 | hypothetical protein | 425 | 99.76 |
| MAP4_2936 | UTP-glucose-1-phosphate uridylyltransferase | 302 | Rv0993 | UTP--glucose-1-phosphate uridylyltr | 88.24 | 306 | Mb1020 | UTP-glucose-1-phosphate uri | 88.56 | 306 | MAV_1102 | GalU protein | 99.66 | 297 | BCG_1048 | UTP--glucose-1-phosphate urid | 88.56 | 306 | MAP0924 | hypothetical protein | 302 | 100 |
| MAP4_2937 | 5-formyltetrahydrofolate cyclo-ligase | 196 | Rv0992c | hypothetical protein | 77.72 | 197 | Mb1019c | hypothetical protein | 77.72 | 197 | MAV_1101 | 5,10-methenyltetrahydrofolate syn | 98.98 | 196 | BCG_1047c | hypothetical protein | 77.2 | 197 | MAP0923c | hypothetical protein | 232 | 100 |
| MAP4_2938 | conserved serine rich protein | 108 | Rv0991c | Conserved serine rich protein | 79.71 | 110 | Mb1018c | serine-rich protein | 79.71 | 110 | MAV_1100 | regulatory protein, FmdB family pr | 99.07 | 108 | BCG_1046c | hypothetical protein | 79.71 | 110 | MAP0922c | hypothetical protein | 108 | 100 |
| MAP4_2939 | hypothetical protein | 226 | Rv0990c | Hypothetical protein | 70.35 | 218 | Mb1017c | hypothetical protein | 70.8 | 218 | MAV_1099 | hypothetical protein | 99.12 | 226 | BCG_1045c | hypothetical protein | 70.8 | 218 | MAP0921c | hypothetical protein | 226 | 100 |
| MAP4_2940 | large-conductance ion mechanosensitive channel mscL | 151 | Rv0985c | Possible large-conductance ion mec | 78.15 | 151 | Mb1011c | large-conductance mechanos | 78.15 | 151 | MAV_1098 | large-conductance mechanosensiti | 100 | 151 | BCG_1040c | large-conductance mechanose | 77.48 | 151 | MAP0920c | large-conductance mechanosensitive ch | 151 | 100 |
| MAP4_2941 | pterin-4-alpha-carbinolamine dehydratase MoaB2 | 185 | Rv0984 | Possible pterin-4-alpha-carbinolami | 94.38 | 181 | Mb1010 | pterin-4-alpha-carbinolamine | 94.38 | 181 | MAV_1097 | molybdenum cofactor synthesis pr | 99.39 | 165 | BCG_1039 | pterin-4-alpha-carbinolamine d | 94.38 | 181 | MAP0919 | MoaB2 | 185 | 100 |
| MAP4_2942 | putative serine protease PepD | 488 | Rv0983 | Probable serine protease PepD (seri | 76.4 | 464 | Mb1009 | serine protease | 76.63 | 464 | MAV_1096 | protease | 99.8 | 488 | BCG_1038 | serine protease | 76.63 | 464 | MAP0918 | hypothetical protein | 488 | 100 |
| MAP4_2943 | two component system sensor kinase mprB | 522 | Rv0982 | Two component sensor kinase MprB | 84.31 | 504 | Mb1008 | two component sensor kinase | 84.51 | 504 | MAV_1095 | sensor histidine kinase | 99.19 | 495 | BCG_1037 | two component sensor kinase | 84.51 | 504 | MAP0917 | hypothetical protein | 511 | 99.8 |
| MAP4_2944 | two component response transcriptional regulatory pr | 228 | Rv0981 | Mycobacterial persistence regulator | 97.81 | 228 | Mb1007 | two component response tra | 97.81 | 230 | MAV_1094 | two component response transcrip | 100 | 228 | BCG_1036 | two component response trans | 97.81 | 230 | MAP0916 | hypothetical protein | 228 | 100 |
| MAP4_2945 | 50S ribosomal protein L32 | 57 | Rv0979A | 50S ribosomal protein L32 RpmF | 85.96 | 57 | Mb1005 | 50S ribosomal protein L32 | 85.96 | 57 | MAV_1093 | 50S ribosomal protein L32 | 98.25 | 57 | BCG_1034 | 50S ribosomal protein L32 | 85.96 | 57 | MAP0915 | 50S ribosomal protein L32 | 57 | 100 |
| MAP4_2946 | hypothetical protein | 573 | Rv0976c | hypothetical protein | 85.18 | 560 | Mb1001c | hypothetical protein | 85.18 | 560 | MAV_1092 | hypothetical protein | 98.95 | 573 | BCG_1030c | hypothetical protein | 85.18 | 560 | MAP0914c | hypothetical protein | 573 | 100 |
| MAP4_2947 | acyl-CoA dehydrogenase | 382 | Rv0975c | Probable acyl-CoA dehydrogenase F | 90.58 | 382 | Mb1000c | acyl-CoA dehydrogenase | 90.83 | 369 | MAV_1091 | acyl-CoA dehydrogenase | 99.74 | 382 | BCG_1029c | acyl-coa dehydrogenase fadE1 | 90.58 | 382 | MAP0913c | FadE13 | 382 | 100 |
| MAP4_2948 | acetyl-propionyl-CoA carboxylase beta subunit accD2 | 531 | Rv0974c | Probable acetyl-/propionyl-CoA carb | 90.93 | 529 | Mb0999c | acetyl-/propionyl-CoA carbox | 91.12 | 529 | MAV_1090 | acetyl-CoA carboxylase carboxyltra | 98.49 | 531 | BCG_1028c | acetyl-/propionyl-coa carboxyl | 91.12 | 529 | MAP0912c | AccD2 | 531 | 99.81 |
| MAP4_2949 | acetyl-propionyl-CoA carboxylase alpha subunit accA2 | 663 | Rv0973c | Probable acetyl-/propionyl-coenzym | 82.21 | 667 | Mb0998c | acetyl-/propionyl-coenzyme A | 82.06 | 667 | MAV_1089 | carbamoyl-phosphate synthase L su | 99.1 | 663 | BCG_1027c | acetyl-/propionyl-coenzyme A | 82.06 | 667 | MAP0911c | hypothetical protein | 663 | 100 |
| MAP4_2950 | acyl-CoA dehydrogenase fadE12 | 388 | Rv0972c | Acyl-CoA dehydrogenase FadE12 | 89.69 | 388 | Mb0997c | acyl-CoA dehydrogenase | 89.43 | 388 | MAV_1088 | acyl-CoA dehydrogenase fadE12 | 99.48 | 388 | BCG_1026c | acyl-CoA dehydrogenase fadE1 | 89.43 | 388 | MAP0910c | FadE12_2 | 388 | 100 |
| MAP4_2951 | enoyl-CoA hydratase | 263 | Rv0971c | Probable enoyl-CoA hydratase EchA | 83.27 | 269 | Mb0996c | enoyl-CoA hydratase | 83.27 | 269 | MAV_1087 | enoyl-CoA hydratase | 98.48 | 263 | BCG_1025c | enoyl-CoA hydratase | 83.27 | 269 | MAP0909c | enoyl-CoA hydratase | 263 | 100 |
| MAP4_2952 | hypothetical protein | 212 | Rv0966c | hypothetical protein | 81.91 | 200 | Mb0991c | hypothetical protein | 81.91 | 200 | MAV_1086 | hypothetical protein | 99.5 | 201 | BCG_1020c | hypothetical protein | 81.91 | 200 | MAP0908c | hypothetical protein | 212 | 100 |
| MAP4_2953 | putative oxidoreductase, Aldoketo reductase family | 282 | Rv2971 | Probable oxidoreductase | 42.34 | 282 | Mb2996 | oxidoreductase | 42.7 | 282 | MAV_1085 | morphine 6-dehydrogenase | 97.87 | 282 | BCG_2993 | oxidoreductase | 42.7 | 282 | MAP0907 | hypothetical protein | 282 | 100 |
| MAP4_2954 | hypothetical protein | 661 | Rv0959 | hypothetical protein | 89.53 | 672 | Mb0984 | hypothetical protein | 89.53 | 672 | MAV_1084 | von Willebrand factor type A | 99.37 | 638 | BCG_1013 | hypothetical protein | 89.53 | 672 | MAP0906 | hypothetical protein | 661 | 100 |
| MAP4_2955 | magnesium chelatase | 463 | Rv0958 | Possible magnesium chelatase | 92.41 | 459 | Mb0983 | magnesium chelatase | 92.62 | 459 | MAV_0412 | ATPase | 25.19 | 327 | BCG_1012 | magnesium chelatase | 92.62 | 459 | MAP0905 | hypothetical protein | 463 | 100 |
| MAP4_2956 | hypothetical protein | 246 | Rv2721c | Possible conserved transmembrane | 38.05 | 699 | Mb2740c | hypothetical protein | 38.05 | 699 | MAV_1082 | hypothetical protein | 96.35 | 192 | BCG_2734c | transmembrane alanine and gl | 38.05 | 699 | MAP0904 | hypothetical protein | 246 | 100 |
| MAP4_2957 | bifunctional purine biosynthesis protein purH | 533 | Rv0957 | Probable bifunctional purine biosyn | 86.34 | 523 | Mb0982 | bifunctional phosphoribosyla | 86.34 | 523 | MAV_1081 | bifunctional phosphoribosylaminoi | 99.44 | 533 | BCG_1011 | bifunctional phosphoribosylam | 86.34 | 523 | MAP0903 | bifunctional phosphoribosylaminoimida | 533 | 99.81 |
| MAP4_2958 | 5-phosphoribosylglycinamide formyl transferase purN | 209 | Rv0956 | Probable 5'-phosphoribosylglycinam | 82.3 | 215 | Mb0981 | phosphoribosylglycinamide fo | 82.3 | 215 | MAV_1080 | phosphoribosylglycinamide formylt | 100 | 209 | BCG_1010 | phosphoribosylglycinamide for | 82.3 | 215 | MAP0902 | phosphoribosylglycinamide formyltrans | 209 | 100 |
| MAP4_2959 | putative conserved membrane protein | 466 | Rv0955 | Probable conserved integral membr | 80.31 | 455 | Mb0980 | hypothetical protein | 80.31 | 455 | MAV_1079 | hypothetical protein | 98.06 | 463 | BCG_1009 | integral membrane protein | 80.31 | 455 | MAP0901 | hypothetical protein | 466 | 100 |
| MAP4_2960 | putative conserved membrane protein | 298 | Rv0954 | Probable conserved transmembrane | 56.57 | 303 | Mb0979 | transmembrane protein | 56.57 | 303 | MAV_1078 | 34 kDa antigenic protein | 99.42 | 302 | BCG_1008 | hypothetical protein | 56.57 | 303 | MAP0900 | hypothetical protein | 298 | 100 |
| MAP4_2961 | oxidoreductase | 282 | Rv0953c | Possible oxidoreductase | 88.3 | 282 | Mb0978c | oxidoreductase | 88.3 | 282 | MAV_1077 | hypothetical protein | 98.92 | 277 | BCG_1007c | oxidoreductase | 87.94 | 282 | MAP0899c | hypothetical protein | 282 | 100 |
| MAP4_2962 | Acetyl-CoA acetyltransferase | 507 | Rv1867 | hypothetical protein | 35.56 | 494 | Mb1898 | acetyl-CoA acetyltransferase | 35.56 | 494 | MAV_1076 | acetyl-CoA acetyltransferase | 98.03 | 508 | BCG_1903 | acetyl-CoA acetyltransferase | 35.56 | 494 | MAP0898 | acetyl-CoA acetyltransferase | 507 | 100 |
| MAP4_2963 | succinyl-CoA synthetase alpha chain sucD | 300 | Rv0952 | Probable succinyl-CoA synthetase (a | 84.67 | 303 | Mb0977 | succinyl-CoA synthetase subu | 85 | 303 | MAV_1075 | succinyl-CoA synthetase subunit al | 99.67 | 300 | BCG_1006 | succinyl-CoA synthetase subun | 85 | 303 | MAP0897 | succinyl-CoA synthetase subunit alpha | 300 | 100 |
| MAP4_2964 | succinyl-CoA synthetase beta chain sucC | 387 | Rv0951 | Probable succinyl-CoA synthetase (b | 89.12 | 387 | Mb0976 | succinyl-CoA synthetase subu | 89.38 | 387 | MAV_1074 | succinyl-CoA synthetase subunit be | 99.48 | 387 | BCG_1005 | succinyl-CoA synthetase subun | 89.38 | 387 | MAP0896 | succinyl-CoA synthetase subunit beta | 406 | 100 |
| MAP4_2965 | putative peptidase, peptidase M23 family protein | 375 | Rv0950c | hypothetical protein | 69.21 | 332 | Mb0975c | hypothetical protein | 69.21 | 332 | MAV_1073 | M23 peptidase domain-containing | 99.14 | 350 | BCG_1004c | hypothetical protein | 69.21 | 332 | MAP0895c | hypothetical protein | 375 | 100 |
| MAP4_2966 | hypothetical protein | 196 | Rv2306A | Possible conserved membrane prote | 36.54 | 197 | Mb2328 | hypothetical protein | 36.54 | 197 | MAV_1072 | hypothetical protein | 99.49 | 196 | BCG_2322 | hypothetical protein | 36.54 | 197 | MAP0894c | hypothetical protein | 207 | 99.49 |
| MAP4_2967 | ATP-dependent DNA helicase UvrD PcrA | 774 | Rv0949 | Probable ATP-dependent DNA helica | 88.79 | 771 | Mb0974 | ATP dependent DNA helicase | 88.79 | 771 | MAV_1071 | ATP-dependent DNA helicase PcrA | 99.87 | 774 | BCG_1003 | ATP dependent DNA helicase u | 88.79 | 771 | MAP0893 | hypothetical protein | 774 | 100 |
| MAP4_2968 | chorismate mutase | 106 | Rv0948c | Chorismate mutase | 72.34 | 105 | Mb0973c | hypothetical protein | 72.34 | 105 | MAV_1069 | hypothetical protein | 100 | 90 | BCG_1002c | hypothetical protein | 72.34 | 105 | MAP0892c | hypothetical protein | 106 | 100 |
| MAP4_2969 | Glucose-6-phosphate isomerase | 554 | Rv0946c | Probable glucose-6-phosphate isom | 90.94 | 553 | Mb0971c | glucose-6-phosphate isomera | 90.94 | 553 | MAV_1068 | glucose-6-phosphate isomerase | 99.82 | 554 | BCG_1000c | glucose-6-phosphate isomeras | 90.94 | 553 | MAP0891c | glucose-6-phosphate isomerase | 554 | 100 |
| MAP4_2970 | short-chain type dehydrogenasereductase | 253 | Rv0945 | Probable short-chain type dehydrog | 86.56 | 253 | Mb0970 | short chain dehydrogenase | 86.96 | 253 | MAV_1067 | short chain dehydrogenase | 99.21 | 253 | BCG_0999 | short chain dehydrogenase | 86.96 | 253 | MAP0890 | short chain dehydrogenase | 253 | 100 |
| MAP4_2971 | Formamidopyrimidine-DNA glycosylase | 287 | Rv0944 | Possible formamidopyrimidine-DNA | 87.26 | 158 | Mb0969 | formamidopyrimidine-DNA gl | 87.26 | 158 | MAV_1066 | formamidopyrimidine-DNA glycosy | 99.65 | 287 | BCG_0998 | formamidopyrimidine-DNA gly | 87.26 | 158 | MAP0889 | hypothetical protein | 287 | 100 |
| MAP4_2972 | precorrin-6A synthase | 247 | Rv2066 | Probable bifunctional protein, CobI- | 26.8 | 508 | Mb2092 | bifunctional S-adenosyl-L-me | 26.8 | 508 | MAV_1065 | precorrin 6A synthase | 99.19 | 247 | BCG_2085 | bifunctional protein, CobI-CobJ | 26.8 | 508 | MAP0888 | precorrin 6A synthase | 271 | 99.6 |
| MAP4_2973 | P-aminobenzoate N-oxygenase AurF family protein | 307 | Rv0885 | hypothetical protein | 30.24 | 340 | Mb0909 | hypothetical protein | 30.24 | 340 | MAV_1064 | hypothetical protein | 100 | 316 | BCG_0937 | hypothetical protein | 30.07 | 340 | MAP0887c | hypothetical protein | 307 | 100 |
| MAP4_2975 | hypothetical protein | 254 | Rv0941c | hypothetical protein | 62.99 | 257 | Mb0966c | hypothetical protein | 62.99 | 257 | MAV_1062 | stas domain-containing protein | 99.14 | 232 | BCG_0995c | hypothetical protein | 62.99 | 257 | MAP0885c | hypothetical protein | 254 | 100 |
| MAP4_2976 | oxidoreductase | 288 | Rv0940c | Possible oxidoreductase | 85.42 | 288 | Mb0965c | oxidoreductase | 85.42 | 288 | MAV_1061 | hypothetical protein | 99.65 | 288 | BCG_0994c | oxidoreductase | 85.42 | 288 | MAP0884c | hypothetical protein | 288 | 100 |
| MAP4_2977 | enoyl-CoA hydratase | 268 | Rv1472 | Possible enoyl-CoA hydratase EchA1 | 40.94 | 285 | Mb1507 | enoyl-CoA hydratase | 40.94 | 285 | MAV_1060 | enoyl-CoA hydratase/isomerase | 98.49 | 265 | BCG_1533 | enoyl-CoA hydratase | 40.94 | 285 | MAP0883 | EchA12_1 | 287 | 100 |
| MAP4_2978 | putative methyltransferase, leucine carboxylmethyl tra | 304 | Rv3399 | Possible S-adenosylmethionine-depe | 50.82 | 348 | Mb3432 | hypothetical protein | 53.5 | 348 | MAV_1058 | methyltransferase, putative, family | 99.34 | 304 | BCG_3469 | hypothetical protein | 53.5 | 348 | MAP0882c | hypothetical protein | 304 | 100 |
| MAP4_2979 | bifunctional2-hydroxyhepta-2,4-diene-1,7-dioate isome | 645 | Rv0939 | Possible bifunctional enzyme: 2-hyd | 82.12 | 644 | Mb0964 | bifunctional 2-hydroxyhepta- | 82.12 | 644 | MAV_1057 | fumarylacetoacetate hydrolase, pu | 99.22 | 645 | BCG_0993 | bifunctional enzyme: 2-hydrox | 82.12 | 644 | MAP0881 | hypothetical protein | 645 | 100 |
| MAP4_2980 | ATP-dependent DNA ligase LigD | 764 | Rv0938 | ATP dependent DNA ligase LigD (ATP | 79.37 | 759 | Mb0963 | ATP-dependent DNA ligase | 79.5 | 759 | MAV_1056 | ATP-dependent DNA ligase | 99.09 | 766 | BCG_0992 | ATP-dependent DNA ligase | 79.5 | 759 | MAP0880 | ATP-dependent DNA ligase | 764 | 100 |
| MAP4_2981 | putative mannitol dehydrogenase | 512 | Rv1640c | Lysyl-tRNA synthetase 2 LysX | 35.62 | 1172 | Mb1667c | lysyl-tRNA synthetase | 35.62 | 1172 | MAV_1054 | D-mannonate oxidoreductase | 99.36 | 466 | BCG_1679c | lysyl-tRNA synthetase | 35.62 | 1172 | MAP0879c | hypothetical protein | 512 | 100 |
| MAP4_2982 | hypothetical protein | 286 | Rv3400 | Probable hydrolase | 31.46 | 262 | Mb3433 | hydrolase | 31.46 | 262 | MAV_1053 | hypothetical protein | 99.3 | 286 | BCG_3470 | hydrolase | 31.46 | 262 | MAP0878c | hypothetical protein | 286 | 100 |
| MAP4_2983 | putative mannitol dehydrogenase | 470 | Rv0920c | Probable transposase | 38.24 | 439 | Mb0944c | transposase | 38.24 | 439 | MAV_1052 | mannitol 2-dehydrogenase | 100 | 470 | BCG_0972c | transposase | 38.24 | 439 | MAP0877c | hypothetical protein | 470 | 100 |
| MAP4_2984 | fructokinase, pfkB carbohydrate kinase family protein | 302 | Rv2436 | Ribokinase RbsK | 42.62 | 304 | Mb2462 | ribokinase RBSK | 42.62 | 304 | MAV_1051 | kinase, PfkB family protein | 99.34 | 302 | BCG_2455 | ribokinase rbsK | 42.62 | 304 | MAP0876c | hypothetical protein | 302 | 100 |
| MAP4_2985 | DNA end-binding protein (Ku domain-containing) | 302 | Rv0937c | DNA end-binding protein, Mku | 87.45 | 273 | Mb0962c | hypothetical protein | 87.45 | 273 | MAV_1050 | Ku protein | 99.67 | 302 | BCG_0991c | hypothetical protein | 87.45 | 273 | MAP0875c | hypothetical protein | 302 | 100 |
| MAP4_2986 | phosphate-transport membrane ABC transporter pstA1 | 302 | Rv0930 | Probable phosphate-transport integ | 82.61 | 308 | Mb0953 | phosphate ABC transporter tr | 82.06 | 304 | MAV_1049 | phosphate ABC transporter permea | 99.67 | 302 | BCG_0982 | phosphate-transport integral m | 82.06 | 304 | MAP0874 | PstA1_2 | 302 | 100 |
| MAP4_2987 | phosphate-transport membrane ABC transporter pstC2 | 326 | Rv0929 | Phosphate-transport integral memb | 83.23 | 324 | Mb0952 | phosphate ABC transporter tr | 83.23 | 324 | MAV_1048 | phosphate ABC transporter permea | 98.77 | 328 | BCG_0981 | phosphate-transport integral m | 83.23 | 324 | MAP0873 | PstC2_2 | 326 | 100 |
| MAP4_2988 | periplasmic phosphate-binding lipoprotein pstS3 | 369 | Rv0928 | Periplasmic phosphate-binding lipop | 79.13 | 370 | Mb0951 | periplasmic phosphate-bindin | 79.13 | 370 | MAV_1047 | phosphate ABC transporter phosph | 100 | 369 | BCG_0980 | periplasmic phosphate-binding | 79.13 | 370 | MAP0872 | PhoS2_2 | 369 | 100 |
| MAP4_2989 | short-chain type dehydrogenasereductase | 263 | Rv0927c | Probable short-chain type dehydrog | 87.45 | 263 | Mb0950c | short chain dehydrogenase | 87.45 | 263 | MAV_1046 | short chain dehydrogenase | 98.86 | 263 | BCG_0979c | short chain dehydrogenase | 87.45 | 263 | MAP0871c | short chain dehydrogenase | 263 | 100 |
| MAP4_2990 | hypothetical protein | 358 | Rv0926c | hypothetical protein | 85.35 | 358 | Mb0949c | hypothetical protein | 85.35 | 358 | MAV_1045 | dihydrodipicolinate reductase N-te | 99.44 | 358 | BCG_0978c | hypothetical protein | 85.35 | 358 | MAP0870c | hypothetical protein | 358 | 100 |
| MAP4_2991 | divalent cation-transport membrane protein mntH | 425 | Rv0924c | Divalent cation-transport integral m | 78.43 | 428 | Mb0948c | manganese transport protein | 78.43 | 684 | MAV_1044 | manganese transport protein MntH | 99.75 | 408 | BCG_0976c | manganese transport protein M | 78.19 | 428 | MAP0869c | manganese transport protein MntH | 425 | 100 |
| MAP4_2992 | hypothetical protein | 359 | Rv0923c | hypothetical protein | 77.12 | 354 | Mb0947c | hypothetical protein | 77.12 | 354 | MAV_1043 | hypothetical protein | 99.44 | 359 | BCG_0975c | hypothetical protein | 77.12 | 354 | MAP0868c | hypothetical protein | 359 | 100 |
| MAP4_2993 | putative oxidoreductase | 272 | Rv2893 | Possible oxidoreductase | 32.59 | 325 | Mb2917 | oxidoreductase | 32.59 | 325 | MAV_1042 | hypothetical protein | 100 | 272 | BCG_2914 | oxidoreductase | 32.59 | 325 | MAP0867c | hypothetical protein | 272 | 100 |
| MAP4_2994 | phage integrase | 452 | Rv2659c | Probable PhiRv2 prophage integrase | 26.75 | 375 | Mb2335c | hypothetical protein | 43.7 | 151 | MAV_2217 | integrase fusion protein | 32.1 | 382 | BCG_2329c | integrase | 43.7 | 151 | MAP0866 | hypothetical protein | 267 | 99.63 |
| MAP4_2995 | phage integrase | 423 | Rv2748c | Possible cell division transmembran | 20.69 | 883 | Mb2769c | DNA translocase FtsK | 20.69 | 883 | MAV_3795 | cell divisionftsk/SpoIIIE | 28 | 480 | BCG_2764c | cell division transmembrane pr | 20.69 | 883 | MAP0865 | hypothetical protein | 423 | 100 |
| MAP4_2996 | hypothetical protein | 141 | Rv1028c | Probable sensor protein KdpD | 34.09 | 860 | Mb1056c | sensor protein KDPD | 34.09 | 860 | MAV_1910 | acyl-CoA dehydrogenase | 46.67 | 340 | BCG_1085c | sensor protein kdpD | 34.09 | 860 | MAP0864 | hypothetical protein | 141 | 100 |
| MAP4_2997 | hypothetical protein | 224 | Rv2476c | Probable NAD-dependent glutamate | 31.15 | 1624 | Mb2503c | NAD-dependent glutamate de | 31.15 | 1623 | MAV_1232 | GTP-dependent nucleic acid-bindin | 32.69 | 350 | BCG_2496c | NAD-dependent glutamate deh | 31.15 | 1623 | MAP0863 | hypothetical protein | 224 | 100 |
| MAP4_2998 | hypothetical protein | 360 | Rv0101 | Probable peptide synthetase Nrp (pe | 27.88 | 2512 | Mb0104 | peptide synthetase | 27.88 | 2512 | MAV_2733 | glucose-6-phosphate 1-dehydroger | 36.17 | 505 | BCG_0134 | peptide synthetase nrp | 27.88 | 2512 | MAP0862 | hypothetical protein | 360 | 100 |
| MAP4_2999 | hypothetical protein | 113 | Rv3749c | hypothetical protein | 42.42 | 169 | Mb3775c | hypothetical protein | 42.42 | 169 | MAV_4799 | hypothetical protein | 35.85 | 340 | BCG_3808c | hypothetical protein | 42.42 | 169 | MAP0861 | hypothetical protein | 113 | 100 |
| MAP4_3000 | hypothetical protein | 296 | Rv2101 | Probable helicase HelZ | 30 | 1013 | Mb2127 | helicase HelZ | 30 | 1013 | MAV_3662 | dihydrodipicolinate reductase | 41.18 | 245 | BCG_2120 | helicase helZ | 30 | 1013 | MAP0860c | hypothetical protein | 296 | 100 |
| MAP4_3001 | hypothetical protein | 202 | Rv1163 | Probable respiratory nitrate reducta | 26.62 | 201 | Mb1195 | respiratory nitrate reductase | 26.62 | 201 | MAV_0317 | quaternary amine ABC transporter | 26.92 | 302 | BCG_1225 | respiratory nitrate reductase ( | 26.62 | 201 | MAP0859c | hypothetical protein | 202 | 100 |
| MAP4_3002 | hypothetical protein | 182 | Rv0800 | Probable aminopeptidase PepC | 32.61 | 433 | Mb0823 | aminopeptidase | 32.61 | 433 | MAV_4890 | hypothetical protein | 29.11 | 128 | BCG_0852 | aminopeptidase 2 | 32.61 | 433 | MAP0858 | hypothetical protein | 182 | 100 |
| MAP4_3003 | hypothetical protein | 105 | Rv3197 | Probable conserved ATP-binding pro | 41.46 | 447 | Mb3220 | ABC transporter ATP-binding | 41.46 | 447 | MAV_3717 | class I glutamine amidotransferase, | 32.58 | 236 | BCG_3220 | ABC transporter ATP-binding p | 41.46 | 447 | MAP0857c | hypothetical protein | 105 | 100 |
| MAP4_3004 | hypothetical protein | 575 | Rv2590 | Probable fatty-acid-CoA ligase FadD | 29.17 | 1168 | Mb2621 | fatty-acid--CoA ligase | 29.17 | 1168 | MAV_4434 | preprotein translocase subunit Sec | 26.32 | 453 | BCG_2613 | fatty-acid-CoA ligase fadD9 | 29.17 | 1168 | MAP0856c | hypothetical protein | 575 | 100 |
| MAP4_3005 | hypothetical protein | 314 | Rv3585 | DNA repair protein RadA (DNA repai | 25.88 | 480 | Mb3616 | DNA repair protein RadA | 25.88 | 480 | MAV_0568 | DNA repair protein RadA | 26.79 | 459 | BCG_3650 | DNA repair protein RadA | 25.88 | 480 | MAP0855 | hypothetical protein | 314 | 100 |
| MAP4_3006 | hypothetical protein | 525 | Rv1962c | Possible toxin VapC35 Contains PIN | 36.36 | 135 | Mb1997c | hypothetical protein | 36.36 | 135 | MAV_1968 | retinol dehydrogenase 12 | 32.73 | 273 | BCG_2001c | hypothetical protein | 36.36 | 135 | MAP0854 | hypothetical protein | 525 | 100 |
| MAP4_3007 | hypothetical protein | 219 | Rv1801 | PPE family protein PPE29 | 24.29 | 423 | Mb1829 | PPE family protein | 24.29 | 423 | MAV_0569 | LpqE protein | 26.79 | 188 | BCG_1833 | PPE family protein | 24.29 | 423 | MAP0853 | hypothetical protein | 219 | 100 |
| MAP4_3008 | hypothetical protein | 181 | Rv2333c | Integral membrane drug efflux prote | 32.69 | 537 | Mb2361c | integral membrane transport | 32.69 | 523 | MAV_2736 | hypothetical protein | 37.5 | 503 | BCG_2355c | integral membrane transport p | 32.69 | 523 | MAP0852 | hypothetical protein | 181 | 100 |
| MAP4_3009 | hypothetical protein | 281 | Rv1952 | Possible antitoxin VapB14 | 67.86 | 71 | Mb1987 | hypothetical protein | 67.86 | 71 | MAV_0091 | glyoxalase | 27.16 | 147 | BCG_1991 | hypothetical protein | 67.86 | 71 | MAP0851 | hypothetical protein | 281 | 100 |
| MAP4_3010 | transposase | 395 | Rv0755A | Putative transposase (fragment) | 90.57 | 61 | Mb0778c | transposase | 90.57 | 61 | MAV_0752 | transposase | 28.75 | 345 | BCG_0807c | transposase | 90.57 | 61 | MAP0428 | hypothetical protein | 395 | 100 |
| MAP4_3011 | transposase, IS1311 | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 100 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0104 | hypothetical protein | 411 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3012 | hypothetical protein | 128 | Rv2524c | Probable fatty acid synthase Fas (fat | 29.85 | 3069 | Mb2553c | fatty acid synthase | 29.85 | 3069 | MAV_1036 | hypothetical protein | 98.44 | 128 | BCG_2545c | fatty acid synthase fas | 29.85 | 3069 | MAP0848 | hypothetical protein | 128 | 100 |
| MAP4_3013 | hypothetical protein | 539 | Rv1754c | hypothetical protein | 61.48 | 563 | Mb1783c | hypothetical protein | 61.48 | 563 | MAV_1035 | hypothetical protein | 100 | 527 | BCG_1793c | hypothetical protein | 61.29 | 563 | MAP0847 | hypothetical protein | 539 | 100 |
| MAP4_3014 | putative conserved membrane protein | 144 | Rv0912 | Probable conserved transmembrane | 74.31 | 149 | Mb0936 | transmembrane protein | 74.31 | 149 | MAV_1034 | hypothetical protein | 99.22 | 129 | BCG_0964 | hypothetical protein | 74.31 | 149 | MAP0846 | hypothetical protein | 144 | 100 |
| MAP4_3015 | hypothetical protein | 153 | Rv0910 | hypothetical protein | 84.62 | 144 | Mb0934 | hypothetical protein | 84.62 | 144 | MAV_1033 | hypothetical protein | 100 | 153 | BCG_0962 | hypothetical protein | 84.62 | 144 | MAP0845 | hypothetical protein | 153 | 100 |
| MAP4_3016 | hypothetical protein | 62 | Rv0909 | hypothetical protein | 62.5 | 59 | Mb0933 | hypothetical protein | 64.29 | 59 | MAV_1032 | hypothetical protein | 100 | 62 | BCG_0961 | hypothetical protein | 64.29 | 59 | MAP0844 | hypothetical protein | 62 | 100 |
| MAP4_3017 | metal cation transporter ATPase P-type CtpE | 790 | Rv0908 | Probable metal cation transporter A | 81.85 | 797 | Mb0932 | metal cation transporter ATPa | 81.85 | 797 | MAV_1031 | cation-transporting ATPase Exp7 | 98.99 | 790 | BCG_0960 | metal cation transporter atpas | 81.85 | 797 | MAP0843 | CtpE | 790 | 100 |
| MAP4_3018 | beta-lactamasepenicillin-binding protein | 528 | Rv0907 | hypothetical protein | 72.57 | 532 | Mb0931 | hypothetical protein | 72.59 | 516 | MAV_1030 | penicillin-binding protein 4 | 99.05 | 528 | BCG_0959 | hypothetical protein | 72.21 | 526 | MAP0842 | hypothetical protein | 528 | 100 |
| MAP4_3019 | putative beta-lactamase superfamily protein | 369 | Rv0906 | hypothetical protein | 78.17 | 372 | Mb0930 | hypothetical protein | 78.17 | 372 | MAV_1029 | metallo-beta-lactamase | 99.46 | 369 | BCG_0958 | hypothetical protein | 78.17 | 372 | MAP0841 | hypothetical protein | 369 | 100 |
| MAP4_3020 | enoyl-CoA hydratase | 243 | Rv0905 | Possible enoyl-CoA hydratase EchA6 | 90.53 | 243 | Mb0929 | enoyl-CoA hydratase | 90.53 | 243 | MAV_1028 | enoyl-CoA hydratase | 99.59 | 243 | BCG_0957 | enoyl-CoA hydratase | 90.53 | 243 | MAP0840 | enoyl-CoA hydratase | 243 | 100 |
| MAP4_3021 | acetyl-CoA carboxylase carboxyl transferase subunit be | 490 | Rv0904c | Putative acetyl-coenzyme A carboxy | 83.98 | 495 | Mb0928c | acetyl-coenzyme A carboxylas | 83.98 | 495 | MAV_4250 | propionyl-CoA carboxylase beta ch | 24.07 | 546 | BCG_0956c | acetyl-coenzyme A carboxylase | 83.98 | 495 | MAP0839c | AccD3 | 490 | 100 |
| MAP4_3022 | hypothetical protein | 137 | Rv1751 | Probable oxidoreductase | 48.65 | 460 | Mb0590c | hypothetical protein | 35.56 | 378 | MAV_2736 | hypothetical protein | 50 | 503 | BCG_0620c | hypothetical protein | 35.56 | 378 | MAP0838c | hypothetical protein | 137 | 100 |
| MAP4_3023 | putative glycogen debranching enzyme | 706 | Rv3130c | Triacylglycerol synthase (diacylglyce | 28 | 463 | Mb3154c | hypothetical protein | 28 | 463 | MAV_1025 | hypothetical protein | 99.29 | 706 | BCG_3153c | hypothetical protein | 28 | 463 | MAP0837 | hypothetical protein | 706 | 100 |
| MAP4_3024 | putative glycosyltransferase | 396 | Rv1212c | Putative glycosyl transferase GlgA | 28.89 | 387 | Mb1244c | glycosyl transferase family pr | 28.64 | 387 | MAV_1024 | glycosyl transferase, group 1 family | 99.75 | 396 | BCG_1272c | glycosyl transferase family prot | 28.64 | 387 | MAP0836 | hypothetical protein | 396 | 100 |
| MAP4_3025 | putative transporter, major facilitator super family prot | 424 | Rv2456c | Probable conserved integral membr | 37.98 | 418 | Mb2483c | integral membrane transport | 37.98 | 418 | MAV_1023 | MFS transporter | 99.76 | 424 | BCG_2476c | integral membrane transport p | 37.98 | 418 | MAP0835c | hypothetical protein | 424 | 100 |
| MAP4_3026 | two component system transcriptional regulator prrA | 233 | Rv0903c | Two component response transcript | 97 | 236 | Mb0927c | two component response tra | 97 | 236 | MAV_1022 | PrrA family transcriptional regulato | 100 | 233 | BCG_0955c | two component response trans | 97 | 236 | MAP0834c | hypothetical protein | 233 | 100 |
| MAP4_3027 | two component system sensor histidine kinase prrB | 445 | Rv0902c | Two component sensor histidine kin | 82.51 | 446 | Mb0926c | two component sensor histid | 82.51 | 446 | MAV_1021 | sensor histidine kinase | 99.78 | 445 | BCG_0954c | two component sensor histidin | 82.51 | 446 | MAP0833c | hypothetical protein | 451 | 99.51 |
| MAP4_3028 | Transposase, IS1601_B | 407 | Rv2014 | Transposase | 31.65 | 196 | Mb2037 | transposase | 31.65 | 196 | MAV_0496 | transposase IS116/IS110/IS902 | 46.4 | 404 | BCG_2031 | transposase | 31.65 | 196 | MAP0832c | IS1601_B_1 transposase | 407 | 100 |
| MAP4_3029 | hypothetical protein | 87 | Rv0898c | hypothetical protein | 70.59 | 87 | Mb0922c | hypothetical protein | 70.59 | 87 | MAV_1020 | hypothetical protein | 100 | 87 | BCG_0950c | hypothetical protein | 70.59 | 87 | MAP0831c | hypothetical protein | 87 | 100 |
| MAP4_3030 | oxidoreductase | 516 | Rv0897c | Probable oxidoreductase | 73.5 | 535 | Mb0921c | oxidoreductase | 73.5 | 535 | MAV_1019 | phytoene dehydrogenase | 97.67 | 516 | BCG_0949c | oxidoreductase | 73.5 | 535 | MAP0830c | hypothetical protein | 516 | 100 |
| MAP4_3031 | citrate synthase I | 431 | Rv0896 | Probable citrate synthase I GltA2 | 90.95 | 431 | Mb0920 | type II citrate synthase | 90.72 | 431 | MAV_0344 | citrate synthase | 33.42 | 375 | BCG_0948 | type II citrate synthase | 90.72 | 431 | MAP0829 | type II citrate synthase | 431 | 100 |
| MAP4_3032 | Pyridoxamine 5'-phosphate oxidase | 220 | Rv2607 | Probable pyridoxamine 5'-phosphate | 69.16 | 224 | Mb2639 | pyridoxamine 5'-phosphate o | 69.16 | 224 | MAV_1017 | pyridoxamine 5'-phosphate oxidase | 99.03 | 207 | BCG_2632 | pyridoxamine 5'-phosphate oxi | 69.16 | 224 | MAP0828 | pyridoxamine 5'-phosphate oxidase | 220 | 100 |
| MAP4_3033 | citrate synthase II | 373 | Rv0889c | Probable citrate synthase II CitA | 92.76 | 373 | Mb0913c | citrate synthase 2 | 92.76 | 373 | MAV_1016 | citrate synthase 2 | 100 | 373 | BCG_0941c | citrate synthase 2 | 92.76 | 373 | MAP0827c | citrate synthase 2 | 373 | 100 |
| MAP4_3034 | hypothetical protein | 158 | Rv0887c | hypothetical protein | 81.08 | 152 | Mb0911c | hypothetical protein | 81.08 | 152 | MAV_1014 | glyoxalase | 100 | 158 | BCG_0939c | hypothetical protein | 81.08 | 152 | MAP0826c | hypothetical protein | 158 | 100 |
| MAP4_3035 | NADPH:adrenodoxin oxidoreductase FprB | 566 | Rv0886 | Probable NADPH:adrenodoxin oxido | 79.02 | 575 | Mb0910 | NADPH:adrenodoxin oxidored | 79.02 | 575 | MAV_1015 | ferredoxin/ferredoxin--NADP reduc | 99.27 | 546 | BCG_0938 | NADPH:adrenodoxin oxidoredu | 79.02 | 575 | MAP0825 | FprB | 566 | 100 |
| MAP4_3036 | P-aminobenzoate N-oxygenase AurF family protein | 328 | Rv0885 | hypothetical protein | 88.72 | 340 | Mb0909 | hypothetical protein | 88.72 | 340 | MAV_1013 | hypothetical protein | 99.7 | 336 | BCG_0937 | hypothetical protein | 88.41 | 340 | MAP0824 | hypothetical protein | 341 | 100 |
| MAP4_3037 | Phosphoserine aminotransferase | 374 | Rv0884c | Possible phosphoserine aminotransf | 85.11 | 376 | Mb0908c | phosphoserine aminotransfer | 85.11 | 376 | MAV_1012 | phosphoserine aminotransferase | 99.47 | 374 | BCG_0936c | phosphoserine aminotransfera | 85.11 | 376 | MAP0823c | phosphoserine aminotransferase | 374 | 100 |
| MAP4_3038 | hypothetical protein | 254 | Rv0883c | hypothetical protein | 73.36 | 253 | Mb0907c | hypothetical protein | 73.36 | 253 | MAV_1010 | hypothetical protein | 96.14 | 259 | BCG_0935c | hypothetical protein | 73.36 | 253 | MAP0822c | hypothetical protein | 254 | 100 |
| MAP4_3039 | transmembrane protein | 90 | Rv0882 | Probable transmembrane protein | 81.58 | 94 | Mb0906 | hypothetical protein | 81.58 | 94 | MAV_1011 | hypothetical protein | 100 | 99 | BCG_0934 | hypothetical protein | 81.58 | 94 | MAP0821 | hypothetical protein | 99 | 100 |
| MAP4_3040 | rRNA methyltransferase | 289 | Rv0881 | Possible rRNA methyltransferase (rR | 82.72 | 288 | Mb0905 | rRNA methyltransferase | 83.09 | 288 | MAV_1009 | SpoU rRNA methylase | 98.96 | 432 | BCG_0933 | rRNA methyltransferase | 83.09 | 288 | MAP0820 | hypothetical protein | 289 | 100 |
| MAP4_3041 | Transcriptional regulator, MarR family | 143 | Rv0880 | Possible transcriptional regulatory p | 86.01 | 143 | Mb0904 | MarR family transcriptional re | 86.01 | 143 | MAV_1009 | SpoU rRNA methylase | 99.15 | 432 | BCG_0932 | MarR family transcriptional reg | 86.01 | 143 | MAP0819 | hypothetical protein | 143 | 100 |
| MAP4_3042 | putative conserved membrane protein | 91 | Rv0879c | Possible conserved transmembrane | 66.29 | 91 | Mb0903c | transmembrane protein | 66.29 | 91 | MAV_1008 | hypothetical protein | 100 | 91 | BCG_0931c | hypothetical protein | 66.29 | 91 | MAP0818c | hypothetical protein | 91 | 100 |
| MAP4_3043 | hypothetical protein | 154 | Rv1883c | hypothetical protein | 30.41 | 153 | Mb1915c | hypothetical protein | 29.8 | 158 | MAV_1006 | hypothetical protein | 98.7 | 154 | BCG_1920c | hypothetical protein | 29.8 | 158 | MAP0817c | hypothetical protein | 154 | 100 |
| MAP4_3044 | hypothetical protein | 310 | Rv0877 | hypothetical protein | 82.76 | 262 | Mb0901 | hypothetical protein | 82.76 | 262 | MAV_1007 | hypothetical protein | 91.29 | 297 | BCG_0929 | hypothetical protein | 82.76 | 262 | MAP0816 | hypothetical protein | 310 | 100 |
| MAP4_3045 | hypothetical protein | 567 | Rv0876c | Possible conserved transmembrane | 83.36 | 548 | Mb0900c | transmembrane protein | 83.55 | 548 | MAV_1005 | hypothetical protein | 99.65 | 567 | BCG_0928c | hypothetical protein | 83.36 | 548 | MAP0815c | hypothetical protein | 567 | 100 |
| MAP4_3046 | hypothetical protein | 166 | Rv0875c | Possible conserved exported protei | 74.53 | 162 | Mb0899c | hypothetical protein | 74.53 | 162 | MAV_1004 | hypothetical protein | 98.8 | 166 | BCG_0927c | hypothetical protein | 74.53 | 162 | MAP0814c | hypothetical protein | 166 | 100 |
| MAP4_3047 | hypothetical protein | 315 | Rv3555c | hypothetical protein | 51.6 | 289 | Mb3585c | hypothetical protein | 51.96 | 289 | MAV_1002 | hypothetical protein | 98.25 | 293 | BCG_3619c | hypothetical protein | 51.96 | 289 | MAP0813c | hypothetical protein | 315 | 100 |
| MAP4_3048 | putative glutathione S-transferase | 334 | Rv0865 | Probable molybdopterin biosynthesi | 42.86 | 160 | Mb0889 | molybdopterin biosynthesis m | 42.86 | 160 | MAV_1003 | glutathione S-transferase | 99.4 | 334 | BCG_0917 | molybdopterin biosynthesis mo | 42.86 | 160 | MAP0812 | hypothetical protein | 334 | 100 |
| MAP4_3049 | acyl-CoA dehydrogenase | 642 | Rv0873 | Probable acyl-CoA dehydrogenase F | 85.67 | 650 | Mb0897 | acyl-CoA dehydrogenase | 85.67 | 650 | MAV_1001 | acyl-CoA dehydrogenase | 99.53 | 642 | BCG_0925 | acyl-CoA dehydrogenase fadE1 | 85.67 | 650 | MAP0811 | FadE10 | 642 | 100 |
| MAP4_3050 | cold shock protein B cspB | 138 | Rv0871 | Probable cold shock-like protein B C | 88.89 | 135 | Mb0895 | cold shock-like protein B Csp | 88.89 | 135 | MAV_1000 | cold shock DNA-binding domain-co | 99.26 | 135 | BCG_0923 | cold shock-like protein B cspB | 88.89 | 135 | MAP0810 | CspB | 138 | 100 |
| MAP4_3051 | hypothetical protein | 135 | Rv0870c | Possible conserved integral membra | 85.94 | 129 | Mb0894c | hypothetical protein | 85.16 | 129 | MAV_0999 | hypothetical protein | 99.26 | 135 | BCG_0922c | hypothetical protein | 85.94 | 129 | MAP0809c | hypothetical protein | 135 | 100 |
| MAP4_3053 | molybdenum cofactor biosynthesis protein MoaD | 93 | Rv0868c | Probable molybdenum cofactor bios | 65.59 | 92 | Mb0892c | molybdenum cofactor biosyn | 65.59 | 92 | MAV_0997 | ThiS family protein | 96.77 | 92 | BCG_0920c | molybdenum cofactor biosynth | 65.59 | 92 | MAP0806c | MoaD2 | 93 | 100 |
| MAP4_3054 | hypothetical protein | 250 | Rv0867c | Possible resuscitation-promoting fac | 74.71 | 407 | Mb1036 | resuscitation-promoting facto | 69.01 | 362 | MAV_0996 | resuscitation-promoting factor Rpf | 92.66 | 234 | BCG_0919c | resuscitation-promoting factor | 74.71 | 407 | MAP0805c | hypothetical protein | 250 | 100 |
| MAP4_3055 | molybdenum cofactor biosynthesis protein E2MoaE2 | 141 | Rv0866 | Probable molybdenum cofactor bios | 80 | 141 | Mb0890 | molybdenum cofactor biosyn | 80 | 141 | MAV_0995 | molybdopterin converting factor, s | 98.58 | 141 | BCG_0918 | molybdenum cofactor biosynth | 80 | 141 | MAP0804 | MoaE2 | 141 | 100 |
| MAP4_3056 | molybdenum cofactor biosynthesis protein Mog | 160 | Rv0865 | Probable molybdopterin biosynthesi | 76.25 | 160 | Mb0889 | molybdopterin biosynthesis m | 76.25 | 160 | MAV_0994 | molybdenum cofactor synthesis do | 99.38 | 160 | BCG_0917 | molybdopterin biosynthesis mo | 76.25 | 160 | MAP0803 | Mog | 160 | 100 |
| MAP4_3057 | molybdenum cofactor biosynthesis protein MoaC2 | 176 | Rv0864 | Probable molybdenum cofactor bios | 84.15 | 167 | Mb0888 | molybdenum cofactor biosyn | 85.82 | 142 | MAV_0993 | molybdenum cofactor biosynthesis | 99.3 | 142 | BCG_0916 | molybdenum cofactor biosynth | 85.82 | 142 | MAP0802 | molybdenum cofactor biosynthesis prot | 176 | 100 |
| MAP4_3058 | hypothetical protein | 87 | Rv0863 | hypothetical protein | 86.36 | 93 | Mb0886 | hypothetical protein | 86.36 | 93 | MAV_0992 | hypothetical protein | 98.48 | 66 | BCG_0915 | hypothetical protein | 86.36 | 93 | MAP0801 | hypothetical protein | 87 | 100 |
| MAP4_3059 | hypothetical protein | 752 | Rv0862c | hypothetical protein | 79.89 | 756 | Mb0885c | hypothetical protein | 80.03 | 756 | MAV_0991 | hypothetical protein | 98.67 | 752 | BCG_0914c | hypothetical protein | 79.89 | 756 | MAP0800c | hypothetical protein | 752 | 100 |
| MAP4_3060 | DNA helicase ErcC3 | 549 | Rv0861c | DNA helicase Ercc3 | 95.39 | 542 | Mb0884c | DNA helicase | 95.2 | 542 | MAV_0990 | DNA or RNA helicase of superfamily | 99.64 | 549 | BCG_0913c | DNA helicase | 95.2 | 542 | MAP0799c | hypothetical protein | 549 | 100 |
| MAP4_3061 | putative thiolase | 381 | Rv1627c | Probable nonspecific lipid-transfer p | 33.42 | 402 | Mb1653c | lipid-transfer protein | 33.42 | 402 | MAV_0989 | thiolase | 99.48 | 381 | BCG_1665c | lipid-transfer protein | 33.42 | 402 | MAP0798 | hypothetical protein | 381 | 100 |
| MAP4_3062 | hypothetical protein | 137 | Rv1628c | hypothetical protein | 34.4 | 163 | Mb1654c | hypothetical protein | 34.4 | 163 | MAV_0988 | hypothetical protein | 99.27 | 137 | BCG_1666c | hypothetical protein | 34.4 | 163 | MAP0797 | hypothetical protein | 150 | 100 |
| MAP4_3063 | hypothetical protein | 97 | Rv0793 | Possible monooxygenase | 29.76 | 101 | Mb0817 | hypothetical protein | 29.76 | 101 | MAV_0987 | antibiotic biosynthesis monooxyge | 97.94 | 97 | BCG_0846 | hypothetical protein | 29.76 | 101 | MAP0796c | hypothetical protein | 97 | 100 |
| MAP4_3064 | putative monooxygenase | 330 | Rv1855c | Possible oxidoreductase | 35.38 | 307 | Mb1886c | oxidoreductase | 35.38 | 307 | MAV_0986 | hypothetical protein | 98.79 | 345 | BCG_1891c | oxidoreductase | 35.38 | 307 | MAP0795 | hypothetical protein | 318 | 99.69 |
| MAP4_3065 | Transcriptional regulator, TetR family | 182 | Rv2506 | Probable transcriptional regulatory | 32.22 | 215 | Mb2534 | TetR family transcriptional re | 32.22 | 215 | MAV_0985 | TetR family transcriptional regulato | 98.1 | 158 | BCG_2526 | TetR family transcriptional regu | 32.22 | 215 | MAP0794 | hypothetical protein | 182 | 100 |
| MAP4_3066 | putative oxidoreductase | 402 | Rv1260 | Probable oxidoreductase | 41.33 | 372 | Mb0590c | hypothetical protein | 38.72 | 378 | MAV_0984 | hypothetical protein | 99.5 | 402 | BCG_0620c | hypothetical protein | 38.72 | 378 | MAP0793c | hypothetical protein | 404 | 100 |
| MAP4_3067 | hypothetical protein | 286 | Rv3463 | hypothetical protein | 45.53 | 285 | Mb3492 | hypothetical protein | 45.53 | 285 | MAV_0983 | hypothetical protein | 98.95 | 286 | BCG_3528 | hypothetical protein | 45.53 | 285 | MAP0792c | hypothetical protein | 286 | 100 |
| MAP4_3068 | putative methyltransferase | 200 | Rv1377c | Putative transferase | 33.99 | 212 | Mb1412c | transferase | 33.99 | 212 | MAV_0982 | methyltransferase type 12 | 99.5 | 200 | BCG_1438c | transferase | 33.99 | 212 | MAP0791c | hypothetical protein | 200 | 100 |
| MAP4_3069 | fatty oxidation protein FadB | 715 | Rv0860 | Probable fatty oxidation protein Fad | 86.25 | 720 | Mb0883 | fatty oxidation protein FadB | 86.11 | 720 | MAV_0981 | acyl-CoA dehydrogenase | 99.16 | 715 | BCG_0912 | fatty oxidation protein fadB | 86.11 | 720 | MAP0790 | FadB_1 | 715 | 100 |
| MAP4_3070 | acyl-CoA thiolase fadA | 403 | Rv0859 | Possible acyl-CoA thiolase FadA | 90.32 | 403 | Mb0882 | acetyl-CoA acetyltransferase | 90.57 | 403 | MAV_0980 | acetyl-CoA acetyltransferase | 99.75 | 403 | BCG_0911 | acetyl-CoA acetyltransferase | 90.57 | 403 | MAP0789 | acetyl-CoA acetyltransferase | 403 | 100 |
| MAP4_3071 | putative aminotransferase | 393 | Rv0858c | Probable N-succinyldiaminopimelate | 85.93 | 397 | Mb0881c | aminotransferase | 85.93 | 397 | MAV_0979 | aminotransferase | 99.24 | 393 | BCG_0910c | aminotransferase | 85.93 | 397 | MAP0788c | aminotransferase | 393 | 100 |
| MAP4_3072 | hypothetical protein | 151 | Rv0857 | hypothetical protein | 76.19 | 157 | Mb0880 | hypothetical protein | 76.19 | 157 | MAV_0978 | hypothetical protein | 99.34 | 151 | BCG_0909 | hypothetical protein | 76.19 | 157 | MAP0787 | hypothetical protein | 151 | 100 |
| MAP4_3073 | hypothetical protein | 154 | Rv0856 | hypothetical protein | 74.22 | 134 | Mb0879 | hypothetical protein | 74.22 | 134 | MAV_0977 | cyclase/dehydrase | 100 | 154 | BCG_0908 | hypothetical protein | 74.22 | 134 | MAP0786 | hypothetical protein | 154 | 100 |
| MAP4_3074 | fatty-acid-CoA racemase Far | 359 | Rv0855 | Probable fatty-acid-CoA racemase F | 83.57 | 359 | Mb0878 | fatty-acid-CoA racemase | 83.57 | 359 | MAV_0976 | alpha-methylacyl-CoA racemase | 99.16 | 359 | BCG_0907 | fatty-acid-CoA racemase far | 83.57 | 359 | MAP0785 | Far | 359 | 100 |
| MAP4_3075 | hypothetical protein | 147 | Rv0854 | hypothetical protein | 74.83 | 147 | Mb0877 | hypothetical protein | 74.83 | 147 | MAV_0975 | cyclase/dehydrase | 99.32 | 147 | BCG_0906 | hypothetical protein | 74.83 | 147 | MAP0784 | hypothetical protein | 147 | 100 |
| MAP4_3076 | pyruvate or indole-3-pyruvate decarboxylase pdc | 563 | Rv0853c | Probable pyruvate or indole-3-pyruv | 86.46 | 560 | Mb0876c | pyruvate or indole-3-pyruvate | 86.46 | 560 | MAV_0973 | indole-3-pyruvate decarboxylase | 99.29 | 561 | BCG_0905c | pyruvate or indole-3-pyruvate | 86.46 | 560 | MAP0783c | Pdc | 563 | 100 |
| MAP4_3077 | hypothetical protein | 61 | Rv1702c | hypothetical protein | 40 | 454 | Mb1728c | hypothetical protein | 40 | 454 | MAV_0974 | hypothetical protein | 100 | 61 | BCG_1740c | hypothetical protein | 40 | 454 | MAP0782 | hypothetical protein | 61 | 100 |
| MAP4_3078 | putative fatty-acid-CoA ligase | 208 | Rv0852 | Possible fatty-acid-CoA ligase FadD1 | 80.48 | 278 | Mb0875 | fatty-acid--CoA ligase | 80.48 | 278 | MAV_0972 | acyl-CoA dehydrogenase | 98.08 | 208 | BCG_0904 | fatty-acid-CoA ligase fadD16 | 80.48 | 278 | MAP0781 | FadD16 | 208 | 100 |
| MAP4_3079 | fatty-acid-CoA ligase fadD3 | 478 | Rv3561 | Probable fatty-acid-CoA ligase FadD | 46.09 | 507 | Mb3591 | long-chain-fatty-acid--CoA lig | 46.09 | 507 | MAV_0971 | long-chain-fatty-acid--CoA ligase | 99.58 | 491 | BCG_3625 | long-chain-fatty-acid--CoA ligas | 46.09 | 507 | MAP0780 | long-chain-fatty-acid--CoA ligase | 478 | 100 |
| MAP4_3080 | amidohydrolase family protein | 396 | Rv2303c | Probable antibiotic-resistance prote | 33.9 | 307 | Mb2325c | antibiotic-resistance protein | 33.9 | 307 | MAV_0970 | amidohydrolase | 100 | 396 | BCG_2319c | antibiotic-resistance protein | 33.9 | 307 | MAP0779 | hypothetical protein | 396 | 100 |
| MAP4_3081 | putative lipoprotein | 174 | Rv3763 | 19 kDa lipoprotein antigen precurso | 33.77 | 159 | Mb3789 | hypothetical protein | 33.77 | 159 | MAV_0969 | hypothetical protein | 98.56 | 139 | BCG_3822 | 19 kDa lipoprotein antigen pre | 33.77 | 159 | MAP0778 | hypothetical protein | 174 | 100 |
| MAP4_3082 | enoyl-CoA hydratase | 251 | Rv1070c | Probable enoyl-CoA hydratase EchA | 36.11 | 257 | Mb1099c | enoyl-CoA hydratase | 36.11 | 257 | MAV_0967 | enoyl-CoA hydratase/isomerase | 99.6 | 251 | BCG_1128c | enoyl-CoA hydratase | 36.11 | 257 | MAP0777c | hypothetical protein | 251 | 100 |
| MAP4_3083 | hypothetical protein | 147 | Rv2576c | Possible conserved membrane prote | 37.1 | 154 | Mb2606c | hypothetical protein | 37.1 | 154 | MAV_0965 | hypothetical protein | 98.64 | 147 | BCG_2599c | hypothetical protein | 37.1 | 154 | MAP0776c | hypothetical protein | 147 | 100 |
| MAP4_3084 | Transcriptional regulator, TetR family | 245 | Rv3208 | Probable transcriptional regulatory | 31.51 | 228 | Mb3233 | TetR family transcriptional re | 31.51 | 228 | MAV_0966 | TetR family transcriptional regulato | 99.59 | 245 | BCG_3234 | TetR family transcriptional regu | 31.51 | 228 | MAP0775 | hypothetical protein | 245 | 100 |
| MAP4_3085 | cytochrome P450 | 431 | Rv1777 | Probable cytochrome P450 144 Cyp | 32.9 | 434 | Mb1806 | cytochrome p450 144 CYP14 | 32.9 | 434 | MAV_0964 | cytochrome p450 | 99.77 | 431 | BCG_1810 | cytochrome p450 144 CYP144 | 32.9 | 434 | MAP0774c | hypothetical protein | 462 | 100 |
| MAP4_3086 | hypothetical protein | 92 | Rv0541c | Probable conserved integral membr | 27.78 | 449 | Mb2049c | hypothetical protein | 64.29 | 1606 | MAV_0963 | hypothetical protein | 98.91 | 92 | BCG_2043c | hypothetical protein | 64.29 | 1606 | MAP2386c | hypothetical protein | 348 | 41.67 |
| MAP4_3087 | cytochrome c oxidase polypeptide III | 192 | Rv2193 | Probable cytochrome C oxidase (sub | 26.47 | 203 | Mb2216 | cytochrome C oxidase subuni | 26.47 | 203 | MAV_0962 | cytochrome C oxidase, subunit III | 100 | 192 | BCG_2209 | cytochrome C oxidase (subunit | 26.47 | 203 | MAP0773 | hypothetical protein | 192 | 100 |
| MAP4_3088 | hypothetical protein | 268 | | | | | | | | | MAV_0961 | hypothetical protein | 99.62 | 265 | | | | | MAP0772 | hypothetical protein | 222 | 100 |
| MAP4_3089 | hypothetical protein | 254 | Rv2734 | hypothetical protein | 27.83 | 284 | Mb2753 | hypothetical protein | 27.83 | 284 | MAV_0960 | hypothetical protein | 99.61 | 254 | BCG_2747 | hypothetical protein | 27.83 | 284 | MAP0771 | hypothetical protein | 226 | 99.56 |
| MAP4_3090 | Transcriptional regulator, TetR family | 200 | Rv0238 | Possible transcriptional regulatory p | 33.8 | 204 | Mb0244 | TetR family transcriptional re | 33.8 | 204 | MAV_0959 | TetR family transcriptional regulato | 99.5 | 200 | BCG_0276 | TetR family transcriptional regu | 33.8 | 204 | MAP0770c | hypothetical protein | 176 | 99.43 |
| MAP4_3091 | hypothetical protein | 139 | Rv1891 | hypothetical protein | 30.4 | 135 | Mb1924 | hypothetical protein | 30.4 | 135 | MAV_0958 | hypothetical protein | 100 | 43 | BCG_1929 | hypothetical protein | 30.4 | 135 | MAP0769 | hypothetical protein | 139 | 100 |
| MAP4_3092 | hypothetical protein | 298 | Rv1363c | Possible membrane protein | 41.56 | 261 | Mb1398c | hypothetical protein | 41.56 | 261 | MAV_0956 | hypothetical protein | 98.38 | 247 | BCG_1425c | hypothetical protein | 41.56 | 261 | MAP0768c | hypothetical protein | 298 | 100 |
| MAP4_3093 | hypothetical protein | 201 | Rv1362c | Possible membrane protein | 50.54 | 220 | Mb1397c | hypothetical protein | 50 | 220 | MAV_0955 | hypothetical protein | 99.5 | 201 | BCG_1424c | hypothetical protein | 50 | 220 | MAP0767c | hypothetical protein | 224 | 100 |
| MAP4_3094 | hypothetical protein | 173 | Rv2379c | Peptide synthetase MbtF (peptide sy | 45 | 1461 | Mb2400c | peptide synthetase mbtF | 45 | 1461 | MAV_0954 | hypothetical protein | 100 | 173 | BCG_2393c | peptide synthetase mbtF | 45 | 1461 | MAP0766c | hypothetical protein | 173 | 100 |
| MAP4_3095 | mce family protein | 576 | Rv1971 | Mce-family protein Mce3F | 43.25 | 437 | Mb0180 | MCE-family protein MCE1F | 36 | 515 | MAV_0953 | mce-family protein mce1f | 99.65 | 575 | BCG_0211 | MCE-family protein mce1F | 36 | 515 | MAP0765 | hypothetical protein | 576 | 99.83 |
| MAP4_3096 | mce family lipoprotein | 435 | Rv1970 | Possible Mce-family lipoprotein Lpr | 41.14 | 377 | Mb3525c | MCE-family lipoprotein LprN | 36.61 | 384 | MAV_2536 | virulence factor Mce | 41.39 | 386 | BCG_3559c | mce family lipoprotein LprN | 36.61 | 384 | MAP0764 | hypothetical protein | 426 | 99.77 |
| MAP4_3099 | mce family protein | 372 | Rv3497c | Mce-family protein Mce4C | 37.72 | 357 | Mb3527c | MCE-family protein MCE4C | 37.72 | 357 | MAV_0950 | virulence factor Mce | 99.73 | 372 | BCG_3561c | Mce-family protein mce4C | 37.72 | 357 | MAP0761 | hypothetical protein | 372 | 100 |
| MAP4_3100 | mce family protein | 340 | Rv3498c | Mce-family protein Mce4B | 43.32 | 350 | Mb3528c | MCE-family protein MCE4B | 43.32 | 350 | MAV_0949 | virulence factor Mce | 100 | 340 | BCG_3562c | Mce-family protein mce4B | 43.32 | 350 | MAP0760 | hypothetical protein | 340 | 100 |
| MAP4_3101 | Mce family protein | 420 | Rv3499c | Mce-family protein Mce4A | 39.59 | 400 | Mb3529c | MCE-family protein MCE4A | 39.59 | 400 | MAV_0948 | virulence factor Mce | 99.29 | 420 | BCG_3563c | Mce-family protein mce4A | 39.59 | 400 | MAP0759 | hypothetical protein | 420 | 100 |
| MAP4_3102 | hypothetical protein | 281 | Rv3500c | Conserved integral membrane prote | 64 | 280 | Mb3530c | hypothetical protein | 64 | 280 | MAV_0947 | TrnB2 protein | 99.64 | 281 | BCG_3564c | integral membrane protein Yrb | 64 | 280 | MAP0758 | hypothetical protein | 281 | 100 |
| MAP4_3103 | hypothetical protein | 272 | Rv3501c | Conserved integral membrane prote | 71.95 | 254 | Mb3531c | hypothetical protein | 71.95 | 254 | MAV_0946 | TrnB1 protein | 99.63 | 272 | BCG_3565c | integral membrane protein Yrb | 71.95 | 254 | MAP0757 | hypothetical protein | 260 | 99.62 |
| MAP4_3104 | putative acyl-CoA transferasecarnitinedehydratase | 401 | Rv3272 | hypothetical protein | 32.76 | 394 | Mb3300 | hypothetical protein | 32.76 | 394 | MAV_0945 | L-carnitine dehydratase/bile acid-i | 99.75 | 401 | BCG_3301 | hypothetical protein | 33.14 | 394 | MAP0756 | hypothetical protein | 401 | 100 |
| MAP4_3105 | aldehyde dehydrogenase | 523 | Rv0768 | Probable aldehyde dehydrogenase | 54.6 | 489 | Mb0791 | aldehyde dehydrogenase | 54.6 | 489 | MAV_0944 | aldehyde dehydrogenase (NAD) fa | 99.04 | 523 | BCG_0820 | aldehyde dehydrogenase AldA | 54.6 | 489 | MAP0755 | AldA_2 | 523 | 100 |
| MAP4_3106 | putative short-chain dehydrogenasereductase | 233 | Rv1483 | 3-oxoacyl-[acyl-carrier protein] redu | 38.36 | 247 | Mb1519 | 3-oxoacyl-ACP reductase | 38.36 | 247 | MAV_0942 | 3-oxoacyl-(acyl-carrier-protein) red | 100 | 233 | BCG_1545 | 3-oxoacyl-ACP reductase | 38.36 | 247 | MAP0754c | hypothetical protein | 233 | 100 |
| MAP4_3107 | ferredoxin | 66 | Rv3503c | Probable ferredoxin FdxD | 41.67 | 63 | Mb3533c | ferredoxin FdxD | 41.67 | 63 | MAV_0941 | hypothetical protein | 100 | 66 | BCG_3567c | ferredoxin fdxD | 41.67 | 63 | MAP0753c | hypothetical protein | 66 | 100 |
| MAP4_3108 | cytochrome P450 | 414 | Rv1785c | Probable cytochrome P450 143 Cyp | 31.85 | 393 | Mb1813c | cytochrome P450 143 | 31.85 | 393 | MAV_0940 | cytochrome P450 superfamily prot | 99.52 | 454 | BCG_1817c | cytochrome P450 143 cyp143 | 31.85 | 393 | MAP0752c | hypothetical protein | 414 | 100 |
| MAP4_3109 | hypothetical protein | 138 | | | | | Mb3356 | hypothetical protein | 34.21 | 116 | MAV_0939 | hypothetical protein | 100 | 138 | BCG_3393 | hypothetical protein | 34.21 | 116 | MAP2179 | hypothetical protein | 153 | 43.09 |
| MAP4_3110 | hypothetical protein | 295 | Rv1363c | Possible membrane protein | 74.34 | 261 | Mb1398c | hypothetical protein | 73.68 | 261 | MAV_0938 | hypothetical protein | 96.62 | 296 | BCG_1425c | hypothetical protein | 74.34 | 261 | MAP0751c | hypothetical protein | 295 | 100 |
| MAP4_3111 | hypothetical protein | 187 | Rv1362c | Possible membrane protein | 66.11 | 220 | Mb1397c | hypothetical protein | 65.56 | 220 | MAV_0937 | hypothetical protein | 99.47 | 187 | BCG_1424c | hypothetical protein | 65.56 | 220 | MAP0750c | hypothetical protein | 187 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3112 | putative conserved membrane protein | 461 | Rv1639c | hypothetical protein | 65.87 | 489 | Mb1666c | hypothetical protein | 65.87 | 489 | MAV_0936 | esterase | 97.14 | 454 | BCG_1678c | hypothetical protein | 65.87 | 489 | MAP0749c | hypothetical protein | 461 | 100 |
| MAP4_3113 | acyl-CoA dehydrogenase | 391 | Rv1934c | Probable acyl-CoA dehydrogenase F | 34.72 | 409 | Mb1969c | acyl-CoA dehydrogenase | 34.72 | 409 | MAV_0935 | acyl-CoA dehydrogenase | 98.98 | 391 | BCG_1973c | acyl-CoA dehydrogenase fadE1 | 34.72 | 409 | MAP0748 | hypothetical protein | 391 | 100 |
| MAP4_3114 | putative acyl-CoA dehydrogenase | 332 | Rv1933c | Probable acyl-CoA dehydrogenase F | 31.59 | 363 | Mb1968c | acyl-CoA dehydrogenase | 31.59 | 363 | MAV_0934 | acyl-CoA dehydrogenase | 99.1 | 332 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 31.59 | 363 | MAP0747 | hypothetical protein | 346 | 100 |
| MAP4_3115 | putative nitroreductase | 216 | Rv3368c | Possible oxidoreductase | 27.27 | 214 | Mb3403c | oxidoreductase | 27.27 | 214 | MAV_0933 | nitroreductase | 99.51 | 206 | BCG_3440c | oxidoreductase | 27.27 | 214 | MAP0746 | hypothetical protein | 216 | 100 |
| MAP4_3116 | putative carboxymuconolactone decarboxylase | 128 | Rv1767 | hypothetical protein | 30 | 119 | Mb1796 | hypothetical protein | 30 | 119 | MAV_3552 | hypothetical protein | 31.13 | 271 | BCG_2133 | lipoprotein lppK | 31.15 | 189 | MAP0745c | hypothetical protein | 175 | 99.22 |
| MAP4_3117 | 3-hydroxyisobutyrate dehydrogenase | 297 | Rv0751c | Probable 3-hydroxyisobutyrate dehy | 33.33 | 294 | Mb0773c | 3-hydroxyisobutyrate dehydr | 33.33 | 294 | MAV_0931 | 3-hydroxyisobutyrate dehydrogena | 99.33 | 297 | BCG_0802c | 3-hydroxyisobutyrate dehydrog | 33.33 | 294 | MAP0744c | hypothetical protein | 297 | 100 |
| MAP4_3118 | amidohydrolase, amidohydrolase 2 family protein | 366 | Rv1381 | Probable dihydroorotase PyrC (DHO | 48 | 430 | Mb1975 | riboflavin biosynthesis protei | 25 | 353 | MAV_0930 | amidohydrolase | 98.62 | 363 | BCG_1442 | dihydroorotase | 48 | 430 | MAP0743c | hypothetical protein | 366 | 100 |
| MAP4_3119 | amidohydrolase, amidohydrolase 2 family protein | 380 | Rv0127 | Maltokinase Mak | 28.99 | 455 | Mb0132 | hypothetical protein | 28.99 | 455 | MAV_0929 | amidohydrolase | 99.74 | 380 | BCG_0161 | hypothetical protein | 28.99 | 455 | MAP0742c | hypothetical protein | 380 | 100 |
| MAP4_3120 | rieske (2Fe-2S) domain-containing protein | 137 | Rv3526 | Oxygenase component of 3-ketoster | 23.85 | 386 | Mb3556 | oxidoreductase | 23.85 | 386 | MAV_0928 | Rieske (2Fe-2S) domain-containing | 99.27 | 137 | BCG_3590 | oxidoreductase | 23.85 | 386 | MAP0741c | hypothetical protein | 113 | 99.12 |
| MAP4_3121 | hypothetical protein | 288 | Rv1123c | Possible peroxidase BpoB (non-haen | 23.42 | 302 | Mb1154c | peroxidase BpoB | 23.42 | 302 | MAV_0927 | hypothetical protein | 100 | 288 | BCG_1184c | peroxidase bpoB | 23.42 | 302 | MAP0740c | hypothetical protein | 288 | 100 |
| MAP4_3122 | hypothetical protein | 157 | Rv0271c | Probable acyl-CoA dehydrogenase F | 28.85 | 731 | Mb0277c | acyl-CoA dehydrogenase | 28.85 | 731 | MAV_0926 | hypothetical protein | 96.73 | 153 | BCG_0309c | acyl-CoA dehydrogenase fadE6 | 28.85 | 731 | MAP0739 | hypothetical protein | 157 | 100 |
| MAP4_3123 | putative respiratory-chain NADH dehydrogenase I subu | 436 | Rv3150 | Probable NADH dehydrogenase I (ch | 31.25 | 445 | Mb3174 | NADH dehydrogenase I subur | 31.25 | 445 | MAV_0925 | respiratory-chain NADH dehydroge | 98.17 | 436 | BCG_3173 | NADH dehydrogenase I subunit | 31.25 | 445 | MAP0738c | hypothetical protein | 436 | 100 |
| MAP4_3124 | ferredoxin | 98 | Rv3503c | Probable ferredoxin FdxD | 34.43 | 63 | Mb3533c | ferredoxin FdxD | 34.43 | 63 | MAV_0924 | hypothetical protein | 100 | 98 | BCG_3567c | ferredoxin fdxD | 34.43 | 63 | MAP0667 | hypothetical protein | 72 | 37.88 |
| MAP4_3125 | putative monooxygenase, luciferase-like monooxygena | 318 | Rv3520c | Possible coenzyme F420-dependent | 29.29 | 347 | Mb3550c | coenzyme F420-dependent o | 29.29 | 347 | MAV_0923 | hypothetical protein | 98.74 | 318 | BCG_3584c | coenzyme F420-dependent oxi | 29.29 | 347 | MAP0737 | hypothetical protein | 318 | 100 |
| MAP4_3126 | hypothetical protein | 247 | Rv2970c | Probable lipase/esterase LipN | 30.85 | 376 | Mb2994c | lipase/esterase | 30.85 | 376 | MAV_0922 | hypothetical protein | 98.38 | 247 | BCG_2991c | lipase/esterase lipN | 30.85 | 376 | MAP0736 | hypothetical protein | 247 | 100 |
| MAP4_3127 | NAD dependent epimerasedehydratase family protein | 356 | Rv3784 | Possible dTDP-glucose 4,6-dehydrat | 25.52 | 326 | Mb3813 | dTDP-glucose 4,6-dehydratas | 25.52 | 326 | MAV_0921 | hypothetical protein | 98.18 | 330 | BCG_3846 | dTDP-glucose 4,6-dehydratase | 25.52 | 326 | MAP0735 | hypothetical protein | 356 | 100 |
| MAP4_3128 | hypothetical protein | 132 | Rv0982 | Two component sensor kinase MprB | 29.49 | 504 | Mb1834c | hypothetical protein | 55.56 | 115 | MAV_0652 | acyl-CoA dehydrogenase | 37.5 | 392 | BCG_1838c | hypothetical protein | 55.56 | 115 | MAP0734 | hypothetical protein | 132 | 100 |
| MAP4_3129 | hypothetical protein | 550 | Rv3540c | Probable lipid transfer protein or ke | 33.83 | 386 | Mb3570c | lipid-transfer protein | 33.83 | 386 | MAV_0919 | hypothetical protein | 99.09 | 550 | BCG_3604c | lipid-transfer protein | 33.83 | 386 | MAP0733c | hypothetical protein | 550 | 100 |
| MAP4_3130 | hypothetical protein | 328 | Rv1938 | Probable epoxide hydrolase EphB (e | 30.34 | 356 | Mb1973 | epoxide hydrolase | 30.34 | 356 | MAV_0918 | hypothetical protein | 93.6 | 344 | BCG_1977 | epoxide hydrolase ephB | 30.34 | 356 | MAP0732c | hypothetical protein | 328 | 100 |
| MAP4_3131 | 6-phosphogluconate dehydrogenase | 271 | Rv0770 | Probable dehydrogenase/reductase | 37.14 | 295 | Mb0793 | dehydrogenase/reductase | 36.57 | 295 | MAV_0917 | 6-phosphogluconate dehydrogenas | 98.89 | 271 | BCG_0822 | dehydrogenase/reductase | 37.14 | 295 | MAP0731c | hypothetical protein | 272 | 100 |
| MAP4_3132 | putative cytochrome P450 hydroxylase | 401 | Rv0766c | Probable cytochrome P450 123 Cyp1 | 38.69 | 402 | Mb0789c | cytochrome P450 123 | 38.69 | 402 | MAV_0916 | cytochrome P450 monooxygenase | 99.25 | 401 | BCG_0818c | cytochrome P450 123 cyp123 | 38.18 | 541 | MAP0730c | hypothetical protein | 401 | 100 |
| MAP4_3133 | ferredoxin | 66 | Rv3503c | Probable ferredoxin FdxD | 40.68 | 63 | Mb3533c | ferredoxin FdxD | 40.68 | 63 | MAV_0915 | hypothetical protein | 100 | 66 | BCG_3567c | ferredoxin fdxD | 40.68 | 63 | MAP0729c | hypothetical protein | 66 | 100 |
| MAP4_3134 | hypothetical protein | 97 | Rv3755c | hypothetical protein | 45.16 | 199 | Mb3781c | hypothetical protein | 45.16 | 199 | MAV_0914 | hypothetical protein | 98.97 | 97 | BCG_3814c | hypothetical protein | 45.16 | 199 | MAP0728 | hypothetical protein | 97 | 100 |
| MAP4_3135 | ferredoxin | 62 | Rv3503c | Probable ferredoxin FdxD | 41.67 | 63 | Mb3533c | ferredoxin FdxD | 41.67 | 63 | MAV_0913 | hypothetical protein | 100 | 48 | BCG_3567c | ferredoxin fdxD | 41.67 | 63 | MAP0753c | hypothetical protein | 66 | 51.67 |
| MAP4_3136 | putative cytochrome P450 hydroxylase | 424 | Rv1777 | Probable cytochrome P450 144 Cyp1 | 31.73 | 434 | Mb1806 | cytochrome p450 144 CYP144 | 31.73 | 434 | MAV_0912 | cytochrome p450 | 99.76 | 424 | BCG_1810 | cytochrome p450 144 CYP144 | 31.73 | 434 | MAP0727 | hypothetical protein | 424 | 100 |
| MAP4_3137 | hypothetical protein | 175 | Rv0893c | Possible S-adenosylmethionine-depe | 50 | 325 | Mb0917c | hypothetical protein | 50 | 325 | MAV_0911 | hypothetical protein | 100 | 175 | BCG_0945c | hypothetical protein | 50 | 325 | MAP0726 | hypothetical protein | 175 | 100 |
| MAP4_3138 | Transcriptional regulator, TetR family | 204 | Rv0302 | Probable transcriptional regulatory | 33.33 | 210 | Mb0310 | TetR/ACRR family transcriptio | 33.33 | 210 | MAV_0910 | TetR family transcriptional regulato | 100 | 204 | BCG_0342 | TetR family transcriptional regu | 33.33 | 210 | MAP0725 | hypothetical protein | 204 | 100 |
| MAP4_3139 | Acetyl-CoA acetyltransferase | 384 | Rv3556c | Probable acetyl-CoA acetyltransfera | 50.13 | 386 | Mb3586c | acetyl-CoA acetyltransferase | 50.13 | 386 | MAV_0909 | acetyl-CoA acetyltransferase | 99.48 | 384 | BCG_3620c | acetyl-CoA acetyltransferase | 50.13 | 386 | MAP0724 | FadA6_2 | 384 | 100 |
| MAP4_3140 | acyl-CoA dehydrogenase | 388 | Rv0972c | Acyl-CoA dehydrogenase FadE12 | 35.97 | 388 | Mb0997c | acyl-CoA dehydrogenase | 35.97 | 388 | MAV_1088 | acyl-CoA dehydrogenase fadE12 | 35.71 | 388 | BCG_1026c | acyl-CoA dehydrogenase fadE1 | 35.97 | 388 | MAP0723 | FadE12_1 | 388 | 100 |
| MAP4_3141 | putative amidohydrolase 2 | 432 | Rv3510c | hypothetical protein | 22.54 | 278 | Mb3540c | hypothetical protein | 22.54 | 278 | MAV_0907 | amidohydrolase | 99.77 | 432 | BCG_3574c | hypothetical protein | 22.54 | 278 | MAP0722 | hypothetical protein | 432 | 100 |
| MAP4_3142 | hypothetical protein | 177 | Rv1531 | hypothetical protein | 28.57 | 188 | Mb1558 | hypothetical protein | 28.57 | 188 | MAV_0906 | hypothetical protein | 99.44 | 177 | BCG_1583 | hypothetical protein | 28.57 | 188 | MAP0721c | hypothetical protein | 177 | 100 |
| MAP4_3143 | putative dioxygenase, Rieske (2Fe-2S) domain-containi | 427 | Rv3161c | Possible dioxygenase | 32.08 | 382 | Mb3186c | dioxygenase | 32.55 | 382 | MAV_0905 | Rieske (2Fe-2S) domain-containing | 99.53 | 427 | BCG_3185c | dioxygenase | 32.55 | 382 | MAP0720c | hypothetical protein | 427 | 100 |
| MAP4_3144 | hypothetical protein | 109 | Rv0777 | Probable adenylosuccinate lyase Pu | 31.82 | 472 | Mb0800 | adenylosuccinate lyase | 31.82 | 472 | MAV_0904 | hypothetical protein | 100 | 109 | BCG_0829 | adenylosuccinate lyase | 31.82 | 472 | MAP0719c | hypothetical protein | 109 | 100 |
| MAP4_3145 | putative amidohydrolase | 409 | Rv2915c | hypothetical protein | 29.3 | 370 | Mb2939c | hypothetical protein | 29.3 | 370 | MAV_0903 | Xaa-Pro dipeptidase | 99.27 | 409 | BCG_2936c | hypothetical protein | 29.3 | 370 | MAP0718c | hypothetical protein | 409 | 100 |
| MAP4_3146 | hypothetical protein | 148 | Rv2910c | hypothetical protein | 34.59 | 147 | Mb2934c | hypothetical protein | 34.59 | 147 | MAV_0902 | hypothetical protein | 100 | 148 | BCG_2931c | hypothetical protein | 34.59 | 147 | MAP0717c | hypothetical protein | 148 | 100 |
| MAP4_3147 | Acyl-CoA dehydrogenase | 359 | Rv3560c | Probable acyl-CoA dehydrogenase F | 37.88 | 385 | Mb3590c | acyl-CoA dehydrogenase | 37.88 | 385 | MAV_0901 | acyl-CoA dehydrogenase | 99.06 | 365 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 37.88 | 385 | MAP0716c | hypothetical protein | 359 | 100 |
| MAP4_3148 | putative acyl-CoA dehydrogenase | 272 | Rv0271c | Probable acyl-CoA dehydrogenase F | 36.23 | 731 | Mb0277c | acyl-CoA dehydrogenase | 36.23 | 731 | MAV_0900 | acyl-CoA dehydrogenase | 98.9 | 272 | BCG_0309c | acyl-CoA dehydrogenase fadE6 | 36.23 | 731 | MAP0715c | hypothetical protein | 228 | 100 |
| MAP4_3149 | hypothetical protein | 89 | Rv3761c | Possible acyl-CoA dehydrogenase Fa | 35.29 | 351 | Mb3787c | acyl-CoA dehydrogenase | 35.29 | 351 | MAV_0899 | hypothetical protein | 100 | 89 | BCG_3820c | acyl-CoA dehydrogenase fadE3 | 35.29 | 351 | MAP0714c | hypothetical protein | 89 | 100 |
| MAP4_3150 | putative acyl-CoA dehydrogenase | 391 | Rv3560c | Probable acyl-CoA dehydrogenase F | 38.23 | 385 | Mb3590c | acyl-CoA dehydrogenase | 38.23 | 385 | MAV_0898 | acyl-CoA dehydrogenase | 99.49 | 391 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 38.23 | 385 | MAP0713 | hypothetical protein | 403 | 99.74 |
| MAP4_3151 | Transcriptional regulator, TetR family | 216 | Rv3208 | Probable transcriptional regulatory | 27.94 | 228 | Mb3233 | TetR family transcriptional re | 27.94 | 228 | MAV_1626 | hypothetical protein | 34.22 | 343 | BCG_3234 | TetR family transcriptional regu | 27.94 | 228 | MAP0712c | hypothetical protein | 216 | 100 |
| MAP4_3152 | putative dehydrogenase | 282 | Rv2750 | Probable dehydrogenase | 48.23 | 272 | Mb2771 | 3-ketoacyl-ACP reductase | 48.23 | 272 | MAV_0896 | carveol dehydrogenase | 100 | 282 | BCG_2766 | 3-ketoacyl-ACP reductase | 48.23 | 272 | MAP0711c | hypothetical protein | 282 | 99.65 |
| MAP4_3153 | short-chain dehydrogenase | 280 | Rv0851c | Probable short-chain type dehydrog | 78.62 | 275 | Mb0874c | short chain dehydrogenase | 78.62 | 275 | MAV_0895 | short chain dehydrogenase | 100 | 280 | BCG_0903c | short chain dehydrogenase | 78.99 | 275 | MAP0710c | short chain dehydrogenase | 280 | 100 |
| MAP4_3154 | short chain dehydrogenasereductase family oxido redu | 269 | Rv1928c | Probable short-chain type dehydrog | 35.92 | 255 | Mb1963c | short chain dehydrogenase | 35.92 | 255 | MAV_0894 | oxidoreductase, short chain dehydr | 98.88 | 269 | BCG_1967c | short chain dehydrogenase | 35.92 | 255 | MAP0709 | hypothetical protein | 269 | 100 |
| MAP4_3155 | CoA-transferase family III protein | 815 | Rv1866 | hypothetical protein | 28.1 | 778 | Mb1897 | hypothetical protein | 27.98 | 778 | MAV_0893 | caib/baif family protein | 98.51 | 805 | BCG_1902 | hypothetical protein | 27.98 | 778 | MAP0708 | hypothetical protein | 815 | 100 |
| MAP4_3156 | peptidase, M24 family protein | 375 | Rv2535c | Probable cytoplasmic peptidase Pep | 25.78 | 372 | Mb2564c | peptidase PepQ | 25.78 | 372 | MAV_0892 | peptidase, M24 family protein | 98.93 | 375 | BCG_2557c | cytoplasmic peptidase pepQ | 25.78 | 372 | MAP0707 | hypothetical protein | 375 | 100 |
| MAP4_3157 | peptidase, M24 family protein | 417 | Rv2089c | Dipeptidase PepE | 26.85 | 375 | Mb2116c | dipeptidase PepE | 26.85 | 375 | MAV_0891 | peptidase, M24 family protein | 100 | 417 | BCG_2109c | dipeptidase PepE | 26.85 | 375 | MAP0706 | hypothetical protein | 392 | 99.74 |
| MAP4_3158 | putative amidohydrolase | 390 | Rv1551 | Possible acyltransferase PlsB1 | 25.27 | 621 | Mb1577 | glycerol-3-phosphate acyltrar | 25.27 | 621 | MAV_0890 | amidohydrolase | 99.72 | 353 | BCG_1603 | glycerol-3-phosphate acyltrans | 25.27 | 621 | MAP0705 | hypothetical protein | 390 | 100 |
| MAP4_3159 | putative cytochrome P450 | 414 | Rv3121 | Probable cytochrome P450 141 Cyp1 | 29.14 | 400 | Mb1912c | cytochrome p450 140 CYP140 | 32.83 | 438 | MAV_2968 | cytochrome P450-SU2 | 71.95 | 409 | BCG_1917c | cytochrome p450 140 CYP140 | 32.83 | 438 | MAP0704 | hypothetical protein | 425 | 100 |
| MAP4_3160 | Ferredoxin | 64 | Rv3503c | Probable ferredoxin FdxD | 40 | 63 | Mb3533c | ferredoxin FdxD | 40 | 63 | MAV_0888 | hypothetical protein | 96.77 | 62 | BCG_3567c | ferredoxin fdxD | 40 | 63 | MAP0560 | FdxD | 63 | 45 |
| MAP4_3161 | Transcriptional regulator, TetR family | 225 | Rv1685c | hypothetical protein | 34.78 | 207 | Mb1711c | hypothetical protein | 34.78 | 207 | MAV_0887 | TetR family transcriptional regulato | 99.11 | 225 | BCG_1723c | hypothetical protein | 34.78 | 207 | MAP0703 | hypothetical protein | 225 | 100 |
| MAP4_3162 | 3-ketoacyl-ACP reductase | 268 | Rv1350 | Probable 3-oxoacyl-[acyl-carrier pro | 42.08 | 247 | Mb1385 | 3-ketoacyl-ACP reductase | 42.08 | 247 | MAV_0886 | short chain dehydrogenase/reducta | 99.25 | 268 | BCG_1412 | 3-ketoacyl-ACP reductase | 42.08 | 247 | MAP0702 | hypothetical protein | 268 | 100 |
| MAP4_3163 | multicopper oxidase | 533 | Rv0846c | Probable oxidase | 69.6 | 504 | Mb0869c | oxidase | 69.41 | 504 | MAV_3048 | multicopper oxidase | 28.32 | 482 | BCG_0898c | oxidase | 69.6 | 504 | MAP0701c | hypothetical protein | 533 | 100 |
| MAP4_3164 | putative alphabeta hydrolase | 273 | Rv3569c | 4,9-DHSA hydrolase | 28.16 | 291 | Mb3600c | 2-hydroxy-6-oxo-6-phenylhex | 28.16 | 291 | MAV_0884 | alpha/beta hydrolase | 99.27 | 273 | BCG_3634c | 2-hydroxy-6-oxo-6-phenylhexa | 28.16 | 291 | MAP0700 | hypothetical protein | 273 | 100 |
| MAP4_3165 | putative cyclase family protein | 329 | Rv1716 | hypothetical protein | 27.59 | 276 | Mb1744 | hypothetical protein | 27.59 | 276 | MAV_0883 | cyclase | 99.39 | 329 | BCG_1755 | hypothetical protein | 27.59 | 276 | MAP0699 | hypothetical protein | 329 | 99.7 |
| MAP4_3166 | 3-alpha-hydroxysteroid dehydrogenase | 275 | Rv0769 | Probable dehydrogenase/reductase | 29.14 | 248 | Mb0792 | short chain dehydrogenase | 29.14 | 248 | MAV_0882 | 3-alpha-hydroxysteroid dehydroge | 99.27 | 275 | BCG_0821 | short chain dehydrogenase | 29.14 | 248 | MAP0698 | 3-alpha-hydroxysteroid dehydrogenase | 275 | 100 |
| MAP4_3167 | monooxygenase | 436 | Rv3618 | Possible monooxygenase | 32.45 | 395 | Mb1971 | monooxygenase | 27.12 | 369 | MAV_0881 | hypothetical protein | 99.54 | 436 | BCG_1975 | monooxygenase | 27.12 | 369 | MAP0697 | hypothetical protein | 436 | 100 |
| MAP4_3168 | putative dehydrogenase | 575 | Rv3537 | Probable dehydrogenase | 42.21 | 563 | Mb3567 | 3-ketosteroid-delta-1-dehydr | 42.21 | 563 | MAV_0880 | 3-ketosteroid-delta-1-dehydrogena | 99.3 | 575 | BCG_3601 | 3-ketosteroid-delta-1-dehydrog | 42.21 | 563 | MAP0696 | 3-ketosteroid-delta-1-dehydrogenase | 575 | 100 |
| MAP4_3169 | 2,3-dihydroxyphenylpropionate 1,2-dioxygenase | 316 | Rv2471 | Probable alpha-glucosidase AglA (m | 30.77 | 546 | Mb2498 | alpha-glucosidase | 30.77 | 546 | MAV_1947 | 3-(2,3-dihydroxyphenyl)propionate | 34.52 | 297 | BCG_2491 | alpha-glucosidase aglA | 30.77 | 546 | MAP0695 | 3-(2,3-dihydroxyphenyl)propionate dio | 316 | 100 |
| MAP4_3170 | 3-(3-hydroxy-phenyl)propionate hydroxylase | 580 | Rv1751 | Probable oxidoreductase | 23.58 | 460 | Mb1780 | hypothetical protein | 24.17 | 460 | MAV_0878 | 3-(3-hydroxyphenyl)propionate hy | 99.31 | 580 | BCG_1790 | hypothetical protein | 24.17 | 460 | MAP0694 | 3-(3-hydroxyphenyl)propionate hydrox | 580 | 100 |
| MAP4_3171 | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase | 287 | Rv3569c | 4,9-DHSA hydrolase | 29.93 | 291 | Mb3600c | 2-hydroxy-6-oxo-6-phenylhex | 29.93 | 291 | MAV_0877 | 2-hydroxy-6-ketonona-2,4-dienedo | 100 | 287 | BCG_3634c | 2-hydroxy-6-oxo-6-phenylhexa | 29.93 | 291 | MAP0693 | hypothetical protein | 287 | 100 |
| MAP4_3172 | Transcriptional regulator, IclR family | 225 | Rv2989 | Probable transcriptional regulatory | 26.84 | 233 | Mb3013 | transcriptional regulator | 26.84 | 233 | MAV_0876 | transcriptional regulator | 100 | 225 | BCG_3010 | transcriptional regulatory prot | 26.84 | 233 | MAP0692c | hypothetical protein | 225 | 100 |
| MAP4_3173 | 3-oxosteroid 1-dehydrogenase | 538 | Rv3537 | Probable dehydrogenase | 39.39 | 563 | Mb3567 | 3-ketosteroid-delta-1-dehydr | 39.39 | 563 | MAV_0875 | FAD binding domain-containing pro | 99.26 | 538 | BCG_3601 | 3-ketosteroid-delta-1-dehydrog | 39.39 | 563 | MAP0691c | hypothetical protein | 507 | 99.8 |
| MAP4_3174 | two component sensor kinase | 429 | Rv0845 | Possible two component sensor kina | 71.01 | 425 | Mb0868 | two component sensor kinase | 71.26 | 425 | MAV_0874 | hypothetical protein | 99.01 | 406 | BCG_0897 | two component sensor kinase | 71.26 | 425 | MAP0690 | hypothetical protein | 429 | 100 |
| MAP4_3175 | nitratenitrite response transcriptional regulator narL | 217 | Rv0844c | Possible nitrate/nitrite response tra | 85.65 | 216 | Mb0867c | nitrate/nitrite response trans | 85.19 | 216 | MAV_0872 | LuxR family transcriptional regulato | 99.45 | 183 | BCG_0896c | nitrate/nitrite response transcr | 85.65 | 216 | MAP0689c | NarL_1 | 217 | 100 |
| MAP4_3176 | putative dehydrogenase | 297 | Rv0843 | Probable dehydrogenase | 44.05 | 334 | Mb0866 | dehydrogenase | 43.73 | 334 | MAV_0873 | dehydrogenase E1 component supe | 97.98 | 297 | BCG_0895 | dehydrogenase | 44.05 | 334 | MAP0688 | hypothetical protein | 297 | 100 |
| MAP4_3177 | LAOAO transport system ATPasekinase | 295 | Rv1496 | Possible transport system kinase | 38.46 | 334 | Mb1533 | arginine/ornithine transport s | 38.46 | 334 | MAV_0871 | LAO/AO transport system ATPase | 99.32 | 295 | BCG_1559 | arginine/ornithine transport sy | 38.46 | 334 | MAP0687 | hypothetical protein | 295 | 100 |
| MAP4_3178 | acetyl-CoA acetyltransferase | 379 | Rv1074c | Probable beta-ketoacyl CoA thiolase | 39.71 | 405 | Mb1103c | acetyl-CoA acetyltransferase | 39.71 | 405 | MAV_1863 | beta-ketoadipyl CoA thiolase | 53.59 | 395 | BCG_1132c | acetyl-CoA acetyltransferase | 39.71 | 405 | MAP0686 | hypothetical protein | 389 | 99.74 |
| MAP4_3179 | phenolic acid decarboxylase | 177 | | | | | | | | | MAV_0869 | phenolic acid decarboxylase | 99.42 | 172 | | | | | MAP0685 | hypothetical protein | 177 | 100 |
| MAP4_3180 | proline iminopeptidase | 287 | Rv0840c | Probable proline iminopeptidase Pip | 71.93 | 286 | Mb0863c | proline iminopeptidase | 71.93 | 286 | MAV_0868 | proline imino-peptidase | 99.29 | 283 | BCG_0892c | proline iminopeptidase pip | 71.93 | 286 | MAP0684c | hypothetical protein | 287 | 100 |
| MAP4_3181 | acyl-CoA hydratase | 254 | Rv2679 | Probable enoyl-CoA hydratase EchA | 32.79 | 276 | Mb2698 | enoyl-CoA hydratase | 32.79 | 276 | MAV_0867 | enoyl-CoA hydratase/isomerase | 99.61 | 254 | BCG_2692 | enoyl-CoA hydratase | 32.79 | 276 | MAP0683 | hypothetical protein | 254 | 100 |
| MAP4_3182 | acyl-CoA dehydrogenase | 360 | Rv3560c | Probable acyl-CoA dehydrogenase F | 38.92 | 385 | Mb3590c | acyl-CoA dehydrogenase | 38.92 | 385 | MAV_0865 | acyl-CoA dehydrogenase middle do | 100 | 360 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 38.92 | 385 | MAP0682 | hypothetical protein | 360 | 100 |
| MAP4_3183 | acyl-CoA dehydrogenase | 301 | Rv1933c | Probable acyl-CoA dehydrogenase F | 29.43 | 363 | Mb1968c | acyl-CoA dehydrogenase | 29.43 | 363 | MAV_0864 | acyl-CoA dehydrogenase domain-co | 98.34 | 301 | BCG_1972c | acyl-CoA dehydrogenase fadE1 | 29.43 | 363 | MAP0681 | hypothetical protein | 301 | 100 |
| MAP4_3184 | AMP-dependent synthetase and ligase | 467 | Rv3089 | Probable chain-fatty-acid-CoA ligase | 31.12 | 503 | Mb3116 | chain-fatty-acid-CoA ligase | 31.12 | 503 | MAV_0863 | AMP-binding enzyme | 99.57 | 467 | BCG_3114 | chain-fatty-acid-CoA ligase fad | 31.12 | 503 | MAP0680 | hypothetical protein | 467 | 100 |
| MAP4_3185 | ferredoxin, 2Fe-2S iron-sulfur cluster binding domain-c | 112 | Rv3554 | Possible electron transfer protein Fd | 46 | 685 | Mb3584 | electron transfer protein Fdx | 46 | 685 | MAV_0862 | FdxB protein | 100 | 112 | BCG_3618 | electron transfer protein fdxB | 46 | 685 | MAP0679c | FdxB | 112 | 100 |
| MAP4_3186 | hypothetical protein | 104 | Rv3592 | Possible heme degrading protein M | 26.47 | 105 | Mb3623 | hypothetical protein | 26.47 | 105 | MAV_0861 | hypothetical protein | 100 | 104 | BCG_3657 | hypothetical protein | 26.47 | 105 | MAP0678c | hypothetical protein | 104 | 100 |
| MAP4_3187 | putative amidohydrolase | 421 | Rv3510c | hypothetical protein | 30.28 | 278 | Mb3540c | hypothetical protein | 30.28 | 278 | MAV_0860 | amidohydrolase | 99.76 | 421 | BCG_3574c | hypothetical protein | 30.28 | 278 | MAP0677c | hypothetical protein | 421 | 100 |
| MAP4_3188 | putative acyl-CoA transferasecarnitine dehydratase | 346 | Rv3272 | hypothetical protein | 27.51 | 394 | Mb3300 | hypothetical protein | 27.51 | 394 | MAV_0859 | caib/baif family protein | 99.42 | 346 | BCG_3301 | hypothetical protein | 27.22 | 394 | MAP0676 | hypothetical protein | 346 | 100 |
| MAP4_3189 | putative oxidoreductase | 318 | Rv1360 | Probable oxidoreductase | 28.19 | 340 | Mb1395 | oxidoreductase | 28.19 | 340 | MAV_0923 | hypothetical protein | 53.46 | 318 | BCG_1422 | oxidoreductase | 28.19 | 340 | MAP0675 | hypothetical protein | 318 | 99.69 |
| MAP4_3190 | Methylmalonyl-CoA mutase, B12 binding domain prote | 146 | Rv1493 | Probable methylmalonyl-CoA mutas | 45.95 | 750 | Mb1530 | methylmalonyl-CoA mutase | 45.95 | 750 | MAV_0857 | methylmalonyl-CoA mutase | 99.32 | 146 | BCG_1556 | methylmalonyl-CoA mutase | 45.95 | 750 | MAP0674 | McmA2 | 146 | 100 |
| MAP4_3191 | Methylmalonyl-CoA mutase | 523 | Rv1493 | Probable methylmalonyl-CoA mutas | 44.17 | 750 | Mb1530 | methylmalonyl-CoA mutase | 44.17 | 750 | MAV_0856 | methylmalonyl-CoA mutase, N-terr | 99.24 | 525 | BCG_1556 | methylmalonyl-CoA mutase | 44.17 | 750 | MAP0673 | hypothetical protein | 530 | 99.81 |
| MAP4_3192 | short chain dehydrogenase | 274 | Rv3224 | Possible iron-regulated short-chain | 53.31 | 282 | Mb3251 | short chain dehydrogenase | 53.31 | 282 | MAV_0855 | short chain dehydrogenase | 99.27 | 274 | BCG_3252 | short chain dehydrogenase | 53.31 | 282 | MAP0672c | short chain dehydrogenase | 274 | 100 |
| MAP4_3193 | methyltransferase-UbiE family protein | 324 | Rv0839 | hypothetical protein | 75.19 | 270 | Mb0862 | hypothetical protein | 75.19 | 270 | MAV_0854 | methyltransferase-UbiE family prot | 99.26 | 270 | BCG_0891 | hypothetical protein | 75.19 | 270 | MAP0671 | hypothetical protein | 324 | 100 |
| MAP4_3194 | lipoprotein LpqR | 245 | Rv0838 | Probable conserved lipoprotein Lpq | 75.24 | 256 | Mb0861 | lipoprotein LpqR | 74.53 | 258 | MAV_0853 | D-alanyl-D-alanine dipeptidase | 98.71 | 232 | BCG_0890 | lipoprotein lpqR | 73.83 | 260 | MAP0670 | hypothetical protein | 245 | 100 |
| MAP4_3195 | Cold shock protein CspA | 67 | Rv3648c | Probable cold shock protein A CspA | 64.18 | 67 | Mb3672c | cold shock protein A | 64.18 | 67 | MAV_0852 | hypothetical protein | 100 | 67 | BCG_3706c | cold shock protein A cspA | 64.18 | 67 | MAP0669 | CspA_2 | 67 | 100 |
| MAP4_3196 | hypothetical protein | 77 | Rv3568c | 3,4-DHSA dioxygenase | 35.48 | 300 | Mb3599c | biphenyl-2,3-diol 1,2-dioxyge | 38.71 | 300 | MAV_0850 | hypothetical protein | 98.7 | 77 | BCG_3633c | biphenyl-2,3-diol 1,2-dioxygen | 35.48 | 300 | MAP4220 | hypothetical protein | 306 | 29.82 |
| MAP4_3197 | putative cytochrome P450 hydroxylase | 426 | Rv1777 | Probable cytochrome P450 144 Cyp1 | 34.26 | 434 | Mb1806 | cytochrome p450 144 CYP144 | 34.26 | 434 | MAV_0849 | cytochrome p450 | 99.3 | 426 | BCG_1810 | cytochrome p450 144 CYP144 | 34.26 | 434 | MAP0668 | hypothetical protein | 426 | 100 |
| MAP4_3198 | ferredoxin | 72 | Rv3503c | Probable ferredoxin FdxD | 45 | 63 | Mb3533c | ferredoxin FdxD | 45 | 63 | MAV_0848 | hypothetical protein | 100 | 72 | BCG_3567c | ferredoxin fdxD | 45 | 63 | MAP0667 | hypothetical protein | 72 | 100 |
| MAP4_3199 | Transcriptional regulator, TetR family | 215 | Rv2506 | Probable transcriptional regulatory | 36.11 | 215 | Mb2534 | TetR family transcriptional re | 36.11 | 215 | MAV_0847 | TetR family transcriptional regulato | 97.28 | 184 | BCG_2526 | TetR family transcriptional regu | 36.11 | 215 | MAP0666c | hypothetical protein | 215 | 100 |
| MAP4_3200 | short-chain dehydrogenasereductase (SDR) family prot | 279 | Rv0687 | Probable short-chain type dehydrog | 48.2 | 275 | Mb0706 | 3-ketoacyl-ACP reductase | 48.2 | 275 | MAV_0846 | carveol dehydrogenase | 98.21 | 279 | BCG_0736 | 3-ketoacyl-ACP reductase | 48.2 | 275 | MAP0665c | hypothetical protein | 279 | 100 |
| MAP4_3201 | transposase, ISmav2 | 395 | Rv0755A | Putative transposase (fragment) | 83.02 | 61 | Mb0778c | transposase | 83.02 | 61 | MAV_0752 | transposase | 29.57 | 345 | BCG_0807c | transposase | 83.02 | 61 | MAP0664c | hypothetical protein | 395 | 100 |
| MAP4_3203 | putative deaminase | 166 | Rv0828c | Possible deaminase | 66.15 | 140 | Mb0851c | deaminase | 66.15 | 140 | MAV_0777 | cytidine/deoxycytidylate deaminas | 100 | 166 | BCG_0881c | deaminase | 66.15 | 140 | MAP0662c | hypothetical protein | 166 | 100 |
| MAP4_3204 | transcriptional regulator, ArsR family | 135 | Rv0827c | Metal sensor transcriptional regulat | 83.08 | 130 | Mb0850c | transcriptional regulator | 83.08 | 130 | MAV_0776 | ArsR family transcriptional regulato | 99.09 | 110 | BCG_0880c | transcriptional regulatory prot | 83.08 | 130 | MAP0661c | hypothetical protein | 135 | 100 |
| MAP4_3205 | hypothetical protein | 67 | Rv1359 | Probable transcriptional regulatory | 34.21 | 250 | Mb1394 | transcriptional regulator | 34.21 | 250 | MAV_0775 | zinc transporter | 98.51 | 67 | BCG_1421 | transcriptional regulator | 34.21 | 250 | MAP2803c | 1-deoxy-D-xylulose-5-phosphate syntha | 641 | 32.65 |
| MAP4_3206 | hypothetical protein | 357 | Rv0826 | hypothetical protein | 82.63 | 351 | Mb0849 | hypothetical protein | 82.07 | 351 | MAV_0774 | hypothetical protein | 98.6 | 357 | BCG_0879 | hypothetical protein | 82.35 | 351 | MAP0660 | hypothetical protein | 357 | 100 |
| MAP4_3207 | hypothetical protein | 204 | Rv0825c | hypothetical protein | 81.37 | 213 | Mb0848c | hypothetical protein | 81.37 | 213 | MAV_0773 | hypothetical protein | 98.96 | 192 | BCG_0878c | hypothetical protein | 81.37 | 213 | MAP0659c | hypothetical protein | 204 | 100 |
| MAP4_3208 | acyl-ACP desaturase | 340 | Rv0824c | Probable acyl-[acyl-carrier protein] | 83.82 | 338 | Mb0847c | acyl-ACP desaturase | 83.82 | 338 | MAV_0772 | fatty acid desaturase | 100 | 340 | BCG_0877c | acyl-ACP desaturase | 83.82 | 338 | MAP0658c | DesA1 | 340 | 100 |
| MAP4_3209 | putative transcriptional regulatory protein,dihyd rouric | 377 | Rv0823c | Possible transcriptional regulatory p | 88.59 | 389 | Mb0846c | transcriptional regulator | 88.59 | 389 | MAV_0771 | dihydrouridine synthase | 98.41 | 377 | BCG_0876c | transcriptional regulatory prot | 88.59 | 389 | MAP0657c | hypothetical protein | 377 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3210 | putative cell envelope-associatedtranscriptional attenu | 674 | Rv0822c | hypothetical protein | 63.41 | 684 | Mb0845c | hypothetical protein | 63.36 | 684 | MAV_0769 | LytR/CpsA/Psr family protein | 98.95 | 662 | BCG_0875c | hypothetical protein | 63.36 | 684 | MAP0656c | hypothetical protein | 674 | 99.85 |
| MAP4_3211 | phosphate-transport system transcriptional regulator p | 222 | Rv0821c | Probable phosphate-transport syste | 93.9 | 213 | Mb0844c | phosphate transport regulato | 93.9 | 213 | MAV_0768 | phosphate transport system regula | 100 | 222 | BCG_0874c | phosphate-transport system tr | 93.9 | 213 | MAP0655c | PhoY2_2 | 222 | 100 |
| MAP4_3212 | phosphate-transport ATP-binding protein ABC transpor | 258 | Rv0820 | Probable phosphate-transport ATP-b | 89.92 | 258 | Mb0843 | phosphate transporter ATP-b | 89.53 | 258 | MAV_0767 | phosphate transporter ATP-binding | 99.61 | 258 | BCG_0872 | phosphate-transport ATP-bindi | 87.59 | 170 | MAP0654 | phosphate transporter ATP-binding pro | 258 | 100 |
| MAP4_3213 | phosphate-transport membrane ABC transporter pstA1 | 304 | Rv0930 | Probable phosphate-transport integ | 54.82 | 308 | Mb0953 | phosphate ABC transporter tr | 54.82 | 304 | MAV_0766 | phosphate ABC transporter permea | 99.34 | 304 | BCG_0982 | phosphate-transport integral m | 54.82 | 304 | MAP0653 | PstA1_1 | 304 | 100 |
| MAP4_3214 | phosphate-transport membrane ABC transporter pstC2 | 331 | Rv0929 | Phosphate-transport integral memb | 57.23 | 324 | Mb0952 | phosphate ABC transporter tr | 57.23 | 324 | MAV_1048 | phosphate ABC transporter permea | 64 | 328 | BCG_0981 | phosphate-transport integral m | 57.23 | 324 | MAP0652 | PstC2_1 | 331 | 100 |
| MAP4_3215 | periplasmic phosphate-binding lipoprotein pstS3 | 365 | Rv0928 | Periplasmic phosphate-binding lipop | 46.48 | 370 | Mb0951 | periplasmic phosphate-bindir | 46.48 | 370 | MAV_1047 | phosphate ABC transporter phosph | 48.25 | 369 | BCG_0980 | periplasmic phosphate-binding | 46.48 | 370 | MAP0651 | PhoS2_1 | 365 | 100 |
| MAP4_3216 | putative acetyltransferase, GNAT family protein | 316 | Rv0819 | GCN5-related N-acetyltransferase, N | 72.06 | 315 | Mb0842 | hypothetical protein | 72.06 | 315 | MAV_0761 | acetyltransferase, GNAT family pro | 99.68 | 316 | BCG_0871 | hypothetical protein | 72.06 | 315 | MAP0650 | hypothetical protein | 316 | 100 |
| MAP4_3217 | transcriptional regulatory protein | 260 | Rv0818 | Transcriptional regulatory protein | 81.2 | 255 | Mb0841 | transcriptional regulator | 81.6 | 255 | MAV_0760 | transcriptional regulator | 100 | 260 | BCG_0870 | transcriptional regulatory prote | 81.6 | 255 | MAP0649 | hypothetical protein | 260 | 100 |
| MAP4_3218 | hypothetical protein | 289 | Rv0817c | Probable conserved exported protei | 71.48 | 270 | Mb0840c | hypothetical protein | 71.48 | 270 | MAV_0759 | hypothetical protein | 100 | 270 | BCG_0869c | hypothetical protein | 71.48 | 270 | MAP0648c | hypothetical protein | 289 | 100 |
| MAP4_3219 | thioredoxin | 139 | Rv0816c | Probable thioredoxin ThiX | 66.43 | 140 | Mb0839c | thioredoxin | 66.43 | 140 | MAV_0758 | thioredoxin | 99.28 | 139 | BCG_0868c | thioredoxin thiX | 66.43 | 140 | MAP0647c | ThiX | 139 | 100 |
| MAP4_3220 | hypothetical protein | 156 | Rv3581c | Probable 2C-methyl-D-erythritol 2,4 | 40.54 | 159 | Mb3612c | 2-C-methyl-D-erythritol 2,4-cy | 40.54 | 159 | MAV_0757 | integral membrane protein | 99.36 | 156 | BCG_3646c | 2-C-methyl-D-erythritol 2,4-cyc | 40.54 | 159 | MAP0646c | hypothetical protein | 156 | 100 |
| MAP4_3221 | thiosulfate sulfurtransferase | 277 | Rv0815c | Probable thiosulfate sulfurtransferas | 90.25 | 277 | Mb0838c | thiosulfate sulfurtransferase | 90.25 | 277 | MAV_0756 | thiosulfate sulfurtransferase | 99.28 | 277 | BCG_0867c | thiosulfate sulfurtransferase cy | 90.25 | 277 | MAP0645c | CysA3 | 277 | 100 |
| MAP4_3222 | hypothetical protein | 100 | Rv0814c | Conserved protein SseC2 | 94.95 | 100 | Mb0837c | hypothetical protein | 94.95 | 100 | MAV_0755 | SseC protein | 98.91 | 92 | BCG_0866c | hypothetical protein | 94.95 | 100 | MAP0644c | SseC | 100 | 100 |
| MAP4_3223 | hypothetical protein | 235 | Rv0813c | hypothetical protein | 88.29 | 226 | Mb0836c | hypothetical protein | 88.29 | 226 | MAV_0753 | hypothetical protein | 98.51 | 202 | BCG_0865c | hypothetical protein | 88.29 | 226 | MAP0643c | hypothetical protein | 235 | 100 |
| MAP4_3224 | amino acid aminotransferase | 289 | Rv0812 | Probable amino acid aminotransfera | 82.35 | 289 | Mb0835 | 4-amino-4-deoxychorismate l | 82.35 | 289 | MAV_0751 | 4-amino-4-deoxychorismate lyase | 99.31 | 289 | BCG_0864 | 4-amino-4-deoxychorismate ly | 82.35 | 289 | MAP0642 | 4-amino-4-deoxychorismate lyase | 289 | 100 |
| MAP4_3225 | glycine cleavage T-protein, aminomethyltransferase | 364 | Rv0811c | hypothetical protein | 79.61 | 368 | Mb0834c | hypothetical protein | 79.61 | 368 | MAV_0750 | glycine cleavage T-protein (aminom | 99.18 | 364 | BCG_0863c | hypothetical protein | 79.61 | 368 | MAP0641c | hypothetical protein | 364 | 100 |
| MAP4_3226 | hypothetical protein | 61 | Rv0810c | hypothetical protein | 97.44 | 60 | Mb0833c | hypothetical protein | 97.44 | 60 | MAV_0749 | hypothetical protein | 100 | 61 | BCG_0862c | hypothetical protein | 97.44 | 60 | MAP0640c | hypothetical protein | 61 | 100 |
| MAP4_3227 | phosphoribosylformylglycinamidine cyclo-ligase purM | 364 | Rv0809 | Probable phosphoribosylformylglyci | 89.84 | 364 | Mb0832 | phosphoribosylaminoimidazo | 89.84 | 364 | MAV_0748 | phosphoribosylaminoimidazole syn | 100 | 364 | BCG_0861 | phosphoribosylaminoimidazole | 89.84 | 364 | MAP0639 | phosphoribosylaminoimidazole synthet | 364 | 100 |
| MAP4_3228 | amidophosphoribosyltransferase | 551 | Rv0808 | Amidophosphoribosyltransferase Pu | 93.26 | 527 | Mb0831 | amidophosphoribosyltransfer | 93.26 | 527 | MAV_0747 | amidophosphoribosyltransferase | 99.8 | 508 | BCG_0860 | amidophosphoribosyltransfera | 93.26 | 527 | MAP0638 | amidophosphoribosyltransferase | 551 | 100 |
| MAP4_3229 | hypothetical protein | 131 | Rv0807 | hypothetical protein | 71.09 | 129 | Mb0830 | hypothetical protein | 71.09 | 129 | MAV_0746 | hypothetical protein | 99.22 | 129 | BCG_0859 | hypothetical protein | 71.09 | 129 | MAP0637 | hypothetical protein | 131 | 100 |
| MAP4_3230 | conserved hypothetical protein, CAAX protease family | 216 | Rv0804 | hypothetical protein | 65.84 | 209 | Mb0827 | hypothetical protein | 65.84 | 209 | MAV_0745 | caax amino protease | 97.22 | 216 | BCG_0856 | hypothetical protein | 65.84 | 209 | MAP0636 | hypothetical protein | 216 | 100 |
| MAP4_3231 | phosphoribosylformylglycinamidine synthase II | 765 | Rv0803 | Phosphoribosylformylglycinamidine | 91.63 | 754 | Mb0826 | phosphoribosylformylglycinar | 91.63 | 754 | MAV_0744 | phosphoribosylformylglycinamidine | 99.48 | 765 | BCG_0855 | phosphoribosylformylglycinam | 91.63 | 754 | MAP0635 | phosphoribosylformylglycinamidine syn | 765 | 100 |
| MAP4_3232 | hypothetical protein | 84 | Rv2024c | hypothetical protein | 44.44 | 515 | Mb2049c | hypothetical protein | 44.44 | 1606 | MAV_2170 | acyl carrier protein | 23.81 | 80 | BCG_2043c | hypothetical protein | 44.44 | 1606 | MAP0634c | hypothetical protein | 84 | 100 |
| MAP4_3233 | putative glyoxalase family protein | 115 | Rv0801 | hypothetical protein | 75.89 | 115 | Mb0824 | hypothetical protein | 75.89 | 115 | MAV_0743 | glyoxalase | 98.26 | 115 | BCG_0853 | hypothetical protein | 75.89 | 115 | MAP0633 | hypothetical protein | 115 | 100 |
| MAP4_3234 | aminopeptidase | 432 | Rv0800 | Probable aminopeptidase PepC | 82.63 | 433 | Mb0823 | aminopeptidase | 82.86 | 433 | MAV_0742 | aminopeptidase | 99.31 | 435 | BCG_0852 | aminopeptidase 2 | 82.86 | 433 | MAP0632 | aminopeptidase 2 | 432 | 100 |
| MAP4_3235 | Dyp-type peroxidase | 336 | Rv0799c | hypothetical protein | 79.76 | 335 | Mb0822c | hypothetical protein | 79.76 | 335 | MAV_0741 | Dyp-type peroxidase | 99.11 | 336 | BCG_0851c | hypothetical protein | 79.76 | 335 | MAP0631c | hypothetical protein | 354 | 99.7 |
| MAP4_3236 | 29 kDa antigen | 265 | Rv0798c | 29 KDa antigen CFP29 | 86.74 | 265 | Mb0821c | hypothetical protein | 86.74 | 265 | MAV_0740 | 29 kDa antigen Cfp29 | 100 | 265 | BCG_0850c | 29 kDa antigen cfp29 | 86.74 | 265 | MAP0630c | hypothetical protein | 265 | 100 |
| MAP4_3237 | hypothetical protein | 155 | Rv0035 | Probable fatty-acid-CoA ligase FadD | 29.67 | 562 | Mb0036 | fatty-acid--CoA ligase | 29.67 | 562 | MAV_0739 | cupin domain-containing protein | 98.71 | 155 | BCG_0066 | fatty-acid-CoA ligase | 29.67 | 562 | MAP0629c | hypothetical protein | 155 | 100 |
| MAP4_3238 | Transcriptional regulator, GntR family | 273 | Rv0792c | Probable transcriptional regulatory | 70.85 | 269 | Mb0816c | GntR family transcriptional re | 70.85 | 269 | MAV_0738 | mercuric reductase/transcriptional | 98.9 | 273 | BCG_0845c | GntR family transcriptional reg | 70.85 | 269 | MAP0628c | hypothetical protein | 273 | 100 |
| MAP4_3239 | hypothetical protein | 172 | Rv0789c | Hypothetical protein | 56.96 | 199 | Mb0813c | hypothetical protein | 56.96 | 199 | MAV_0737 | hypothetical protein | 98.21 | 168 | BCG_0842c | hypothetical protein | 56.96 | 199 | MAP0627c | hypothetical protein | 172 | 100 |
| MAP4_3240 | phosphoribosylformylglycinamidine synthase I | 224 | Rv0788 | Probable phosphoribosylformylglyci | 91.52 | 224 | Mb0812 | phosphoribosylformylglycinar | 91.52 | 224 | MAV_0736 | phosphoribosylformylglycinamidine | 100 | 224 | BCG_0841 | phosphoribosylformylglycinam | 91.52 | 224 | MAP0626 | phosphoribosylformylglycinamidine syn | 224 | 100 |
| MAP4_3241 | phosphoribosylformylglycinamidine synthase,PurS sub | 79 | Rv0787A | hypothetical protein | 88.61 | 79 | Mb0811 | phosphoribosylformylglycinar | 88.61 | 79 | MAV_0735 | phosphoribosylformylglycinamidine | 100 | 79 | BCG_0840 | phosphoribosylformylglycinam | 88.61 | 79 | MAP0625 | phosphoribosylformylglycinamidine syn | 79 | 100 |
| MAP4_3242 | hypothetical protein | 244 | Rv0787 | hypothetical protein | 67.62 | 319 | Mb0810 | hypothetical protein | 68.03 | 319 | MAV_0734 | hypothetical protein | 99.13 | 230 | BCG_0839 | hypothetical protein | 68.03 | 319 | MAP0624 | hypothetical protein | 244 | 100 |
| MAP4_3243 | putative metallo-beta-lactamase superfamily protein | 212 | Rv0786c | hypothetical protein | 87.6 | 129 | Mb0809c | hypothetical protein | 87.6 | 129 | MAV_0733 | metallo-beta-lactamase, putative | 99.53 | 212 | BCG_0838c | hypothetical protein | 87.6 | 129 | MAP0622c | hypothetical protein | 129 | 99.22 |
| MAP4_3244 | putative FAD-binding dehydrogenase | 550 | Rv0785 | hypothetical protein | 86.95 | 566 | Mb0808 | hypothetical protein | 85.56 | 368 | MAV_0732 | FAD-binding dehydrogenase | 99.45 | 555 | BCG_0837 | hypothetical protein | 85.56 | 368 | MAP0621 | FAD-binding dehydrogenase | 550 | 100 |
| MAP4_3245 | hypothetical protein | 234 | Rv0784 | hypothetical protein | 84.21 | 228 | Mb0806 | hypothetical protein | 84.21 | 228 | MAV_0731 | hypothetical protein | 98.26 | 230 | BCG_0835 | hypothetical protein | 84.21 | 228 | MAP0620 | hypothetical protein | 234 | 100 |
| MAP4_3246 | multidrug resistance membrane efflux protein emrB | 538 | Rv0783c | Possible multidrug resistance integra | 66.36 | 540 | Mb0805c | multidrug resistance integral | 66.36 | 540 | MAV_0730 | EmrB efflux protein | 98.88 | 560 | BCG_0834c | multidrug resistance integral m | 66.36 | 540 | MAP0619c | hypothetical protein | 538 | 100 |
| MAP4_3247 | multidrug resistance membrane efflux protein emrB | 537 | Rv0783c | Possible multidrug resistance integra | 63.13 | 540 | Mb0805c | multidrug resistance integral | 63.13 | 540 | MAV_0729 | EmrB efflux protein | 99.81 | 537 | BCG_0834c | multidrug resistance integral m | 63.13 | 540 | MAP0618c | hypothetical protein | 537 | 99.81 |
| MAP4_3248 | Transcriptional regulator, TetR family | 187 | Rv0653c | Possible transcriptional regulatory p | 31.25 | 231 | Mb0672c | TetR family transcriptional re | 31.25 | 231 | MAV_0728 | TetR family transcriptional regulato | 98.4 | 187 | BCG_0702c | TetR family transcriptional regu | 31.25 | 231 | MAP0617 | hypothetical protein | 187 | 100 |
| MAP4_3249 | hypothetical protein | 148 | Rv1254 | Probable acyltransferase | 29.31 | 383 | Mb1286 | acyltransferase | 29.31 | 383 | MAV_0726 | hypothetical protein | 99.32 | 158 | BCG_1314 | acyltransferase | 29.31 | 383 | MAP0616c | hypothetical protein | 148 | 100 |
| MAP4_3250 | Protease II PtrBb | 720 | Rv0782 | Probable protease II PtrBb [second p | 79.96 | 552 | Mb0804 | oligopeptidase B | 80.37 | 719 | MAV_0727 | protease 2 | 99.03 | 720 | BCG_0833 | protease II ptrB (oligopeptidase | 80.37 | 719 | MAP0615 | PtrBa | 720 | 100 |
| MAP4_3251 | phosphoribosylaminoimidazole-succinocarboxamide sy | 296 | Rv0780 | Phosphoribosylaminoimidazole-succ | 87.8 | 297 | Mb0803 | phosphoribosylaminoimidazo | 87.8 | 297 | MAV_0725 | phosphoribosylaminoimidazole-suc | 99.66 | 296 | BCG_0832 | phosphoribosylaminoimidazole | 87.8 | 297 | MAP0614 | phosphoribosylaminoimidazole-succino | 296 | 100 |
| MAP4_3252 | hypothetical protein | 206 | Rv0779c | Possible conserved transmembrane | 71.71 | 206 | Mb0802c | transmembrane protein | 71.71 | 206 | MAV_0724 | hypothetical protein | 99.03 | 206 | BCG_0831c | hypothetical protein | 71.71 | 206 | MAP0613c | hypothetical protein | 206 | 100 |
| MAP4_3253 | putative cytochrome P450 hydroxylase | 415 | Rv0778 | Possible cytochrome P450 126 Cyp1 | 80.15 | 414 | Mb0801 | cytochrome P450 126 | 80.15 | 414 | MAV_0723 | P450 monooxygenase | 99.28 | 415 | BCG_0830 | cytochrome P450 126 cyp126 | 79.9 | 414 | MAP0612 | hypothetical protein | 415 | 100 |
| MAP4_3254 | adenylosuccinate lyase | 472 | Rv0777 | Probable adenylosuccinate lyase Pu | 88.35 | 472 | Mb0800 | adenylosuccinate lyase | 88.56 | 472 | MAV_0722 | adenylosuccinate lyase | 99.36 | 472 | BCG_0829 | adenylosuccinate lyase | 88.56 | 472 | MAP0611 | adenylosuccinate lyase | 472 | 100 |
| MAP4_3255 | hypothetical protein | 263 | Rv0776c | hypothetical protein | 69.02 | 259 | Mb0799c | hypothetical protein | 69.02 | 259 | MAV_0720 | hypothetical protein | 98.48 | 263 | BCG_0828c | hypothetical protein | 69.02 | 259 | MAP0610c | hypothetical protein | 263 | 100 |
| MAP4_3256 | Transcriptional regulator, TetR family | 205 | Rv0775 | hypothetical protein | 89.66 | 207 | Mb0798 | hypothetical protein | 89.66 | 207 | MAV_0721 | TetR family transcriptional regulato | 99.47 | 189 | BCG_0827 | hypothetical protein | 89.66 | 207 | MAP0609 | hypothetical protein | 205 | 100 |
| MAP4_3257 | hypothetical protein | 319 | Rv0774c | Probable conserved exported protei | 78.69 | 303 | Mb0797c | hypothetical protein | 78.69 | 303 | MAV_0719 | esterase | 99.35 | 306 | BCG_0826c | hypothetical protein | 79.02 | 303 | MAP0608c | hypothetical protein | 319 | 100 |
| MAP4_3258 | bifunctional acylase GgtA | 542 | Rv0773c | Probable bifunctional acylase GgtA: | 80.78 | 512 | Mb0796c | bifunctional cephalosporin ac | 80.78 | 512 | MAV_0717 | gamma-glutamyltransferase | 98.1 | 527 | BCG_0825c | bifunctional acylase ggtA: ceph | 80.78 | 512 | MAP0607c | GgtA | 542 | 100 |
| MAP4_3259 | phosphoribosylamine-glycine ligase PurD | 422 | Rv0772 | Probable phosphoribosylamine--gly | 84.83 | 422 | Mb0795 | phosphoribosylamine--glycine | 84.83 | 422 | MAV_0718 | phosphoribosylamine--glycine ligas | 99.29 | 422 | BCG_0824 | phosphoribosylamine--glycine | 84.83 | 422 | MAP0606 | phosphoribosylamine--glycine ligase | 422 | 100 |
| MAP4_3260 | 4-carboxymuconolactone decarboxylase | 145 | Rv0771 | Possible 4-carboxymuconolactone d | 60.28 | 144 | Mb0794 | 4-carboxymuconolactone dec | 60.28 | 144 | MAV_0716 | hypothetical protein | 100 | 146 | BCG_0823 | 4-carboxymuconolactone deca | 60.28 | 144 | MAP0605 | hypothetical protein | 146 | 100 |
| MAP4_3261 | dehydrogenasereductase | 292 | Rv0770 | Probable dehydrogenase/reductase | 68.77 | 295 | Mb0793 | dehydrogenase/reductase | 68.42 | 295 | MAV_0715 | oxidoreductase | 99.32 | 292 | BCG_0822 | dehydrogenase/reductase | 68.77 | 295 | MAP0604 | hypothetical protein | 292 | 100 |
| MAP4_3262 | dehydrogenasereductase | 249 | Rv0769 | Probable dehydrogenase/reductase | 80.57 | 248 | Mb0792 | short chain dehydrogenase | 80.16 | 248 | MAV_0714 | short chain dehydrogenase | 100 | 249 | BCG_0821 | short chain dehydrogenase | 80.16 | 248 | MAP0603 | short chain dehydrogenase | 249 | 100 |
| MAP4_3263 | aldehyde dehydrogenase NAD-dependent AldA | 489 | Rv0768 | Probable aldehyde dehydrogenase N | 83.78 | 489 | Mb0791 | aldehyde dehydrogenase | 83.78 | 489 | MAV_0713 | aldehyde dehydrogenase (NAD) far | 99.18 | 489 | BCG_0820 | aldehyde dehydrogenase AldA | 83.78 | 489 | MAP0602 | AldA_1 | 489 | 100 |
| MAP4_3264 | Transcriptional regulator, TetR family | 215 | Rv0767c | hypothetical protein | 75.96 | 213 | Mb0790c | hypothetical protein | 75.96 | 213 | MAV_0711 | TetR family transcriptional regulato | 100 | 215 | BCG_0819c | hypothetical protein | 75.96 | 213 | MAP0601c | hypothetical protein | 215 | 100 |
| MAP4_3265 | putative cytochrome P450 hydroxylase | 408 | Rv0766c | Probable cytochrome P450 123 Cyp1 | 72.3 | 402 | Mb0789c | cytochrome P450 123 | 72.3 | 402 | MAV_0916 | cytochrome P450 monooxygenase | 37.47 | 401 | BCG_0818c | cytochrome P450 123 cyp123 | 71.51 | 541 | MAP0600c | hypothetical protein | 408 | 100 |
| MAP4_3266 | oxidoreductase, short-chaindehydrogenase/reductase | 275 | Rv0765c | Probable oxidoreductase | 72.73 | 275 | Mb0788c | short chain dehydrogenase | 72.73 | 275 | MAV_0709 | short chain dehydrogenase | 100 | 275 | BCG_0817c | short chain dehydrogenase | 72.73 | 275 | MAP0599c | short chain dehydrogenase | 275 | 100 |
| MAP4_3267 | cytochrome P450 51 Cyp51 | 451 | Rv0764c | Cytochrome P450 51 Cyp51 (CYPL1) | 79.29 | 451 | Mb0787c | cytochrome P450 sterol 14-al | 79.29 | 451 | MAV_0708 | cytochrome P450 51 | 99.78 | 451 | BCG_0816c | cytochrome P450 51 cyp51 | 79.29 | 451 | MAP0598c | hypothetical protein | 451 | 100 |
| MAP4_3268 | ferredoxin | 69 | Rv0763c | Possible ferredoxin | 75 | 68 | Mb0786c | ferredoxin | 75 | 68 | MAV_0707 | hypothetical protein | 100 | 69 | BCG_0815c | ferredoxin | 75 | 68 | MAP0597c | hypothetical protein | 69 | 100 |
| MAP4_3269 | hypothetical protein | 182 | Rv0762c | hypothetical protein | 65.56 | 181 | Mb0785c | hypothetical protein | 65.56 | 181 | MAV_0706 | hypothetical protein | 99.45 | 182 | BCG_0814c | hypothetical protein | 65.56 | 181 | MAP0596c | hypothetical protein | 182 | 100 |
| MAP4_3270 | zinc-containing alcohol dehydrogenase NAD dependen | 375 | Rv0761c | Possible zinc-containing alcohol deh | 87.2 | 375 | Mb0784c | NAD dependent zinc-containi | 87.2 | 375 | MAV_0705 | alcohol dehydrogenase B | 100 | 375 | BCG_0813c | zinc-containing alcohol dehydr | 87.2 | 375 | MAP0595c | AdhB | 375 | 100 |
| MAP4_3271 | conserved hypothetical protein, nuclear transport fact | 136 | Rv0760c | hypothetical protein | 78.42 | 139 | Mb0783c | hypothetical protein | 78.42 | 139 | MAV_0704 | steroid delta-isomerase | 97.14 | 140 | BCG_0812c | hypothetical protein | 78.42 | 139 | MAP0594c | hypothetical protein | 136 | 100 |
| MAP4_3272 | conserved hypothetical protein, histidine triad (HIT) do | 134 | Rv0759c | hypothetical protein | 85.45 | 110 | Mb0782c | hypothetical protein | 85.45 | 110 | MAV_0702 | HIT domain-containing protein | 99.25 | 134 | BCG_0811c | hypothetical protein | 85.45 | 110 | MAP0593c | hypothetical protein | 134 | 100 |
| MAP4_3273 | two component system sensor kinase PhoR | 478 | Rv0758 | Possible two component system res | 77.16 | 485 | Mb0781 | two component system respo | 76.94 | 485 | MAV_0703 | sensor histidine kinase | 99.79 | 478 | BCG_0810 | two component system respon | 76.94 | 485 | MAP0592 | PhoR | 478 | 100 |
| MAP4_3274 | two component system transcriptional regulator PhoP | 239 | Rv0757 | Possible two component system res | 93.75 | 247 | Mb0780 | two component system respo | 93.75 | 247 | MAV_0701 | DNA-binding response regulator Ph | 99.58 | 239 | BCG_0809 | two component system respon | 93.75 | 247 | MAP0591 | PhoP | 239 | 100 |
| MAP4_3275 | hypothetical protein | 238 | Rv0756c | hypothetical protein | 80.45 | 241 | Mb0779c | hypothetical protein | 80.45 | 241 | MAV_0700 | hypothetical protein | 100 | 238 | BCG_0808c | hypothetical protein | 80.45 | 241 | MAP3452c | hypothetical protein | 342 | 57.89 |
| MAP4_3276 | transposase | 395 | Rv0755A | Putative transposase (fragment) | 90.57 | 61 | Mb0778c | transposase | 90.57 | 61 | MAV_0752 | transposase | 28.75 | 345 | BCG_0807c | transposase | 90.57 | 61 | MAP0428 | hypothetical protein | 395 | 100 |
| MAP4_3277 | hypothetical protein | 632 | Rv3762c | Possible hydrolase | 31.58 | 626 | Mb3788c | hydrolase | 31.58 | 626 | MAV_0683 | hypothetical protein | 98.1 | 632 | BCG_3821c | hydrolase | 31.58 | 626 | MAP0588 | hypothetical protein | 632 | 100 |
| MAP4_3278 | hypothetical protein | 249 | Rv1291c | Conserved hypothetical secreted pr | 35.71 | 111 | Mb1323c | hypothetical protein | 35.71 | 111 | MAV_0682 | hypothetical protein | 97.99 | 249 | BCG_1351c | hypothetical protein | 35.71 | 111 | MAP0587 | hypothetical protein | 157 | 100 |
| MAP4_3279 | hypothetical protein | 313 | Rv1230c | Possible membrane protein | 30.32 | 411 | Mb1262c | hypothetical protein | 30.32 | 411 | MAV_0681 | transglycosylase | 99.36 | 313 | BCG_1290c | hypothetical protein | 30.32 | 411 | MAP0586c | hypothetical protein | 313 | 100 |
| MAP4_3280 | hypothetical protein | 341 | Rv0352 | Probable chaperone protein DnaJ1 | 52 | 395 | Mb0360 | molecular chaperone DnaJ | 52 | 395 | MAV_0680 | hypothetical protein | 88.34 | 319 | BCG_0391 | chaperone protein DnaJ | 52 | 395 | MAP0585 | hypothetical protein | 341 | 100 |
| MAP4_3281 | 19 kda lipoprotein antigen precursor | 156 | Rv3763 | 19 kDa lipoprotein antigen precurso | 47.53 | 159 | Mb3789 | hypothetical protein | 47.53 | 159 | MAV_0679 | lipoprotein LpqH | 98.65 | 148 | BCG_3822 | 19 kDa lipoprotein antigen pre | 47.53 | 159 | MAP0584 | hypothetical protein | 156 | 100 |
| MAP4_3282 | hypothetical protein | 222 | Rv1815 | hypothetical protein | 27.32 | 221 | Mb1845 | hypothetical protein | 27.18 | 221 | MAV_0678 | hypothetical protein | 100 | 222 | BCG_1849 | hypothetical protein | 27.18 | 221 | MAP0583 | hypothetical protein | 222 | 100 |
| MAP4_3283 | peroxidase BpoA | 289 | Rv3473c | Possible peroxidase BpoA (non-haer | 80 | 261 | Mb3502c | peroxidase BpoA | 80 | 261 | MAV_0677 | alpha/beta hydrolase | 98.96 | 289 | BCG_3538c | peroxidase bpoA | 80 | 261 | MAP0582 | BpoA | 261 | 99.62 |
| MAP4_3284 | putative amidase | 498 | Rv2888c | Probable amidase AmiC (aminohydr | 38.29 | 473 | Mb2912c | amidase | 38.29 | 473 | MAV_0676 | 6-aminohexanoate-cyclic-dimer hy | 99.19 | 492 | BCG_2909c | amidase | 38.29 | 473 | MAP0581c | hypothetical protein | 498 | 100 |
| MAP4_3285 | hypothetical protein | 58 | Rv1832 | Probable glycine dehydrogenase Gc | 46.43 | 941 | Mb1863 | glycine dehydrogenase | 46.43 | 941 | MAV_0675 | hypothetical protein | 100 | 58 | BCG_1867 | glycine dehydrogenase | 46.43 | 941 | MAP4222c | AtfA_1 | 381 | 52.94 |
| MAP4_3286 | hypothetical protein | 81 | Rv1844c | Probable 6-phosphogluconate dehy | 28.81 | 485 | Mb1875c | 6-phosphogluconate dehydro | 43.33 | 685 | MAV_0674 | hypothetical protein | 98.77 | 80 | BCG_1880c | 6-phosphogluconate dehydrog | 43.33 | 685 | MAP0580c | hypothetical protein | 80 | 98.77 |
| MAP4_3287 | putative cell envelope-associated transcriptional atten | 520 | Rv3484 | Possible conserved protein CpsA | 76.15 | 512 | Mb3514 | hypothetical protein | 76.15 | 512 | MAV_0673 | cell envelope-related function tran | 99.81 | 521 | BCG_3548 | protein cpsA | 76.15 | 512 | MAP0579c | CpsA | 520 | 100 |
| MAP4_3288 | oxidoreductase | 263 | Rv1350 | Probable 3-oxoacyl-[acyl-carrier pro | 34.11 | 247 | Mb1385 | 3-ketoacyl-ACP reductase | 34.11 | 247 | MAV_0672 | oxidoreductase | 99.62 | 263 | BCG_1412 | 3-ketoacyl-ACP reductase | 34.11 | 247 | MAP0578 | hypothetical protein | 263 | 100 |
| MAP4_3289 | short-chain type dehydrogenasereductase | 281 | Rv3485c | Probable short-chain type dehydrog | 79.36 | 314 | Mb3515c | short chain dehydrogenase | 79.36 | 314 | MAV_0671 | short chain dehydrogenase | 99.64 | 281 | BCG_3549c | short chain dehydrogenase | 79.36 | 314 | MAP0577 | short chain dehydrogenase | 281 | 100 |
| MAP4_3290 | Enoyl-CoA hydratase EchA13 | 314 | Rv1935c | Possible enoyl-CoA hydratase EchA1 | 62.33 | 318 | Mb1970c | enoyl-CoA hydratase | 62.33 | 318 | MAV_0670 | enoyl-CoA hydratase | 100 | 311 | BCG_1974c | enoyl-CoA hydratase | 62.33 | 318 | MAP0576 | enoyl-CoA hydratase | 314 | 100 |
| MAP4_3291 | hypothetical protein | 260 | Rv3000 | Possible conserved transmembrane | 50.52 | 219 | Mb3025 | transmembrane protein | 50.52 | 219 | MAV_0669 | hypothetical protein | 100 | 260 | BCG_3022 | hypothetical protein | 50.52 | 219 | MAP0575 | hypothetical protein | 260 | 100 |
| MAP4_3292 | phosphate-transport ATP-binding protein ABC transpor | 228 | Rv0933 | Phosphate-transport ATP-binding pr | 42.11 | 276 | Mb0843 | phosphate transporter ATP-b | 38.5 | 258 | MAV_0668 | ABC transporter ATP-binding prote | 99.12 | 234 | BCG_2412c | sulfate-transport ATP-binding p | 39.23 | 351 | MAP0574 | hypothetical protein | 222 | 99.55 |
| MAP4_3293 | hypothetical protein | 54 | Rv3489 | hypothetical protein | 88.89 | 54 | Mb3519 | hypothetical protein | 88.89 | 54 | MAV_0667 | hypothetical protein | 100 | 54 | BCG_3553 | hypothetical protein | 88.89 | 54 | MAP0798 | hypothetical protein | 381 | 32.5 |
| MAP4_3294 | alpha,alpha-trehalose-phosphate synthase OtsA | 492 | Rv3490 | Alpha, alpha-trehalose-phosphate sy | 82.49 | 500 | Mb3520 | alpha,alpha-trehalose-phosph | 82.7 | 500 | MAV_0666 | UDP-forming alpha,alpha-trehalose | 99.59 | 492 | BCG_3554 | alpha, alpha-trehalose-phospha | 82.7 | 500 | MAP0573c | hypothetical protein | 492 | 100 |
| MAP4_3295 | hypothetical protein | 192 | Rv3491 | hypothetical protein | 74.48 | 192 | Mb3521 | hypothetical protein | 74.48 | 192 | MAV_0665 | hypothetical protein | 99.48 | 192 | BCG_3555 | hypothetical protein | 74.48 | 192 | MAP0572c | hypothetical protein | 192 | 100 |
| MAP4_3296 | Mce associated protein | 163 | Rv3492c | Conserved hypothetical Mce associa | 76.73 | 160 | Mb3522c | Mce associated protein | 76.73 | 160 | MAV_0664 | hypothetical protein | 99.39 | 163 | BCG_3556c | Mce-associated protein | 76.73 | 160 | MAP0571 | hypothetical protein | 164 | 100 |
| MAP4_3297 | Mce associated alanine and valine rich protein | 243 | Rv3493c | Conserved hypothetical Mce associa | 72.03 | 242 | Mb3523c | Mce associated alanine and v | 72.03 | 242 | MAV_0663 | hypothetical protein | 99.59 | 243 | BCG_3557c | Mce-associated protein | 72.03 | 242 | MAP0570 | hypothetical protein | 243 | 100 |
| MAP4_3298 | MCE-family protein MCE4F | 533 | Rv3494c | Mce-family protein Mce4F | 85.78 | 564 | Mb3524c | MCE-family protein MCE4F | 85.78 | 564 | MAV_0953 | mce-family protein mce1f | 38.63 | 575 | BCG_3558c | Mce-family protein mce4F | 85.78 | 564 | MAP0569 | hypothetical protein | 533 | 100 |
| MAP4_3299 | MCE-family lipoprotein LprN | 384 | Rv3495c | Possible Mce-family lipoprotein Lpr | 82.03 | 384 | Mb3525c | MCE-family lipoprotein LprN | 82.03 | 384 | MAV_0661 | virulence factor Mce | 100 | 381 | BCG_3559c | mce family lipoprotein LprN | 82.03 | 384 | MAP0568 | hypothetical protein | 384 | 100 |
| MAP4_3300 | MCE-family protein MCE4D | 475 | Rv3496c | Mce-family protein Mce4D | 79.53 | 451 | Mb3526c | MCE-family protein MCE4D | 79.53 | 451 | MAV_0660 | virulence factor Mce | 99.37 | 475 | BCG_3560c | Mce-family protein mce4D | 79.53 | 451 | MAP0567 | hypothetical protein | 475 | 100 |
| MAP4_3301 | MCE-family protein MCE4C | 354 | Rv3497c | Mce-family protein Mce4C | 81.2 | 357 | Mb3527c | MCE-family protein MCE4C | 81.2 | 357 | MAV_0659 | virulence factor Mce | 99.44 | 354 | BCG_3561c | Mce-family protein mce4C | 81.2 | 357 | MAP0566 | hypothetical protein | 354 | 100 |
| MAP4_3302 | MCE-family protein MCE4B | 350 | Rv3498c | Mce-family protein Mce4B | 83.43 | 350 | Mb3528c | MCE-family protein MCE4B | 83.43 | 350 | MAV_0658 | virulence factor Mce | 99.43 | 350 | BCG_3562c | Mce-family protein mce4B | 83.43 | 350 | MAP0565 | hypothetical protein | 350 | 100 |
| MAP4_3303 | MCE-family protein MCE4A | 400 | Rv3499c | Mce-family protein Mce4A | 84.25 | 400 | Mb3529c | MCE-family protein MCE4A | 84.25 | 400 | MAV_0657 | virulence factor Mce | 99.48 | 384 | BCG_3563c | Mce-family protein mce4A | 84.25 | 400 | MAP0564 | Mce4 | 379 | 100 |
| MAP4_3304 | putative membrane protein YrbE4B | 280 | Rv3500c | Conserved integral membrane prote | 92.14 | 280 | Mb3530c | hypothetical protein | 92.14 | 280 | MAV_0656 | ABC transporter transmembrane pr | 99.64 | 280 | BCG_3564c | integral membrane protein Yrb | 92.14 | 280 | MAP0563 | hypothetical protein | 280 | 100 |
| MAP4_3305 | putative membrane protein YrbE4A | 254 | Rv3501c | Conserved integral membrane prote | 94.88 | 254 | Mb3531c | hypothetical protein | 94.88 | 254 | MAV_0655 | hypothetical protein | 100 | 254 | BCG_3565c | integral membrane protein Yrb | 94.88 | 254 | MAP0562 | hypothetical protein | 254 | 100 |
| MAP4_3306 | short-chain type dehydrogenasereductase | 304 | Rv3502c | Probable short-chain type dehydrog | 80.39 | 317 | Mb3532c | 3-ketoacyl-ACP reductase | 80.39 | 317 | MAV_0654 | 3-ketoacyl-(acyl-carrier-protein) re | 99.65 | 289 | BCG_3566c | 3-ketoacyl-ACP reductase | 80.39 | 317 | MAP0561 | 3-ketoacyl-ACP reductase | 304 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3307 | ferredoxin | 63 | Rv3503c | Probable ferredoxin FdxD | 93.65 | 63 | Mb3533c | ferredoxin FdxD | 93.65 | 63 | MAV_0653 | hypothetical protein | 100 | 63 | BCG_3567c | ferredoxin fdxD | 93.65 | 63 | MAP0560 | FdxD | 63 | 100 |
| MAP4_3308 | acyl-CoA dehydrogenase FadE26 | 392 | Rv3504 | Probable acyl-CoA dehydrogenase F | 88.16 | 400 | Mb3534 | acyl-CoA dehydrogenase | 88.16 | 400 | MAV_0652 | acyl-CoA dehydrogenase | 99.74 | 392 | BCG_3568 | acyl-CoA dehydrogenase fadE2 | 88.16 | 400 | MAP0559c | FadE26_1 | 392 | 100 |
| MAP4_3311 | fatty-acid-CoA synthetase FadD17 | 503 | Rv3506 | Fatty-acid-CoA synthetase FadD17 (f | 83.87 | 502 | Mb3536 | acyl-CoA synthetase | 83.87 | 502 | MAV_0650 | acyl-CoA synthetase | 99.6 | 503 | BCG_3570 | acyl-CoA synthetase | 83.87 | 502 | MAP0556c | acyl-CoA synthetase | 503 | 100 |
| MAP4_3312 | hypothetical protein | 70 | Rv1619 | hypothetical protein | 33.33 | 484 | Mb1645 | hypothetical protein | 33.33 | 484 | MAV_0649 | hypothetical protein | 98.57 | 93 | BCG_1657 | hypothetical protein | 33.33 | 484 | MAP0555c | hypothetical protein | 70 | 100 |
| MAP4_3313 | hypothetical protein | 252 | Rv0355c | PPE family protein PPE8 | 30.65 | 3300 | Mb0362c | PPE family protein | 30.65 | 3507 | MAV_0647 | hypothetical protein | 99.58 | 237 | BCG_0393c | PPE family protein | 30.65 | 3507 | MAP0554c | hypothetical protein | 252 | 100 |
| MAP4_3315 | putative amidohydrolase 2 | 275 | Rv3510c | hypothetical protein | 85.66 | 278 | Mb3540c | hypothetical protein | 85.66 | 278 | MAV_0646 | amidohydrolase | 99.27 | 275 | BCG_3574c | hypothetical protein | 85.66 | 278 | MAP0552 | hypothetical protein | 275 | 100 |
| MAP4_3316 | fructosamine kinase family protein | 255 | Rv2079 | hypothetical protein | 25.31 | 656 | Mb2105 | hypothetical protein | 27.92 | 656 | MAV_0645 | phosphotransferase enzyme family | 99.22 | 255 | BCG_2098 | hypothetical protein | 27.92 | 656 | MAP0551 | hypothetical protein | 255 | 100 |
| MAP4_3317 | fatty-acid-CoA ligase FadD19 | 546 | Rv3515c | Fatty-acid-CoA ligase FadD19 (fatty- | 90.11 | 548 | Mb3544c | acyl-CoA synthetase | 90.11 | 548 | MAV_0644 | acyl-CoA synthetase | 99.63 | 546 | BCG_3578c | acyl-CoA synthetase | 90.11 | 548 | MAP0550 | acyl-CoA synthetase | 546 | 100 |
| MAP4_3318 | Enoyl-CoA hydratase EchA19 | 270 | Rv3516 | Possible enoyl-CoA hydratase EchA1 | 91.6 | 263 | Mb3545 | enoyl-CoA hydratase | 91.98 | 263 | MAV_0643 | enoyl-CoA hydratase | 100 | 270 | BCG_3579 | enoyl-CoA hydratase | 91.98 | 263 | MAP0549c | enoyl-CoA hydratase | 270 | 100 |
| MAP4_3319 | hypothetical protein | 290 | Rv3517 | hypothetical protein | 67.38 | 279 | Mb3546 | hypothetical protein | 67.38 | 279 | MAV_0642 | hypothetical protein | 98.28 | 290 | BCG_3580 | hypothetical protein | 67.38 | 279 | MAP0548c | hypothetical protein | 290 | 100 |
| MAP4_3320 | putative cytochrome P450 hydroxylase Cyp142 | 406 | Rv3518c | Probable cytochrome P450 monoox | 80.51 | 398 | Mb3547c | cytochrome P450 monooxyge | 83.85 | 193 | MAV_0641 | P450 heme-thiolate protein | 100 | 406 | BCG_3581c | cytochrome P450 monooxygen | 83.85 | 193 | MAP0547 | hypothetical protein | 406 | 100 |
| MAP4_3321 | acetoacetate decarboxylase (ADC) family protein | 240 | Rv3519 | hypothetical protein | 69.87 | 236 | Mb3549 | hypothetical protein | 69.87 | 236 | MAV_0640 | hypothetical protein | 100 | 226 | BCG_3583 | hypothetical protein | 69.87 | 236 | MAP0546c | hypothetical protein | 240 | 100 |
| MAP4_3322 | putative coenzyme F420-dependent oxidoreductase | 343 | Rv3520c | Possible coenzyme F420-dependent | 86.01 | 347 | Mb3550c | coenzyme F420-dependent o | 86.01 | 347 | MAV_0639 | FMN-dependent monooxygenase | 98.54 | 343 | BCG_3584c | coenzyme F420-dependent oxi | 86.01 | 347 | MAP0545 | hypothetical protein | 343 | 100 |
| MAP4_3323 | hypothetical protein | 344 | Rv3521 | hypothetical protein | 83.83 | 303 | Mb3551 | hypothetical protein | 84.16 | 303 | MAV_0638 | hypothetical protein | 99.69 | 322 | BCG_3585 | hypothetical protein | 84.16 | 303 | MAP0544c | hypothetical protein | 344 | 100 |
| MAP4_3324 | lipid transfer protein or keto acyl-CoA thiolase Ltp4 | 354 | Rv3522 | Possible lipid transfer protein or ket | 88.67 | 354 | Mb3552 | lipid-transfer protein | 88.95 | 354 | MAV_0637 | lipid-transfer protein | 100 | 354 | BCG_3586 | lipid-transfer protein | 88.95 | 354 | MAP0543c | lipid-transfer protein | 354 | 100 |
| MAP4_3325 | lipid carrier protein or keto acyl-CoA thiolase Ltp3 | 397 | Rv3523 | Probable lipid carrier protein or keto | 91.71 | 394 | Mb3553 | acetyl-CoA acetyltransferase | 91.71 | 394 | MAV_0636 | acetyl-CoA acetyltransferase | 99.75 | 397 | BCG_3587 | acetyl-CoA acetyltransferase | 91.71 | 394 | MAP0542c | acetyl-CoA acetyltransferase | 397 | 100 |
| MAP4_3326 | hypothetical protein | 135 | Rv0760c | hypothetical protein | 38.1 | 139 | Mb0783c | hypothetical protein | 38.1 | 139 | MAV_0635 | hypothetical protein | 98.52 | 135 | BCG_0812c | hypothetical protein | 38.1 | 139 | MAP0541c | hypothetical protein | 135 | 100 |
| MAP4_3327 | putative siderophore-binding protein | 174 | Rv3525c | Possible siderophore-binding protei | 83.33 | 174 | Mb3555c | siderophore-binding protein | 83.33 | 174 | MAV_0634 | carnitine operon protein CaiE | 100 | 174 | BCG_3589c | siderophore-binding protein | 83.33 | 174 | MAP0540 | hypothetical protein | 174 | 100 |
| MAP4_3328 | oxidoreductase, Rieske (2Fe-2S) domain-containing pro | 385 | Rv3526 | Oxygenase component of 3-ketoster | 90.93 | 386 | Mb3556 | oxidoreductase | 90.93 | 386 | MAV_0633 | Rieske (2Fe-2S) domain-containing | 99.74 | 385 | BCG_3590 | oxidoreductase | 90.93 | 386 | MAP1434 | hypothetical protein | 372 | 61.75 |
| MAP4_3329 | hypothetical protein | 145 | Rv3527 | Hypothetical protein | 77.08 | 149 | Mb3557 | hypothetical protein | 77.08 | 149 | MAV_0632 | hypothetical protein | 97.93 | 145 | BCG_3591 | hypothetical protein | 77.08 | 149 | MAP0538c | hypothetical protein | 145 | 100 |
| MAP4_3330 | hypothetical protein | 381 | Rv3529c | hypothetical protein | 88.65 | 384 | Mb3559c | hypothetical protein | 88.65 | 384 | MAV_0631 | hypothetical protein | 100 | 381 | BCG_3593c | hypothetical protein | 88.65 | 384 | MAP0537 | hypothetical protein | 381 | 100 |
| MAP4_3331 | oxidoreductase | 260 | Rv3530c | Possible oxidoreductase | 82.31 | 260 | Mb3560c | short chain dehydrogenase | 82.31 | 260 | MAV_0630 | short chain dehydrogenase | 99.22 | 257 | BCG_3594c | short chain dehydrogenase | 82.31 | 260 | MAP0536 | short chain dehydrogenase | 260 | 100 |
| MAP4_3332 | hypothetical protein | 375 | Rv3531c | Hypothetical protein | 87.73 | 375 | Mb3561c | hypothetical protein | 87.73 | 375 | MAV_0629 | hypothetical protein | 100 | 375 | BCG_3595c | hypothetical protein | 87.73 | 375 | MAP0535 | hypothetical protein | 375 | 100 |
| MAP4_3333 | hypothetical protein | 101 | Rv0203 | Possible exported protein | 29.67 | 136 | Mb0209 | hypothetical protein | 29.67 | 136 | MAV_0628 | hypothetical protein | 99.01 | 101 | BCG_0240 | hypothetical protein | 29.67 | 136 | MAP0534 | hypothetical protein | 101 | 100 |
| MAP4_3334 | 4-hydroxy-2-oxovalerate aldolase | 352 | Rv3534c | Probable 4-hydroxy-2-oxovalerate a | 92.65 | 346 | Mb3564c | 4-hydroxy-2-ketovalerate ald | 92.65 | 346 | MAV_0627 | 4-hydroxy-2-ketovalerate aldolase | 99.15 | 352 | BCG_3598c | 4-hydroxy-2-ketovalerate aldol | 92.65 | 346 | MAP0533 | 4-hydroxy-2-ketovalerate aldolase | 352 | 100 |
| MAP4_3335 | acetaldehyde dehydrogenase | 305 | Rv3535c | Probable acetaldehyde dehydrogena | 92.13 | 303 | Mb3565c | acetaldehyde dehydrogenase | 92.13 | 303 | MAV_0626 | acetaldehyde dehydrogenase | 97.35 | 304 | BCG_3599c | acetaldehyde dehydrogenase | 92.13 | 303 | MAP0532 | acetaldehyde dehydrogenase | 305 | 100 |
| MAP4_3336 | hydratase | 261 | Rv3536c | Probable hydratase | 81.99 | 261 | Mb3566c | hydratase | 81.99 | 261 | MAV_0625 | 2-keto-4-pentenoate hydratase | 99.62 | 261 | BCG_3600c | hydratase | 81.99 | 261 | MAP0531 | hypothetical protein | 261 | 100 |
| MAP4_3337 | 3-oxosteroid 1-dehydrogenase | 563 | Rv3537 | Probable dehydrogenase | 89.09 | 563 | Mb3567 | 3-ketosteroid-delta-1-dehydr | 89.09 | 563 | MAV_0624 | 3-ketosteroid-delta-1-dehydrogena | 99.46 | 560 | BCG_3601 | 3-ketosteroid-delta-1-dehydro | 89.09 | 563 | MAP0530c | 3-ketosteroid-delta-1-dehydrogenase | 560 | 100 |
| MAP4_3338 | dehydrogenase | 286 | Rv3538 | Probable dehydrogenase Possible 2- | 85.31 | 286 | Mb3568 | dehydrogenase | 85.31 | 286 | MAV_0623 | MaoC like domain-containing prote | 98.95 | 286 | BCG_3602 | dehydrogenase | 85.31 | 286 | MAP0529c | UfaA2 | 286 | 100 |
| MAP4_3339 | hypothetical protein | 279 | Rv1482c | hypothetical protein | 57.35 | 280 | Mb1518c | hypothetical protein | 57.35 | 280 | MAV_0622 | hypothetical protein | 96.68 | 222 | BCG_1544c | hypothetical protein | 57.35 | 280 | MAP0528 | hypothetical protein | 279 | 100 |
| MAP4_3340 | lipid transfer protein or keto acyl-CoA thiolase Ltp2 | 389 | Rv3540c | Probable lipid transfer protein or ke | 89.23 | 386 | Mb3570c | lipid-transfer protein | 89.23 | 386 | MAV_0621 | lipid-transfer protein | 99.49 | 389 | BCG_3604c | lipid-transfer protein | 89.23 | 386 | MAP0527 | lipid-transfer protein | 389 | 100 |
| MAP4_3341 | hypothetical protein | 133 | Rv3541c | hypothetical protein | 88.1 | 129 | Mb3571c | hypothetical protein | 88.1 | 129 | MAV_0620 | hypothetical protein | 100 | 133 | BCG_3605c | hypothetical protein | 88.1 | 129 | MAP0526 | hypothetical protein | 133 | 100 |
| MAP4_3342 | hypothetical protein | 317 | Rv3542c | hypothetical protein | 81.33 | 311 | Mb3572c | hypothetical protein | 81.33 | 311 | MAV_0619 | hypothetical protein | 100 | 317 | BCG_3606c | hypothetical protein | 81.33 | 311 | MAP0525 | hypothetical protein | 317 | 100 |
| MAP4_3343 | acyl-CoA dehydrogenase FadE29 | 387 | Rv3543c | Probable acyl-CoA dehydrogenase F | 87.6 | 387 | Mb3573c | acyl-CoA dehydrogenase | 87.6 | 387 | MAV_0618 | acyl-CoA dehydrogenase | 100 | 387 | BCG_3607c | acyl-CoA dehydrogenase fadE2 | 87.6 | 387 | MAP0524 | FadE29 | 387 | 100 |
| MAP4_3344 | putative acyl-CoA dehydrogenase FadE28 | 362 | Rv3544c | Probable acyl-CoA dehydrogenase F | 82.53 | 339 | Mb3574c | acyl-CoA dehydrogenase | 82.53 | 339 | MAV_0617 | acyl-CoA dehydrogenase | 99.72 | 362 | BCG_3608c | acyl-CoA dehydrogenase fadE2 | 82.53 | 339 | MAP0523 | FadE28 | 362 | 100 |
| MAP4_3345 | putative cytochrome P450 125 | 416 | Rv3545c | Probable cytochrome P450 125 Cyp1 | 82.49 | 433 | Mb3575c | cytochrome P450 125 | 82.49 | 433 | MAV_0616 | cytochrome P450 124 | 99.76 | 416 | BCG_3609c | cytochrome P450 125 cyp125 | 82.49 | 433 | MAP0522 | hypothetical protein | 416 | 100 |
| MAP4_3346 | acetyl-CoA acetyltransferase FadA5 | 386 | Rv3546 | Probable acetyl-CoA acetyltransfera | 85.93 | 391 | Mb3576 | acetyl-CoA acetyltransferase | 85.93 | 391 | MAV_0615 | acetyl-CoA acetyltransferase | 99.74 | 386 | BCG_3610 | acetyl-CoA acetyltransferase | 85.93 | 391 | MAP0521c | acetyl-CoA acetyltransferase | 386 | 100 |
| MAP4_3347 | hypothetical protein | 133 | Rv1412 | Probable riboflavin synthase alpha c | 24.62 | 201 | Mb1447 | riboflavin synthase subunit al | 24.62 | 201 | MAV_0614 | hypothetical protein | 100 | 133 | BCG_1473 | riboflavin synthase subunit alp | 24.62 | 201 | MAP0520c | hypothetical protein | 133 | 100 |
| MAP4_3348 | hypothetical protein | 148 | Rv3547 | Deazaflavin-dependent nitroreducta | 72.6 | 151 | Mb3577 | hypothetical protein | 72.6 | 151 | MAV_0613 | AclJ protein | 99.3 | 142 | BCG_3611 | hypothetical protein | 72.6 | 151 | MAP0519c | hypothetical protein | 148 | 100 |
| MAP4_3349 | short-chain type dehydrogenasereductase | 301 | Rv3548c | Probable short-chain type dehydrog | 88.82 | 304 | Mb3578c | short chain dehydrogenase | 88.49 | 304 | MAV_0612 | short chain dehydrogenase | 98.67 | 301 | BCG_3612c | short chain dehydrogenase | 88.49 | 304 | MAP0518 | short chain dehydrogenase | 301 | 100 |
| MAP4_3350 | short-chain type dehydrogenasereductase | 265 | Rv3549c | Probable short-chain type dehydrog | 75.19 | 259 | Mb3579c | short chain dehydrogenase | 75.19 | 259 | MAV_0611 | short chain dehydrogenase | 99.59 | 244 | BCG_3613c | short chain dehydrogenase | 75.19 | 259 | MAP0517 | short chain dehydrogenase | 265 | 100 |
| MAP4_3351 | enoyl-CoA hydratase EchA20 | 251 | Rv3550 | Probable enoyl-CoA hydratase EchA | 91.36 | 247 | Mb3580 | enoyl-CoA hydratase | 91.36 | 247 | MAV_0610 | enoyl-CoA hydratase | 98.41 | 251 | BCG_3614 | enoyl-CoA hydratase | 91.36 | 247 | MAP0516c | enoyl-CoA hydratase | 251 | 100 |
| MAP4_3352 | putative CoA-transferase alpha subunit | 293 | Rv3551 | Possible CoA-transferase (alpha sub | 87.5 | 292 | Mb3581 | CoA-transferase subunit alph | 87.85 | 292 | MAV_0609 | coenzyme A transferase, subunit A | 99.66 | 293 | BCG_3615 | CoA-transferase subunit alpha | 87.85 | 292 | MAP0515c | hypothetical protein | 293 | 100 |
| MAP4_3353 | putative CoA-transferase beta subunit | 247 | Rv3552 | Possible CoA-transferase (beta subu | 85.89 | 250 | Mb3582 | CoA-transferase subunit beta | 85.89 | 250 | MAV_0608 | coenzyme A transferase, subunit B | 99.19 | 247 | BCG_3616 | CoA-transferase subunit beta | 85.89 | 250 | MAP0514c | hypothetical protein | 247 | 100 |
| MAP4_3354 | oxidoreductase, 2-nitropropane dioxygenase | 358 | Rv3553 | Possible oxidoreductase | 88.45 | 355 | Mb3583 | oxidoreductase | 88.45 | 355 | MAV_0607 | oxidoreductase, 2-nitropropane dic | 99.44 | 358 | BCG_3617 | oxidoreductase | 88.45 | 355 | MAP0513c | hypothetical protein | 358 | 100 |
| MAP4_3355 | hypothetical protein | 215 | Rv3530c | Possible oxidoreductase | 36.84 | 260 | Mb3560c | short chain dehydrogenase | 36.84 | 260 | MAV_0606 | hypothetical protein | 98.02 | 202 | BCG_3594c | short chain dehydrogenase | 36.84 | 260 | MAP0512c | hypothetical protein | 215 | 100 |
| MAP4_3356 | hypothetical protein | 246 | Rv0906 | hypothetical protein | 33.33 | 372 | Mb0930 | hypothetical protein | 33.33 | 372 | MAV_0605 | hypothetical protein | 97.97 | 246 | BCG_0958 | hypothetical protein | 33.33 | 372 | MAP0511c | hypothetical protein | 246 | 100 |
| MAP4_3357 | acetyl-CoA acetyltransferase FadA6 | 386 | Rv3556c | Probable acetyl-CoA acetyltransfera | 95.34 | 386 | Mb3586c | acetyl-CoA acetyltransferase | 95.34 | 386 | MAV_0604 | acetyl-CoA acetyltransferase | 99.74 | 386 | BCG_3620c | acetyl-CoA acetyltransferase | 95.34 | 386 | MAP0510 | acetyl-CoA acetyltransferase | 386 | 100 |
| MAP4_3358 | TetR family transcriptional regulator | 202 | Rv3557c | Transcriptional regulatory protein (p | 87.76 | 200 | Mb3587c | TetR family transcriptional re | 87.76 | 200 | MAV_0603 | TetR family transcriptional regulato | 99.5 | 199 | BCG_3621c | TetR family transcriptional regu | 87.76 | 200 | MAP0509 | hypothetical protein | 202 | 100 |
| MAP4_3359 | oxidoreductase | 262 | Rv3559c | Probable oxidoreductase | 90.84 | 262 | Mb3589c | short chain dehydrogenase | 90.84 | 262 | MAV_0602 | short chain dehydrogenase | 100 | 262 | BCG_3623c | short chain dehydrogenase | 90.84 | 262 | MAP0508 | short chain dehydrogenase | 262 | 100 |
| MAP4_3360 | FadE30 | 382 | Rv3560c | Probable acyl-CoA dehydrogenase F | 92.47 | 385 | Mb3590c | acyl-CoA dehydrogenase | 92.47 | 385 | MAV_0601 | acyl-CoA dehydrogenase | 100 | 382 | BCG_3624c | acyl-CoA dehydrogenase fadE3 | 92.47 | 385 | MAP0507 | FadE30 | 382 | 100 |
| MAP4_3361 | Long-chain-fatty-acid--CoA ligase | 421 | Rv3561 | Probable fatty-acid-CoA ligase FadD | 83.37 | 507 | Mb3591 | long-chain-fatty-acid--CoA lig | 83.37 | 507 | MAV_0600 | long-chain-fatty-acid--CoA ligase | 99.49 | 509 | BCG_3625 | long-chain-fatty-acid--CoA ligas | 83.37 | 507 | MAP0506c | acyl-CoA synthase | 421 | 100 |
| MAP4_3362 | acyl-CoA dehydrogenase FadE31 | 381 | Rv3562 | Probable acyl-CoA dehydrogenase F | 88.33 | 377 | Mb3592 | acyl-CoA dehydrogenase | 88.33 | 377 | MAV_0599 | acyl-CoA dehydrogenase | 100 | 381 | BCG_3626 | acyl-CoA dehydrogenase fadE3 | 88.33 | 377 | MAP0505c | FadE31 | 381 | 100 |
| MAP4_3363 | acyl-CoA dehydrogenase FadE32 | 314 | Rv3563 | Probable acyl-CoA dehydrogenase F | 78.55 | 319 | Mb3593 | acyl-CoA dehydrogenase | 78.86 | 319 | MAV_0598 | acyl-CoA dehydrogenase | 98.09 | 314 | BCG_3627 | acyl-CoA dehydrogenase fadE3 | 78.86 | 319 | MAP0504c | FadE32 | 314 | 100 |
| MAP4_3364 | acyl-CoA dehydrogenase FadE33 | 319 | Rv3564 | Probable acyl-CoA dehydrogenase F | 80.25 | 318 | Mb3594 | acyl-CoA dehydrogenase | 80.25 | 318 | MAV_0597 | acyl-CoA dehydrogenase | 99.69 | 319 | BCG_3628 | acyl-CoA dehydrogenase fadE3 | 80.25 | 318 | MAP0503c | FadE33 | 319 | 100 |
| MAP4_3365 | aspartate aminotransferase AspB | 388 | Rv3565 | Possible aspartate aminotransferase | 85.71 | 388 | Mb3595 | aspartate aminotransferase | 85.71 | 388 | MAV_0596 | aspartate aminotransferase | 99.48 | 388 | BCG_3629 | aspartate aminotransferase | 85.71 | 388 | MAP0502c | aspartate aminotransferase | 388 | 100 |
| MAP4_3366 | Arylamine N-acetyltransferase Nat | 276 | Rv3566c | Arylamine N-acetyltransferase Nat ( | 67.88 | 283 | Mb3596c | arylamine acetylase | 67.88 | 283 | MAV_0595 | arylamine N-acetyltransferase | 98.19 | 276 | BCG_3630c | arylamine n-acetyltransferase | 67.88 | 283 | MAP0501 | NhoA | 276 | 100 |
| MAP4_3367 | oxidoreductase | 187 | Rv3567c | Possible oxidoreductase Possible 3-h | 88.24 | 187 | Mb3598c | oxidoreductase | 88.77 | 187 | MAV_0594 | flavin reductase | 100 | 187 | BCG_3632c | oxidoreductase | 88.77 | 187 | MAP0500 | hypothetical protein | 187 | 100 |
| MAP4_3368 | biphenyl-2,3-diol 1,2-dioxygenase | 303 | Rv3568c | 3,4-DHSA dioxygenase | 89.63 | 300 | Mb3599c | biphenyl-2,3-diol 1,2-dioxyge | 89.3 | 300 | MAV_0593 | extradiol ring-cleavage dioxygenase | 100 | 303 | BCG_3633c | biphenyl-2,3-diol 1,2-dioxygena | 89.63 | 300 | MAP0499 | hypothetical protein | 303 | 100 |
| MAP4_3369 | 2-hydroxy-6-oxo-6-phenylhexa-2, 4-dienoatehydrolase | 293 | Rv3569c | 4,9-DHSA hydrolase | 89.38 | 291 | Mb3600c | 2-hydroxy-6-oxo-6-phenylhex | 89.38 | 291 | MAV_0592 | 2-hydroxy-6-oxo-6-phenylhexa-2,4- | 100 | 293 | BCG_3634c | 2-hydroxy-6-oxo-6-phenylhexa | 89.38 | 291 | MAP0498 | hypothetical protein | 293 | 100 |
| MAP4_3370 | oxidoreductase | 394 | Rv3570c | Possible oxidoreductase Possible 3-h | 90.61 | 394 | Mb3601c | oxidoreductase | 90.86 | 394 | MAV_0591 | pigment production hydroxylase | 99.75 | 394 | BCG_3635c | oxidoreductase | 90.86 | 394 | MAP0497 | hypothetical protein | 394 | 100 |
| MAP4_3371 | oxidoreductase, hemoglobin-related protein hmp | 364 | Rv3571 | Reductase component of 3-ketoster | 84.34 | 358 | Mb3602 | hemoglobine-like protein | 84.34 | 358 | MAV_0590 | oxidoreductase, electron transfer c | 99.45 | 364 | BCG_3636 | hemoglobine-related protein h | 84.34 | 358 | MAP0496c | hypothetical protein | 364 | 100 |
| MAP4_3372 | hypothetical protein | 186 | Rv3572 | hypothetical protein | 65.54 | 176 | Mb3603 | hypothetical protein | 65.54 | 176 | MAV_0589 | hypothetical protein | 99.44 | 177 | BCG_3637 | hypothetical protein | 65.54 | 176 | MAP0495c | hypothetical protein | 186 | 100 |
| MAP4_3373 | putative oxidoreductase | 293 | Rv2047c | hypothetical protein | 35.44 | 854 | Mb2073c | hypothetical protein | 35.44 | 854 | MAV_0588 | oxidoreductase | 98.98 | 293 | BCG_2066c | hypothetical protein | 35.44 | 854 | MAP0494 | hypothetical protein | 317 | 99.66 |
| MAP4_3374 | Transcriptional regulator, TetR family | 190 | Rv3295 | Probable transcriptional regulatory | 31.91 | 221 | Mb3323 | TetR family transcriptional re | 31.91 | 221 | MAV_0586 | TetR family transcriptional regulato | 98.95 | 190 | BCG_3324 | TetR family transcriptional regu | 31.91 | 221 | MAP0493c | hypothetical protein | 190 | 100 |
| MAP4_3375 | acyl-CoA dehydrogenase FadE34 | 707 | Rv3573c | Probable acyl-CoA dehydrogenase F | 81.43 | 711 | Mb3604c | acyl-CoA dehydrogenase | 81.43 | 711 | MAV_0587 | acyl-CoA dehydrogenase | 99.58 | 707 | BCG_3638c | acyl-CoA dehydrogenase fadE3 | 81.43 | 711 | MAP0492 | FadE34 | 707 | 100 |
| MAP4_3376 | TetR family transcriptional regulator | 248 | Rv3574 | Transcriptional regulatory protein K | 95.41 | 199 | Mb3605 | transcriptional regulatory pro | 95.41 | 199 | MAV_0584 | TetR family transcriptional regulato | 98.98 | 197 | BCG_3639 | TetR family transcriptional regu | 95.41 | 199 | MAP0491c | hypothetical protein | 248 | 100 |
| MAP4_3377 | Transcriptional regulator, laci-family | 359 | Rv3575c | Transcriptional regulatory protein (p | 90.53 | 359 | Mb3606c | LacI family transcriptional reg | 90.53 | 359 | MAV_0585 | LacI family transcriptional regulator | 99.72 | 359 | BCG_3640c | LacI family transcriptional regu | 90.53 | 359 | MAP0490 | hypothetical protein | 398 | 99.72 |
| MAP4_3378 | putative Zinc ABC transporter, periplasmic-binding pro | 311 | Rv2059 | hypothetical protein | 63.07 | 511 | Mb2085 | hypothetical protein | 63.07 | 511 | MAV_0583 | periplasmic solute binding protein | 99.04 | 311 | BCG_2078 | hypothetical protein | 63.07 | 511 | MAP0489c | hypothetical protein | 311 | 100 |
| MAP4_3379 | pitative Zinc ABC transporter, ATP-binding protein Znu | 273 | Rv2397c | Sulfate-transport ATP-binding prote | 33.03 | 351 | Mb2419c | sulfate-transport ABC transpo | 33.03 | 351 | MAV_0582 | ABC transporter ATP-binding prote | 99.27 | 273 | BCG_2412c | sulfate-transport ATP-binding | 33.03 | 351 | MAP0488c | hypothetical protein | 273 | 100 |
| MAP4_3380 | putative Zinc ABC transporter, transmembrane protein | 286 | Rv2060 | Possible conserved integral membra | 85.83 | 133 | Mb2086 | hypothetical protein | 85.83 | 133 | MAV_0581 | Mn2+/Zn2+ ABC transporter perme | 99.65 | 286 | BCG_1905c | reductase | 26.32 | 411 | MAP0487c | hypothetical protein | 286 | 100 |
| MAP4_3381 | lactam utilization protein, LamBYcsF family | 252 | Rv1996 | Universal stress protein family prote | 48.39 | 317 | Mb2019 | hypothetical protein | 48.39 | 317 | MAV_0580 | LamB/YcsF family protein | 98.81 | 252 | BCG_2013 | hypothetical protein | 48.39 | 317 | MAP0486c | LamB/YcsF family protein | 252 | 100 |
| MAP4_3382 | hypothetical protein | 305 | Rv3577 | hypothetical protein | 83.09 | 288 | Mb3608 | hypothetical protein | 83.09 | 288 | MAV_0579 | hypothetical protein | 98.69 | 305 | BCG_3642 | hypothetical protein | 83.09 | 288 | MAP0485c | hypothetical protein | 305 | 100 |
| MAP4_3383 | putative arsenical PUMP integral membrane protein Ar | 413 | Rv3578 | Possible arsenical pump integral me | 75.73 | 413 | Mb3609 | arsenical PUMP integral mem | 75.49 | 413 | MAV_0577 | arsenical pump membrane protein | 99.76 | 413 | BCG_3643 | arsenical pump integral memb | 75.49 | 413 | MAP0484c | ArsB2 | 413 | 100 |
| MAP4_3386 | hypothetical protein | 477 | Rv3254 | hypothetical protein | 38.98 | 462 | Mb3282 | hypothetical protein | 38.98 | 462 | MAV_0575 | hypothetical protein | 99.37 | 477 | BCG_3283 | hypothetical protein | 38.98 | 462 | MAP0481c | hypothetical protein | 477 | 100 |
| MAP4_3387 | glycerophosphoryl diester phosphodiesterase | 297 | Rv3842c | Probable glycerophosphoryl diester | 27.84 | 274 | Mb3872c | glycerophosphoryl diester ph | 27.84 | 274 | MAV_0576 | glycerophosphoryl diester phospho | 98.99 | 314 | BCG_3905c | glycerophosphoryl diester phos | 27.84 | 274 | MAP0480 | hypothetical protein | 297 | 100 |
| MAP4_3388 | tRNArRNA methyltransferase | 309 | Rv3579c | Possible tRNA/rRNA methyltransfera | 88.16 | 322 | Mb3610c | tRNA/rRNA methyltransferas | 87.5 | 402 | MAV_0574 | RNA methyltransferase, TrmH fami | 99.35 | 309 | BCG_3644c | tRNA/rRNA methyltransferase | 87.83 | 322 | MAP0479 | hypothetical protein | 309 | 100 |
| MAP4_3389 | Cysteinyl-tRNA synthetase 1 | 468 | Rv3580c | Cysteinyl-tRNA synthetase 1 CysS1 ( | 88.91 | 469 | Mb3611c | cysteinyl-tRNA synthetase | 88.91 | 469 | MAV_0573 | cysteinyl-tRNA synthetase | 99.57 | 468 | BCG_3645c | cysteinyl-tRNA synthetase | 88.91 | 469 | MAP0478 | cysteinyl-tRNA synthetase | 468 | 100 |
| MAP4_3390 | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase | 159 | Rv3581c | Probable 2C-methyl-D-erythritol 2,4 | 82.05 | 159 | Mb3612c | 2-C-methyl-D-erythritol 2,4-c | 82.05 | 159 | MAV_0572 | 2-C-methyl-D-erythritol 2,4-cyclodi | 100 | 159 | BCG_3646c | 2-C-methyl-D-erythritol 2,4-cyc | 82.05 | 159 | MAP0477 | 2-C-methyl-D-erythritol 2,4-cyclodiphos | 159 | 100 |
| MAP4_3391 | 4-diphosphocytidyl-2-C-methyl-D-erythritol synthase is | 235 | Rv3582c | 4-diphosphocytidyl-2C-methyl-D-ery | 71.81 | 231 | Mb3613c | 2-C-methyl-D-erythritol 4-pho | 72.25 | 231 | MAV_0571 | 2-C-methyl-D-erythritol 4-phosphat | 98.25 | 229 | BCG_3647c | 2-C-methyl-D-erythritol 4-phos | 71.81 | 231 | MAP0476 | 2-C-methyl-D-erythritol 4-phosphate cy | 235 | 100 |
| MAP4_3392 | transcriptional regulator | 162 | Rv3583c | Possible transcription factor | 100 | 162 | Mb3614c | transcription factor | 100 | 162 | MAV_0570 | CarD family transcriptional regulato | 100 | 162 | BCG_3648c | transcription factor | 100 | 162 | MAP0475 | hypothetical protein | 162 | 100 |
| MAP4_3393 | putative lipoprotein LpqE | 188 | Rv3584 | Possible conserved lipoprotein LpqE | 70.17 | 182 | Mb3615 | lipoprotein LpqE | 70.17 | 182 | MAV_0569 | LpqE protein | 99.47 | 188 | BCG_3649 | lipoprotein lpqE | 70.17 | 182 | MAP0474c | hypothetical protein | 188 | 100 |
| MAP4_3394 | DNA repair protein RadA | 474 | Rv3585 | DNA repair protein RadA (DNA repai | 81.39 | 480 | Mb3616 | DNA repair protein RadA | 81.39 | 480 | MAV_0568 | DNA repair protein RadA | 99.35 | 459 | BCG_3650 | DNA repair protein RadA | 81.39 | 480 | MAP0473c | DNA repair protein RadA | 474 | 100 |
| MAP4_3395 | DNA integrity scanning protein DisA | 357 | Rv3586 | hypothetical protein | 90.68 | 358 | Mb3617 | DNA integrity scanning protei | 90.68 | 358 | MAV_0567 | DNA integrity scanning protein Dis | 99.72 | 357 | BCG_3651 | DNA integrity scanning protein | 90.68 | 358 | MAP0472c | DNA integrity scanning protein DisA | 357 | 100 |
| MAP4_3396 | putative conserved membrane protein | 277 | Rv3587c | Probable conserved membrane prot | 87.45 | 264 | Mb3618c | hypothetical protein | 87.45 | 264 | MAV_0566 | hypothetical protein | 99.64 | 277 | BCG_3652c | hypothetical protein | 87.45 | 263 | MAP0471 | hypothetical protein | 277 | 100 |
| MAP4_3397 | Carbonic anhydrase | 205 | Rv3588c | Beta-carbonic anhydrase CanB | 78.05 | 207 | Mb3619c | carbonic anhydrase | 77.56 | 207 | MAV_0565 | carbonic anhydrase | 100 | 205 | BCG_3653c | carbonic anhydrase | 78.05 | 207 | MAP0470 | hypothetical protein | 205 | 100 |
| MAP4_3398 | adenine glycosylase MutY | 303 | Rv3589 | Probable adenine glycosylase MutY | 80.13 | 304 | Mb3620 | adenine glycosylase | 80.13 | 304 | MAV_0563 | A/G-specific adenine glycosylase | 98.02 | 303 | BCG_3654 | adenine glycosylase | 80.13 | 304 | MAP0469c | MutY | 303 | 100 |
| MAP4_3399 | putative hydrolase | 251 | Rv3591c | Possible hydrolase | 84.06 | 257 | Mb3622c | hydrolase | 84.06 | 257 | MAV_0564 | hydrolase, alpha/beta hydrolase fa | 97.57 | 247 | BCG_3656c | hydrolase | 84.06 | 257 | MAP0468 | hypothetical protein | 272 | 100 |
| MAP4_3400 | hypothetical protein | 106 | Rv3592 | Possible heme degrading protein Mh | 89.22 | 105 | Mb3623 | hypothetical protein | 89.22 | 105 | MAV_0562 | antibiotic biosynthesis monooxyge | 99.02 | 102 | BCG_3657 | hypothetical protein | 89.22 | 105 | MAP0467c | hypothetical protein | 106 | 100 |
| MAP4_3401 | lipoprotein LpqF | 429 | Rv3593 | Probable conserved lipoprotein Lpq | 80.38 | 452 | Mb3624 | lipoprotein LpqF | 80.38 | 452 | MAV_0561 | LpqF protein | 99.53 | 437 | BCG_3658 | lipoprotein lpqF | 80.38 | 452 | MAP0466c | hypothetical protein | 429 | 100 |
| MAP4_3402 | putative dioxygenase | 479 | Rv0654 | Probable dioxygenase | 57.55 | 501 | Mb0673 | dioxygenase | 57.55 | 501 | MAV_0560 | carotenoid oxygenase | 99.16 | 479 | BCG_0703 | dioxygenase | 57.55 | 501 | MAP0465 | hypothetical protein | 479 | 100 |
| MAP4_3403 | putative phosphoglycerate mutase | 182 | Rv2419c | Glucosyl-3-phosphoglycerate phosp | 32.28 | 223 | Mb2442c | phosphoglycerate mutase | 32.28 | 223 | MAV_0559 | phosphoglycerate mutase, putative | 92.73 | 165 | BCG_2435c | phosphoglycerate mutase | 32.28 | 223 | MAP0464 | hypothetical protein | 182 | 100 |
| MAP4_3404 | putative cobalt transporter subunit (CbtA) family prote | 258 | Rv1692 | Probable phosphatase | 32.98 | 353 | Mb1718 | phosphatase | 32.98 | 353 | MAV_0558 | hypothetical protein | 98.45 | 258 | BCG_1730 | phosphatase | 32.98 | 353 | MAP0463 | hypothetical protein | 249 | 99.6 |
| MAP4_3405 | hypothetical protein | 71 | Rv2222c | Probable glutamine synthetase GlnA | 26.98 | 446 | Mb2246c | glutamine synthetase | 26.98 | 446 | MAV_0557 | hypothetical protein | 98.59 | 71 | BCG_2239c | glutamine synthetase glnA2 | 26.98 | 446 | MAP0462 | hypothetical protein | 71 | 100 |
| MAP4_3406 | ATP-dependent protease ATP-binding subunit ClpC | 843 | Rv3596c | Probable ATP-dependent protease A | 98.1 | 848 | Mb3627c | ATP-dependent Clp protease | 98.1 | 848 | MAV_0556 | negative regulator of genetic comp | 99.88 | 822 | BCG_3661c | ATP-dependent Clp protease A | 98.1 | 848 | MAP0461 | ClpC | 843 | 100 |
| MAP4_3407 | iron-regulated protein precursor LSR2 | 112 | Rv3597c | Iron-regulated H-NS-like protein Lsr | 94.64 | 112 | Mb3628c | LSR2 protein precursor | 94.64 | 112 | MAV_0555 | Lsr2 protein | 99.07 | 108 | BCG_3662c | lsr2 protein precursor | 94.64 | 112 | MAP0460 | Lsr2 | 112 | 100 |
| MAP4_3408 | Lysyl-tRNA synthetase 1 | 499 | Rv3598c | Lysyl-tRNA synthetase 1 LysS (lysine | 87.1 | 505 | Mb3629c | lysyl-tRNA synthetase | 87.1 | 505 | MAV_0554 | lysyl-tRNA synthetase | 99.8 | 499 | BCG_3663c | lysyl-tRNA synthetase | 87.1 | 505 | MAP0459 | lysyl-tRNA synthetase | 499 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3409 | type III pantothenate kinase family protein | 271 | Rv3600c | hypothetical protein | 91.18 | 272 | Mb3630c | pantothenate kinase | 91.18 | 272 | MAV_0553 | pantothenate kinase | 100 | 271 | BCG_3664c | pantothenate kinase | 91.18 | 272 | MAP0458 | pantothenate kinase | 271 | 100 |
| MAP4_3410 | aspartate 1-decarboxylase precursor panD | 143 | Rv3601c | Probable aspartate 1-decarboxylase | 87.86 | 139 | Mb3631c | aspartate alpha-decarboxylas | 87.86 | 139 | MAV_0552 | aspartate alpha-decarboxylase | 100 | 143 | BCG_3665c | aspartate alpha-decarboxylase | 87.86 | 139 | MAP0457 | aspartate alpha-decarboxylase | 143 | 100 |
| MAP4_3411 | pantoate-beta-alanine ligase PanC | 308 | Rv3602c | Pantoate--beta-alanine ligase PanC ( | 81.7 | 309 | Mb3632c | pantoate--beta-alanine ligase | 81.7 | 309 | MAV_0551 | pantoate--beta-alanine ligase | 99.68 | 308 | BCG_3666c | pantoate--beta-alanine ligase | 81.7 | 309 | MAP0456 | pantoate--beta-alanine ligase | 308 | 100 |
| MAP4_3412 | conserved alanine and leucine rich protein | 303 | Rv3603c | Conserved hypothetical alanine and | 88.37 | 303 | Mb3633c | hypothetical protein | 88.37 | 303 | MAV_0550 | chalcone/stilbene synthase | 99.67 | 303 | BCG_3667c | hypothetical protein | 88.37 | 303 | MAP0455 | hypothetical protein | 303 | 100 |
| MAP4_3413 | conserved alanine, arginine and proline rich membrane | 462 | Rv3604c | Probable conserved transmembrane | 51.74 | 397 | Mb3634c | transmembrane protein | 51.74 | 397 | MAV_0549 | hypothetical protein | 99.05 | 421 | BCG_3668c | transmembrane protein rich in | 51.74 | 397 | MAP0454 | hypothetical protein | 462 | 100 |
| MAP4_3414 | conserved secreted protein | 158 | Rv3605c | Probable conserved secreted protei | 87.34 | 158 | Mb3635c | hypothetical protein | 87.34 | 158 | MAV_0548 | hypothetical protein | 98.73 | 158 | BCG_3669c | hypothetical protein | 87.34 | 158 | MAP0453 | hypothetical protein | 158 | 100 |
| MAP4_3415 | 2-amino-4-hydroxy-6- hydroxymethyldihydropteridine | 182 | Rv3606c | 2-amino-4-hydroxy-6- hydroxymeth | 74.4 | 188 | Mb3636c | 2-amino-4-hydroxy-6- hydrox | 74.4 | 188 | MAV_0546 | 2-amino-4-hydroxy-6- hydroxymeth | 98.9 | 182 | BCG_3670c | 2-amino-4-hydroxy-6- hydroxy | 73.81 | 188 | MAP0452 | hypothetical protein | 182 | 100 |
| MAP4_3416 | dihydroneopterin aldolase FolB | 133 | Rv3607c | Probable dihydroneopterin aldolase | 79.7 | 133 | Mb3637c | dihydroneopterin aldolase Fo | 79.7 | 133 | MAV_0545 | dihydroneopterin aldolase | 99.25 | 133 | BCG_3671c | dihydroneopterin aldolase folB | 79.7 | 133 | MAP0451 | FolX | 133 | 100 |
| MAP4_3417 | Dihydropteroate synthase FolP | 270 | Rv3608c | Dihydropteroate synthase 1 FolP (D | 81.27 | 280 | Mb3638c | dihydropteroate synthase | 81.27 | 280 | MAV_0544 | dihydropteroate synthase | 99.24 | 264 | BCG_3672c | dihydropteroate synthase | 81.27 | 280 | MAP0450 | hypothetical protein | 270 | 100 |
| MAP4_3418 | GTP cyclohydrolase I FolE | 204 | Rv3609c | GTP cyclohydrolase I FolE (GTP-ch-I) | 89.23 | 202 | Mb3639c | GTP cyclohydrolase I | 89.23 | 202 | MAV_0543 | GTP cyclohydrolase I | 99.51 | 204 | BCG_3673c | GTP cyclohydrolase I | 89.23 | 202 | MAP0449 | GTP cyclohydrolase I | 204 | 100 |
| MAP4_3419 | membrane-bound cell division protein FtsH | 799 | Rv3610c | Membrane-bound protease FtsH (ce | 85.41 | 760 | Mb3640c | membrane-bound protease F | 85.41 | 760 | MAV_0542 | ATP-dependent metallopeptidase H | 99.87 | 799 | BCG_3674c | membrane-bound protease fts | 85.41 | 760 | MAP0448 | hypothetical protein | 799 | 100 |
| MAP4_3420 | putative dioxygenase | 137 | Rv0274 | hypothetical protein | 24.83 | 193 | Mb0280 | hypothetical protein | 24.83 | 193 | MAV_0540 | dioxygenase | 100 | 137 | BCG_0312 | hypothetical protein | 24.83 | 193 | MAP0447 | hypothetical protein | 137 | 100 |
| MAP4_3421 | epoxide hydrolase EphA | 327 | Rv3617 | Probable epoxide hydrolase EphA (e | 81.5 | 322 | Mb1973 | epoxide hydrolase | 36.47 | 356 | MAV_0539 | alpha/beta hydrolase | 98.38 | 309 | BCG_1977 | epoxide hydrolase ephB | 36.47 | 356 | MAP0446c | EphA | 327 | 100 |
| MAP4_3422 | monooxygenase | 395 | Rv3618 | Possible monooxygenase | 87.02 | 395 | Mb1971 | monooxygenase | 32.36 | 369 | MAV_0538 | limonene 1,2-monooxygenase | 100 | 395 | BCG_1975 | monooxygenase | 32.36 | 369 | MAP0445c | hypothetical protein | 395 | 100 |
| MAP4_3423 | dehydrogenase | 337 | Rv3726 | Possible dehydrogenase | 42.36 | 397 | Mb3753 | dehydrogenase | 42.36 | 397 | MAV_0537 | zinc-binding dehydrogenase | 99.7 | 337 | BCG_3786 | dehydrogenase | 42.36 | 397 | MAP0444c | hypothetical protein | 337 | 100 |
| MAP4_3424 | 13E12 repeat family protein | 526 | Rv0336 | Conserved 13E12 repeat family prot | 38.15 | 503 | Mb0343 | hypothetical protein | 38.15 | 503 | MAV_0536 | hypothetical protein | 97.91 | 526 | BCG_0375 | hypothetical protein | 38.15 | 503 | MAP0443c | hypothetical protein | 526 | 100 |
| MAP4_3425 | PPE family protein | 424 | Rv3621c | PPE family protein PPE65 | 53.3 | 413 | Mb3159 | PPE family protein | 38.9 | 381 | MAV_0535 | PPE family protein | 97.36 | 421 | BCG_3158 | PPE family protein | 38.9 | 381 | MAP0442 | hypothetical protein | 424 | 100 |
| MAP4_3426 | PE family protein | 99 | Rv3622c | PE family protein PE32 | 52.87 | 99 | Mb3504 | PE family protein | 47.47 | 98 | MAV_0534 | PE family protein | 96.97 | 99 | BCG_3540 | PE family protein | 47.47 | 98 | MAP0441 | hypothetical protein | 99 | 100 |
| MAP4_3427 | lipoprotein LpqG | 249 | Rv3623 | Probable conserved lipoprotein Lpq | 73.76 | 240 | Mb3647 | lipoprotein LpqG | 74.42 | 171 | MAV_0533 | LpqG protein | 99.6 | 249 | BCG_3681 | lipoprotein lpqG | 74.42 | 171 | MAP0440c | hypothetical protein | 249 | 100 |
| MAP4_3428 | hypoxanthine-guanine phosphoribosyltransferase Hpt | 203 | Rv3624c | Hypoxanthine-guanine phosphoribo | 88 | 216 | Mb3648c | hypoxanthine-guanine phosp | 88 | 216 | MAV_0532 | hypoxanthine phosphoribosyltrans | 99.51 | 203 | BCG_3682c | hypoxanthine-guanine phosph | 87 | 216 | MAP0439 | hypoxanthine-guanine phosphoribosylt | 203 | 100 |
| MAP4_3429 | cell cycle protein MesJ | 320 | Rv3625c | Possible cell cycle protein MesJ | 74.61 | 323 | Mb3649c | cell cycle protein MESJ | 74.61 | 323 | MAV_0531 | tRNA(Ile)-lysidine synthetase | 97.5 | 320 | BCG_3683c | cell cycle protein mesJ | 74.61 | 323 | MAP0438 | hypothetical protein | 320 | 100 |
| MAP4_3430 | hypothetical protein | 357 | Rv3626c | hypothetical protein | 77.31 | 350 | Mb3650c | hypothetical protein | 77.31 | 350 | MAV_0530 | hypothetical protein | 99.44 | 357 | BCG_3684c | hypothetical protein | 77.31 | 350 | MAP0437 | hypothetical protein | 357 | 100 |
| MAP4_3431 | D-alanyl-D-alanine carboxypeptidase | 461 | Rv3627c | hypothetical protein | 80.26 | 461 | Mb3651c | hypothetical protein | 79.18 | 461 | MAV_0529 | D-alanyl-D-alanine carboxypeptidas | 99.78 | 450 | BCG_3685c | hypothetical protein | 79.18 | 461 | MAP0436 | hypothetical protein | 461 | 100 |
| MAP4_3432 | inorganic pyrophosphatase | 162 | Rv3628 | Inorganic pyrophosphatase Ppa (pyr | 87.04 | 162 | Mb3652 | inorganic pyrophosphatase | 87.04 | 162 | MAV_0527 | inorganic pyrophosphatase | 98.77 | 162 | BCG_3686 | inorganic pyrophosphatase pp | 87.04 | 162 | MAP0435c | inorganic pyrophosphatase | 162 | 100 |
| MAP4_3433 | hypothetical protein | 359 | Rv3629c | Probable conserved integral membr | 75.43 | 365 | Mb3653c | hypothetical protein | 75.43 | 365 | MAV_0528 | hypothetical protein | 99.16 | 362 | BCG_3687c | hypothetical protein | 75.43 | 365 | MAP0434 | hypothetical protein | 359 | 100 |
| MAP4_3434 | hypothetical protein | 438 | Rv3630 | Probable conserved integral membr | 80.43 | 431 | Mb3654 | hypothetical protein | 80.67 | 431 | MAV_0526 | hypothetical protein | 99.28 | 416 | BCG_3688 | integral membrane protein | 80.67 | 431 | MAP0433c | hypothetical protein | 438 | 100 |
| MAP4_3435 | putative glycosyl transferase | 233 | Rv3631 | Possible transferase (possibly glycos | 84.39 | 241 | Mb3655 | transferase | 84.39 | 241 | MAV_0525 | glycosyl transferase | 99.55 | 221 | BCG_3689 | transferase | 84.39 | 241 | MAP0432c | hypothetical protein | 233 | 100 |
| MAP4_3436 | hypothetical protein | 113 | Rv3632 | Possible conserved membrane prote | 87.5 | 114 | Mb3656 | hypothetical protein | 87.5 | 114 | MAV_0523 | hypothetical protein | 100 | 113 | BCG_3690 | hypothetical protein | 87.5 | 114 | MAP0431c | hypothetical protein | 113 | 100 |
| MAP4_3437 | UDP-glucose 4-epimerase GalE1 | 318 | Rv3634c | UDP-glucose 4-epimerase GalE1 (gal | 88.82 | 314 | Mb3658c | UDP-glucose 4-epimerase | 88.82 | 314 | MAV_0524 | nucleoside-diphosphate-sugar epim | 99.04 | 313 | BCG_3692c | UDP-glucose 4-epimerase | 88.82 | 314 | MAP0430 | RmlB2 | 318 | 100 |
| MAP4_3438 | hypothetical protein | 584 | Rv3635 | Probable conserved transmembrane | 79.11 | 591 | Mb3659 | transmembrane protein | 79.11 | 591 | MAV_0522 | hypothetical protein | 97.41 | 580 | BCG_3693 | hypothetical protein | 79.11 | 591 | MAP0429c | hypothetical protein | 584 | 100 |
| MAP4_3441 | DNA polymerase | 401 | Rv3644c | Possible DNA polymerase | 87.75 | 401 | Mb3668c | DNA polymerase III subunit d | 87.75 | 401 | MAV_0520 | DNA polymerase III subunit delta' | 99.23 | 388 | BCG_3702c | DNA polymerase III subunit del | 87.75 | 401 | MAP0427 | DNA polymerase III subunit delta' | 401 | 100 |
| MAP4_3442 | hypothetical protein | 553 | Rv3645 | Probable conserved transmembrane | 84.43 | 549 | Mb3669 | transmembrane protein | 84.43 | 549 | MAV_0518 | adenylate cyclase, family protein 3 | 99.81 | 534 | BCG_3703 | hypothetical protein | 84.43 | 549 | MAP0426c | hypothetical protein | 553 | 100 |
| MAP4_3443 | DNA topoisomerase I TopA | 932 | Rv3646c | DNA topoisomerase I TopA (omega- | 86.3 | 934 | Mb3670c | DNA topoisomerase I | 86.3 | 934 | MAV_0519 | DNA topoisomerase I | 99.68 | 932 | BCG_3704c | DNA topoisomerase I | 86.19 | 934 | MAP0425 | DNA topoisomerase I | 932 | 100 |
| MAP4_3444 | hypothetical protein | 196 | Rv3647c | hypothetical protein | 82.05 | 192 | Mb3671c | hypothetical protein | 82.05 | 192 | MAV_0517 | hypothetical protein | 99.49 | 196 | BCG_3705c | hypothetical protein | 82.05 | 192 | MAP0424 | hypothetical protein | 196 | 100 |
| MAP4_3445 | Cold shock protein CspA | 67 | Rv3648c | Probable cold shock protein A CspA | 100 | 67 | Mb3672c | cold shock protein A | 100 | 67 | MAV_0516 | hypothetical protein | 100 | 67 | BCG_3706c | cold shock protein A cspA | 100 | 67 | MAP0423 | CspA_1 | 67 | 100 |
| MAP4_3446 | ATP-dependent helicase | 776 | Rv3649 | Probable helicase | 84.59 | 771 | Mb3673 | helicase | 84.72 | 771 | MAV_0515 | ATP-dependent rna helicase, dead/ | 98.97 | 776 | BCG_3707 | helicase | 84.59 | 771 | MAP0422c | hypothetical protein | 776 | 100 |
| MAP4_3447 | hypothetical protein | 345 | Rv3651 | hypothetical protein | 76.74 | 345 | Mb3675 | hypothetical protein | 76.74 | 345 | MAV_0513 | hypothetical protein | 99.39 | 328 | BCG_3709 | hypothetical protein | 76.74 | 345 | MAP0421c | hypothetical protein | 345 | 99.71 |
| MAP4_3448 | hypothetical protein | 97 | Rv3654c | hypothetical protein | 67.53 | 84 | Mb3678c | hypothetical protein | 67.53 | 84 | MAV_0514 | hypothetical protein | 98.97 | 97 | BCG_3712c | hypothetical protein | 67.53 | 84 | MAP0914c | hypothetical protein | 573 | 48.39 |
| MAP4_3449 | hypothetical protein | 89 | Rv3655c | hypothetical protein | 68.75 | 125 | Mb3679c | hypothetical protein | 68.75 | 99 | MAV_0512 | hypothetical protein | 95.51 | 89 | BCG_3713c | hypothetical protein | 68.75 | 99 | MAP0420 | hypothetical protein | 89 | 100 |
| MAP4_3450 | hypothetical protein | 67 | Rv3656c | hypothetical protein | 79.37 | 68 | Mb3680c | hypothetical protein | 79.37 | 68 | MAV_0511 | hypothetical protein | 98.48 | 66 | BCG_3714c | hypothetical protein | 79.37 | 68 | MAP0419 | hypothetical protein | 67 | 100 |
| MAP4_3451 | putative conserved alanine rich membrane protein | 195 | Rv3657c | Possible conserved alanine rich mem | 69.47 | 191 | Mb3681c | hypothetical protein | 69.47 | 191 | MAV_0510 | type II secretion system protein F | 99.49 | 195 | BCG_3715c | alanine rich membrane protein | 69.47 | 191 | MAP0418 | hypothetical protein | 193 | 99.48 |
| MAP4_3452 | conserved transmembrane protein | 267 | Rv3658c | Probable conserved transmembrane | 67.42 | 266 | Mb3682c | transmembrane protein | 67.42 | 266 | MAV_0509 | type II secretion system protein F | 98.5 | 267 | BCG_3716c | hypothetical protein | 67.42 | 266 | MAP0417 | hypothetical protein | 267 | 100 |
| MAP4_3453 | type IIIV secretion system protein | 391 | Rv3659c | hypothetical protein | 87.68 | 352 | Mb3683c | hypothetical protein | 87.68 | 352 | MAV_0471 | Type II/IV secretion system protein | 99.7 | 362 | BCG_3717c | hypothetical protein | 87.68 | 352 | MAP0416 | hypothetical protein | 352 | 100 |
| MAP4_3454 | hypothetical protein | 351 | Rv3660c | hypothetical protein | 74.36 | 350 | Mb3684c | hypothetical protein | 74.36 | 350 | MAV_0470 | hypothetical protein | 98.01 | 350 | BCG_3718c | hypothetical protein | 74.36 | 350 | MAP0415 | hypothetical protein | 351 | 100 |
| MAP4_3455 | haloacid dehalogenase (HAD)-like hydrolase family pro | 285 | Rv3661 | hypothetical protein | 87.37 | 287 | Mb3685 | hypothetical protein | 87.02 | 287 | MAV_0469 | HAD-superfamily protein subfamily | 100 | 285 | BCG_3719 | hypothetical protein | 87.02 | 287 | MAP0414c | hypothetical protein | 285 | 100 |
| MAP4_3456 | hypothetical protein | 252 | Rv3662c | hypothetical protein | 79.92 | 256 | Mb3686c | hypothetical protein | 79.53 | 256 | MAV_0468 | hypothetical protein | 100 | 243 | BCG_3720c | hypothetical protein | 79.53 | 256 | MAP0413 | hypothetical protein | 252 | 100 |
| MAP4_3457 | dipeptide-transport ATP-binding protein ABC transport | 548 | Rv3663c | Probable dipeptide-transport ATP-bi | 78.64 | 548 | Mb3687c | peptide ABC transporter ATP- | 78.64 | 548 | MAV_0467 | ABC transporter ATP-binding prote | 99.27 | 551 | BCG_3721c | dipeptide-transport ATP-bindin | 78.64 | 548 | MAP0412 | DppD_1 | 548 | 100 |
| MAP4_3458 | dipeptide-transport membrane protein ABC transporte | 291 | Rv3664c | Probable dipeptide-transport integra | 90.04 | 266 | Mb3688c | peptide ABC transporter | 90.04 | 266 | MAV_0466 | ABC transporter permease | 99.31 | 291 | BCG_3722c | dipeptide-transport integral m | 90.04 | 266 | MAP0411 | hypothetical protein | 291 | 100 |
| MAP4_3459 | dipeptide-transport membrane protein ABC transporte | 308 | Rv3665c | Probable dipeptide-transport integra | 90.26 | 308 | Mb3689c | peptide ABC transporter | 90.26 | 308 | MAV_0465 | ABC transporter permease | 99.03 | 308 | BCG_3723c | dipeptide-transport integral m | 90.26 | 308 | MAP0410 | hypothetical protein | 308 | 100 |
| MAP4_3460 | periplasmic dipeptide-binding lipoprotein DppA | 541 | Rv3666c | Probable periplasmic dipeptide-bind | 84.42 | 541 | Mb3690c | periplasmic dipeptide-binding | 84.42 | 541 | MAV_0464 | extracellular solute-binding protein | 99.25 | 534 | BCG_3724c | periplasmic dipeptide-binding | 84.62 | 541 | MAP0409 | hypothetical protein | 541 | 100 |
| MAP4_3461 | hypothetical protein | 180 | Rv2158c | Probable UDP-N-acetylmuramoylala | 35.04 | 535 | Mb2182c | UDP-N-acetylmuramoylalanyl | 35.04 | 535 | MAV_0463 | hypothetical protein | 99.44 | 180 | BCG_2175c | UDP-N-acetylmuramoylalanyl- | 35.04 | 535 | MAP0408 | hypothetical protein | 180 | 100 |
| MAP4_3462 | acetyl-coA synthetase Acs | 650 | Rv3667 | Acetyl-coenzyme A synthetase Acs ( | 80.03 | 651 | Mb3691 | acetyl-CoA synthetase | 80.03 | 651 | MAV_0462 | acetyl-CoA synthetase | 99.08 | 650 | BCG_3725 | acetyl-CoA synthetase | 80.03 | 651 | MAP0407c | acetyl-CoA synthetase | 650 | 100 |
| MAP4_3463 | putative protease | 232 | Rv3668c | Possible protease | 79.22 | 232 | Mb3692c | protease | 79.22 | 232 | MAV_0461 | hypothetical protein | 99.1 | 223 | BCG_3726c | protease | 79.22 | 232 | MAP0406 | hypothetical protein | 232 | 100 |
| MAP4_3464 | hypothetical protein | 179 | Rv3669 | Probable conserved transmembrane | 78.77 | 172 | Mb3693 | transmembrane protein | 78.77 | 172 | MAV_0460 | hypothetical protein | 99.44 | 179 | BCG_3727 | hypothetical protein | 78.77 | 172 | MAP0405c | hypothetical protein | 179 | 100 |
| MAP4_3465 | epoxide hydrolase EphE | 321 | Rv3670 | Possible epoxide hydrolase EphE (ep | 81.17 | 327 | Mb3694 | epoxide hydrolase | 81.17 | 327 | MAV_0458 | alpha/beta hydrolase | 97.82 | 321 | BCG_3728 | epoxide hydrolase ephE | 81.17 | 327 | MAP0404c | EphE | 321 | 100 |
| MAP4_3466 | membrane-associated serine protease | 397 | Rv3671c | Membrane-associated serine protea | 85.64 | 397 | Mb3695c | membrane-associated serine | 85.89 | 397 | MAV_0459 | serine protease | 100 | 402 | BCG_3729c | membrane-associated serine p | 85.39 | 397 | MAP0403 | hypothetical protein | 397 | 100 |
| MAP4_3467 | putative phosphohydrolase, NUDIX family protein | 272 | Rv3672c | hypothetical protein | 79.7 | 273 | Mb3696c | hypothetical protein | 79.7 | 273 | MAV_0457 | hydrolase, nudix family protein | 99.63 | 272 | BCG_3730c | hypothetical protein | 79.7 | 273 | MAP0402 | hypothetical protein | 272 | 100 |
| MAP4_3468 | membrane-anchored thioredoxin | 222 | Rv3673c | Possible membrane-anchored thiore | 71.76 | 227 | Mb3697c | membrane-anchored thiored | 71.76 | 227 | MAV_0456 | hypothetical protein | 99.1 | 222 | BCG_3731c | membrane-anchored thioredo | 71.76 | 227 | MAP0401 | hypothetical protein | 222 | 100 |
| MAP4_3469 | Endonuclease III Nth | 265 | Rv3674c | Probable endonuclease III Nth (DNA | 83.88 | 245 | Mb3698c | endonuclease III | 83.88 | 245 | MAV_0455 | endonuclease III | 98.28 | 232 | BCG_3732c | endonuclease III nth | 83.88 | 245 | MAP0400 | hypothetical protein | 265 | 100 |
| MAP4_3470 | hypothetical protein | 131 | Rv3675 | Possible membrane protein | 57.25 | 125 | Mb3699 | hypothetical protein | 57.25 | 125 | MAV_0454 | hypothetical protein | 99.21 | 126 | BCG_3733 | hypothetical protein | 57.25 | 125 | MAP0399c | hypothetical protein | 131 | 100 |
| MAP4_3471 | transcriptional regulator, crpfnr-family | 224 | Rv3676 | Transcriptional regulatory protein C | 96.88 | 224 | Mb3700 | Crp/Fnr family transcriptional | 96.88 | 224 | MAV_0453 | Crp/Fnr family transcriptional regul | 100 | 224 | BCG_3734 | CRP/FNR family transcriptional | 95.98 | 224 | MAP0398c | hypothetical protein | 224 | 100 |
| MAP4_3472 | putative hydrolase | 267 | Rv3677c | Possible hydrolase | 77.95 | 264 | Mb3701c | hydrolase | 77.95 | 264 | MAV_0452 | metallo-beta-lactamase | 98.5 | 267 | BCG_3735c | hydrolase | 77.95 | 264 | MAP0397 | hypothetical protein | 267 | 100 |
| MAP4_3473 | putative endoribonuclease, L-PSP domain-containing p | 158 | Rv3678c | hypothetical protein | 82 | 151 | Mb3702c | hypothetical protein | 82 | 151 | MAV_0451 | translation initiation inhibitor | 98.73 | 158 | BCG_3736c | hypothetical protein | 82 | 151 | MAP0396 | hypothetical protein | 158 | 100 |
| MAP4_3474 | hypothetical protein | 53 | Rv3678A | hypothetical protein | 96.23 | 53 | Mb3703c | hypothetical protein | 96.23 | 53 | MAV_0450 | hypothetical protein | 100 | 53 | BCG_3737c | hypothetical protein | 96.23 | 53 | MAP0391c | hypothetical protein | 315 | 47.62 |
| MAP4_3475 | anion transporter ATPase | 340 | Rv3679 | Probable anion transporter ATPase | 88.53 | 340 | Mb3704 | anion transporter ATPase | 88.53 | 340 | MAV_0449 | anion-transporting ATPase | 99.69 | 323 | BCG_3738 | anion transporter atpase | 88.53 | 340 | MAP0395c | hypothetical protein | 340 | 100 |
| MAP4_3476 | anion transporter ATPase | 380 | Rv3680 | Probable anion transporter ATPase | 88.8 | 386 | Mb3705 | anion transporter ATPase | 88.8 | 386 | MAV_0448 | anion-transporting ATPase | 99.73 | 371 | BCG_3739 | anion transporter atpase | 88.8 | 386 | MAP0394c | hypothetical protein | 380 | 100 |
| MAP4_3477 | transcriptional regulator whib-like whiB4 | 116 | Rv3681c | Probable transcriptional regulatory | 87.72 | 118 | Mb3706c | transcriptional regulatory pro | 87.72 | 118 | MAV_0447 | transcription factor WhiB | 98.57 | 70 | BCG_3740c | transcriptional regulatory prote | 87.72 | 118 | MAP0393 | WhiB4 | 116 | 100 |
| MAP4_3478 | bifunctional membrane-associated penicillin-binding p | 813 | Rv3682 | Probable bifunctional membrane-as | 89.37 | 810 | Mb3707 | bifunctional membrane-assoc | 89.37 | 810 | MAV_0446 | transglycosylase | 99.07 | 786 | BCG_3741 | bifunctional membrane-associa | 89.37 | 810 | MAP0392c | PonA_2 | 809 | 99.23 |
| MAP4_3479 | hypothetical protein | 315 | Rv3683 | hypothetical protein | 86.98 | 319 | Mb3708 | hypothetical protein | 86.98 | 319 | MAV_0445 | secreted protein | 99.68 | 337 | BCG_3742 | hypothetical protein | 86.98 | 319 | MAP0391c | hypothetical protein | 315 | 100 |
| MAP4_3480 | putative lyase | 367 | Rv3684 | Probable lyase | 87.83 | 346 | Mb3709 | lyase | 87.83 | 346 | MAV_0444 | cysteine synthase/cystathionine be | 99.46 | 367 | BCG_3743 | lyase | 87.83 | 346 | MAP0390c | hypothetical protein | 367 | 100 |
| MAP4_3481 | hypothetical protein | 337 | Rv2131c | Monophosphatase CysQ | 41.94 | 267 | Mb2155c | hypothetical protein | 41.94 | 267 | MAV_3248 | Mmp14A protein | 26.44 | 963 | BCG_2148c | hypothetical protein | 41.94 | 267 | MAP0389 | hypothetical protein | 337 | 100 |
| MAP4_3482 | hypothetical protein | 441 | Rv1292 | Probable arginyl-tRNA synthetase A | 32.76 | 550 | Mb2835 | transposase | 30.34 | 226 | MAV_2370 | mycocerosic acid synthase | 29.59 | 2098 | BCG_1352 | arginyl-tRNA synthetase | 32.76 | 550 | MAP0388 | hypothetical protein | 398 | 99.75 |
| MAP4_3483 | hypothetical protein | 186 | Rv2969c | Possible conserved membrane or se | 75 | 255 | Mb2993c | hypothetical protein | 75 | 255 | MAV_1379 | magnesium and cobalt transport pr | 26 | 366 | BCG_2990c | membrane or hypothetical pro | 75 | 255 | MAP0387 | hypothetical protein | 186 | 100 |
| MAP4_3484 | transcription antitermination regulator (ANTAR)do mai | 229 | Rv1724c | Hypothetical protein | 32.73 | 139 | Mb1753c | hypothetical protein | 32.73 | 139 | MAV_0441 | ANTAR domain-containing protein | 99.56 | 229 | BCG_1763c | hypothetical protein | 32.73 | 139 | MAP0386c | hypothetical protein | 229 | 100 |
| MAP4_3485 | hypothetical protein | 197 | Rv1077 | Probable cystathionine beta-synthas | 32.43 | 464 | Mb1106 | cystathionine beta-synthase | 32.43 | 464 | MAV_0440 | restriction endonuclease | 98.48 | 197 | BCG_1135 | cystathionine beta-synthase | 32.43 | 464 | MAP0385 | hypothetical protein | 197 | 100 |
| MAP4_3486 | hypothetical protein | 100 | Rv2699c | hypothetical protein | 57.73 | 100 | Mb2718c | hypothetical protein | 57.73 | 100 | MAV_3591 | hypothetical protein | 58.76 | 100 | BCG_2712c | hypothetical protein | 57.73 | 100 | MAP0384 | hypothetical protein | 100 | 100 |
| MAP4_3487 | hypothetical protein | 114 | Rv3288c | Putative protein UsfY | 35.96 | 137 | Mb3316c | hypothetical protein | 35.96 | 137 | MAV_0438 | hypothetical protein | 98.06 | 103 | BCG_3317c | protein usfY | 35.96 | 137 | MAP0383 | hypothetical protein | 114 | 100 |
| MAP4_3488 | putative hydrolase, haloacid dehalogenase-like hydrola | 215 | Rv2496c | Probable branched-chain keto acid d | 33.87 | 348 | Mb2524c | pyruvate dehydrogenase E1 c | 33.87 | 348 | MAV_0437 | hydrolase | 96.67 | 210 | BCG_2516c | pyruvate dehydrogenase E1 co | 33.87 | 348 | MAP0382c | hypothetical protein | 215 | 100 |
| MAP4_3489 | hypothetical protein | 173 | Rv1718 | hypothetical protein | 33.33 | 272 | Mb1746 | hypothetical protein | 33.33 | 207 | MAV_0436 | hypothetical protein | 99.41 | 169 | BCG_1757 | hypothetical protein | 33.33 | 207 | MAP0381 | hypothetical protein | 173 | 100 |
| MAP4_3490 | putative anti-anti-sigma factor rsfB | 122 | Rv3687c | Anti-anti-sigma factor RsfB (anti-sig | 73.55 | 122 | Mb3712c | hypothetical protein | 73.75 | 81 | MAV_0435 | anti-anti-sigma factor | 99.12 | 113 | BCG_3746c | hypothetical protein | 73.75 | 81 | MAP0380 | hypothetical protein | 122 | 99.18 |
| MAP4_3491 | putative anti-sigma-factor antagonist RsbR | 300 | Rv2043c | Pyrazinamidase/nicotinamidase Pnc | 29.85 | 186 | Mb2069c | pyrazinamidase | 29.85 | 186 | MAV_0434 | anti-anti-sigma factor | 100 | 300 | BCG_2062c | pyrazinamidase/nicotinamidas | 29.85 | 186 | MAP0379c | hypothetical protein | 300 | 100 |
| MAP4_3492 | putative antagonist protein RsbS | 129 | Rv2638 | hypothetical protein | 32.5 | 148 | Mb2671 | hypothetical protein | 32.5 | 148 | MAV_0433 | antagonist protein RsbS | 100 | 129 | BCG_2665 | hypothetical protein | 32.5 | 148 | MAP0378c | hypothetical protein | 129 | 100 |
| MAP4_3493 | serinethreonine-protein kinase RsbT | 136 | Rv0490 | Putative two component sensor hist | 28.92 | 410 | Mb0500 | two component sensor histid | 28.92 | 410 | MAV_0432 | serine/threonine protein kinase | 100 | 136 | BCG_0531 | two component sensor histidin | 28.92 | 410 | MAP0377c | hypothetical protein | 136 | 100 |
| MAP4_3494 | stage II sporulation protein E family protein | 207 | Rv3564 | Probable acyl-CoA dehydrogenase F | 30.65 | 318 | Mb3594 | acyl-CoA dehydrogenase | 30.65 | 318 | MAV_0431 | stage II sporulation protein E (SpoII | 98.62 | 190 | BCG_3628 | acyl-CoA dehydrogenase fadE3 | 30.65 | 318 | MAP0376c | hypothetical protein | 207 | 100 |
| MAP4_3495 | stage II sporulation protein E (SpoIIE) | 736 | Rv1364c | Possible sigma factor regulatory pro | 31.25 | 653 | Mb1399c | hypothetical protein | 31.25 | 653 | MAV_0430 | stage II sporulation protein E (SpoII | 100 | 736 | BCG_1426c | hypothetical protein | 31.25 | 653 | MAP0375c | hypothetical protein | 736 | 100 |
| MAP4_3497 | putative methyltransferase | 229 | Rv1300 | Probable HemK protein homolog He | 29.32 | 325 | Mb1332 | hypothetical protein | 29.32 | 325 | MAV_0427 | methylase, putative | 99.56 | 229 | BCG_1360 | hemk protein hemK | 29.32 | 325 | MAP0373 | hypothetical protein | 229 | 100 |
| MAP4_3498 | putative protease, ThiJPfpI family protein | 184 | Rv0052 | hypothetical protein | 27.47 | 187 | Mb0053 | hypothetical protein | 27.47 | 187 | MAV_0426 | intracellular protease, PfpI family p | 98.89 | 180 | BCG_0083 | hypothetical protein | 27.47 | 187 | MAP0372 | PfpI | 184 | 100 |
| MAP4_3499 | putative oxidoreductase | 328 | Rv0407 | F420-dependent glucose-6-phospha | 34.52 | 336 | Mb0415 | F420-dependent glucose-6-ph | 34.52 | 336 | MAV_0425 | dehydrogenase | 99.7 | 336 | BCG_0446 | glucose-6-phosphate dehydrog | 34.52 | 336 | MAP0371 | hypothetical protein | 328 | 100 |
| MAP4_3500 | putative polysulfide reductase, NrfD family protein | 361 | Rv0364 | Possible conserved transmembrane | 40 | 227 | Mb0371 | transmembrane protein | 40 | 227 | MAV_0424 | polysulphide reductase | 99.72 | 361 | BCG_0402 | hypothetical protein | 40 | 227 | MAP0370 | hypothetical protein | 361 | 100 |
| MAP4_3501 | 4Fe-4S ferredoxin iron-sulfur binding domain-containin | 324 | Rv1162 | Probable respiratory nitrate reducta | 36.36 | 558 | Mb1194 | respiratory nitrate reductase | 36.36 | 558 | MAV_0423 | 4Fe-4S ferredoxin iron-sulfur bindin | 99.69 | 330 | BCG_1224 | respiratory nitrate reductase su | 36.36 | 558 | MAP0369 | hypothetical protein | 324 | 100 |
| MAP4_3502 | formate dehydrogenase, alpha subunit | 887 | Rv2900c | Possible formate dehydrogenase H F | 29.03 | 779 | Mb2924c | formate dehydrogenase H | 29.03 | 779 | MAV_0422 | formate dehydrogenase, alpha sub | 99.77 | 887 | BCG_2921c | formate dehydrogenase H fdhF | 29.03 | 779 | MAP0368 | hypothetical protein | 874 | 100 |
| MAP4_3503 | molybdopterin oxidoreductase Fe4S4 domain protein | 193 | Rv0197 | Possible oxidoreductase | 30.85 | 762 | Mb0203 | oxidoreductase | 30 | 748 | MAV_0421 | molybdopterin oxidoreductase Fe4 | 100 | 193 | BCG_0234 | oxidoreductase | 30 | 748 | MAP0367 | hypothetical protein | 193 | 100 |
| MAP4_3504 | selenide, water dikinase SelD | 330 | Rv0809 | Probable phosphoribosylformylglyci | 30.34 | 364 | Mb0832 | phosphoribosylaminoimidazo | 30.34 | 364 | MAV_0420 | selenide, water dikinase | 99.7 | 330 | BCG_0861 | phosphoribosylaminoimidazole | 30.34 | 364 | MAP0366 | hypothetical protein | 305 | 99.67 |
| MAP4_3505 | L-seryl-tRNA(Sec) selenium transferase | 428 | Rv3700c | hypothetical protein | 38.1 | 390 | Mb3726c | hypothetical protein | 38.1 | 390 | MAV_0418 | selenocysteine synthase | 98.12 | 426 | BCG_3759c | hypothetical protein | 38.1 | 390 | MAP0365c | selenocysteine synthase | 361 | 99.72 |
| MAP4_3506 | selenocysteine-specific translation elongation factor | 570 | Rv0685 | Probable iron-regulated elongation f | 30.95 | 396 | Mb0704 | elongation factor Tu | 30.95 | 396 | MAV_0417 | elongation factor Tu GTP binding d | 98.25 | 570 | BCG_0734 | elongation factor Tu | 30.95 | 396 | MAP0364c | hypothetical protein | 570 | 100 |
| MAP4_3507 | hypothetical protein | 154 | Rv3688c | hypothetical protein | 86.36 | 154 | Mb3713c | hypothetical protein | 86.36 | 154 | MAV_0416 | GatB/Yqey domain-containing prot | 100 | 154 | BCG_3747c | hypothetical protein | 86.36 | 154 | MAP0363 | hypothetical protein | 154 | 100 |
| MAP4_3508 | putative conserved membrane protein | 419 | Rv3689 | Probable conserved transmembrane | 63.22 | 451 | Mb3714 | transmembrane protein | 63.22 | 451 | MAV_0415 | hypothetical protein | 97.14 | 418 | BCG_3748 | hypothetical protein | 63.22 | 451 | MAP0362c | hypothetical protein | 419 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3509 | putative conserved membrane protein | 217 | Rv3690 | Probable conserved membrane prot | 68.2 | 217 | Mb3715 | hypothetical protein | 68.2 | 217 | MAV_0414 | hypothetical protein | 98.62 | 217 | BCG_3749 | hypothetical protein | 68.2 | 217 | MAP0361c | hypothetical protein | 217 | 100 |
| MAP4_3510 | hypothetical protein | 377 | Rv3691 | hypothetical protein | 66.87 | 333 | Mb3716 | hypothetical protein | 66.87 | 333 | MAV_0413 | hypothetical protein | 99.2 | 377 | BCG_3750 | hypothetical protein | 66.87 | 333 | MAP0360c | hypothetical protein | 377 | 100 |
| MAP4_3511 | Putative methanol dehydrogenase transcriptional regu | 327 | Rv3692 | Probable methanol dehydrogenase t | 88.27 | 358 | Mb3717 | methanol dehydrogenase tra | 88.27 | 358 | MAV_0412 | ATPase | 99.69 | 327 | BCG_3751 | methanol dehydrogenase trans | 88.27 | 358 | MAP0359c | MoxR2 | 327 | 100 |
| MAP4_3512 | putative conserved membrane protein | 440 | Rv3693 | Possible conserved membrane prote | 82.5 | 440 | Mb3718 | hypothetical protein | 82.5 | 440 | MAV_0411 | lipoprotein | 99.09 | 440 | BCG_3752 | hypothetical protein | 82.5 | 440 | MAP0358c | hypothetical protein | 440 | 100 |
| MAP4_3513 | hypothetical protein | 330 | Rv3694c | Possible conserved transmembrane | 79.09 | 330 | Mb3719c | transmembrane protein | 79.09 | 330 | MAV_0410 | integral membrane protein | 99.7 | 330 | BCG_3753c | hypothetical protein | 79.09 | 330 | MAP0357 | hypothetical protein | 330 | 100 |
| MAP4_3514 | putative conserved membrane protein | 289 | Rv3695 | Possible conserved membrane prote | 78.93 | 310 | Mb3720 | hypothetical protein | 78.93 | 310 | MAV_0408 | integral membrane protein | 99.31 | 290 | BCG_3754 | hypothetical protein | 78.93 | 310 | MAP0356c | hypothetical protein | 289 | 100 |
| MAP4_3515 | hypothetical protein | 129 | Rv0961 | Probable integral membrane protein | 45.45 | 115 | Mb0986 | hypothetical protein | 45.45 | 115 | MAV_0409 | hypothetical protein | 99.22 | 129 | BCG_1015 | integral membrane protein | 45.45 | 115 | MAP0355 | hypothetical protein | 129 | 100 |
| MAP4_3516 | Transcriptional regulator, PadR family | 238 | Rv0047c | hypothetical protein | 35.62 | 180 | Mb0048c | hypothetical protein | 35.62 | 180 | MAV_0407 | PadR family transcriptional regulato | 99.58 | 256 | BCG_0078c | hypothetical protein | 35.62 | 180 | MAP0354c | hypothetical protein | 238 | 100 |
| MAP4_3517 | Glycerol kinase GlpK | 515 | Rv3696c | Probable glycerol kinase GlpK (ATP:g | 87.4 | 517 | Mb3722c | glycerol kinase | 85.79 | 251 | MAV_0406 | glycerol kinase | 99.21 | 508 | BCG_3755c | glycerol kinase | 87.43 | 518 | MAP0353 | glycerol kinase | 515 | 100 |
| MAP4_3518 | D-3-phosphoglycerate dehydrogenase | 328 | Rv2996c | Probable D-3-phosphoglycerate deh | 36.21 | 528 | Mb3020c | D-3-phosphoglycerate dehydr | 36.21 | 528 | MAV_0349 | D-isomer specific 2-hydroxyacid de | 98.85 | 329 | BCG_3017c | D-3-phosphoglycerate dehydro | 36.21 | 528 | MAP0352c | hypothetical protein | 328 | 100 |
| MAP4_3519 | Transcriptional regulator, TetR family | 198 | Rv3830c | Transcriptional regulatory protein (p | 38.04 | 209 | Mb3860c | transcriptional regulatory pro | 38.04 | 209 | MAV_0350 | TetR family transcriptional regulato | 100 | 198 | BCG_3893c | TetR family transcriptional regu | 38.04 | 209 | MAP0351 | hypothetical protein | 198 | 100 |
| MAP4_3520 | putative dehydrogenasereductase | 257 | Rv0769 | Probable dehydrogenase/reductase | 35.92 | 248 | Mb0792 | short chain dehydrogenase | 35.92 | 248 | MAV_0351 | short chain dehydrogenase/reducta | 99.61 | 257 | BCG_0821 | short chain dehydrogenase | 35.92 | 248 | MAP0350 | hypothetical protein | 257 | 100 |
| MAP4_3521 | hypothetical protein | 367 | Rv1059 | hypothetical protein | 60.91 | 354 | Mb1088 | hypothetical protein | 60.91 | 354 | MAV_0353 | hypothetical protein | 99.44 | 359 | BCG_1117 | hypothetical protein | 60.91 | 354 | MAP0349 | hypothetical protein | 367 | 100 |
| MAP4_3522 | putative oxidoreductase, short-chain type dehydrogena | 297 | Rv3549c | Probable short-chain type dehydrog | 38.58 | 259 | Mb3579c | short chain dehydrogenase | 38.58 | 259 | MAV_0354 | oxidoreductase, short chain dehydr | 97.89 | 285 | BCG_3613c | short chain dehydrogenase | 38.58 | 259 | MAP0348c | hypothetical protein | 297 | 100 |
| MAP4_3523 | putative acyltransferase, wax estersynthase-like Acyl-C | 451 | Rv3734c | Putative triacylglycerol synthase (dia | 73.51 | 454 | Mb3761c | hypothetical protein | 73.51 | 454 | MAV_0355 | bifunctional wax ester synthase/ac | 99.78 | 451 | BCG_3794c | hypothetical protein | 73.51 | 454 | MAP0347c | hypothetical protein | 451 | 100 |
| MAP4_3524 | hypothetical protein | 161 | Rv3733c | hypothetical protein | 79.38 | 166 | Mb3760c | hypothetical protein | 79.38 | 166 | MAV_0356 | nudix hydrolase | 98.76 | 161 | BCG_3793c | hypothetical protein | 79.38 | 166 | MAP0346c | hypothetical protein | 161 | 100 |
| MAP4_3525 | haloalkane dehalogenase | 301 | Rv2296 | Probable haloalkane dehalogenase | 51 | 300 | Mb2318 | haloalkane dehalogenase | 51 | 300 | MAV_0357 | haloalkane dehalogenase | 99.34 | 301 | BCG_2312 | haloalkane dehalogenase | 51 | 300 | MAP0345c | haloalkane dehalogenase | 301 | 100 |
| MAP4_3526 | putative cytochrome P450 hydroxylase | 411 | Rv1880c | Probable cytochrome P450 140 Cyp1 | 38.26 | 438 | Mb1912c | cytochrome p450 140 CYP140 | 38.26 | 438 | MAV_0358 | cytochrome P450 | 99.03 | 411 | BCG_1917c | cytochrome p450 140 CYP140 | 38.26 | 438 | MAP0344c | hypothetical protein | 411 | 100 |
| MAP4_3527 | hypothetical protein | 122 | Rv3042c | Probable phosphoserine phosphatas | 37.14 | 409 | Mb3865 | hypothetical protein | 26.32 | 449 | MAV_0359 | hypothetical protein | 98.33 | 120 | BCG_3898 | hypothetical protein | 26.32 | 452 | MAP0343 | hypothetical protein | 122 | 100 |
| MAP4_3528 | hypothetical protein | 115 | Rv3312A | Secreted protein antigen | 32.35 | 103 | Mb3341c | hypothetical protein | 32.35 | 103 | MAV_0361 | hypothetical protein | 98.26 | 115 | BCG_3378c | hypothetical protein | 32.35 | 103 | MAP0342c | hypothetical protein | 115 | 100 |
| MAP4_3529 | ATP-dependent DNA ligase LigC | 369 | Rv3731 | Possible ATP-dependent DNA ligase | 87.11 | 358 | Mb3758 | ATP-dependent DNA ligase | 87.39 | 358 | MAV_0360 | ATP-dependent DNA ligase | 99.45 | 364 | BCG_3791 | ATP-dependent DNA ligase | 87.39 | 358 | MAP0341 | ATP-dependent DNA ligase | 369 | 100 |
| MAP4_3530 | hypothetical protein | 342 | Rv3730c | hypothetical protein | 87.1 | 346 | Mb3757c | hypothetical protein | 87.1 | 346 | MAV_0362 | DNA polymerase LigD polymerase s | 99.71 | 342 | BCG_3790c | hypothetical protein | 87.1 | 346 | MAP0340c | hypothetical protein | 342 | 100 |
| MAP4_3531 | hypothetical protein | 697 | Rv1420 | Probable excinuclease ABC (subunit | 32.76 | 646 | Mb1455 | excinuclease ABC subunit C | 32.76 | 646 | MAV_0365 | hypothetical protein | 98.96 | 670 | BCG_1481 | excinuclease ABC subunit C | 32.76 | 646 | MAP0339c | hypothetical protein | 697 | 100 |
| MAP4_3532 | transposase, IS4 family | 557 | Rv3386 | Possible transposase | 25.95 | 234 | Mb3418 | transposase | 25.95 | 234 | MAV_3010 | ABC transporter ATP-binding prote | 29.31 | 862 | BCG_3455 | transposase | 25.95 | 234 | MAP0338c | hypothetical protein | 557 | 100 |
| MAP4_3533 | putative transmembrane protein | 331 | Rv1648 | Probable transmembrane protein | 50.72 | 268 | Mb1675 | transmembrane protein | 50.72 | 268 | MAV_0364 | hypothetical protein | 98.17 | 351 | BCG_1687 | hypothetical protein | 50.72 | 268 | MAP0337 | hypothetical protein | 331 | 100 |
| MAP4_3534 | putative cytochrome P450 | 400 | Rv0766c | Probable cytochrome P450 123 Cyp1 | 38.63 | 402 | Mb0789c | cytochrome P450 123 | 38.63 | 402 | MAV_0366 | cytochrome P450 superfamily prot | 99.25 | 400 | BCG_0818c | cytochrome P450 123 cyp123 | 36.76 | 541 | MAP0336c | hypothetical protein | 400 | 100 |
| MAP4_3535 | Transcriptional regulator, TetR family | 191 | Rv0328 | Possible transcriptional regulatory p | 26.06 | 200 | Mb0335 | TetR/AcrR family transcriptio | 26.06 | 200 | MAV_0367 | TetR family transcriptional regulato | 98.43 | 191 | BCG_0367 | TetR family transcriptional regu | 26.06 | 200 | MAP0335 | hypothetical protein | 191 | 100 |
| MAP4_3536 | oxidoreductase | 330 | Rv3725 | Possible oxidoreductase | 84.49 | 309 | Mb3752 | oxidoreductase | 82.97 | 333 | MAV_1849 | dihydroflavonol-4-reductase | 25.56 | 327 | BCG_3785 | oxidoreductase | 82.97 | 333 | MAP0334 | hypothetical protein | 330 | 100 |
| MAP4_3537 | cutinase | 209 | Rv3724B | Probable cutinase [second part] Cut | 70.24 | 187 | Mb3751 | cutinase | 71.22 | 233 | MAV_0369 | serine esterase cutinase | 99.52 | 231 | BCG_3784 | cutinase precursor cut5 | 71.22 | 233 | MAP0333 | hypothetical protein | 209 | 100 |
| MAP4_3538 | hypothetical protein | 355 | Rv1059 | hypothetical protein | 35.98 | 354 | Mb1088 | hypothetical protein | 35.98 | 354 | MAV_0371 | dihydrodipicolinate reductase | 99.44 | 355 | BCG_1117 | hypothetical protein | 35.98 | 354 | MAP0332 | hypothetical protein | 355 | 100 |
| MAP4_3539 | hypothetical protein | 378 | Rv0642c | Methoxy mycolic acid synthase 4 Mr | 40 | 301 | Mb0661c | methoxy mycolic acid synthas | 40 | 301 | MAV_0372 | hypothetical protein | 98.15 | 378 | BCG_0691c | methoxy mycolic acid synthase | 40 | 301 | MAP0331 | hypothetical protein | 378 | 100 |
| MAP4_3540 | hypothetical protein | 442 | Rv3079c | hypothetical protein | 39.13 | 275 | Mb3106c | hypothetical protein | 39.13 | 275 | MAV_0373 | hypothetical protein | 97.51 | 444 | BCG_3104c | hypothetical protein | 39.13 | 275 | MAP0330 | hypothetical protein | 442 | 100 |
| MAP4_3541 | hypothetical protein | 112 | Rv1517 | hypothetical protein | 33.33 | 254 | Mb1544 | hypothetical protein | 33.33 | 254 | MAV_0374 | hypothetical protein | 100 | 110 | BCG_1569 | hypothetical protein | 33.33 | 254 | MAP0329c | hypothetical protein | 112 | 100 |
| MAP4_3542 | hypothetical protein | 462 | Rv3331 | Probable sugar-transport integral m | 30.12 | 502 | Mb3364 | sugar-transport integral mem | 30.12 | 502 | MAV_0375 | hypothetical protein | 99.13 | 460 | BCG_3401 | sugar-transport integral memb | 30.12 | 497 | MAP0328 | hypothetical protein | 462 | 100 |
| MAP4_3543 | hypothetical protein | 561 | Rv2402 | hypothetical protein | 31.96 | 642 | Mb2425 | hypothetical protein | 31.96 | 642 | MAV_0376 | hypothetical protein | 98.4 | 562 | BCG_2418 | hypothetical protein | 31.96 | 642 | MAP0327 | hypothetical protein | 561 | 100 |
| MAP4_3544 | putative 19 kda lipoprotein antigen precursor lpqH | 163 | Rv3763 | 19 kDa lipoprotein antigen precurso | 40.59 | 159 | Mb3789 | hypothetical protein | 40.59 | 159 | MAV_0377 | hypothetical protein | 99.34 | 152 | BCG_3822 | 19 kDa lipoprotein antigen pre | 40.59 | 159 | MAP0326 | hypothetical protein | 163 | 100 |
| MAP4_3545 | hypothetical protein | 125 | Rv3543c | Probable acyl-CoA dehydrogenase F | 34.48 | 387 | Mb3573c | acyl-CoA dehydrogenase | 34.48 | 387 | MAV_0379 | hypothetical protein | 100 | 125 | BCG_3607c | acyl-CoA dehydrogenase fadE2 | 34.48 | 387 | MAP0325c | hypothetical protein | 125 | 100 |
| MAP4_3546 | putative conserved membrane protein | 277 | Rv3723 | Probable conserved transmembrane | 65.88 | 254 | Mb3750 | transmembrane protein | 65.88 | 254 | MAV_0378 | hypothetical protein | 97.83 | 277 | BCG_3783 | hypothetical protein | 65.88 | 254 | MAP0324 | hypothetical protein | 277 | 100 |
| MAP4_3547 | putative aminotransferase | 428 | Rv3722c | hypothetical protein | 86.76 | 435 | Mb3749c | hypothetical protein | 86.76 | 435 | MAV_0381 | aspartate transaminase | 100 | 428 | BCG_3782c | hypothetical protein | 86.52 | 435 | MAP0323c | hypothetical protein | 428 | 100 |
| MAP4_3548 | DNA polymerase III subunits gamma tau subunit | 612 | Rv3721c | DNA polymerase III (subunit gamma | 79.42 | 578 | Mb3748c | DNA polymerase III subunits g | 79.42 | 578 | MAV_0382 | DNA polymerase III subunits gamm | 97.55 | 608 | BCG_3781c | DNA polymerase III subunits ga | 79.42 | 578 | MAP0322c | DNA polymerase III subunits gamma an | 612 | 100 |
| MAP4_3549 | fatty acid synthase | 436 | Rv3720 | Possible fatty acid synthase | 86.67 | 420 | Mb3747 | fatty acid synthase | 86.67 | 420 | MAV_0383 | cyclopropane-fatty-acyl-phospholip | 100 | 436 | BCG_3780 | fatty acid synthase | 86.67 | 420 | MAP0321 | hypothetical protein | 436 | 100 |
| MAP4_3550 | hypothetical protein | 474 | Rv3719 | hypothetical protein | 79.75 | 470 | Mb3746 | hypothetical protein | 79.75 | 470 | MAV_0384 | FAD/FMN-containing dehydrogena | 99.16 | 474 | BCG_3779 | hypothetical protein | 79.75 | 470 | MAP0320 | hypothetical protein | 474 | 100 |
| MAP4_3551 | hypothetical protein | 145 | Rv3718c | hypothetical protein | 86.81 | 147 | Mb3745c | hypothetical protein | 86.81 | 147 | MAV_0386 | KanY protein | 99.31 | 145 | BCG_3778c | hypothetical protein | 86.81 | 147 | MAP0319c | hypothetical protein | 145 | 100 |
| MAP4_3552 | putative N-acetylmuramoyl-L-alanine amidase | 257 | Rv3717 | hypothetical protein | 81.89 | 241 | Mb3744 | hypothetical protein | 81.89 | 241 | MAV_0385 | N-acetylmuramoyl-L-alanine amida | 99.59 | 245 | BCG_3777 | hypothetical protein | 81.89 | 241 | MAP0318 | hypothetical protein | 257 | 100 |
| MAP4_3553 | hypothetical protein | 116 | Rv3716c | hypothetical protein | 86.17 | 133 | Mb3743c | hypothetical protein | 86.17 | 133 | MAV_0387 | hypothetical protein | 100 | 108 | BCG_3776c | hypothetical protein | 86.17 | 133 | MAP0317c | hypothetical protein | 116 | 100 |
| MAP4_3554 | recombination protein RecR | 203 | Rv3715c | Probable recombination protein Rec | 94.55 | 203 | Mb3742c | recombination protein RecR | 94.55 | 203 | MAV_0388 | recombination protein RecR | 100 | 203 | BCG_3775c | recombination protein RecR | 94.55 | 203 | MAP0316c | recombination protein RecR | 203 | 100 |
| MAP4_3555 | putative cobyric acid synthase CobQ2 | 235 | Rv3713 | Possible cobyric acid synthase CobQ | 87.01 | 231 | Mb3740 | cobyric acid synthase CobQ2 | 87.01 | 231 | MAV_0389 | CobB/CobQ-like glutamine amidotr | 98.72 | 235 | BCG_3773 | cobyric acid synthase cobQ2 | 87.01 | 231 | MAP0315 | CobQ2 | 225 | 99.56 |
| MAP4_3556 | putative ligase | 416 | Rv3712 | Possible ligase | 86.19 | 413 | Mb3739 | ligase | 86.19 | 413 | MAV_0390 | mur ligase | 99.52 | 416 | BCG_3772 | ligase | 86.19 | 413 | MAP1901c | hypothetical protein | 519 | 30.47 |
| MAP4_3557 | DNA polymerase III epsilon subunit dnaQ | 329 | Rv3711c | Probable DNA polymerase III (epsilo | 81.85 | 329 | Mb3738c | DNA polymerase III subunit ep | 82.77 | 329 | MAV_0391 | DNA polymerase III subunit epsilon | 99.7 | 329 | BCG_3771c | DNA polymerase III subunit eps | 82.77 | 329 | MAP0313c | DNA polymerase III subunit epsilon | 329 | 100 |
| MAP4_3558 | 2-isopropylmalate synthase | 614 | Rv3710 | 2-isopropylmalate synthase LeuA (al | 83.07 | 644 | Mb3737 | 2-isopropylmalate synthase | 90.11 | 661 | MAV_0392 | 2-isopropylmalate synthase | 99.17 | 599 | BCG_3770 | 2-isopropylmalate synthase | 87.85 | 834 | MAP0312 | 2-isopropylmalate synthase | 564 | 100 |
| MAP4_3559 | aspartokinase Ask | 421 | Rv3709c | Aspartokinase Ask (aspartate kinase | 93.35 | 421 | Mb3736c | aspartate kinase | 93.35 | 421 | MAV_0393 | aspartate kinase | 99.76 | 421 | BCG_3769c | aspartate kinase | 93.35 | 421 | MAP0311c | aspartate kinase | 421 | 100 |
| MAP4_3560 | Aspartate-semialdehyde dehydrogenase Asd | 344 | Rv3708c | Aspartate-semialdehyde dehydroge | 89.8 | 345 | Mb3735c | aspartate-semialdehyde dehy | 89.8 | 345 | MAV_0394 | aspartate-semialdehyde dehydroge | 99.71 | 344 | BCG_3768c | aspartate-semialdehyde dehyd | 89.8 | 345 | MAP0310c | aspartate-semialdehyde dehydrogenase | 344 | 100 |
| MAP4_3561 | hypothetical protein | 335 | Rv3707c | hypothetical protein | 84.04 | 336 | Mb3734c | hypothetical protein | 84.04 | 336 | MAV_0395 | hypothetical protein | 99.1 | 382 | BCG_3767c | hypothetical protein | 84.04 | 336 | MAP0309c | hypothetical protein | 335 | 100 |
| MAP4_3562 | hypothetical protein | 181 | Rv3705A | Conserved hypothetical proline rich | 51.67 | 129 | Mb3732c | hypothetical protein | 51.67 | 129 | MAV_0396 | hypothetical protein | 98.37 | 144 | BCG_3765c | hypothetical protein | 51.67 | 129 | MAP0308c | hypothetical protein | 181 | 100 |
| MAP4_3563 | hypothetical protein | 172 | Rv3705A | Conserved hypothetical proline rich | 51.52 | 129 | Mb3732c | hypothetical protein | 51.52 | 129 | MAV_0397 | hypothetical protein | 99.42 | 172 | BCG_3765c | hypothetical protein | 51.52 | 129 | MAP0308c | hypothetical protein | 181 | 44.62 |
| MAP4_3564 | hypothetical protein | 235 | Rv3705c | hypothetical protein | 81.69 | 214 | Mb3731c | hypothetical protein | 81.69 | 214 | MAV_0398 | hypothetical protein | 99.09 | 220 | BCG_3764c | hypothetical protein | 81.69 | 214 | MAP0307c | hypothetical protein | 235 | 100 |
| MAP4_3565 | glutamate-cysteine ligase GshA | 436 | Rv3704c | Glutamate--cysteine ligase GshA (ga | 75.79 | 432 | Mb3730c | glutamate--cysteine ligase | 75.79 | 432 | MAV_0399 | glutamate--cysteine ligase | 99.31 | 436 | BCG_3763c | glutamate--cysteine ligase | 75.79 | 432 | MAP0306c | GshA | 436 | 100 |
| MAP4_3566 | putative sulfatase enzyme | 433 | Rv3703c | hypothetical protein | 83.1 | 425 | Mb3729c | hypothetical protein | 83.1 | 425 | MAV_0400 | hypothetical protein | 98.85 | 433 | BCG_3762c | hypothetical protein | 83.1 | 425 | MAP0305c | hypothetical protein | 433 | 100 |
| MAP4_3567 | hypothetical protein | 232 | Rv3702c | hypothetical protein | 80.52 | 233 | Mb3728c | hypothetical protein | 80.52 | 233 | MAV_0401 | hypothetical protein | 98.28 | 232 | BCG_3761c | hypothetical protein | 80.52 | 233 | MAP0304c | hypothetical protein | 232 | 100 |
| MAP4_3568 | putative methyltransferase | 321 | Rv3701c | hypothetical protein | 81.62 | 321 | Mb3727c | hypothetical protein | 81.62 | 321 | MAV_0402 | hypothetical protein | 99.38 | 322 | BCG_3760c | hypothetical protein | 81.62 | 321 | MAP0303c | hypothetical protein | 322 | 100 |
| MAP4_3569 | putative aminotransferase, class V | 381 | Rv3700c | hypothetical protein | 76.13 | 390 | Mb3726c | hypothetical protein | 76.13 | 390 | MAV_0403 | pyridoxal-phosphate-dependent tra | 99.21 | 381 | BCG_3759c | hypothetical protein | 76.13 | 390 | MAP0302c | hypothetical protein | 381 | 100 |
| MAP4_3570 | putative methyltransferase | 229 | Rv3699 | hypothetical protein | 76.62 | 233 | Mb3725 | hypothetical protein | 76.62 | 233 | MAV_0404 | thiopurine S-methyltransferase (tp | 99.12 | 226 | BCG_3758 | hypothetical protein | 76.62 | 233 | MAP0301 | hypothetical protein | 229 | 99.56 |
| MAP4_3571 | hypothetical protein | 424 | Rv3698 | hypothetical protein | 80.66 | 509 | Mb3724 | hypothetical protein | 80.42 | 509 | MAV_0405 | CBS domain-containing protein | 99.06 | 490 | BCG_3757 | hypothetical protein | 80.19 | 509 | MAP0300 | hypothetical protein | 424 | 100 |
| MAP4_3572 | putative kinase, pfkB family carbohydrate kinase family | 294 | Rv2436 | Ribokinase RbsK | 30.72 | 304 | Mb2462 | ribokinase RBSK | 30.99 | 304 | MAV_0347 | kinase, PfkB family protein | 98.97 | 292 | BCG_2455 | ribokinase rbsK | 30.99 | 304 | MAP0299c | hypothetical protein | 294 | 100 |
| MAP4_3573 | putative transcriptional regulator | 502 | Rv1129c | Probable transcriptional regulator p | 65.39 | 486 | Mb1160c | transcriptional regulator | 65.39 | 486 | MAV_0348 | XRE family transcriptional regulato | 99.16 | 474 | BCG_1190c | transcriptional regulator protei | 65.39 | 486 | MAP0298 | hypothetical protein | 502 | 100 |
| MAP4_3574 | putative 2-methylcitrate dehydratase | 507 | Rv1130 | Possible methylcitrate dehydratase | 79.29 | 526 | Mb1161 | hypothetical protein | 79.29 | 526 | MAV_0346 | 2-methylcitrate dehydratase 2 | 99.2 | 501 | BCG_1191 | hypothetical protein | 79.29 | 526 | MAP0297c | hypothetical protein | 507 | 100 |
| MAP4_3575 | methylisocitrate lyase | 300 | Rv0467 | Isocitrate lyase Icl (isocitrase) (isocit | 29.84 | 428 | Mb0476 | isocitrate lyase | 29.84 | 428 | MAV_0345 | methylisocitrate lyase | 95.67 | 300 | BCG_0507 | isocitrate lyase icl | 29.84 | 428 | MAP0296c | hypothetical protein | 300 | 100 |
| MAP4_3576 | citrate synthase I | 375 | Rv1131 | Probable methylcitrate synthase Prp | 79.67 | 393 | Mb1162 | citrate synthase | 79.67 | 393 | MAV_0344 | citrate synthase | 99.73 | 375 | BCG_1192 | citrate synthase | 79.67 | 393 | MAP0295c | citrate synthase | 375 | 100 |
| MAP4_3577 | pyruvate carboxylase Pca | 1127 | Rv2967c | Probable pyruvate carboxylase Pca ( | 83.48 | 1127 | Mb2991c | pyruvate carboxylase | 83.48 | 1127 | MAV_0342 | pyruvate carboxylase | 99.29 | 1127 | BCG_2988c | pyruvate carboxylase | 83.48 | 1127 | MAP0294c | pyruvate carboxylase | 1127 | 100 |
| MAP4_3578 | putative citrate lyase | 308 | Rv3075c | hypothetical protein | 36.12 | 307 | Mb3102c | hypothetical protein | 36.12 | 307 | MAV_0343 | malyl-CoA lyase | 99.03 | 308 | BCG_3100c | hypothetical protein | 36.12 | 307 | MAP0293 | hypothetical protein | 308 | 100 |
| MAP4_3579 | putative CoA-transferase family protein | 394 | Rv1143 | Probable alpha-methylacyl-CoA race | 29.17 | 360 | Mb1175 | alpha-methylacyl-CoA racema | 29.17 | 360 | MAV_0341 | caib/baif family protein | 98.73 | 394 | BCG_1205 | alpha-methylacyl-CoA racemas | 29.17 | 360 | MAP0292 | hypothetical protein | 394 | 100 |
| MAP4_3580 | hypothetical protein | 150 | Rv0817c | Probable conserved exported protei | 52.17 | 270 | Mb0840c | hypothetical protein | 52.17 | 270 | MAV_0340 | nitrilotriacetate monooxygenase co | 91.59 | 451 | BCG_0869c | hypothetical protein | 52.17 | 270 | MAP0291 | hypothetical protein | 150 | 100 |
| MAP4_3581 | hypothetical protein | 160 | Rv2241 | Pyruvate dehydrogenase E1 compor | 30.51 | 901 | Mb2265 | pyruvate dehydrogenase subu | 30.51 | 901 | MAV_0337 | hypothetical protein | 98.12 | 160 | BCG_2258 | pyruvate dehydrogenase subun | 30.51 | 901 | MAP0290 | hypothetical protein | 160 | 100 |
| MAP4_3582 | metallo-beta-lactamase superfamily protein | 398 | Rv3762c | Possible hydrolase | 28.95 | 626 | Mb3788c | hydrolase | 28.07 | 626 | MAV_0336 | metallo-beta-lactamase | 98.49 | 412 | BCG_3821c | hydrolase | 28.36 | 626 | MAP0289 | hypothetical protein | 398 | 100 |
| MAP4_3585 | hypothetical protein | 128 | Rv3745c | hypothetical protein | 75 | 70 | Mb3771c | hypothetical protein | 75 | 70 | MAV_0334 | hypothetical protein | 98.84 | 86 | BCG_3804c | hypothetical protein | 75 | 70 | MAP0286 | hypothetical protein | 86 | 98.84 |
| MAP4_3586 | hypothetical protein | 377 | Rv3096 | hypothetical protein | 75.33 | 379 | Mb3123 | hypothetical protein | 75.07 | 379 | MAV_0332 | hypothetical protein | 100 | 377 | BCG_3121 | hypothetical protein | 75.07 | 379 | MAP0285c | hypothetical protein | 377 | 100 |
| MAP4_3587 | hypothetical protein | 540 | Rv2079 | hypothetical protein | 56.78 | 656 | Mb2105 | hypothetical protein | 57.29 | 656 | MAV_0331 | hypothetical protein | 68.6 | 545 | BCG_2098 | hypothetical protein | 57.29 | 656 | MAP0284c | hypothetical protein | 540 | 100 |
| MAP4_3588 | hypothetical protein | 170 | Rv1591 | Probable transmembrane protein | 29.17 | 221 | Mb1617 | hypothetical protein | 29.17 | 221 | MAV_0330 | hypothetical protein | 56.32 | 172 | BCG_1629 | hypothetical protein | 29.17 | 221 | MAP0283c | hypothetical protein | 170 | 100 |
| MAP4_3589 | hypothetical protein | 263 | Rv0391 | Probable O-succinylhomoserine sulf | 34.78 | 406 | Mb0397 | O-succinylhomoserine sulfhy | 34.78 | 406 | MAV_3690 | hypothetical protein | 43.21 | 188 | BCG_0428 | O-succinylhomoserine sulfhydr | 34.78 | 406 | MAP0282c | hypothetical protein | 263 | 100 |
| MAP4_3590 | hypothetical protein | 157 | Rv1975 | hypothetical protein | 31.37 | 221 | Mb0317 | hypothetical protein | 32.79 | 218 | MAV_0327 | hypothetical protein | 96.18 | 157 | BCG_0349 | hypothetical protein | 32.79 | 218 | MAP0281 | hypothetical protein | 157 | 100 |
| MAP4_3591 | cellulase celA1 | 329 | Rv0062 | Possible cellulase CelA1 (endoglucar | 70.75 | 380 | Mb0063 | endo-1,4-beta-glucanase | 70.75 | 380 | MAV_0326 | endoglucanase A | 97.05 | 305 | BCG_0093 | cellulase celA1 (endoglucanase | 70.75 | 380 | MAP0280 | hypothetical protein | 329 | 100 |
| MAP4_3592 | cytidinedeoxycytidylate deaminase | 152 | Rv3752c | Possible cytidine/deoxycytidylate de | 92.11 | 152 | Mb3778c | cytidine/deoxycytidylate dea | 92.11 | 152 | MAV_0324 | cytidine and deoxycytidylate deami | 99.34 | 152 | BCG_3811c | cytidine/deoxycytidylate deam | 92.11 | 152 | MAP0279 | hypothetical protein | 152 | 100 |
| MAP4_3593 | hypothetical protein | 173 | Rv3753c | hypothetical protein | 92.73 | 166 | Mb3779c | hypothetical protein | 92.49 | 173 | MAV_0323 | hypothetical protein | 100 | 173 | BCG_3812c | hypothetical protein | 92.49 | 173 | MAP0278 | hypothetical protein | 173 | 100 |
| MAP4_3594 | prephenate dehydrogenase TyrA | 327 | Rv3754 | Prephenate dehydrogenase TyrA (PD | 79.4 | 301 | Mb3780 | prephenate dehydrogenase | 79.4 | 301 | MAV_0321 | prephenate dehydrogenase | 99.04 | 314 | BCG_3813 | prephenate dehydrogenase | 79.4 | 301 | MAP0277c | prephenate dehydrogenase | 327 | 100 |
| MAP4_3595 | hypothetical protein | 199 | Rv3755c | hypothetical protein | 77.89 | 199 | Mb3781c | hypothetical protein | 77.89 | 199 | MAV_0322 | hypothetical protein | 99.4 | 166 | BCG_3814c | hypothetical protein | 77.89 | 199 | MAP0276 | hypothetical protein | 199 | 100 |
| MAP4_3596 | osmoprotectant ProZ | 238 | Rv3756c | Possible osmoprotectant (glycine be | 85.14 | 239 | Mb3782c | glycine betaine/carnitine/cho | 85.14 | 239 | MAV_0320 | ABC transporter permease | 100 | 238 | BCG_3815c | osmoprotectant (glycine betai | 85.14 | 239 | MAP0275 | ProZ | 238 | 100 |
| MAP4_3597 | osmoprotectant ProW | 228 | Rv3757c | Possible osmoprotectant (glycine be | 72.93 | 229 | Mb3783c | glycine betaine/carnitine/cho | 72.93 | 229 | MAV_0319 | ABC transporter permease | 99.12 | 228 | BCG_3816c | osmoprotectant (glycine betai | 72.93 | 229 | MAP0274 | ProW | 228 | 100 |
| MAP4_3600 | osmoprotectant ProX | 315 | Rv3759c | Possible osmoprotectant (glycine be | 75.59 | 315 | Mb3785c | osmoprotectant (glycine beta | 75.59 | 315 | MAV_0317 | quaternary amine ABC transporter | 98.34 | 302 | BCG_3818c | osmoprotectant (glycine betai | 75.59 | 315 | MAP0271 | ProX | 338 | 100 |
| MAP4_3601 | acyl-CoA dehydrogenase FadE36 | 350 | Rv3761c | Possible acyl-CoA dehydrogenase Fa | 84.9 | 351 | Mb3787c | acyl-CoA dehydrogenase | 84.9 | 351 | MAV_0316 | phosphotransferase enzyme family | 99.71 | 350 | BCG_3820c | acyl-CoA dehydrogenase fadE3 | 84.9 | 351 | MAP0270 | FadE36 | 350 | 100 |
| MAP4_3602 | putative phosphoglycerate mutase | 202 | Rv2135c | hypothetical protein | 33.91 | 236 | Mb2159c | hypothetical protein | 33.91 | 236 | MAV_0314 | phosphoglycerate mutase, putative | 98.51 | 202 | BCG_2152c | hypothetical protein | 33.91 | 236 | MAP0269 | hypothetical protein | 202 | 100 |
| MAP4_3603 | hypothetical protein | 227 | Rv3699 | hypothetical protein | 52.14 | 233 | Mb3725 | hypothetical protein | 52.14 | 233 | MAV_0313 | thiopurine S-methyltransferase (tp | 98.68 | 227 | BCG_3758 | hypothetical protein | 52.14 | 233 | MAP0268c | hypothetical protein | 227 | 100 |
| MAP4_3604 | phosphotransferase enzyme family protein | 352 | Rv3761c | Possible acyl-CoA dehydrogenase Fa | 29.01 | 351 | Mb3787c | acyl-CoA dehydrogenase | 29.01 | 351 | MAV_0312 | phosphotransferase enzyme family | 98.86 | 352 | BCG_3820c | acyl-CoA dehydrogenase fadE3 | 29.01 | 351 | MAP0267c | hypothetical protein | 352 | 100 |
| MAP4_3605 | oxidoreductase, short-chaindehydrogenase/reductase | 254 | Rv2766c | Probable short-chain type dehydrog | 34.02 | 260 | Mb2788c | 3-ketoacyl-ACP reductase | 34.02 | 260 | MAV_0311 | short chain dehydrogenase/reducta | 98.43 | 254 | BCG_2783c | 3-ketoacyl-ACP reductase | 34.02 | 260 | MAP0266c | hypothetical protein | 254 | 100 |
| MAP4_3606 | acyl-CoA dehydrogenase FadE1 | 427 | Rv0131c | Probable acyl-CoA dehydrogenase F | 50.59 | 447 | Mb0136c | acyl-CoA dehydrogenase | 50.59 | 447 | MAV_5173 | acyl-CoA dehydrogenase | 52.71 | 431 | BCG_0165c | acyl-CoA dehydrogenase fadE1 | 50.59 | 447 | MAP0265c | FadE1_1 | 427 | 100 |
| MAP4_3607 | Transcriptional regulator, TetR family | 207 | Rv0653c | Possible transcriptional regulatory p | 33.33 | 231 | Mb0672c | TetR family transcriptional re | 33.33 | 231 | MAV_0309 | TetR family transcriptional regulato | 99.51 | 204 | BCG_0702c | TetR family transcriptional regu | 33.33 | 231 | MAP0264c | hypothetical protein | 207 | 100 |
| MAP4_3608 | oxidoreductase | 322 | Rv3141 | Probable NADPH quinone oxidoredu | 35.38 | 323 | Mb3165 | NADPH quinone oxidoreducta | 35.38 | 323 | MAV_0308 | alcohol dehydrogenase, zinc-bindin | 98.76 | 322 | BCG_3164 | NADPH quinone oxidoreductas | 35.38 | 323 | MAP0263c | hypothetical protein | 322 | 100 |
| MAP4_3609 | hydrolase | 624 | Rv3762c | Possible hydrolase | 78.85 | 626 | Mb3788c | hydrolase | 78.53 | 626 | MAV_0307 | metallo-beta-lactamase | 98.72 | 624 | BCG_3821c | hydrolase | 78.69 | 626 | MAP0262 | hypothetical protein | 624 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3610 | 19 kDa lipoprotein antigen precursor LpqH | 161 | Rv3763 | 19 kDa lipoprotein antigen precurso | 76.73 | 159 | Mb3789 | hypothetical protein | 76.73 | 159 | MAV_0306 | lipoprotein LpqH | 100 | 161 | BCG_3822 | 19 kDa lipoprotein antigen pre | 76.73 | 159 | MAP0261c | hypothetical protein | 161 | 100 |
| MAP4_3611 | two component system sensor kinase | 496 | Rv3764c | Possible two component sensor kina | 81.82 | 475 | Mb3790c | two component sensor kinase | 81.82 | 475 | MAV_0305 | sensor histidine kinase | 99.6 | 496 | BCG_3823c | two component sensor kinase | 81.82 | 475 | MAP0260 | hypothetical protein | 496 | 100 |
| MAP4_3612 | two component system transcriptional regulator | 246 | Rv3765c | Probable two component transcripti | 94.02 | 234 | Mb3791c | two component transcription | 94.02 | 234 | MAV_0304 | DNA-binding response regulator | 100 | 246 | BCG_3824c | two component transcriptional | 94.02 | 234 | MAP0259 | hypothetical protein | 246 | 100 |
| MAP4_3613 | hypothetical protein | 51 | Rv0344c | Probable lipoprotein LpqJ | 44.44 | 186 | Mb1630 | inositol-monophosphatase | 38.46 | 270 | MAV_0303 | hypothetical protein | 100 | 51 | BCG_1642 | inositol-monophosphatase imp | 38.46 | 270 | MAP0258 | hypothetical protein | 51 | 100 |
| MAP4_3614 | hypothetical protein | 79 | Rv2852c | Probable malate:quinone oxidoredu | 33.33 | 493 | Mb2877c | malate:quinone oxidoreducta | 33.33 | 493 | MAV_0302 | hypothetical protein | 100 | 75 | BCG_2872c | malate:quinone oxidoreductas | 33.33 | 493 | MAP0257 | hypothetical protein | 79 | 100 |
| MAP4_3615 | putative methyltransferase | 314 | Rv3767c | Possible S-adenosylmethionine-depe | 78.14 | 314 | Mb3793c | hypothetical protein | 78.14 | 314 | MAV_0301 | methyltransferase, putative, family | 99.04 | 314 | BCG_3826c | hypothetical protein | 78.14 | 314 | MAP0256 | hypothetical protein | 314 | 100 |
| MAP4_3616 | putative acyl-CoA dehydrogenase | 359 | Rv3761c | Possible acyl-CoA dehydrogenase Fa | 33.33 | 351 | Mb3787c | acyl-CoA dehydrogenase | 33.33 | 351 | MAV_0300 | phosphotransferase enzyme family | 99.72 | 354 | BCG_3820c | acyl-CoA dehydrogenase fadE3 | 33.33 | 351 | MAP0255c | hypothetical protein | 359 | 100 |
| MAP4_3617 | hypothetical protein | 104 | Rv2264c | Conserved hypothetical proline rich | 35.71 | 592 | Mb2287c | hypothetical protein | 35.71 | 592 | MAV_4815 | hypothetical protein | 30.49 | 207 | BCG_2281c | hypothetical protein | 35.71 | 592 | MAP0254c | hypothetical protein | 104 | 100 |
| MAP4_3618 | transposase, ISMav2 | 395 | Rv0755A | Putative transposase (fragment) | 83.02 | 61 | Mb0778c | transposase | 83.02 | 61 | MAV_0752 | transposase | 29.88 | 345 | BCG_0807c | transposase | 83.02 | 61 | MAP0253 | hypothetical protein | 395 | 100 |
| MAP4_3619 | aminotransferase HisC2 | 355 | Rv3772 | Probable histidinol-phosphate amin | 75.07 | 353 | Mb3800 | aminotransferase | 75.36 | 353 | MAV_0250 | aminotransferase | 99.44 | 355 | BCG_3833 | aminotransferase | 75.36 | 353 | MAP0252c | aminotransferase | 355 | 100 |
| MAP4_3620 | hypothetical protein | 153 | Rv1405c | Putative methyltransferase | 26.44 | 274 | Mb1440c | methyltransferase | 26.44 | 274 | MAV_0249 | hypothetical protein | 100 | 153 | BCG_1466c | methyltransferase | 26.44 | 274 | MAP0251c | hypothetical protein | 153 | 100 |
| MAP4_3621 | hypothetical protein | 195 | Rv3773c | hypothetical protein | 58.46 | 194 | Mb0591 | ArsR family transcriptional re | 48.9 | 434 | MAV_0248 | hypothetical protein | 97.44 | 198 | BCG_0621 | ArsR family transcriptional regu | 48.9 | 434 | MAP0250 | hypothetical protein | 195 | 100 |
| MAP4_3622 | enoyl-CoA hydrataseisomerase EchA21 | 274 | Rv3774 | Possible enoyl-CoA hydratase EchA2 | 83.94 | 274 | Mb3803 | enoyl-CoA hydratase | 83.94 | 274 | MAV_0247 | enoyl-CoA hydratase | 99.27 | 274 | BCG_3836 | enoyl-CoA hydratase | 83.94 | 274 | MAP0249c | enoyl-CoA hydratase | 274 | 100 |
| MAP4_3623 | lipase LipE | 414 | Rv3775 | Probable lipase LipE | 81.57 | 415 | Mb3804 | lipase LIPE | 81.57 | 415 | MAV_0246 | beta-lactamase | 98.79 | 414 | BCG_3837 | lipase lipE | 81.57 | 415 | MAP0248c | hypothetical protein | 414 | 100 |
| MAP4_3624 | hypothetical protein | 63 | Rv3667 | Acetyl-coenzyme A synthetase Acs ( | 38.71 | 651 | Mb3691 | acetyl-CoA synthetase | 38.71 | 651 | MAV_0245 | hypothetical protein | 100 | 63 | BCG_3725 | acetyl-CoA synthetase | 38.71 | 651 | MAP0247c | hypothetical protein | 63 | 100 |
| MAP4_3625 | hypothetical protein | 372 | Rv2629 | hypothetical protein | 52.46 | 374 | Mb2662 | hypothetical protein | 52.46 | 374 | MAV_0244 | hypothetical protein | 98.92 | 372 | BCG_2656 | hypothetical protein | 52.46 | 374 | MAP0246c | hypothetical protein | 372 | 100 |
| MAP4_3626 | oxidoreductase | 323 | Rv3777 | Probable oxidoreductase | 77.23 | 328 | Mb3806 | oxidoreductase | 77.54 | 328 | MAV_0242 | quinone oxidoreductase | 98.76 | 326 | BCG_3839 | oxidoreductase | 77.54 | 328 | MAP0245c | hypothetical protein | 323 | 100 |
| MAP4_3627 | aminotransferase | 398 | Rv3778c | Possible aminotransferase | 87.44 | 398 | Mb3807c | aminotransferase | 87.44 | 398 | MAV_0241 | cysteine desulfurase | 100 | 398 | BCG_3840c | aminotransferase | 87.44 | 398 | MAP0244 | hypothetical protein | 398 | 100 |
| MAP4_3628 | conserved alanine and leucine rich membrane protein | 657 | Rv3779 | Probable conserved transmembrane | 76.73 | 666 | Mb3808 | transmembrane protein alani | 76.73 | 666 | MAV_3054 | GNAT family acetyltransferase | 32.88 | 597 | BCG_3841 | transmembrane protein alanin | 76.73 | 666 | MAP0243c | hypothetical protein | 657 | 100 |
| MAP4_3629 | hypothetical protein | 168 | Rv3780 | hypothetical protein | 85.29 | 178 | Mb3809 | hypothetical protein | 85.29 | 178 | MAV_0239 | hypothetical protein | 98.82 | 169 | BCG_3842 | hypothetical protein | 85.29 | 178 | MAP0242c | hypothetical protein | 168 | 100 |
| MAP4_3630 | O-antigenlipopolysaccharide transport ATP-binding pro | 268 | Rv3781 | Probable O-antigen/lipopolysacchar | 90.15 | 273 | Mb3810 | o-antigen/lipopolysaccharide | 90.15 | 273 | MAV_0238 | O-antigen export system ATP-bindi | 98.81 | 253 | BCG_3843 | O-antigen/lipopolysaccharide t | 90.15 | 273 | MAP0241c | hypothetical protein | 268 | 100 |
| MAP4_3631 | L-rhamnosyltransferase | 304 | Rv3782 | UDP-galactofuranosyl transferase Gl | 87.13 | 304 | Mb3811 | L-rhamnosyltransferase | 87.13 | 304 | MAV_0237 | glycosyl transferase | 99.67 | 304 | BCG_3844 | L-rhamnosyltransferase | 87.13 | 304 | MAP0240c | RfbE | 304 | 100 |
| MAP4_3632 | O-antigenlipopolysaccharide transport membrane prot | 276 | Rv3783 | Probable O-antigen/lipopolysacchar | 89.64 | 280 | Mb3812 | O-antigen/lipopolysaccharide | 89.64 | 280 | MAV_0236 | O-antigen ABC transporter permea | 100 | 276 | BCG_3845 | O-antigen/lipopolysaccharide t | 89.64 | 280 | MAP0239c | hypothetical protein | 276 | 100 |
| MAP4_3633 | putative dioxygenase | 295 | Rv3406 | Probable dioxygenase | 29.29 | 295 | Mb3440 | dioxygenase | 29.29 | 295 | MAV_0235 | taurine catabolism dioxygenase Ta | 98.31 | 295 | BCG_3476 | dioxygenase | 29.29 | 295 | MAP0238c | hypothetical protein | 295 | 100 |
| MAP4_3634 | putative nucleoside diphosphate kinase regulator | 158 | Rv3788 | Hypothetical protein | 80 | 161 | Mb3817 | nucleoside diphosphate kinas | 80 | 161 | MAV_0234 | nucleoside diphosphate kinase regu | 98.73 | 158 | BCG_3850 | nucleoside diphosphate kinase | 80 | 161 | MAP0237c | nucleoside diphosphate kinase regulato | 158 | 100 |
| MAP4_3635 | putative conserved membrane protein | 134 | Rv3789 | GTRA family protein | 88.43 | 121 | Mb3818 | hypothetical protein | 88.43 | 121 | MAV_0233 | membrane protein | 99.25 | 134 | BCG_3851 | hypothetical protein | 88.43 | 121 | MAP0236c | hypothetical protein | 121 | 100 |
| MAP4_3636 | putative oxidoreductase | 466 | Rv3790 | Decaprenylphosphoryl-beta-D-ribos | 73.61 | 461 | Mb3819 | oxidoreductase | 73.61 | 461 | MAV_0232 | oxidoreductase, FAD-binding | 99.79 | 466 | BCG_3852 | oxidoreductase | 73.61 | 461 | MAP0235c | hypothetical protein | 466 | 100 |
| MAP4_3637 | short-chain type dehydrogenasereductase | 254 | Rv3791 | Decaprenylphosphoryl-D-2-keto ery | 88.19 | 254 | Mb3820 | short chain dehydrogenase | 88.19 | 254 | MAV_0231 | short chain dehydrogenase | 100 | 254 | BCG_3853 | short chain dehydrogenase | 88.19 | 254 | MAP0234c | short chain dehydrogenase | 254 | 100 |
| MAP4_3638 | putative conserved membrane protein | 697 | Rv3792 | Arabinofuranosyltransferase AftA | 77.38 | 643 | Mb3821 | transmembrane protein | 77.38 | 643 | MAV_0230 | hypothetical protein | 96.7 | 682 | BCG_3854 | hypothetical protein | 77.38 | 643 | MAP0233c | hypothetical protein | 697 | 100 |
| MAP4_3639 | membrane indolylacetylinositol arabinosyltransferase | 1091 | Rv3793 | Integral membrane indolylacetylinos | 85.23 | 1094 | Mb3822 | indolylacetylinositol arabinos | 85.32 | 1094 | MAV_0229 | arabinosyltransferase A | 99.62 | 1052 | BCG_3855 | integral membrane indolylacet | 85.32 | 1094 | MAP0232c | EmbC | 1091 | 100 |
| MAP4_3640 | hypothetical protein | 226 | Rv2036 | hypothetical protein | 71.57 | 213 | Mb2062 | hypothetical protein | 71.57 | 213 | MAV_0227 | hypothetical protein | 100 | 207 | BCG_2055 | hypothetical protein | 71.57 | 213 | MAP0231c | hypothetical protein | 226 | 100 |
| MAP4_3641 | transcriptional regulatory protein EmbR | 384 | Rv1267c | Probable transcriptional regulatory | 59.68 | 388 | Mb1298c | transcriptional regulator Emb | 59.68 | 388 | MAV_0226 | EmbR protein | 99.48 | 384 | BCG_1326c | transcriptional regulatory prote | 59.68 | 388 | MAP0230 | EmbR_1 | 379 | 99.74 |
| MAP4_3642 | membrane indolylacetylinositolarabinosyl transferase | 1108 | Rv3794 | Integral membrane indolylacetylinos | 81.97 | 1094 | Mb3823 | indolylacetylinositol arabinos | 81.97 | 1094 | MAV_0225 | arabinosyltransferase C | 99.63 | 1093 | BCG_3856 | integral membrane indolylacet | 81.97 | 1094 | MAP0229c | EmbA | 1108 | 100 |
| MAP4_3643 | membrane indolylacetylinositolarabinosyl transferase | 1065 | Rv3795 | Integral membrane indolylacetylinos | 83.09 | 1098 | Mb3824 | indolylacetylinositol arabinos | 83.18 | 1098 | MAV_0229 | arabinosyltransferase A | 45.43 | 1052 | BCG_3857 | integral membrane indolylacet | 83.18 | 1098 | MAP0228c | EmbB | 1065 | 99.91 |
| MAP4_3644 | hypothetical protein | 171 | Rv1031 | Probable potassium-transporting AT | 30.77 | 189 | Mb1060 | potassium-transporting ATPa | 30.77 | 189 | MAV_0223 | hypothetical protein | 98.25 | 171 | BCG_1089 | potassium-transporting ATPase | 30.77 | 189 | MAP0227c | hypothetical protein | 171 | 100 |
| MAP4_3645 | putative luciferase-like monooxygenase | 309 | Rv0940c | Possible oxidoreductase | 32.79 | 288 | Mb0965c | oxidoreductase | 32.79 | 288 | MAV_3379 | MmcJ protein | 54.55 | 288 | BCG_0994c | oxidoreductase | 32.79 | 288 | MAP0226 | hypothetical protein | 309 | 100 |
| MAP4_3646 | transcriptional regulator, AsnC-family | 351 | Rv3291c | Probable transcriptional regulatory | 33.05 | 150 | Mb3319c | AsnC family transcriptional re | 33.05 | 150 | MAV_3380 | AsnC family transcriptional regulat | 54.27 | 327 | BCG_3320c | AsnC family transcriptional reg | 33.05 | 150 | MAP0225c | hypothetical protein | 351 | 100 |
| MAP4_3647 | acyl-CoA dehydrogenase fadE35 FadE35 | 589 | Rv3797 | Probable acyl-CoA dehydrogenase F | 83.5 | 593 | Mb3826 | acyl-CoA dehydrogenase | 83.5 | 593 | MAV_0222 | acyl-CoA dehydrogenase | 99.15 | 589 | BCG_3859 | acyl-CoA dehydrogenase fadE3 | 83.5 | 593 | MAP0224c | FadE35 | 589 | 100 |
| MAP4_3648 | Transcriptional regulator, AraC family | 273 | Rv3833 | Transcriptional regulatory protein (p | 25.85 | 263 | Mb3863 | AraC family transcriptional re | 25.85 | 263 | MAV_0221 | AraC family transcriptional regulat | 96.64 | 268 | BCG_3896 | AraC family transcriptional regu | 25.85 | 263 | MAP0223c | hypothetical protein | 273 | 100 |
| MAP4_3649 | putative methyltransferase | 297 | Rv3767c | Possible S-adenosylmethionine-depe | 48.61 | 314 | Mb3793c | hypothetical protein | 48.61 | 314 | MAV_0219 | methyltransferase, putative, family | 96.77 | 279 | BCG_3826c | hypothetical protein | 48.61 | 314 | MAP0222c | hypothetical protein | 297 | 100 |
| MAP4_3650 | propionyl-CoA carboxylase beta chain 4 AccD4 | 524 | Rv3799c | Probable propionyl-CoA carboxylase | 85.3 | 522 | Mb3829c | propionyl-CoA carboxylase su | 85.3 | 522 | MAV_0220 | propionyl-CoA carboxylase beta ch | 99.62 | 524 | BCG_3861c | propionyl-CoA carboxylase bet | 85.3 | 522 | MAP0221 | AccD4_1 | 524 | 100 |
| MAP4_3651 | putative polyketide synthase Pks13 | 1791 | Rv3800c | Polyketide synthase Pks13 | 81.32 | 1733 | Mb3830c | polyketide synthase | 81.26 | 1733 | MAV_0218 | polyketide synthase | 99.61 | 1791 | BCG_3862c | polyketide synthase | 81.2 | 1733 | MAP0220 | hypothetical protein | 1774 | 99.94 |
| MAP4_3652 | fatty-acid-CoA ligase FadD32 | 632 | Rv3801c | Fatty-acid-AMP ligase FadD32 (fatty | 83.17 | 637 | Mb3831c | long-chain-fatty-acid--CoA lig | 83.33 | 637 | MAV_0217 | long-chain-fatty-acid--CoA ligase | 99.68 | 632 | BCG_3863c | long-chain-fatty-acid--CoA ligas | 83.33 | 637 | MAP0219 | long-chain-fatty-acid--CoA ligase | 632 | 100 |
| MAP4_3653 | hypothetical protein | 336 | Rv3802c | Probable conserved membrane prot | 75.82 | 336 | Mb3832c | hypothetical protein | 75.82 | 336 | MAV_0216 | cutinase | 100 | 336 | BCG_3864c | hypothetical protein | 75.82 | 336 | MAP0218 | hypothetical protein | 336 | 100 |
| MAP4_3654 | secreted fibronectin-binding protein antigenprote in Fb | 300 | Rv3803c | Secreted MPT51/MPB51 antigen pro | 82.57 | 299 | Mb3833c | secreted MPT51/MPB51 anti | 82.57 | 299 | MAV_0215 | antigen 85-C | 99.33 | 305 | BCG_3865c | hypothetical protein | 82.57 | 299 | MAP0217 | FbpC1 | 300 | 100 |
| MAP4_3655 | secreted fibronectin-binding protein antigen 85A FbpA | 347 | Rv3804c | Secreted antigen 85-a FbpA (mycoly | 82.25 | 338 | Mb3834c | secreted antigen 85-A FbpA | 82.25 | 338 | MAV_0214 | antigen 85-A | 99.71 | 347 | BCG_3866c | hypothetical protein | 82.25 | 338 | MAP0216 | FbpA | 347 | 100 |
| MAP4_3656 | hypothetical protein | 639 | Rv3805c | Possible arabinofuranosyltransferas | 82.28 | 627 | Mb3835c | transmembrane protein | 82.11 | 627 | MAV_0212 | hypothetical protein | 99.53 | 660 | BCG_3867c | hypothetical protein | 82.11 | 627 | MAP0215 | hypothetical protein | 639 | 100 |
| MAP4_3657 | putative conserved membrane protein | 305 | Rv3806c | Decaprenylphosphoryl-5-phosphori | 78.74 | 302 | Mb3836c | phosphoribose diphosphate: | 79.07 | 302 | MAV_0211 | phosphoribose diphosphate:decap | 99.67 | 305 | BCG_3868c | phosphoribose diphosphate:de | 79.07 | 302 | MAP0214 | phosphoribose diphosphate:decapreny | 305 | 100 |
| MAP4_3658 | putative conserved membrane protein | 166 | Rv3807c | Possible conserved transmembrane | 73.51 | 165 | Mb3837c | transmembrane protein | 73.51 | 165 | MAV_0210 | PAP2 superfamily protein | 99.33 | 150 | BCG_3869c | hypothetical protein | 73.51 | 165 | MAP0213 | hypothetical protein | 166 | 100 |
| MAP4_3659 | bifunctional UDP-galactofuranosyl transferase GlfT | 628 | Rv3808c | Bifunctional UDP-galactofuranosyl t | 85.99 | 637 | Mb3838c | galactofuranosyl transferase | 85.99 | 637 | MAV_0209 | bifunctional udp-galactofuranosyl t | 99.68 | 625 | BCG_3870c | galactofuranosyl transferase | 85.99 | 637 | MAP0212 | hypothetical protein | 628 | 100 |
| MAP4_3660 | UDP-galactopyranose mutase Glf | 402 | Rv3809c | UDP-galactopyranose mutase Glf (U | 93.64 | 399 | Mb3839c | UDP-galactopyranose mutase | 93.64 | 399 | MAV_0208 | UDP-galactopyranose mutase | 100 | 402 | BCG_3871c | UDP-galactopyranose mutase | 93.64 | 399 | MAP0211 | Glf | 402 | 100 |
| MAP4_3661 | exported repetitive protein PirG | 336 | Rv3810 | Exported repetitive protein precurs | 60.14 | 284 | Mb3840 | exported repetitive protein P | 60.14 | 284 | MAV_0207 | Erp protein | 98.27 | 348 | BCG_3872 | hypothetical protein | 60.14 | 284 | MAP0210c | PirG | 336 | 100 |
| MAP4_3662 | hypothetical protein | 536 | Rv3811 | hypothetical protein | 77.45 | 539 | Mb3841 | hypothetical protein | 77.45 | 539 | MAV_0206 | N-acetylmuramoyl-L-alanine amida | 98.32 | 542 | BCG_3873 | hypothetical protein | 77.45 | 539 | MAP0209c | Csp | 536 | 100 |
| MAP4_3663 | putative hydrolase, haloacid dehydrogenase(HAD) supe | 272 | Rv3813c | hypothetical protein | 79.63 | 273 | Mb3843c | hypothetical protein | 79.63 | 273 | MAV_0205 | hypothetical protein | 98.9 | 271 | BCG_3875c | hypothetical protein | 79.63 | 273 | MAP0208 | hypothetical protein | 272 | 100 |
| MAP4_3664 | putative acyltransferase | 261 | Rv3814c | Possible acyltransferase | 69.35 | 261 | Mb3844c | acyltransferase | 69.35 | 261 | MAV_0204 | acyltransferase | 99.62 | 261 | BCG_3876c | acyltransferase | 69.35 | 261 | MAP0207 | hypothetical protein | 261 | 100 |
| MAP4_3665 | putative acyltransferase | 259 | Rv3815c | Possible acyltransferase | 77.68 | 251 | Mb3845c | acyltransferase | 77.68 | 251 | MAV_0203 | acyltransferase | 98.46 | 259 | BCG_3877c | acyltransferase | 77.68 | 251 | MAP0206 | hypothetical protein | 259 | 100 |
| MAP4_3666 | acyltransferase | 252 | Rv3816c | Possible acyltransferase | 86.7 | 259 | Mb3846c | acyltransferase | 86.7 | 259 | MAV_0202 | acyltransferase | 99.6 | 255 | BCG_3878c | acyltransferase | 86.7 | 259 | MAP0205 | hypothetical protein | 252 | 100 |
| MAP4_3667 | hypothetical protein | 51 | Rv3817 | Possible phosphotransferase | 61.9 | 251 | Mb3847 | phosphotransferase | 61.9 | 251 | MAV_0201 | hypothetical protein | 91.49 | 47 | BCG_3879 | phosphotransferase | 61.9 | 251 | MAP3232 | hypothetical protein | 309 | 66.67 |
| MAP4_3668 | hypothetical protein | 512 | Rv3818 | hypothetical protein | 86.6 | 516 | Mb3848 | hypothetical protein | 86.6 | 516 | MAV_0200 | Rieske 2Fe-2S family protein | 99.02 | 512 | BCG_3880 | hypothetical protein | 86.6 | 516 | MAP0204c | hypothetical protein | 512 | 100 |
| MAP4_3669 | hypothetical protein | 111 | Rv3819 | hypothetical protein | 74.77 | 111 | Mb3849 | hypothetical protein | 74.77 | 111 | MAV_0199 | hypothetical protein | 100 | 111 | BCG_3881 | hypothetical protein | 74.77 | 111 | MAP0203c | hypothetical protein | 111 | 100 |
| MAP4_3670 | putative dehydrogenase | 524 | Rv3829c | Probable dehydrogenase | 80 | 536 | Mb3859c | dehydrogenase | 79.81 | 536 | MAV_0198 | FAD dependent oxidoreductase, pu | 99.24 | 524 | BCG_3892c | dehydrogenase | 79.81 | 536 | MAP0202 | hypothetical protein | 524 | 100 |
| MAP4_3671 | Transcriptional regulator, TetR family | 212 | Rv3830c | Transcriptional regulatory protein (p | 81.25 | 209 | Mb3860c | transcriptional regulatory pro | 81.25 | 209 | MAV_0197 | TetR family transcriptional regulat | 100 | 212 | BCG_3893c | TetR family transcriptional regu | 81.25 | 209 | MAP0201 | hypothetical protein | 212 | 100 |
| MAP4_3672 | hypothetical protein | 161 | Rv3831 | Hypothetical protein | 80.12 | 160 | Mb3861 | hypothetical protein | 80.12 | 160 | MAV_0195 | hypothetical protein | 100 | 161 | BCG_3894 | hypothetical protein | 80.12 | 160 | MAP0200c | hypothetical protein | 161 | 100 |
| MAP4_3673 | hypothetical protein | 190 | Rv3832c | hypothetical protein | 75.13 | 191 | Mb3862c | hypothetical protein | 75.13 | 191 | MAV_0196 | hypothetical protein | 98.95 | 193 | BCG_3895c | hypothetical protein | 75.13 | 191 | MAP0199 | hypothetical protein | 190 | 100 |
| MAP4_3674 | transcriptional regulator, AraC family | 249 | Rv3833 | Transcriptional regulatory protein (p | 78.78 | 263 | Mb3863 | AraC family transcriptional re | 79.18 | 263 | MAV_0193 | AraC family transcriptional regulat | 98.8 | 249 | BCG_3896 | AraC family transcriptional regu | 79.18 | 263 | MAP0198c | hypothetical protein | 249 | 100 |
| MAP4_3675 | seryl-tRNA synthetase SerS | 425 | Rv3834c | SERYL-tRNA synthetase SerS (serine- | 87.65 | 419 | Mb3864c | seryl-tRNA synthetase | 87.65 | 419 | MAV_0194 | seryl-tRNA synthetase | 99.53 | 425 | BCG_3897c | seryl-tRNA synthetase | 87.65 | 419 | MAP0197 | seryl-tRNA synthetase | 425 | 100 |
| MAP4_3676 | putative conserved membrane protein | 450 | Rv3835 | hypothetical protein | 72.95 | 449 | Mb3865 | hypothetical protein | 72.95 | 449 | MAV_0192 | hypothetical protein | 99.02 | 448 | BCG_3898 | hypothetical protein | 73.47 | 452 | MAP0196c | hypothetical protein | 450 | 100 |
| MAP4_3677 | hypothetical protein | 116 | Rv3836 | hypothetical protein | 80 | 137 | Mb3866 | hypothetical protein | 80.17 | 116 | MAV_0191 | hypothetical protein | 99.12 | 114 | BCG_3899 | hypothetical protein | 80.17 | 116 | MAP0195c | hypothetical protein | 116 | 100 |
| MAP4_3678 | hypothetical protein | 63 | Rv0995 | Ribosomal-protein-alanine acetyltra | 55 | 203 | Mb1022 | ribosomal-protein-alanine ac | 55 | 203 | MAV_0190 | hypothetical protein | 98.08 | 52 | BCG_1050 | ribosomal-protein-alanine acet | 55 | 203 | MAP0926 | RimJ | 217 | 55 |
| MAP4_3679 | putative phosphoglycerate mutase | 231 | Rv3837c | Probable phosphoglycerate mutase | 73.28 | 232 | Mb3867c | phosphoglycerate mutase | 73.28 | 232 | MAV_0189 | phosphoglycerate mutase | 100 | 231 | BCG_3900c | phosphoglycerate mutase | 73.28 | 232 | MAP0194 | hypothetical protein | 231 | 100 |
| MAP4_3680 | prephenate dehydratase PheA | 315 | Rv3838c | Prephenate dehydratase PheA | 80.84 | 321 | Mb3868c | prephenate dehydratase | 80.84 | 321 | MAV_0188 | prephenate dehydratase | 100 | 315 | BCG_3901c | prephenate dehydratase | 80.84 | 321 | MAP0193 | prephenate dehydratase | 315 | 100 |
| MAP4_3681 | hypothetical protein | 264 | Rv3839 | hypothetical protein | 73.21 | 258 | Mb3869 | hypothetical protein | 73.21 | 258 | MAV_0187 | hypothetical protein | 98.48 | 264 | BCG_3902 | hypothetical protein | 73.21 | 258 | MAP0192c | hypothetical protein | 264 | 100 |
| MAP4_3682 | cell envelope-related transcriptional regulator | 401 | Rv3267 | Conserved protein (CPSA-related pr | 35.8 | 498 | Mb3295 | hypothetical protein | 35.8 | 498 | MAV_0185 | transcriptional regulator | 98.31 | 317 | BCG_3296 | hypothetical protein | 35.8 | 498 | MAP0191c | hypothetical protein | 401 | 100 |
| MAP4_3683 | glycerophosphoryl diester phosphodiesterase GlpQ1 | 272 | Rv3842c | Probable glycerophosphoryl diester | 91.04 | 274 | Mb3872c | glycerophosphoryl diester ph | 91.04 | 274 | MAV_0186 | glycerophosphoryl diester phospho | 99.63 | 272 | BCG_3905c | glycerophosphoryl diester pho | 91.04 | 274 | MAP0190 | GlpQ1 | 272 | 100 |
| MAP4_3684 | putative conserved membrane protein | 334 | Rv3843c | Probable conserved transmembrane | 62.68 | 342 | Mb3873c | transmembrane protein | 62.68 | 342 | MAV_0184 | hypothetical protein | 96.12 | 273 | BCG_3906c | hypothetical protein | 62.68 | 342 | MAP0189 | hypothetical protein | 334 | 100 |
| MAP4_3685 | hypothetical protein | 59 | Rv3211 | Probable ATP-dependent RNA helica | 37.5 | 527 | Mb3237 | ATP-dependent RNA helicase | 37.5 | 527 | MAV_0183 | hypothetical protein | 100 | 51 | BCG_3238 | ATP-dependent RNA helicase r | 37.5 | 527 | MAP0188c | hypothetical protein | 59 | 100 |
| MAP4_3686 | superoxide dismutase SodA | 207 | Rv3846 | Superoxide dismutase [FE] SodA | 82.13 | 207 | Mb3876 | superoxide dismutase [Fe] SO | 81.64 | 207 | MAV_0182 | [Mn]-superoxide dismutase | 99.52 | 207 | BCG_3909 | superoxide dismutase [Fe] sod | 81.64 | 207 | MAP0187c | hypothetical protein | 207 | 100 |
| MAP4_3687 | hypothetical protein | 177 | Rv3847 | Hypothetical protein | 96.61 | 177 | Mb3877 | hypothetical protein | 96.61 | 177 | MAV_0181 | hypothetical protein | 99.35 | 154 | BCG_3910 | hypothetical protein | 96.61 | 177 | MAP0186c | hypothetical protein | 177 | 100 |
| MAP4_3688 | hypothetical protein | 132 | Rv3849 | ESX-1 transcriptional regulatory pro | 83.33 | 132 | Mb3879 | hypothetical protein | 83.33 | 132 | MAV_0180 | hypothetical protein | 100 | 132 | BCG_3912 | hypothetical protein | 83.33 | 132 | MAP0185c | hypothetical protein | 132 | 100 |
| MAP4_3689 | hypothetical protein | 218 | Rv3850 | hypothetical protein | 82.57 | 218 | Mb3880 | hypothetical protein | 82.57 | 218 | MAV_0179 | hypothetical protein | 98.17 | 218 | BCG_3913 | hypothetical protein | 82.57 | 218 | MAP0184c | hypothetical protein | 229 | 100 |
| MAP4_3690 | hypothetical protein | 210 | Rv1286 | Probable bifunctional enzyme CysN/ | 36.36 | 614 | Mb1317 | bifunctional sulfate adenylylt | 36.36 | 614 | MAV_0178 | nuclear export factor GLE1 family p | 99.52 | 210 | BCG_1345 | bifunctional sulfate adenylyltra | 36.36 | 614 | MAP0183c | hypothetical protein | 210 | 100 |
| MAP4_3691 | copper resistance protein CopC | 168 | Rv0328 | Possible transcriptional regulatory p | 29.79 | 200 | Mb0335 | TetR/AcrR family transcriptio | 29.79 | 200 | MAV_0177 | copper resistance protein CopC | 98.21 | 168 | BCG_0367 | TetR family transcriptional regu | 29.79 | 200 | MAP2170c | hypothetical protein | 428 | 23.53 |
| MAP4_3692 | putative histone-like protein Hns | 136 | Rv3852 | Possible histone-like protein Hns | 61.63 | 134 | Mb3882 | histone-like protein HNS | 61.63 | 134 | MAV_0176 | hypothetical protein | 100 | 136 | BCG_3915 | histone-like protein hns | 61.63 | 134 | MAP0182c | hypothetical protein | 136 | 100 |
| MAP4_3693 | S-adenosylmethionine:2-demethylmenaquinone methy | 160 | Rv3853 | Regulator of RNase E activity a RraA | 87.18 | 157 | Mb3883 | ribonuclease activity regulato | 87.18 | 157 | MAV_0174 | ribonuclease activity regulator prot | 98.76 | 161 | BCG_3916 | ribonuclease activity regulator | 87.18 | 157 | MAP0181c | ribonuclease activity regulator protein | 160 | 100 |
| MAP4_3694 | monooxygenase EthA | 489 | Rv3854c | Monooxygenase EthA | 67.48 | 489 | Mb3884c | monooxygenase ETHA | 67.48 | 489 | MAV_0175 | monooxygenase, flavin-binding fam | 99.15 | 473 | BCG_3917c | monooxygenase ethA | 67.48 | 489 | MAP0180 | hypothetical protein | 489 | 100 |
| MAP4_3695 | Transcriptional repressor EthR, TetR family | 213 | Rv3855 | Transcriptional regulatory repressor | 60.27 | 216 | Mb3885 | TetR family transcriptional re | 60.27 | 216 | MAV_0173 | TetR family transcriptional regulat | 99.06 | 213 | BCG_3918 | TetR family transcriptional regu | 60.27 | 216 | MAP0179c | hypothetical protein | 213 | 100 |
| MAP4_3696 | DNA polymerase IV | 400 | Rv1537 | Probable DNA polymerase IV DinX ( | 41.43 | 463 | Mb1564 | DNA polymerase IV | 41.43 | 468 | MAV_0172 | DNA polymerase IV | 99 | 400 | BCG_1589 | DNA polymerase IV | 41.43 | 463 | MAP0178c | DNA polymerase IV | 400 | 100 |
| MAP4_3697 | hypothetical protein | 334 | Rv3856c | hypothetical protein | 86.75 | 335 | Mb3886c | hypothetical protein | 86.75 | 335 | MAV_0171 | hypothetical protein | 99.7 | 334 | BCG_3919c | hypothetical protein | 86.75 | 335 | MAP0177 | hypothetical protein | 334 | 100 |
| MAP4_3698 | hypothetical protein | 146 | Rv3857c | Possible membrane protein | 57.14 | 65 | Mb3887c | hypothetical protein | 57.14 | 65 | MAV_0170 | hypothetical protein | 99.32 | 146 | BCG_3920c | hypothetical protein | 57.14 | 65 | MAP0176 | hypothetical protein | 146 | 100 |
| MAP4_3699 | putative oxidoreductase | 283 | Rv1855c | Possible oxidoreductase | 39.03 | 307 | Mb1886c | oxidoreductase | 39.03 | 307 | MAV_0169 | hypothetical protein | 99.65 | 283 | BCG_1891c | oxidoreductase | 39.03 | 307 | MAP0175c | hypothetical protein | 283 | 100 |
| MAP4_3700 | hypothetical protein | 49 | Rv1637c | hypothetical protein | 36 | 264 | Mb1663c | hypothetical protein | 36 | 264 | MAV_0168 | hypothetical protein | 97.83 | 46 | BCG_1675c | hypothetical protein | 36 | 264 | MAP0174 | hypothetical protein | 49 | 100 |
| MAP4_3701 | NADH-dependent glutamate synthase small subunit Gl | 491 | Rv3858c | Probable NADH-dependent glutama | 88.39 | 488 | Mb3888c | glutamate synthase | 88.19 | 488 | MAV_0167 | glutamate synthase subunit beta | 100 | 491 | BCG_3921c | glutamate synthase subunit be | 87.78 | 488 | MAP0173 | glutamate synthase subunit beta | 491 | 100 |
| MAP4_3702 | ferredoxin-dependent glutamate synthase large subun | 1527 | Rv3859c | Probable ferredoxin-dependent glut | 92.34 | 1527 | Mb3889c | ferredoxin-dependent glutam | 92.4 | 1527 | MAV_0166 | ferredoxin-dependent glutamate sy | 99.87 | 1529 | BCG_3922c | ferredoxin-dependent glutama | 92.4 | 1527 | MAP0172 | hypothetical protein | 1527 | 100 |
| MAP4_3703 | hypothetical protein | 384 | Rv3860 | hypothetical protein | 65.8 | 390 | Mb3890 | hypothetical protein | 65.54 | 390 | MAV_0163 | hypothetical protein | 95.05 | 383 | BCG_3923 | hypothetical protein | 65.91 | 353 | MAP0171c | hypothetical protein | 384 | 100 |
| MAP4_3704 | RNA polymerase sigma factor SigI | 285 | Rv1189 | Possible alternative RNA polymerase | 49.65 | 290 | Mb1221 | RNA polymerase sigma factor | 49.65 | 290 | MAV_0164 | RNA polymerase sigma factor SigI | 99.3 | 285 | BCG_1251 | RNA polymerase sigma factor | 49.82 | 401 | MAP0170 | RNA polymerase sigma factor SigI | 285 | 100 |
| MAP4_3705 | hypothetical protein | 286 | Rv2047c | hypothetical protein | 28.23 | 854 | Mb2073c | hypothetical protein | 28.23 | 854 | MAV_0162 | hypothetical protein | 98.6 | 286 | BCG_2066c | hypothetical protein | 28.23 | 854 | MAP0169c | hypothetical protein | 286 | 100 |
| MAP4_3706 | hypothetical protein | 146 | Rv0523c | hypothetical protein | 37.35 | 131 | Mb0536c | hypothetical protein | 37.35 | 131 | MAV_0161 | hypothetical protein | 99.32 | 146 | BCG_0566c | hypothetical protein | 37.35 | 131 | MAP0168c | hypothetical protein | 146 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3707 | putative CBXXCFQX family protein | 613 | Rv3884c | ESX conserved component EccA2 ES | 88.07 | 619 | Mb3914c | CBXX/CFQX family protein | 88.07 | 619 | MAV_0160 | ATPase AAA | 99.35 | 613 | BCG_3939c | hypothetical protein | 88.07 | 619 | MAP0167 | hypothetical protein | 613 | 100 |
| MAP4_3709 | alanine and proline rich membrane-anchored mycosin | 553 | Rv3886c | Probable alanine and proline rich me | 85.74 | 550 | Mb3916c | secreted alanine and proline | 85.74 | 550 | MAV_0158 | subtilase | 98.89 | 552 | BCG_3941c | hypothetical protein | 85.74 | 550 | MAP0165 | hypothetical protein | 553 | 100 |
| MAP4_3710 | hypothetical protein | 509 | Rv3887c | ESX conserved component EccD2 ES | 84.28 | 509 | Mb3917c | transmembrane protein | 81.94 | 289 | MAV_0157 | secretion protein Snm4 | 98.95 | 476 | BCG_3942c | hypothetical protein | 84.28 | 509 | MAP0164 | hypothetical protein | 509 | 100 |
| MAP4_3711 | hypothetical protein | 341 | Rv3888c | Probable conserved membrane prot | 88.79 | 341 | Mb3890 | hypothetical protein | 33.8 | 390 | MAV_0156 | hypothetical protein | 100 | 307 | BCG_3943c | hypothetical protein | 90.83 | 220 | MAP0163 | hypothetical protein | 341 | 100 |
| MAP4_3712 | ESX-1 EspG family protein | 276 | Rv3889c | ESX-2 secretion-associated protein E | 80.07 | 276 | Mb3918c | hypothetical protein | 88.24 | 72 | MAV_0155 | hypothetical protein | 100 | 276 | BCG_3945c | hypothetical protein | 80.07 | 276 | MAP0162 | hypothetical protein | 276 | 100 |
| MAP4_3713 | ESAT-6 like protein EsxC | 95 | Rv3890c | ESAT-6 like protein EsxC (ESAT-6 like | 76.84 | 95 | Mb3919c | ESAT-6 like protein 11 | 74.55 | 124 | MAV_0154 | hypothetical protein | 100 | 95 | BCG_3946c | ESAT-6 like protein 11 esxC | 74.55 | 124 | MAP0161 | hypothetical protein | 95 | 100 |
| MAP4_3714 | ESAT-6 like protein EsxD | 104 | Rv3891c | Possible ESAT-6 like protein EsxD | 76.92 | 107 | Mb3920c | hypothetical protein | 76.92 | 107 | MAV_0153 | hypothetical protein | 100 | 104 | BCG_3947c | hypothetical protein | 76.92 | 107 | MAP0160 | hypothetical protein | 100 | 99 |
| MAP4_3715 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_3716 | PPE family protein | 396 | Rv3892c | PPE family protein PPE69 | 67.84 | 399 | Mb3921c | PPE family protein | 68.09 | 399 | MAV_2746 | PPE family protein | 34.48 | 461 | BCG_3948c | PPE family protein | 67.84 | 399 | MAP0158 | hypothetical protein | 396 | 100 |
| MAP4_3717 | PE family protein | 103 | Rv3893c | PE family protein PE36 | 83.12 | 77 | Mb3922c | PE family protein | 83.12 | 77 | MAV_0151 | PE family protein | 100 | 103 | BCG_3949c | PE family protein | 83.12 | 77 | MAP0157 | hypothetical protein | 103 | 100 |
| MAP4_3718 | hypothetical protein | 132 | Rv1394c | Probable cytochrome P450 132 Cyp | 37.21 | 461 | Mb1429c | cytochrome P450 132 | 37.21 | 461 | MAV_0150 | glyoxalase | 98.48 | 132 | BCG_1455c | cytochrome P450 132 cyp132 | 37.21 | 461 | MAP0156 | hypothetical protein | 132 | 100 |
| MAP4_3719 | Transcriptional regulator, TetR family | 192 | Rv0196 | Possible transcriptional regulatory p | 32.62 | 194 | Mb0202 | transcriptional regulator | 32.62 | 194 | MAV_0149 | TetR family transcriptional regulato | 98.44 | 192 | BCG_0233 | transcriptional regulatory prote | 32.62 | 194 | MAP0155 | hypothetical protein | 192 | 100 |
| MAP4_3720 | enoyl-CoA hydratase | 260 | Rv1070c | Probable enoyl-CoA hydratase EchA | 37.23 | 257 | Mb1099c | enoyl-CoA hydratase | 37.23 | 257 | MAV_0148 | enoyl-CoA hydratase/isomerase | 100 | 260 | BCG_1128c | enoyl-CoA hydratase | 37.23 | 257 | MAP0154 | hypothetical protein | 260 | 100 |
| MAP4_3721 | two component sensor histidine kinase | 442 | Rv0902c | Two component sensor histidine kin | 61.05 | 446 | Mb0926c | two component sensor histid | 61.05 | 446 | MAV_0147 | sensor histidine kinase | 99.55 | 442 | BCG_0954c | two component sensor histidin | 61.05 | 446 | MAP0153 | hypothetical protein | 442 | 100 |
| MAP4_3724 | acyl-CoA dehydrogenase FadE25 | 403 | Rv3274c | Probable acyl-CoA dehydrogenase F | 36.36 | 389 | Mb3302c | acyl-CoA dehydrogenase | 36.36 | 389 | MAV_0145 | acyl-CoA dehydrogenase | 100 | 403 | BCG_3303c | acyl-CoA dehydrogenase fadE2 | 36.36 | 389 | MAP0150c | FadE25_2 | 403 | 100 |
| MAP4_3727 | putative FAD dependent oxidoreductase | 317 | Rv3858c | Probable NADH-dependent glutama | 50 | 488 | Mb3888c | glutamate synthase | 29.71 | 488 | MAV_0142 | FAD dependent oxidoreductase | 97.48 | 317 | BCG_3921c | glutamate synthase subunit be | 50 | 488 | MAP0147c | hypothetical protein | 317 | 100 |
| MAP4_3728 | putative ABC transporter inner membrane protein | 233 | Rv3757c | Possible osmoprotectant (glycine be | 28.72 | 229 | Mb3783c | glycine betaine/carnitine/cho | 28.72 | 229 | MAV_0143 | aliphatic sulfonates ABC transporte | 99.14 | 233 | BCG_3816c | osmoprotectant (glycine betair | 28.72 | 229 | MAP0146 | hypothetical protein | 233 | 100 |
| MAP4_3729 | ABC transporter, sulfonate-binding protein | 321 | Rv0411c | Probable glutamine-binding lipoprot | 30.86 | 328 | Mb0419c | glutamine-binding lipoprotei | 30.86 | 328 | MAV_0141 | sulfonate binding protein | 99.69 | 321 | BCG_0450c | glutamine-binding lipoprotein | 30.86 | 328 | MAP0145 | hypothetical protein | 321 | 100 |
| MAP4_3730 | nitratesulfonatebicarbonate transport ABC transporter | 262 | Rv2397c | Sulfate-transport ATP-binding prote | 44.98 | 351 | Mb2419c | sulfate-transport ABC transpo | 44.98 | 351 | MAV_0140 | nitrate/sulfonate/bicarbonate ABC | 96.28 | 242 | BCG_2412c | sulfate-transport ATP-binding | 44.98 | 351 | MAP0144 | hypothetical protein | 262 | 100 |
| MAP4_3731 | hypothetical protein | 105 | Rv2241 | Pyruvate dehydrogenase E1 compor | 32.26 | 901 | Mb2265 | pyruvate dehydrogenase sub | 32.26 | 901 | MAV_0139 | hypothetical protein | 100 | 93 | BCG_2258 | pyruvate dehydrogenase subur | 32.26 | 901 | MAP0143 | hypothetical protein | 105 | 100 |
| MAP4_3732 | putative transporter, major facilitator family protein | 364 | Rv1410c | Aminoglycosides/tetracycline-transp | 30.97 | 518 | Mb1445c | aminoglycosides/tetracycline | 30.97 | 518 | MAV_0138 | transporter, major facilitator family | 99.43 | 405 | BCG_1471c | aminoglycosides/tetracycline-t | 30.97 | 518 | MAP0142c | hypothetical protein | 405 | 96.09 |
| MAP4_3733 | coenzyme F420-dependent oxidoreductase | 347 | Rv3520c | Possible coenzyme F420-dependent | 43.8 | 347 | Mb3550c | coenzyme F420-dependent o | 43.8 | 347 | MAV_0137 | oxidoreductase | 99.71 | 347 | BCG_3584c | coenzyme F420-dependent oxi | 43.8 | 347 | MAP0141 | hypothetical protein | 347 | 100 |
| MAP4_3734 | hypothetical protein | 140 | Rv3684 | Probable lyase | 36.36 | 346 | Mb3709 | lyase | 36.36 | 346 | MAV_0136 | hypothetical protein | 100 | 161 | BCG_3743 | lyase | 36.36 | 346 | MAP0140 | hypothetical protein | 140 | 100 |
| MAP4_3735 | Transcriptional regulator, PadR family | 211 | Rv1176c | hypothetical protein | 33.7 | 189 | Mb1209c | hypothetical protein | 33.7 | 189 | MAV_0135 | PadR family transcriptional regulato | 99.51 | 204 | BCG_1239c | hypothetical protein | 33.7 | 189 | MAP0139c | hypothetical protein | 211 | 100 |
| MAP4_3736 | hypothetical protein | 297 | Rv1701 | Probable integrase/recombinase | 43.24 | 311 | Mb1727 | site-specific tyrosine recombi | 43.24 | 311 | MAV_0134 | hypothetical protein | 98.99 | 297 | BCG_1739 | site-specific tyrosine recombin | 43.24 | 311 | MAP0138c | hypothetical protein | 297 | 100 |
| MAP4_3737 | hypothetical protein | 88 | Rv2299c | Probable chaperone protein HtpG (h | 30 | 647 | Mb2321c | heat shock protein 90 | 30 | 647 | MAV_0133 | hypothetical protein | 100 | 88 | BCG_2315c | heat shock protein 90 | 30 | 647 | MAP0137c | hypothetical protein | 88 | 100 |
| MAP4_3738 | hypothetical protein | 117 | Rv1244 | Probable lipoprotein LpqZ | 40 | 286 | Mb1276 | lipoprotein LPQZ | 40 | 286 | MAV_0132 | glyoxalase | 100 | 117 | BCG_1304 | lipoprotein lpqZ | 40 | 286 | MAP0136 | hypothetical protein | 140 | 100 |
| MAP4_3739 | cyclopropane-fatty-acyl-phospholipid synthase1, C ma | 294 | Rv3392c | Cyclopropane-fatty-acyl-phospholipi | 70.32 | 287 | Mb3424c | cyclopropane-fatty-acyl-phos | 70.67 | 287 | MAV_0130 | cyclopropane-fatty-acyl-phospholip | 99.32 | 294 | BCG_3461c | cyclopropane-fatty-acyl-phospl | 70.67 | 287 | MAP0135 | CmaA1 | 294 | 100 |
| MAP4_3740 | hypothetical protein | 191 | Rv0530 | hypothetical protein | 34.48 | 405 | Mb0543 | hypothetical protein | 34.48 | 405 | MAV_0129 | hypothetical protein | 97.38 | 191 | BCG_0573 | hypothetical protein | 34.48 | 405 | MAP0134c | hypothetical protein | 186 | 100 |
| MAP4_3741 | putative transporter protein | 502 | Rv1200 | Probable conserved integral membr | 29.84 | 425 | Mb1232 | integral membrane transport | 29.84 | 425 | MAV_4627 | major facilitator superfamily protei | 33 | 449 | BCG_1260 | integral membrane transport p | 29.84 | 425 | MAP0133c | hypothetical protein | 502 | 100 |
| MAP4_3742 | Phosphate transport system regulatory proteinPhoY 2 | 211 | Rv0821c | Probable phosphate-transport syste | 61.9 | 213 | Mb0844c | phosphate transport regulato | 61.9 | 213 | MAV_0768 | phosphate transport system regula | 63.03 | 222 | BCG_0874c | phosphate-transport system tr | 61.9 | 213 | MAP0132c | PhoY2_1 | 211 | 100 |
| MAP4_3743 | putative acyltransferase, wax estersynthase-like Acyl-C | 451 | Rv3734c | Putative triacylglycerol synthase (dia | 63.96 | 454 | Mb3761c | hypothetical protein | 63.96 | 454 | MAV_0126 | bifunctional wax ester synthase/ac | 98.89 | 451 | BCG_3794c | hypothetical protein | 63.96 | 454 | MAP0131c | hypothetical protein | 451 | 100 |
| MAP4_3744 | hypothetical protein | 152 | Rv1364c | Possible sigma factor regulatory pro | 30.34 | 653 | Mb1399c | hypothetical protein | 30.34 | 653 | MAV_0124 | hypothetical protein | 99.29 | 141 | BCG_1426c | hypothetical protein | 30.34 | 653 | MAP0130 | hypothetical protein | 152 | 100 |
| MAP4_3745 | D-3-phosphoglycerate dehydrogenase | 351 | Rv2996c | Probable D-3-phosphoglycerate deh | 35.09 | 528 | Mb3020c | D-3-phosphoglycerate dehyd | 35.09 | 528 | MAV_0123 | D-isomer specific 2-hydroxyacid de | 99.08 | 325 | BCG_3017c | D-3-phosphoglycerate dehydro | 35.09 | 528 | MAP0129 | hypothetical protein | 351 | 100 |
| MAP4_3746 | luciferase-like monooxygenase | 285 | Rv2161c | hypothetical protein | 35.07 | 288 | Mb2185c | hypothetical protein | 35.07 | 288 | MAV_0122 | hypothetical protein | 98.6 | 285 | BCG_2178c | hypothetical protein | 35.07 | 288 | MAP0128c | hypothetical protein | 285 | 100 |
| MAP4_3747 | transmembrane carbonic anhydrase | 521 | Rv3273 | Probable transmembrane carbonic a | 57.11 | 764 | Mb3301 | transmembrane carbonic anh | 57.11 | 764 | MAV_0121 | carbonate dehydratase | 99.6 | 502 | BCG_3302 | transmembrane carbonic anhy | 57.11 | 764 | MAP0127 | hypothetical protein | 521 | 100 |
| MAP4_3748 | hypothetical protein | 140 | Rv1558 | hypothetical protein | 56.06 | 148 | Mb1584 | hypothetical protein | 56.06 | 148 | MAV_0120 | hypothetical protein | 100 | 140 | BCG_1610 | hypothetical protein | 56.06 | 148 | MAP0126 | hypothetical protein | 140 | 100 |
| MAP4_3749 | benzoquinone methyltransferase | 231 | Rv0560c | Possible benzoquinone methyltrans | 72.49 | 241 | Mb0575c | benzoquinone methyltransfe | 72.49 | 241 | MAV_0119 | thiopurine S-methyltransferase (tp | 99.13 | 231 | BCG_0605c | benzoquinone methyltransfera | 72.49 | 241 | MAP0125c | hypothetical protein | 231 | 100 |
| MAP4_3752 | PE family protein | 101 | Rv0285 | PE family protein PE5 | 65.98 | 102 | Mb0293 | PE family protein | 65.98 | 102 | MAV_0117 | PE family protein | 100 | 101 | BCG_0325 | PE family protein | 65.98 | 102 | MAP0122 | hypothetical protein | 101 | 100 |
| MAP4_3753 | hypothetical protein | 186 | Rv3455c | Probable tRNA pseudouridine synth | 50 | 256 | Mb3484c | tRNA pseudouridine synthase | 50 | 297 | MAV_0116 | hypothetical protein | 98.39 | 186 | BCG_3520c | tRNA pseudouridine synthase | 50 | 256 | MAP0121 | hypothetical protein | 186 | 100 |
| MAP4_3754 | hypothetical protein | 140 | Rv3568c | 3,4-DHSA dioxygenase | 34.04 | 300 | Mb0327 | pyrrolidone-carboxylate pept | 54.84 | 222 | MAV_0115 | hypothetical protein | 99.24 | 131 | BCG_3633c | biphenyl-2,3-diol 1,2-dioxygen | 34.04 | 300 | MAP0120c | hypothetical protein | 140 | 100 |
| MAP4_3755 | hypothetical protein | 262 | Rv2219 | Probable conserved transmembrane | 48.48 | 250 | Mb2242 | transmembrane protein | 43.59 | 250 | MAV_0114 | hypothetical protein | 98.85 | 262 | BCG_2235 | hypothetical protein | 43.59 | 250 | MAP0119c | hypothetical protein | 262 | 100 |
| MAP4_3756 | hypothetical protein | 55 | Rv3604c | Probable conserved transmembrane | 37.5 | 397 | Mb3634c | transmembrane protein | 37.5 | 397 | MAV_0113 | hypothetical protein | 96.36 | 55 | BCG_3668c | transmembrane protein rich in | 37.5 | 397 | MAP3902c | hypothetical protein | 173 | 50 |
| MAP4_3757 | putative transmembrane protein | 122 | Rv0420c | Possible transmembrane protein | 42.55 | 136 | Mb0428c | transmembrane protein | 49.32 | 136 | MAV_0112 | hypothetical protein | 98.25 | 114 | BCG_0459c | hypothetical protein | 42.55 | 136 | MAP0118 | hypothetical protein | 122 | 100 |
| MAP4_3758 | hypothetical protein | 74 | Rv2455c | Probable oxidoreductase (alpha sub | 27.78 | 653 | Mb2482c | oxidoreductase subunit alpha | 27.78 | 653 | MAV_0111 | hypothetical protein | 100 | 74 | BCG_2475c | oxidoreductase subunit alpha | 27.78 | 653 | MAP0117 | hypothetical protein | 74 | 100 |
| MAP4_3759 | Transcriptional regulator, TetR family | 448 | Rv1963c | Probable transcriptional repressor ( | 29.5 | 406 | Mb1998c | transcriptional regulator | 29.5 | 406 | MAV_0110 | TetR family transcriptional regulato | 99.51 | 410 | BCG_2002c | transcriptional regulatory prote | 29.5 | 406 | MAP0116 | hypothetical protein | 448 | 100 |
| MAP4_3760 | hypothetical protein | 261 | Rv1980c | Immunogenic protein Mpt64 (antige | 23.16 | 228 | Mb2002c | hypothetical protein | 23.16 | 228 | MAV_0109 | hypothetical protein | 99.62 | 261 | BCG_1713c | transcriptional regulatory prote | 30.77 | 244 | MAP0115 | hypothetical protein | 261 | 100 |
| MAP4_3761 | putative transmembrane protein | 198 | Rv2390c | hypothetical protein | 49.63 | 185 | Mb2411c | hypothetical protein | 49.63 | 185 | MAV_0108 | hypothetical protein | 98.48 | 198 | BCG_2404c | hypothetical protein | 49.63 | 185 | MAP0114 | hypothetical protein | 198 | 100 |
| MAP4_3762 | Mce family protein | 416 | Rv0174 | Mce-family protein Mce1F | 25.81 | 515 | Mb0180 | MCE-family protein MCE1F | 25.81 | 515 | MAV_0107 | mce related protein | 98.08 | 416 | BCG_0211 | MCE-family protein mce1F | 25.81 | 515 | MAP0113 | hypothetical protein | 416 | 100 |
| MAP4_3763 | Mce family protein | 410 | Rv0593 | Possible Mce-family lipoprotein LprL | 29.04 | 402 | Mb0609 | MCE-family lipoprotein LprL | 34.73 | 188 | MAV_0106 | mce related protein | 99.76 | 410 | BCG_0639 | mce family lipoprotein LprL | 29.04 | 402 | MAP0112 | hypothetical protein | 410 | 100 |
| MAP4_3764 | mce family protein | 371 | Rv3496c | Mce-family protein Mce4D | 32.26 | 451 | Mb3526c | MCE-family protein MCE4D | 32.26 | 451 | MAV_0105 | virulence factor Mce | 100 | 371 | BCG_3560c | Mce-family protein mce4D | 32.26 | 451 | MAP0111 | hypothetical protein | 371 | 100 |
| MAP4_3765 | mce family protein | 348 | Rv3497c | Mce-family protein Mce4C | 29.62 | 357 | Mb3527c | MCE-family protein MCE4C | 29.62 | 357 | MAV_0104 | virulence factor Mce | 99.71 | 348 | BCG_3561c | Mce-family protein mce4C | 28.89 | 357 | MAP0110 | hypothetical protein | 348 | 100 |
| MAP4_3766 | MCE-family protein | 359 | Rv0590 | Mce-family protein Mce2B | 34.19 | 275 | Mb0605 | MCE-family protein MCE2B | 30.25 | 343 | MAV_0103 | virulence factor Mce | 99.72 | 357 | BCG_0635 | mce-family protein mce2B | 30.25 | 343 | MAP0109 | Mce1B | 359 | 100 |
| MAP4_3767 | Mce related protein | 523 | Rv1966 | Mce-family protein Mce3A | 22.33 | 425 | Mb3526c | MCE-family protein MCE4D | 23.3 | 451 | MAV_0102 | mce related protein | 97.51 | 518 | BCG_3560c | Mce-family protein mce4D | 23.3 | 451 | MAP0108 | hypothetical protein | 507 | 99.8 |
| MAP4_3769 | putative phage integrase | 343 | Rv2894c | Probable integrase/recombinase Xe | 33.17 | 298 | Mb2918c | site-specific tyrosine recombi | 33.17 | 298 | MAV_3746 | site-specific tyrosine recombinase | 33.33 | 301 | BCG_2915c | site-specific tyrosine recombin | 33.17 | 298 | MAP0106c | hypothetical protein | 343 | 100 |
| MAP4_3770 | hypothetical protein | 889 | Rv0920c | Probable transposase | 24.19 | 439 | Mb0944c | transposase | 24.19 | 439 | MAV_3024 | IclR family transcriptional regulator | 34.48 | 278 | BCG_0972c | transposase | 24.19 | 439 | MAP0105c | hypothetical protein | 889 | 100 |
| MAP4_3771 | hypothetical protein | 52 | Rv1167c | Probable transcriptional regulatory | 36 | 201 | Mb1199c | transcriptional regulator | 36 | 201 | MAV_2041 | hypothetical protein | 33.33 | 661 | BCG_1229c | transcriptional regulatory prote | 36 | 201 | MAP2937c | hypothetical protein | 284 | 34.21 |
| MAP4_3772 | transposase, IS1311 | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 99.76 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0028c | hypothetical protein | 411 | 100 |
| MAP4_3773 | hypothetical protein | 183 | Rv2520c | Possible conserved membrane prote | 42.42 | 75 | Mb2549c | hypothetical protein | 42.42 | 75 | MAV_2295 | hypothetical protein | 33.33 | 147 | BCG_2541c | hypothetical protein | 42.42 | 75 | MAP0103c | hypothetical protein | 183 | 100 |
| MAP4_3774 | hypothetical protein | 167 | Rv2970c | Probable lipase/esterase LipN | 28 | 376 | Mb2994c | lipase/esterase | 28 | 376 | MAV_2295 | hypothetical protein | 32 | 147 | BCG_2991c | lipase/esterase lipN | 28 | 376 | MAP0102 | hypothetical protein | 167 | 100 |
| MAP4_3777 | Transcriptional regulator, TetR family | 257 | Rv1353c | Probable transcriptional regulatory | 23.45 | 261 | Mb1388c | transcriptional regulator | 23.45 | 261 | MAV_5055 | TetR family transcriptional regulato | 33.77 | 210 | BCG_1415c | transcriptional regulatory prote | 23.45 | 261 | MAP0098c | hypothetical protein | 257 | 100 |
| MAP4_3780 | NADH dehydrogenase chain I | 175 | Rv3153 | Probable NADH dehydrogenase I (ch | 77.91 | 211 | Mb3177 | NADH dehydrogenase subuni | 78.49 | 211 | MAV_4041 | NADH dehydrogenase subunit I | 79.43 | 181 | BCG_3176 | NADH dehydrogenase subunit | 78.49 | 211 | MAP0095c | NADH dehydrogenase subunit I | 175 | 100 |
| MAP4_3781 | hypothetical protein | 94 | Rv0144 | Probable transcriptional regulatory | 47.62 | 280 | Mb0149 | TetR family transcriptional re | 47.62 | 280 | MAV_5151 | TetR family transcriptional regulato | 37.21 | 211 | BCG_0180 | TetR family transcriptional regu | 47.62 | 280 | MAP0094 | hypothetical protein | 94 | 100 |
| MAP4_3783 | putative permease family protein | 289 | Rv3501c | Conserved integral membrane prote | 37.96 | 254 | Mb3531c | hypothetical protein | 37.96 | 254 | MAV_2390 | hypothetical protein | 77.16 | 286 | BCG_3565c | integral membrane protein Yrb | 37.96 | 254 | MAP0092 | hypothetical protein | 289 | 100 |
| MAP4_3784 | hypothetical protein | 227 | Rv1050 | Probable oxidoreductase | 45.45 | 301 | Mb1079 | oxidoreductase | 45.45 | 301 | MAV_0099 | hypothetical protein | 99 | 200 | BCG_1108 | oxidoreductase | 45.45 | 301 | MAP0091c | hypothetical protein | 227 | 100 |
| MAP4_3785 | hypothetical protein | 228 | Rv2390c | hypothetical protein | 60.58 | 185 | Mb2411c | hypothetical protein | 60.58 | 185 | MAV_0098 | hypothetical protein | 96.05 | 229 | BCG_2404c | hypothetical protein | 60.58 | 185 | MAP0090c | hypothetical protein | 212 | 99.53 |
| MAP4_3786 | putative phosphinothricin N-acetyltransferase | 192 | Rv3420c | Ribosomal-protein-alanine acetyltra | 31.03 | 158 | Mb3454c | ribosomal-protein-alanine ac | 31.03 | 158 | MAV_0097 | phosphinothricin N-acetyltransfera | 99.47 | 188 | BCG_3490c | ribosomal-protein-alanine acet | 31.03 | 158 | MAP0089 | hypothetical protein | 192 | 100 |
| MAP4_3787 | hypothetical protein | 145 | Rv2042c | hypothetical protein | 33.96 | 265 | Mb2068c | hypothetical protein | 33.96 | 265 | MAV_0944 | aldehyde dehydrogenase (NAD) fa | 37.21 | 523 | BCG_2061c | hypothetical protein | 33.96 | 265 | MAP0088 | hypothetical protein | 145 | 100 |
| MAP4_3788 | putative conserved secreted protein | 238 | Rv3036c | Probable conserved secreted protei | 45.36 | 227 | Mb3062c | hypothetical protein | 44.85 | 227 | MAV_3901 | immunogenic protein MPB64/MPT | 40.72 | 227 | BCG_3060c | hypothetical protein | 45.36 | 227 | MAP0087 | hypothetical protein | 238 | 100 |
| MAP4_3789 | hypothetical protein | 310 | Rv1394c | Probable cytochrome P450 132 Cyp | 40 | 461 | Mb1429c | cytochrome P450 132 | 40 | 461 | MAV_0095 | hypothetical protein | 98.69 | 305 | BCG_1455c | cytochrome P450 132 cyp132 | 40 | 461 | MAP0086 | hypothetical protein | 310 | 100 |
| MAP4_3790 | transcriptional regulator, LysR family | 283 | Rv0377 | Probable transcriptional regulatory | 30.5 | 321 | Mb0384 | LysR family transcriptional re | 30.5 | 321 | MAV_0094 | LysR family transcriptional regulato | 99.29 | 283 | BCG_0415 | LysR family transcriptional regu | 30.5 | 321 | MAP0085c | hypothetical protein | 280 | 99.64 |
| MAP4_3791 | putative hydrolase, alphabeta hydrolase family protein | 291 | Rv2715 | Possible hydrolase | 33.62 | 341 | Mb2734 | hydrolase | 33.62 | 341 | MAV_0093 | alpha/beta hydrolase | 99.31 | 310 | BCG_2728 | hydrolase | 33.62 | 341 | MAP0084c | hypothetical protein | 291 | 100 |
| MAP4_3792 | hypothetical protein | 147 | Rv1327c | Probable glucanase GlgE | 38.3 | 701 | Mb1362c | glucanase GLGE | 38.3 | 701 | MAV_0091 | glyoxalase | 98.64 | 147 | BCG_1389c | glucanase glgE | 38.3 | 701 | MAP0083c | hypothetical protein | 147 | 100 |
| MAP4_3793 | transcriptional regulator, crpfnr-family | 225 | Rv3676 | Transcriptional regulatory protein C | 67.41 | 224 | Mb3700 | Crp/Fnr family transcriptional | 67.41 | 224 | MAV_0092 | Crp/Fnr family transcriptional regu | 100 | 225 | BCG_3734 | CRP/FNR family transcriptional | 67.41 | 224 | MAP0082 | hypothetical protein | 225 | 100 |
| MAP4_3794 | oxidoreductase | 478 | Rv0063 | Possible oxidoreductase | 82.67 | 479 | Mb0064 | oxidoreductase | 82.67 | 479 | MAV_0089 | FAD binding domain-containing pro | 99.16 | 478 | BCG_0094 | oxidoreductase | 82.67 | 479 | MAP0081 | hypothetical protein | 438 | 99.77 |
| MAP4_3795 | hypothetical protein | 211 | Rv0970 | Probable conserved integral membr | 38.5 | 210 | Mb0995 | hypothetical protein | 38.5 | 210 | MAV_0088 | hypothetical protein | 98.57 | 211 | BCG_1024 | integral membrane protein | 38.5 | 210 | MAP0080c | hypothetical protein | 211 | 100 |
| MAP4_3796 | oxidoreductase, short-chaindehydrogenase/reductase | 246 | Rv2002 | Possible 20-beta-hydroxysteroid deh | 36.73 | 260 | Mb2025 | 20-beta-hydroxysteroid dehy | 36.73 | 260 | MAV_0087 | oxidoreductase, short chain dehydr | 98.78 | 246 | BCG_2019 | 20-beta-hydroxysteroid dehydr | 36.73 | 260 | MAP0079 | hypothetical protein | 246 | 100 |
| MAP4_3797 | hypothetical protein | 91 | Rv1857 | Probable molybdate-binding lipopro | 44.44 | 261 | Mb1888 | molybdate-binding lipoprotei | 44.44 | 261 | MAV_0086 | hypothetical protein | 98.9 | 91 | BCG_1893 | molybdate-binding lipoprotein | 44.44 | 261 | MAP0078 | hypothetical protein | 91 | 100 |
| MAP4_3798 | hypothetical protein | 368 | Rv1002c | hypothetical protein | 24.38 | 503 | Mb1029c | hypothetical protein | 24.38 | 503 | MAV_0085 | hypothetical protein | 98.59 | 354 | BCG_1059c | hypothetical protein | 24.38 | 503 | MAP0077 | hypothetical protein | 368 | 100 |
| MAP4_3799 | putative transmembrane transport protein MmpL4 | 973 | Rv0450c | Probable conserved transmembrane | 54.31 | 967 | Mb0458c | transmembrane transport pro | 54.31 | 967 | MAV_0084 | transport protein MmpL4 | 99.69 | 977 | BCG_0489c | transmembrane transport prot | 54.31 | 967 | MAP0076 | hypothetical protein | 973 | 100 |
| MAP4_3800 | membrane protein mmpS1 | 140 | Rv0403c | Probable conserved membrane prot | 39.13 | 142 | Mb1582 | hypothetical protein | 40.71 | 148 | MAV_3864 | MmpS4 protein | 39.01 | 148 | BCG_1608 | membrane protein mmpS6 | 40.71 | 148 | MAP0075 | hypothetical protein | 140 | 100 |
| MAP4_3801 | Transcriptional regulator, TetR family | 189 | Rv1019 | Probable transcriptional regulatory | 42.86 | 197 | Mb1047 | TetR family transcriptional re | 42.86 | 197 | MAV_0082 | TetR family transcriptional regulato | 99.47 | 189 | BCG_1076 | TetR family transcriptional regu | 42.86 | 197 | MAP0074 | hypothetical protein | 189 | 100 |
| MAP4_3802 | hypothetical protein | 269 | Rv1978 | hypothetical protein | 63.02 | 282 | Mb2000 | hypothetical protein | 62.64 | 282 | MAV_0081 | hypothetical protein | 98.88 | 269 | BCG_2004 | methyltransferase | 64.15 | 174 | MAP0073c | hypothetical protein | 269 | 100 |
| MAP4_3803 | hypothetical protein | 295 | Rv1920 | Probable membrane protein | 40.82 | 287 | Mb1955 | hypothetical protein | 40.82 | 287 | MAV_0080 | acyltransferase domain-containing | 96.95 | 295 | BCG_1959 | hypothetical protein | 40.82 | 287 | MAP0072c | hypothetical protein | 295 | 100 |
| MAP4_3804 | replicative DNA helicase DnaB | 875 | Rv0058 | Probable replicative DNA helicase D | 91.6 | 874 | Mb0059 | replicative DNA helicase | 91.6 | 874 | MAV_0079 | replicative DNA helicase | 92.69 | 795 | BCG_0089 | replicative DNA helicase | 91.6 | 874 | MAP0071 | hypothetical protein | 875 | 100 |
| MAP4_3805 | 50S ribosomal protein L9 RplI | 152 | Rv0056 | 50S ribosomal protein L9 RplI | 86.84 | 152 | Mb0057 | 50S ribosomal protein L9 | 86.84 | 152 | MAV_0077 | 50S ribosomal protein L9 | 98.68 | 152 | BCG_0087 | 50S ribosomal protein L9 | 86.84 | 152 | MAP0070 | 50S ribosomal protein L9 | 152 | 100 |
| MAP4_3806 | 30S ribosomal protein S18 RpsR1 | 84 | Rv0055 | 30S ribosomal protein S18-1 RpsR1 | 95.24 | 84 | Mb0056 | 30S ribosomal protein S18 | 95.24 | 84 | MAV_0076 | 30S ribosomal protein S18 | 100 | 84 | BCG_0086 | 30S ribosomal protein S18 | 95.24 | 84 | MAP0069 | 30S ribosomal protein S18 | 84 | 100 |
| MAP4_3807 | single-stranded DNA-binding protein Ssb | 168 | Rv0054 | Single-strand binding protein Ssb (he | 88.82 | 164 | Mb0055 | single-stranded DNA-binding | 88.82 | 164 | MAV_1694 | hypothetical protein | 31.4 | 160 | BCG_0085 | single-stranded DNA-binding p | 88.82 | 164 | MAP0068 | single-stranded DNA-binding protein | 168 | 100 |
| MAP4_3808 | 30S ribosomal protein S6 RpsF | 96 | Rv0053 | 30S ribosomal protein S6 RpsF | 95.83 | 96 | Mb0054 | 30S ribosomal protein S6 | 95.83 | 96 | MAV_0074 | 30S ribosomal protein S6 | 100 | 96 | BCG_0084 | 30S ribosomal protein S6 | 95.83 | 96 | MAP0067 | 30S ribosomal protein S6 | 96 | 100 |
| MAP4_3809 | putative transcriptional regulator | 213 | Rv0052 | hypothetical protein | 69.89 | 187 | Mb0053 | hypothetical protein | 69.89 | 187 | MAV_0073 | DJ-1/PfpI family protein | 98.12 | 213 | BCG_0083 | hypothetical protein | 69.89 | 187 | MAP0066 | hypothetical protein | 213 | 100 |
| MAP4_3810 | hypothetical protein | 545 | Rv0051 | Probable conserved transmembrane | 80.99 | 560 | Mb0052 | transmembrane protein | 80.99 | 560 | MAV_0072 | hypothetical protein | 98.9 | 545 | BCG_0082 | hypothetical protein | 80.99 | 560 | MAP0065 | hypothetical protein | 545 | 100 |
| MAP4_3811 | bifunctional penicillin-binding protein PonA1 | 877 | Rv0050 | Probable bifunctional penicillin-bind | 87.93 | 678 | Mb0051 | bifunctional penicillin-binding | 87.22 | 680 | MAV_0071 | transglycosylase | 99.54 | 877 | BCG_0081 | bifunctional penicillin-binding | 87.09 | 681 | MAP0064 | PonA_1 | 877 | 100 |
| MAP4_3812 | hypothetical protein | 138 | Rv0049 | hypothetical protein | 89.86 | 137 | Mb0050 | hypothetical protein | 89.86 | 137 | MAV_0070 | hypothetical protein | 99.28 | 147 | BCG_0080 | hypothetical protein | 89.86 | 137 | MAP0063 | hypothetical protein | 138 | 100 |
| MAP4_3813 | hypothetical protein | 294 | Rv0048c | Possible membrane protein | 71.77 | 289 | Mb0049c | hypothetical protein | 71.77 | 289 | MAV_0069 | hypothetical protein | 98.98 | 294 | BCG_0079c | hypothetical protein | 71.77 | 289 | MAP0062c | hypothetical protein | 294 | 100 |
| MAP4_3814 | Transcriptional regulator, PadR family | 180 | Rv0047c | hypothetical protein | 96.11 | 180 | Mb0048c | hypothetical protein | 96.11 | 180 | MAV_0068 | PadR family transcriptional regulato | 100 | 180 | BCG_0078c | hypothetical protein | 96.11 | 180 | MAP0061c | hypothetical protein | 180 | 100 |
| MAP4_3815 | myo-inositol-1-phosphate synthase | 368 | Rv0046c | myo-inositol-1-phosphate synthase | 92.64 | 367 | Mb0047c | myo-inositol-1-phosphate syn | 92.92 | 367 | MAV_0067 | myo-inositol-1-phosphate synthase | 99.73 | 368 | BCG_0077c | myo-inositol-1-phosphate synt | 92.64 | 367 | MAP0060c | hypothetical protein | 368 | 100 |
| MAP4_3816 | oxidoreductase, luciferase-like monooxygenase | 375 | Rv2951c | Possible oxidoreductase | 38.51 | 381 | Mb2975c | oxidoreductase | 38.51 | 381 | MAV_0066 | hypothetical protein | 98.4 | 375 | BCG_2972c | oxidoreductase | 38.51 | 381 | MAP0059c | hypothetical protein | 375 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3817 | hypothetical protein | 389 | Rv3529c | hypothetical protein | 28.28 | 384 | Mb3559c | hypothetical protein | 28.28 | 384 | MAV_0065 | hypothetical protein | 99.74 | 389 | BCG_3593c | hypothetical protein | 28.28 | 384 | MAP0058c | hypothetical protein | 380 | 100 |
| MAP4_3818 | hypothetical protein | 267 | Rv1742 | hypothetical protein | 33.87 | 245 | Mb1771 | hypothetical protein | 33.87 | 221 | MAV_0064 | AP endonuclease, family protein 2 | 97 | 267 | BCG_1781 | hypothetical protein | 33.87 | 221 | MAP0057c | hypothetical protein | 267 | 100 |
| MAP4_3819 | hypothetical protein | 402 | Rv3531c | Hypothetical protein | 25.54 | 375 | Mb3561c | hypothetical protein | 25.54 | 375 | MAV_0063 | hypothetical protein | 97.51 | 404 | BCG_3595c | hypothetical protein | 25.54 | 375 | MAP0056c | hypothetical protein | 411 | 97.81 |
| MAP4_3820 | putative hydrolase | 304 | Rv0045c | Possible hydrolase | 78.07 | 298 | Mb0046c | hydrolase | 78.07 | 298 | MAV_0062 | alpha/beta hydrolase | 99.67 | 304 | BCG_0076c | hydrolase | 78.07 | 298 | MAP0055c | hypothetical protein | 304 | 100 |
| MAP4_3821 | oxidoreductase | 262 | Rv0044c | Possible oxidoreductase | 83.2 | 264 | Mb0045c | oxidoreductase | 83.2 | 264 | MAV_0061 | MmcI protein | 98.84 | 259 | BCG_0075c | oxidoreductase | 83.2 | 264 | MAP0054c | hypothetical protein | 262 | 100 |
| MAP4_3822 | Transcriptional regulator, GntR family | 246 | Rv0043c | Probable transcriptional regulatory | 81 | 244 | Mb0044c | GntR family transcriptional re | 81 | 244 | MAV_0060 | GntR family transcriptional regulat | 99.19 | 246 | BCG_0074c | GntR family transcriptional reg | 81 | 244 | MAP0053c | hypothetical protein | 246 | 100 |
| MAP4_3823 | amino acid ABC transporter, substrate binding and per | 598 | Rv0411c | Probable glutamine-binding lipoprot | 25.24 | 328 | Mb0419c | glutamine-binding lipoprotei | 25.24 | 328 | MAV_0059 | amino acid ABC transporter perme | 99.5 | 598 | BCG_0450c | glutamine-binding lipoprotein | 25.24 | 328 | MAP0052c | hypothetical protein | 579 | 100 |
| MAP4_3824 | amino acid ABC transporter, ATP-binding protein | 248 | Rv0933 | Phosphate-transport ATP-binding pr | 39.74 | 276 | Mb2419c | sulfate-transport ABC transpo | 40.18 | 351 | MAV_0058 | ABC transporter ATP-binding prote | 99.6 | 248 | BCG_2412c | sulfate-transport ATP-binding | 40.18 | 351 | MAP0051c | GluA | 248 | 100 |
| MAP4_3825 | transcriptional regulator, MarR family | 182 | Rv0042c | Possible transcriptional regulatory p | 85.8 | 208 | Mb0043c | MarR family transcriptional re | 85.8 | 208 | MAV_0057 | MarR family transcriptional regulat | 99.4 | 167 | BCG_0073c | transcriptional regulatory prote | 85.8 | 208 | MAP0050c | hypothetical protein | 182 | 100 |
| MAP4_3826 | short chain dehydrogenase | 223 | Rv0484c | Probable short-chain type oxidoredu | 36.8 | 251 | Mb0494c | short-chain type oxidoreduct | 36.8 | 251 | MAV_0056 | short chain dehydrogenase | 99.1 | 223 | BCG_0525c | short-chain type oxidoreductas | 36.8 | 251 | MAP0049c | short chain dehydrogenase | 223 | 100 |
| MAP4_3827 | leucyl-tRNA synthetase LeuS | 969 | Rv0041 | Probable leucyl-tRNA synthetase Leu | 85.79 | 969 | Mb0042 | leucyl-tRNA synthetase | 85.79 | 969 | MAV_0055 | leucyl-tRNA synthetase | 99.48 | 992 | BCG_0072 | leucyl-tRNA synthetase | 85.79 | 969 | MAP0048 | leucyl-tRNA synthetase | 969 | 100 |
| MAP4_3828 | secreted proline rich protein | 361 | Rv0040c | Secreted proline rich protein Mtc28 | 58.22 | 310 | Mb0041c | secreted proline rich protein | 58.22 | 310 | MAV_0054 | proline-rich 28 kDa antigen | 86.89 | 366 | BCG_0071c | hypothetical protein | 58.22 | 310 | MAP0047c | hypothetical protein | 407 | 100 |
| MAP4_3829 | putative conserved membrane protein | 113 | Rv0039c | Possible conserved transmembrane | 69.3 | 115 | Mb0040c | transmembrane protein | 69.3 | 115 | MAV_0053 | hypothetical protein | 100 | 113 | BCG_0070c | hypothetical protein | 69.3 | 115 | MAP0046c | hypothetical protein | 113 | 100 |
| MAP4_3830 | hypothetical protein | 201 | Rv0038 | hypothetical protein | 90.95 | 202 | Mb0039 | hypothetical protein | 90.95 | 202 | MAV_0052 | hypothetical protein | 100 | 201 | BCG_0069 | hypothetical protein | 90.95 | 202 | MAP0045 | hypothetical protein | 201 | 100 |
| MAP4_3831 | hypothetical protein | 428 | Rv0037c | Probable conserved integral membr | 79.67 | 441 | Mb0038c | hypothetical protein | 79.67 | 441 | MAV_0051 | transporter, major facilitator family | 98.83 | 428 | BCG_0068c | integral membrane protein | 79.67 | 441 | MAP0044c | hypothetical protein | 428 | 100 |
| MAP4_3832 | hypothetical protein | 257 | Rv0036c | hypothetical protein | 83.27 | 257 | Mb0037c | hypothetical protein | 83.27 | 257 | MAV_0050 | hypothetical protein | 98.83 | 257 | BCG_0067c | hypothetical protein | 82.84 | 226 | MAP0043c | hypothetical protein | 257 | 100 |
| MAP4_3833 | hypothetical protein | 107 | Rv0030 | hypothetical protein | 80.56 | 109 | Mb0031 | hypothetical protein | 80.56 | 109 | MAV_0049 | hypothetical protein | 100 | 107 | BCG_0061 | hypothetical protein | 80.56 | 109 | MAP0042 | hypothetical protein | 107 | 100 |
| MAP4_3834 | hypothetical protein | 544 | Rv0029 | hypothetical protein | 52.67 | 365 | Mb0030 | hypothetical protein | 52.67 | 365 | MAV_0048 | hypothetical protein | 92.88 | 562 | BCG_0060 | hypothetical protein | 52.67 | 365 | MAP0041 | hypothetical protein | 544 | 100 |
| MAP4_3835 | hypothetical protein | 47 | Rv0926c | hypothetical protein | 37.93 | 358 | Mb0949c | hypothetical protein | 37.93 | 358 | MAV_0047 | hypothetical protein | 100 | 47 | BCG_0978c | hypothetical protein | 37.93 | 358 | MAP2493c | hypothetical protein | 876 | 48.65 |
| MAP4_3836 | hypothetical protein | 103 | Rv0028 | hypothetical protein | 86 | 101 | Mb0029 | hypothetical protein | 86 | 101 | MAV_0046 | hypothetical protein | 100 | 77 | BCG_0059 | hypothetical protein | 86 | 101 | MAP0040 | hypothetical protein | 103 | 100 |
| MAP4_3837 | hypothetical protein | 105 | Rv0027 | hypothetical protein | 73.33 | 105 | Mb0028 | hypothetical protein | 73.33 | 105 | MAV_0045 | hypothetical protein | 100 | 105 | BCG_0058 | hypothetical protein | 73.33 | 105 | MAP0039 | hypothetical protein | 105 | 100 |
| MAP4_3838 | hypothetical protein | 483 | Rv0026 | hypothetical protein | 56.06 | 448 | Mb0027 | hypothetical protein | 57.26 | 477 | MAV_0044 | hypothetical protein | 98.76 | 483 | BCG_0057 | hypothetical protein | 57.26 | 477 | MAP0038 | hypothetical protein | 483 | 100 |
| MAP4_3839 | hypothetical protein | 120 | Rv0025 | hypothetical protein | 58.33 | 120 | Mb0026 | hypothetical protein | 58.62 | 120 | MAV_0043 | hypothetical protein | 94.17 | 120 | BCG_0056 | hypothetical protein | 58.62 | 120 | MAP0037 | hypothetical protein | 120 | 100 |
| MAP4_3840 | putative secreted protein | 274 | Rv0024 | Putative secreted protein P60-relate | 68.35 | 281 | Mb0024 | hypothetical protein | 59.38 | 277 | MAV_0042 | NLP/P60 family protein | 99.64 | 275 | BCG_0054 | hypothetical protein | 59.38 | 277 | MAP0036 | hypothetical protein | 274 | 100 |
| MAP4_3841 | transcriptional regulatory protein | 262 | Rv0023 | Possible transcriptional regulatory p | 87.1 | 256 | Mb0023 | transcriptional regulator | 87.1 | 256 | MAV_0041 | hypothetical protein | 98.09 | 262 | BCG_0053 | transcriptional regulatory prote | 87.1 | 256 | MAP0035 | hypothetical protein | 262 | 100 |
| MAP4_3842 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_3843 | transcriptional regulatory protein WHIB-like WhiB5 | 138 | Rv0022c | Probable transcriptional regulatory | 80.58 | 139 | Mb0022c | transcriptional regulator Whi | 80.58 | 139 | MAV_0040 | transcription factor WhiB family pr | 99.28 | 138 | BCG_0052c | transcriptional regulatory prote | 80.58 | 139 | MAP0033c | hypothetical protein | 138 | 100 |
| MAP4_3844 | acyl-CoA dehydrogenase | 460 | Rv3274c | Probable acyl-CoA dehydrogenase F | 35.56 | 389 | Mb3302c | acyl-CoA dehydrogenase | 35.56 | 389 | MAV_0039 | acyl-CoA dehydrogenase | 100 | 460 | BCG_3303c | acyl-CoA dehydrogenase fadE2 | 35.56 | 389 | MAP0032c | FadE25_1 | 460 | 100 |
| MAP4_3845 | putative pirin domain-containing protein | 330 | Rv0181c | hypothetical protein | 31.06 | 244 | Mb0187c | hypothetical protein | 31.06 | 244 | MAV_0038 | hypothetical protein | 97.58 | 330 | BCG_0218c | hypothetical protein | 31.06 | 244 | MAP0031c | hypothetical protein | 330 | 100 |
| MAP4_3846 | hypothetical protein | 109 | Rv3420c | Ribosomal-protein-alanine acetyltra | 50 | 158 | Mb3454c | ribosomal-protein-alanine ac | 50 | 158 | MAV_0037 | hypothetical protein | 99.08 | 109 | BCG_3490c | ribosomal-protein-alanine acet | 50 | 158 | MAP0030c | hypothetical protein | 109 | 100 |
| MAP4_3847 | conserved hypothetical protein (repetitive sequence co | 414 | Rv2015c | hypothetical protein | 71.29 | 418 | Mb1794c | hypothetical protein | 71.29 | 418 | MAV_0036 | hypothetical protein | 97.52 | 414 | BCG_2032c | hypothetical protein | 71.29 | 418 | MAP0029c | hypothetical protein | 414 | 100 |
| MAP4_3848 | transposase, IS1311 | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 99.76 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0028c | hypothetical protein | 411 | 100 |
| MAP4_3849 | hypothetical protein | 632 | Rv2079 | hypothetical protein | 59.82 | 656 | Mb2105 | hypothetical protein | 60.27 | 656 | MAV_0031 | hypothetical protein | 97.95 | 633 | BCG_2098 | hypothetical protein | 60.27 | 656 | MAP0027 | hypothetical protein | 632 | 100 |
| MAP4_3850 | putative fatty acyl-AMP ligase or polyketide synthase F | 518 | Rv1345 | Probable fatty acyl-AMP ligase Mbt | 59.62 | 521 | Mb1380 | long-chain-fatty-acid--CoA lig | 59.62 | 521 | MAV_0030 | long-chain-fatty-acid--[acyl-carrier- | 97.68 | 518 | BCG_1407 | long-chain-fatty-acid--ACP ligas | 59.62 | 521 | MAP0026 | long-chain-fatty-acid--ACP ligase | 518 | 100 |
| MAP4_3851 | acyl carrier protein | 87 | Rv1344 | Acyl carrier protein (ACP) MbtL | 62.32 | 106 | Mb1379 | acyl carrier protein | 62.32 | 106 | MAV_0029 | acyl carrier protein | 98.85 | 87 | BCG_1406 | acyl carrier protein | 62.32 | 106 | MAP0025 | acyl carrier protein | 87 | 100 |
| MAP4_3852 | hypothetical protein | 221 | Rv0018c | Phosphoserine/threonine phosphata | 36.84 | 514 | Mb0018c | serine/threonine phosphatas | 36.84 | 514 | MAV_0028 | hypothetical protein | 88.62 | 167 | BCG_0048c | Serine/threonine phosphatase | 36.84 | 514 | MAP0024c | hypothetical protein | 221 | 100 |
| MAP4_3853 | conserved hypothetical protein with FHA-domain | 544 | Rv0020c | Conserved protein with FHA domain | 69.12 | 527 | Mb0020c | hypothetical protein | 67.86 | 521 | MAV_0024 | hypothetical protein | 98.53 | 545 | BCG_0050c | hypothetical protein | 68.22 | 521 | MAP0023c | hypothetical protein | 544 | 100 |
| MAP4_3854 | conserved hypothetical protein with FHA-domain | 155 | Rv0019c | Conserved protein with FHA domain | 92.26 | 155 | Mb0019c | hypothetical protein | 92.26 | 155 | MAV_0023 | FHA domain-containing protein | 99.24 | 132 | BCG_0049c | hypothetical protein | 92.26 | 155 | MAP0022c | hypothetical protein | 155 | 100 |
| MAP4_3855 | putative serinethreonine phosphatase Ppp | 499 | Rv0018c | Phosphoserine/threonine phosphata | 75.19 | 514 | Mb0018c | serine/threonine phosphatas | 76.52 | 514 | MAV_0022 | protein phosphatase 2C | 99.8 | 499 | BCG_0048c | Serine/threonine phosphatase | 76.52 | 514 | MAP0021c | Ppp | 499 | 100 |
| MAP4_3856 | cell division protein RodA | 469 | Rv0017c | Probable cell division protein RodA | 85.07 | 469 | Mb0017c | cell division protein RodA | 85.07 | 469 | MAV_0021 | cell cycle protein, FtsW/RodA/SpoV | 99.57 | 469 | BCG_0047c | cell division protein rodA | 85.07 | 469 | MAP0020c | RodA | 469 | 100 |
| MAP4_3857 | penicillin-binding protein PbpA | 492 | Rv0016c | Probable penicillin-binding protein P | 87.8 | 491 | Mb0016c | penicillin-binding protein Pbp | 87.8 | 491 | MAV_0020 | PbpA protein | 100 | 492 | BCG_0046c | penicillin-binding protein pbpA | 87.8 | 491 | MAP0019c | PbpA | 492 | 100 |
| MAP4_3858 | transmembrane serinethreonine-protein kinase A PknA | 427 | Rv0015c | Transmembrane serine/threonine-p | 85.75 | 431 | Mb0015c | Ser/Thr protein kinase | 85.75 | 431 | MAV_0019 | serine/threonine protein kinase | 99.76 | 421 | BCG_0045c | Ser/Thr protein kinase | 85.75 | 431 | MAP0018c | hypothetical protein | 253 | 100 |
| MAP4_3859 | transmembrane serinethreonine-protein kinase B PknB | 626 | Rv0014c | Transmembrane serine/threonine-p | 86.42 | 626 | Mb0014c | Ser/Thr protein kinase | 86.42 | 626 | MAV_0017 | serine/threonine protein kinase | 99.84 | 626 | BCG_0044c | Ser/Thr protein kinase | 86.42 | 626 | MAP0016c | hypothetical protein | 626 | 100 |
| MAP4_3860 | anthranilate synthase component II TrpG | 228 | Rv0013 | Possible anthranilate synthase comp | 81.03 | 232 | Mb0013 | para-aminobenzoate synthas | 81.47 | 232 | MAV_0018 | para-aminobenzoate synthase com | 98.25 | 228 | BCG_0013 | para-aminobenzoate synthase | 81.47 | 232 | MAP0015 | para-aminobenzoate synthase compone | 228 | 100 |
| MAP4_3861 | hypothetical protein | 247 | Rv0012 | Probable conserved membrane prot | 81.38 | 262 | Mb0012 | hypothetical protein | 81.38 | 262 | MAV_0016 | hypothetical protein | 100 | 247 | BCG_0012 | hypothetical protein | 81.38 | 262 | MAP0014 | hypothetical protein | 247 | 100 |
| MAP4_3862 | hypothetical protein | 93 | Rv0011c | Probable conserved transmembrane | 95.7 | 93 | Mb0011c | septation inhibitor protein | 95.7 | 93 | MAV_0015 | septation inhibitor protein | 100 | 93 | BCG_0011c | septation inhibitor protein | 95.7 | 93 | MAP0013c | septation inhibitor protein | 93 | 100 |
| MAP4_3863 | hypothetical protein | 141 | Rv0010c | Probable conserved membrane prot | 71.63 | 141 | Mb0010c | hypothetical protein | 70.64 | 111 | MAV_0014 | hypothetical protein | 95.7 | 93 | BCG_0010c | hypothetical protein | 70.64 | 111 | MAP0012c | hypothetical protein | 141 | 100 |
| MAP4_3864 | iron-regulated peptidyl-prolyl cis-transisomerase PpiA | 182 | Rv0009 | Probable iron-regulated peptidyl-pr | 89.56 | 182 | Mb0009 | iron-regulated peptidyl-prolyl | 89.56 | 182 | MAV_0013 | peptidyl-prolyl cis-trans isomerase | 98.86 | 176 | BCG_0009 | iron-regulated peptidyl-prolyl c | 89.56 | 182 | MAP0011 | PpiA | 182 | 100 |
| MAP4_3865 | hypothetical protein | 144 | Rv0008c | Possible membrane protein | 66.94 | 145 | Mb0008c | hypothetical protein | 64.19 | 145 | MAV_0012 | hypothetical protein | 98.61 | 144 | BCG_0008c | hypothetical protein | 64.19 | 145 | MAP0010c | hypothetical protein | 144 | 100 |
| MAP4_3866 | putative cytochrome P450 | 441 | Rv1777 | Probable cytochrome P450 144 Cyp1 | 64.85 | 434 | Mb1806 | cytochrome p450 144 CYP14 | 64.6 | 434 | MAV_0011 | cytochrome P450 | 99.75 | 404 | BCG_1810 | cytochrome p450 144 CYP144 | 64.6 | 434 | MAP0009 | hypothetical protein | 441 | 100 |
| MAP4_3867 | transcriptional regulator, TetR family | 207 | Rv1776c | Possible transcriptional regulatory p | 49.45 | 186 | Mb1805c | transcriptional regulator | 49.45 | 186 | MAV_0009 | TetR family transcriptional regulat | 98.44 | 192 | BCG_1809c | transcriptional regulatory prote | 49.45 | 186 | MAP0008c | hypothetical protein | 192 | 98.96 |
| MAP4_3868 | Transposase, IS1311 | 411 | Rv3640c | Probable transposase | 60 | 409 | Mb3664c | transposase | 60 | 409 | MAV_2074 | transposase, Mutator family protei | 100 | 425 | BCG_3698c | transposase | 60 | 409 | MAP0104 | hypothetical protein | 411 | 100 |
| MAP4_3870 | hypothetical protein | 242 | Rv1517 | hypothetical protein | 35.47 | 254 | Mb1544 | hypothetical protein | 35.9 | 254 | MAV_3059 | hypothetical protein | 34.24 | 261 | BCG_1569 | hypothetical protein | 35.9 | 254 | MAP3761c | hypothetical protein | 242 | 100 |
| MAP4_3871 | putative glycosyltransferase | 408 | Rv1524 | Probable glycosyltransferase | 56.28 | 414 | Mb1551 | glycosyltransferase | 56.28 | 414 | MAV_3258 | glycosyltransferase 28 | 56.25 | 418 | BCG_1576 | glycosyltransferase | 56.28 | 414 | MAP3762c | hypothetical protein | 408 | 100 |
| MAP4_3872 | polyketide synthase associated protein papA3 | 506 | Rv1182 | Probable conserved polyketide synt | 54.51 | 472 | Mb1214 | polyketide synthase | 54.51 | 472 | MAV_2723 | PapA2 protein | 54.33 | 468 | BCG_1244 | polyketide synthase associated | 54.51 | 472 | MAP3763c | PapA3_2 | 506 | 100 |
| MAP4_3873 | polyketide synthase Pks2 | 2098 | Rv3825c | Polyketide synthase Pks2 | 68.57 | 2126 | Mb3855c | polyketide synthase | 68.57 | 2126 | MAV_2370 | mycocerosic acid synthase | 68.2 | 2098 | BCG_3888c | polyketide synthase | 68.57 | 2126 | MAP3764c | hypothetical protein | 2098 | 99.95 |
| MAP4_3874 | PPE family protein | 538 | Rv0280 | PPE family protein PPE3 | 59.92 | 536 | Mb0288 | PPE family protein | 59.74 | 536 | MAV_4879 | PPE family protein | 71.48 | 527 | BCG_0320 | PPE family protein | 59.74 | 536 | MAP3765 | hypothetical protein | 538 | 100 |
| MAP4_3875 | putative permease | 330 | Rv3910 | Probable conserved transmembrane | 42.22 | 1184 | Mb3940 | transmembrane protein | 42.22 | 1184 | MAV_4878 | permease | 85.06 | 330 | BCG_3967 | hypothetical protein | 42.22 | 1184 | MAP3766 | hypothetical protein | 330 | 100 |
| MAP4_3876 | hypothetical protein | 245 | Rv1631 | Probable dephospho-CoA kinase Co | 32.14 | 407 | Mb1657 | dephospho-CoA kinase/prote | 32.14 | 407 | MAV_4877 | hypothetical protein | 80 | 245 | BCG_1669 | dephospho-CoA kinase/protein | 32.14 | 407 | MAP1802c | FxsA | 171 | 35.9 |
| MAP4_3877 | 30S ribosomal protein S18 RpsR2 | 88 | Rv2055c | 30S ribosomal protein S18 RpsR2 | 89.23 | 88 | Mb2081c | 30S ribosomal protein S18 | 89.23 | 88 | MAV_0076 | 30S ribosomal protein S18 | 53.25 | 84 | BCG_2074c | 30S ribosomal protein S18 | 89.23 | 88 | MAP3767c | 30S ribosomal protein S18 | 88 | 100 |
| MAP4_3878 | 30S ribosomal protein S14 RpsN2 | 101 | Rv2056c | 30S ribosomal protein S14 RpsN2 | 81.19 | 101 | Mb2082c | 30S ribosomal protein S14 | 81.19 | 101 | MAV_4452 | 30S ribosomal protein S14 | 50.82 | 61 | BCG_2075c | 30S ribosomal protein S14 | 81.19 | 101 | MAP3768c | 30S ribosomal protein S14 | 101 | 100 |
| MAP4_3879 | 50S ribosomal protein L33 RpmG | 54 | Rv2057c | 50S ribosomal protein L33 RpmG1 | 85.19 | 54 | Mb2083c | 50S ribosomal protein L33 | 85.19 | 54 | MAV_4876 | 50S ribosomal protein L33 | 94.44 | 54 | BCG_2076c | 50S ribosomal protein L33 | 85.19 | 54 | MAP3769c | 50S ribosomal protein L33 | 54 | 100 |
| MAP4_3880 | putative cobalamin synthesis protein | 398 | Rv0106 | hypothetical protein | 66.14 | 398 | Mb0109 | hypothetical protein | 66.14 | 398 | MAV_4874 | CobW/P47K domain-containing pro | 75.97 | 381 | BCG_0139 | hypothetical protein | 66.14 | 398 | MAP3770 | hypothetical protein | 398 | 100 |
| MAP4_3881 | 50S ribosomal protein L31 | 97 | Rv1298 | 50S ribosomal protein L31 RpmE | 38.82 | 80 | Mb1330 | 50S ribosomal protein L31 | 38.82 | 80 | MAV_1515 | 50S ribosomal protein L31 | 35.11 | 80 | BCG_1358 | 50S ribosomal protein L31 | 38.82 | 80 | MAP3771 | 50S ribosomal protein L31 type B | 97 | 100 |
| MAP4_3882 | putative cobalamin synthesis protein | 380 | Rv0106 | hypothetical protein | 29.63 | 398 | Mb0109 | hypothetical protein | 29.63 | 398 | MAV_4874 | CobW/P47K domain-containing pro | 30 | 381 | BCG_0139 | hypothetical protein | 29.63 | 398 | MAP3772c | hypothetical protein | 380 | 100 |
| MAP4_3883 | ferric uptake regulator, Fur family protein | 139 | Rv2359 | Probable zinc uptake regulation pro | 34.33 | 130 | Mb2380 | ferric uptake regulation prote | 35.07 | 130 | MAV_2036 | FurB protein | 34.59 | 135 | BCG_2373 | ferric uptake regulation protei | 35.07 | 130 | MAP3773c | hypothetical protein | 139 | 100 |
| MAP4_3884 | ABC transporter, ABC 3 transport family protein | 307 | Rv2060 | Possible conserved integral membra | 58.62 | 133 | Mb2086 | hypothetical protein | 58.62 | 133 | MAV_0581 | Mn2+/Zn2+ ABC transporter perme | 37.86 | 286 | BCG_0140c | cation-transporter atpase I ctp | 36.78 | 1625 | MAP3774c | hypothetical protein | 307 | 100 |
| MAP4_3885 | ABC transporter, ATP-binding protein | 242 | Rv2397c | Sulfate-transport ATP-binding protei | 35.78 | 351 | Mb2419c | sulfate-transport ABC transpo | 35.78 | 351 | MAV_0582 | ABC transporter ATP-binding prote | 37.55 | 273 | BCG_2412c | sulfate-transport ATP-binding | 35.78 | 351 | MAP3775c | hypothetical protein | 242 | 100 |
| MAP4_3886 | ABC transporter, periplasmic solute binding protein | 369 | Rv2059 | hypothetical protein | 35.27 | 511 | Mb2085 | hypothetical protein | 35.27 | 511 | MAV_0583 | periplasmic solute binding protein | 36.23 | 311 | BCG_2078 | hypothetical protein | 35.27 | 511 | MAP3776c | hypothetical protein | 369 | 100 |
| MAP4_3888 | putative ESX-3 type VII secretion system protein | 617 | Rv0282 | ESX conserved component EccA3 ES | 86.45 | 631 | Mb0290 | hypothetical protein | 86.45 | 631 | MAV_4871 | ATPase AAA | 95.14 | 617 | BCG_0322 | hypothetical protein | 86.45 | 631 | MAP3778 | hypothetical protein | 617 | 100 |
| MAP4_3889 | hypothetical protein | 539 | Rv0283 | ESX conserved component EccB3 ES | 72.57 | 538 | Mb0291 | hypothetical protein | 72.57 | 538 | MAV_4870 | hypothetical protein | 87.5 | 544 | BCG_0323 | hypothetical protein | 72.57 | 538 | MAP3779 | hypothetical protein | 539 | 100 |
| MAP4_3890 | hypothetical protein | 1329 | Rv0284 | ESX conserved component EccC3 ES | 84.86 | 1330 | Mb0292 | hypothetical protein | 84.93 | 1330 | MAV_4390 | ftsk/SpoIIIE family protein | 34.01 | 1197 | BCG_0324 | hypothetical protein | 85.01 | 1330 | MAP3780 | hypothetical protein | 1329 | 100 |
| MAP4_3891 | PE family protein | 102 | Rv0285 | PE family protein PE5 | 85.15 | 102 | Mb0293 | PE family protein | 85.15 | 102 | MAV_4868 | PE family protein | 99.02 | 102 | BCG_0325 | PE family protein | 85.15 | 102 | MAP3781 | hypothetical protein | 102 | 100 |
| MAP4_3892 | PPE family protein | 493 | Rv0286 | PPE family protein PPE4 | 54.93 | 513 | Mb0294 | PPE family protein | 54.93 | 513 | MAV_4867 | PPE family protein | 98.58 | 493 | BCG_0326 | PPE family protein | 54.93 | 513 | MAP3782 | hypothetical protein | 493 | 100 |
| MAP4_3893 | esat-6 like protein EsxG | 97 | Rv0287 | ESAT-6 like protein EsxG (conserved | 84.54 | 97 | Mb0295 | hypothetical protein | 84.54 | 97 | MAV_4866 | PE family protein | 100 | 95 | BCG_0327 | hypothetical protein | 84.54 | 97 | MAP3783 | hypothetical protein | 97 | 100 |
| MAP4_3894 | Esat-6 like protein EsxH | 96 | Rv3019c | Secreted ESAT-6 like protein EsxR (T | 80.21 | 96 | Mb3045c | secreted ESAT-6 like protein | 80.21 | 96 | MAV_4865 | low molecular weight protein antig | 100 | 97 | BCG_3042c | ESAT-6 like protein 9 esxR | 80.21 | 96 | MAP3784 | hypothetical protein | 96 | 100 |
| MAP4_3895 | putative ESX-3 secretion-associated protein | 293 | Rv0289 | ESX-3 secretion-associated protein E | 76.77 | 295 | Mb0297 | hypothetical protein | 76.77 | 295 | MAV_4864 | hypothetical protein | 99.66 | 293 | BCG_0329 | hypothetical protein | 76.77 | 295 | MAP3785 | hypothetical protein | 293 | 100 |
| MAP4_3896 | hypothetical protein | 480 | Rv0290 | ESX conserved component EccD3 ES | 80.13 | 472 | Mb0298 | transmembrane protein | 79.92 | 472 | MAV_4863 | hypothetical protein | 99.38 | 480 | BCG_0330 | hypothetical protein | 79.92 | 472 | MAP3786 | hypothetical protein | 480 | 100 |
| MAP4_3897 | membrane-anchored mycosin MycP3 | 468 | Rv0291 | Probable membrane-anchored myc | 70.17 | 461 | Mb0299 | protease | 70.17 | 461 | MAV_4862 | subtilase | 98.93 | 468 | BCG_0331 | protease | 70.17 | 461 | MAP3787 | hypothetical protein | 468 | 100 |
| MAP4_3898 | hypothetical protein | 330 | Rv0292 | ESX conserved component EccE3 ES | 60.74 | 331 | Mb0300 | transmembrane protein | 61.04 | 331 | MAV_4860 | hypothetical protein | 98.18 | 330 | BCG_0332 | hypothetical protein | 61.04 | 331 | MAP3788 | hypothetical protein | 240 | 99.16 |
| MAP4_3899 | hypothetical protein | 399 | Rv0293c | hypothetical protein | 76.14 | 400 | Mb0301c | hypothetical protein | 76.14 | 400 | MAV_4861 | hypothetical protein | 99 | 399 | BCG_0333c | hypothetical protein | 75.89 | 400 | MAP3789c | hypothetical protein | 399 | 100 |
| MAP4_3901 | sulfatase | 476 | Rv0296c | Probable sulfatase | 78.43 | 465 | Mb0304c | sulfatase | 78.43 | 465 | MAV_4858 | sulfatase | 100 | 476 | BCG_0336c | sulfatase | 78.43 | 465 | MAP3791c | AtsG | 476 | 100 |
| MAP4_3902 | oxidoreductase | 219 | Rv0306 | Putative oxidoreductase | 80.66 | 223 | Mb0314 | oxidoreductase | 80.66 | 223 | MAV_4857 | cob(II)yrinic acid a,c-diamide reduc | 100 | 219 | BCG_0346 | oxidoreductase | 80.66 | 223 | MAP3792c | hypothetical protein | 219 | 100 |
| MAP4_3903 | hypothetical protein | 94 | Rv2685 | Probable arsenic-transport integral | 30 | 428 | Mb2704 | arsenic-transport integral me | 30 | 428 | MAV_4855 | hypothetical protein | 96.81 | 94 | BCG_2698 | arsenic-transport integral mem | 30 | 428 | MAP3793 | hypothetical protein | 94 | 98.94 |
| MAP4_3904 | hypothetical protein | 160 | Rv0307c | hypothetical protein | 68.12 | 160 | Mb0315c | hypothetical protein | 68.12 | 160 | MAV_4856 | hypothetical protein | 99.35 | 153 | BCG_0347c | hypothetical protein | 68.12 | 160 | MAP3794c | hypothetical protein | 160 | 100 |
| MAP4_3905 | hypothetical protein | 234 | Rv0308 | Probable conserved integral membr | 50.96 | 238 | Mb0316 | hypothetical protein | 50.96 | 238 | MAV_4854 | PAP2 superfamily protein | 99.07 | 214 | BCG_0348 | integral membrane protein | 50.96 | 238 | MAP3795 | hypothetical protein | 234 | 100 |
| MAP4_3906 | putative secreted protein | 219 | Rv0309 | Possible conserved exported protei | 75.8 | 218 | Mb0317 | hypothetical protein | 75.8 | 218 | MAV_4853 | hypothetical protein | 99.51 | 206 | BCG_0349 | hypothetical protein | 75.8 | 218 | MAP3796 | hypothetical protein | 219 | 100 |
| MAP4_3907 | hypothetical protein | 165 | Rv0310c | hypothetical protein | 75.31 | 163 | Mb0318c | hypothetical protein | 75.31 | 163 | MAV_4852 | hypothetical protein | 100 | 159 | BCG_0350c | hypothetical protein | 75.31 | 163 | MAP3797c | hypothetical protein | 165 | 100 |
| MAP4_3908 | transcriptional regulator, TetR family | 206 | Rv0302 | Probable transcriptional regulatory | 25.55 | 210 | Mb0310 | TetR/ACRR family transcripti | 25.55 | 210 | MAV_4851 | TetR family transcriptional regulat | 99.51 | 206 | BCG_0342 | TetR family transcriptional regu | 25.55 | 210 | MAP3798c | hypothetical protein | 206 | 100 |
| MAP4_3909 | hypothetical protein | 408 | Rv0311 | hypothetical protein | 80.15 | 409 | Mb0319 | hypothetical protein | 80.15 | 409 | MAV_4850 | hypothetical protein | 99.02 | 408 | BCG_0351 | hypothetical protein | 80.15 | 409 | MAP3799 | hypothetical protein | 408 | 100 |
| MAP4_3910 | conserved proline and threonine rich protein | 653 | Rv0312 | Conserved hypothetical proline and | 69.78 | 620 | Mb0320 | hypothetical protein | 69.98 | 620 | MAV_4816 | hypothetical protein | 41.72 | 565 | BCG_0352 | hypothetical protein | 69.98 | 620 | MAP3800 | hypothetical protein | 653 | 100 |
| MAP4_3911 | hypothetical protein | 462 | Rv1887 | Hypothetical protein | 32.69 | 380 | Mb1919 | hypothetical protein | 32.69 | 380 | MAV_4848 | hypothetical protein | 99.13 | 462 | BCG_1924 | hypothetical protein | 32.21 | 380 | MAP3801 | hypothetical protein | 488 | 99.78 |
| MAP4_3912 | hypothetical protein | 128 | Rv0313 | hypothetical protein | 81.97 | 128 | Mb0321 | hypothetical protein | 81.97 | 128 | MAV_4847 | hypothetical protein | 99.22 | 128 | BCG_0353 | hypothetical protein | 81.97 | 128 | MAP3018 | hypothetical protein | 187 | 57.14 |
| MAP4_3913 | putative conserved membrane protein | 220 | Rv0314c | Possible conserved membrane prote | 53.3 | 220 | Mb0322c | hypothetical protein | 52.86 | 220 | MAV_4846 | hypothetical protein | 99.09 | 220 | BCG_0354c | hypothetical protein | 52.86 | 220 | MAP3802c | hypothetical protein | 220 | 100 |
| MAP4_3914 | putative oxidoreductase, zinc-binding protein | 339 | Rv3777 | Probable oxidoreductase | 27.13 | 328 | Mb2958 | phenolpthiocerol synthesis ty | 25 | 2188 | MAV_4845 | oxidoreductase, zinc-binding | 99.41 | 339 | BCG_2955 | phenolpthiocerol synthesis typ | 25 | 2188 | MAP3803 | hypothetical protein | 339 | 100 |
| MAP4_3915 | glycosyl hydrolases family protein 16 | 273 | Rv0315 | Possible beta-1,3-glucanase precurs | 48.79 | 294 | Mb0323 | beta-1,3-glucanase | 48.79 | 294 | MAV_4844 | glycosyl hydrolases family protein 1 | 100 | 273 | BCG_0355 | beta-1,3-glucanase | 48.79 | 294 | MAP3804 | hypothetical protein | 273 | 100 |
| MAP4_3916 | hypothetical protein | 506 | Rv1635c | Probable mannosyltransferase Prob | 49.6 | 556 | Mb1661c | hypothetical protein | 49.6 | 556 | MAV_4843 | hypothetical protein | 98.22 | 506 | BCG_1673c | hypothetical protein | 49.6 | 556 | MAP3805c | hypothetical protein | 541 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_3917 | hypothetical protein | 101 | Rv0552 | hypothetical protein | 28.17 | 534 | Mb0567 | hypothetical protein | 28.17 | 534 | MAV_4842 | hypothetical protein | 100 | 101 | BCG_0597 | hypothetical protein | 28.17 | 534 | MAP2524c | hypothetical protein | 309 | 34.43 |
| MAP4_3918 | hypothetical protein | 224 | Rv3481c | Probable integral membrane protei | 61.64 | 229 | Mb3511c | hypothetical protein | 61.64 | 229 | MAV_4841 | hypothetical protein | 97.7 | 217 | BCG_3545c | integral membrane protein | 61.64 | 229 | MAP3806 | hypothetical protein | 224 | 100 |
| MAP4_3919 | hypothetical protein | 229 | Rv3481c | Probable integral membrane protei | 65.5 | 229 | Mb3511c | hypothetical protein | 65.5 | 229 | MAV_4839 | hypothetical protein | 99.55 | 223 | BCG_3545c | integral membrane protein | 65.5 | 229 | MAP3807 | hypothetical protein | 229 | 100 |
| MAP4_3920 | hypothetical protein | 260 | Rv3132c | Two component sensor histidine kin | 32.08 | 578 | Mb3156c | two component sensor histid | 32.08 | 578 | MAV_4840 | hypothetical protein | 99.62 | 260 | BCG_3155c | two component sensor histidin | 32.08 | 578 | MAP3808c | hypothetical protein | 260 | 100 |
| MAP4_3921 | mannitol dehydrogenase | 467 | Rv1709 | Possible segregation and condensati | 27.34 | 278 | Mb1736 | hypothetical protein | 27.34 | 278 | MAV_4838 | mannitol 2-dehydrogenase | 99.79 | 467 | BCG_1748 | hypothetical protein | 27.34 | 278 | MAP3809c | hypothetical protein | 467 | 100 |
| MAP4_3922 | hypothetical protein | 144 | Rv2140c | Conserved protein TB18.6 | 35.48 | 176 | Mb2164c | hypothetical protein | 35.48 | 176 | MAV_4837 | hypothetical protein | 98.98 | 98 | BCG_2157c | hypothetical protein | 35.48 | 176 | MAP3810c | hypothetical protein | 144 | 100 |
| MAP4_3923 | hypothetical protein | 183 | Rv1435c | Probable conserved proline, glycine, | 54.11 | 202 | Mb1470c | proline, glycine, valine-rich se | 55.14 | 209 | MAV_4835 | hypothetical protein | 99.44 | 180 | BCG_1496c | hypothetical protein | 55.14 | 209 | MAP3811 | hypothetical protein | 183 | 100 |
| MAP4_3924 | conserved exported protein | 271 | Rv1433 | Possible conserved exported protei | 74.91 | 271 | Mb1468 | hypothetical protein | 74.91 | 271 | MAV_4834 | ErfK/YbiS/YcfS/YnhG family protein | 98.03 | 254 | BCG_1494 | hypothetical protein | 74.52 | 273 | MAP3812c | hypothetical protein | 271 | 99.63 |
| MAP4_3925 | hypothetical protein | 101 | Rv0611c | Hypothetical protein | 40.32 | 127 | Mb0628c | hypothetical protein | 40.32 | 127 | MAV_4833 | hypothetical protein | 97.1 | 69 | BCG_0658c | hypothetical protein | 40.32 | 127 | MAP3813 | hypothetical protein | 101 | 100 |
| MAP4_3926 | putative transposase | 493 | Rv3845 | Hypothetical protein | 47.37 | 119 | Mb3875 | hypothetical protein | 47.37 | 119 | MAV_0496 | transposase IS116/IS110/IS902 | 28.24 | 404 | BCG_3908 | hypothetical protein | 47.37 | 119 | MAP3814c | hypothetical protein | 493 | 100 |
| MAP4_3927 | hypothetical protein | 284 | Rv1380 | Probable aspartate carbamoyltransf | 28.57 | 319 | Mb1415 | aspartate carbamoyltransfera | 28.57 | 319 | MAV_3143 | hypothetical protein | 28.42 | 353 | BCG_1441 | aspartate carbamoyltransferas | 28.57 | 319 | MAP3815 | hypothetical protein | 284 | 100 |
| MAP4_3928 | hypothetical protein | 216 | Rv0860 | Probable fatty oxidation protein Fad | 46.81 | 720 | Mb0883 | fatty oxidation protein FadB | 46.81 | 720 | MAV_1466 | hypothetical protein | 58.2 | 208 | BCG_0912 | fatty oxidation protein fadB | 46.81 | 720 | MAP3649 | long-chain-fatty-acid--CoA ligase | 505 | 29.27 |
| MAP4_3929 | putative phage integrase family protein | 80 | Rv3751 | Probable integrase (fragment) | 37.21 | 71 | Mb3777 | integrase (fragment) | 37.21 | 71 | MAV_2266 | phage-related integrase | 33.33 | 402 | BCG_3810 | integrase | 37.21 | 71 | MAP3816 | hypothetical protein | 80 | 100 |
| MAP4_3930 | hypothetical protein | 312 | Rv2160A | hypothetical protein | 33.33 | 211 | Mb0555c | hypothetical protein | 26.47 | 449 | MAV_0931 | 3-hydroxyisobutyrate dehydrogena | 31.15 | 297 | BCG_0585c | integral membrane protein | 26.47 | 449 | MAP3817c | hypothetical protein | 312 | 100 |
| MAP4_3931 | putative cytochrome P450 hydroxylase | 432 | Rv2266 | Probable cytochrome P450 124 Cyp1 | 39.49 | 428 | Mb2289 | cytochrome P450 124 CYP124 | 39.49 | 428 | MAV_2174 | P450 heme-thiolate protein | 40.92 | 435 | BCG_2283 | cytochrome P450 124 CYP124 | 39.49 | 428 | MAP3818 | hypothetical protein | 432 | 100 |
| MAP4_3932 | hypothetical protein | 214 | Rv0320 | Possible conserved exported protei | 63.64 | 220 | Mb0328 | hypothetical protein | 63.64 | 220 | MAV_4829 | hypothetical protein | 99.34 | 152 | BCG_0360 | hypothetical protein | 63.64 | 220 | MAP3819 | hypothetical protein | 211 | 99.53 |
| MAP4_3933 | deoxycytidine triphosphate deaminase Dcd | 190 | Rv0321 | Probable deoxycytidine triphosphate | 92.11 | 190 | Mb0329 | deoxycytidine triphosphate d | 91.58 | 190 | MAV_4828 | deoxycytidine triphosphate deamin | 99.47 | 190 | BCG_0361 | deoxycytidine triphosphate de | 91.58 | 190 | MAP3820 | deoxycytidine triphosphate deaminase | 190 | 100 |
| MAP4_3934 | hypothetical protein | 690 | Rv1887 | Hypothetical protein | 29.35 | 380 | Mb1919 | hypothetical protein | 29.35 | 380 | MAV_4827 | hypothetical protein | 99.21 | 644 | BCG_1924 | hypothetical protein | 28.86 | 380 | MAP3821 | hypothetical protein | 690 | 100 |
| MAP4_3935 | hypothetical protein | 502 | Rv1887 | Hypothetical protein | 30.61 | 380 | Mb1919 | hypothetical protein | 30.61 | 380 | MAV_4826 | hypothetical protein | 99.2 | 490 | BCG_1924 | hypothetical protein | 30.1 | 380 | MAP3822 | hypothetical protein | 512 | 100 |
| MAP4_3936 | hypothetical protein | 410 | Rv1887 | Hypothetical protein | 30.5 | 380 | Mb1919 | hypothetical protein | 30.5 | 380 | MAV_4825 | hypothetical protein | 98.66 | 372 | BCG_1924 | hypothetical protein | 30.5 | 380 | MAP3823 | hypothetical protein | 410 | 100 |
| MAP4_3937 | hypothetical protein | 448 | Rv1887 | Hypothetical protein | 29.17 | 380 | Mb1919 | hypothetical protein | 29.17 | 380 | MAV_4824 | hypothetical protein | 100 | 482 | BCG_1924 | hypothetical protein | 28.7 | 380 | MAP3824 | hypothetical protein | 448 | 100 |
| MAP4_3938 | UDP-glucose 6-dehydrogenase UdgA | 441 | Rv0322 | Probable UDP-glucose 6-dehydroger | 88.64 | 443 | Mb0330 | UDP-glucose 6-dehydrogenas | 88.64 | 443 | MAV_4823 | UDP-glucose 6-dehydrogenase | 99.31 | 437 | BCG_0362 | udp-glucose 6-dehydrogenase | 88.64 | 443 | MAP3825 | UdgA | 441 | 100 |
| MAP4_3939 | hypothetical protein | 274 | Rv0332 | hypothetical protein | 72.55 | 261 | Mb0339 | hypothetical protein | 72.16 | 261 | MAV_4822 | hypothetical protein | 98.48 | 264 | BCG_0371 | hypothetical protein | 72.16 | 261 | MAP3826 | hypothetical protein | 274 | 100 |
| MAP4_3940 | hypothetical protein | 116 | Rv0333 | hypothetical protein | 73.33 | 124 | Mb0340 | hypothetical protein | 73.33 | 124 | MAV_4821 | hypothetical protein | 88.61 | 124 | BCG_0372 | hypothetical protein | 73.33 | 124 | MAP3827 | hypothetical protein | 116 | 100 |
| MAP4_3941 | glucose-1-phosphate thymidylyltransferase RmlA | 291 | Rv0334 | Alpha-D-glucose-1-phosphate thymi | 83.68 | 288 | Mb0341 | glucose-1-phosphate thymidy | 83.68 | 288 | MAV_4820 | glucose-1-phosphate thymidylyltra | 100 | 291 | BCG_0373 | glucose-1-phosphate thymidyly | 83.68 | 288 | MAP3828 | RmlA | 291 | 100 |
| MAP4_3942 | putative membrane protein, YibEF-like protein family | 424 | Rv2051c | Polyprenol-monophosphomannose | 31.48 | 874 | Mb2077c | polyprenol-monophosphoma | 31.48 | 874 | MAV_4819 | hypothetical protein | 98.81 | 421 | BCG_2070c | polyprenol-monophosphoman | 31.48 | 874 | MAP3829c | hypothetical protein | 424 | 100 |
| MAP4_3943 | aspartate aminotransferase AspC | 430 | Rv0337c | Probable aspartate aminotransferas | 92.56 | 429 | Mb0344c | aminotransferase | 92.56 | 429 | MAV_4818 | aminotransferase AlaT | 99.28 | 414 | BCG_0376c | aminotransferase | 92.56 | 429 | MAP3830c | aminotransferase AlaT | 430 | 100 |
| MAP4_3944 | iron-sulfur-binding reductase | 959 | Rv0338c | Probable iron-sulfur-binding reducta | 80.07 | 882 | Mb0345c | iron-sulfur-binding reductase | 80.29 | 882 | MAV_4817 | ferredoxin, 4Fe-4S | 94.87 | 975 | BCG_0377c | iron-sulfur-binding reductase | 80.29 | 882 | MAP3831c | hypothetical protein | 959 | 100 |
| MAP4_3945 | putative heat shock protein, hsp70 family | 564 | Rv2264c | Conserved hypothetical proline rich | 37.31 | 592 | Mb2287c | hypothetical protein | 37.31 | 592 | MAV_4816 | hypothetical protein | 97.93 | 565 | BCG_2281c | hypothetical protein | 37.31 | 592 | MAP3832c | hypothetical protein | 565 | 98.55 |
| MAP4_3946 | hypothetical protein | 260 | Rv2264c | Conserved hypothetical proline rich | 35.38 | 592 | Mb2287c | hypothetical protein | 35.38 | 592 | MAV_4815 | hypothetical protein | 97.6 | 207 | BCG_2281c | hypothetical protein | 35.38 | 592 | MAP3833c | hypothetical protein | 260 | 100 |
| MAP4_3947 | putative metabolitesugar transport protein | 476 | Rv3331 | Probable sugar-transport integral m | 30.84 | 502 | Mb3364 | sugar-transport integral mem | 31.06 | 502 | MAV_4814 | metabolite/sugar transport protein | 99.33 | 449 | BCG_3401 | sugar-transport integral memb | 30.84 | 497 | MAP3834 | hypothetical protein | 476 | 100 |
| MAP4_3948 | hypothetical protein | 275 | | | | | | | | | MAV_4813 | hypothetical protein | 96.12 | 206 | | | | | MAP3835c | hypothetical protein | 275 | 100 |
| MAP4_3949 | hypothetical protein | 777 | Rv2079 | hypothetical protein | 53.3 | 656 | Mb2105 | hypothetical protein | 53.3 | 656 | MAV_0331 | hypothetical protein | 53.88 | 545 | BCG_2098 | hypothetical protein | 53.3 | 656 | MAP3836c | hypothetical protein | 777 | 100 |
| MAP4_3950 | lipoprotein LpqJ | 194 | Rv0344c | Probable lipoprotein LpqJ | 74.55 | 186 | Mb0351c | lipoprotein LpqJ | 74.55 | 186 | MAV_4811 | LpqJ protein | 98.97 | 194 | BCG_0383c | lipoprotein lpqJ | 74.55 | 186 | MAP3837c | hypothetical protein | 200 | 99.48 |
| MAP4_3951 | conserved hypothetical protein, (RES) domain-containi | 211 | Rv1635c | Probable mannosyltransferase Prob | 29.9 | 556 | Mb1661c | hypothetical protein | 29.9 | 556 | MAV_4810 | hypothetical protein | 99.53 | 220 | BCG_1673c | hypothetical protein | 29.9 | 556 | MAP3838c | hypothetical protein | 211 | 99.53 |
| MAP4_3952 | hypothetical protein | 199 | Rv2897c | hypothetical protein | 45.45 | 503 | Mb2921c | hypothetical protein | 45.45 | 503 | MAV_4809 | hypothetical protein | 98.99 | 199 | BCG_2918c | hypothetical protein | 45.45 | 503 | MAP3839c | hypothetical protein | 201 | 100 |
| MAP4_3953 | chaperone protein DnaK | 623 | Rv0350 | Probable chaperone protein DnaK (H | 92.64 | 625 | Mb0358 | molecular chaperone DnaK | 92.64 | 625 | MAV_4808 | molecular chaperone DnaK | 99.84 | 623 | BCG_0389 | molecular chaperone DnaK | 92.64 | 625 | MAP3840 | molecular chaperone DnaK | 623 | 100 |
| MAP4_3954 | heat shock protein GrpE | 227 | Rv0351 | Probable GrpE protein (HSP-70 cofa | 84.57 | 235 | Mb0359 | heat shock protein GrpE | 84.57 | 235 | MAV_4807 | heat shock protein GrpE | 99.56 | 227 | BCG_0390 | heat shock protein GrpE | 84.57 | 235 | MAP3841 | heat shock protein GrpE | 227 | 100 |
| MAP4_3955 | chaperone protein DnaJ | 392 | Rv0352 | Probable chaperone protein DnaJ1 | 92.15 | 395 | Mb0360 | molecular chaperone DnaJ | 92.15 | 395 | MAV_4806 | chaperone protein DnaJ | 100 | 392 | BCG_0391 | chaperone protein DnaJ | 91.9 | 395 | MAP3842 | molecular chaperone DnaJ | 392 | 100 |
| MAP4_3956 | merR-family heat shock protein transcriptional repress | 131 | Rv0353 | Probable heat shock protein transcri | 81.75 | 126 | Mb0361 | HEAT shock protein transcript | 81.75 | 126 | MAV_4805 | MerR family transcriptional regulat | 99.24 | 131 | BCG_0392 | heat shock protein transcriptio | 81.75 | 126 | MAP3843 | HspR | 131 | 100 |
| MAP4_3957 | putative ATPase associated adenylateguanylate cyclase | 1425 | Rv3645 | Probable conserved transmembrane | 30.46 | 549 | Mb3669 | transmembrane protein | 30.46 | 549 | MAV_4804 | GAF domain-containing protein | 99.09 | 1432 | BCG_3703 | hypothetical protein | 30.46 | 549 | MAP3844 | hypothetical protein | 1425 | 100 |
| MAP4_3958 | hypothetical protein | 268 | Rv0425c | Possible metal cation transporting P | 35.14 | 1539 | Mb0433c | metal cation transporting P-ty | 35.14 | 1539 | MAV_4803 | hypothetical protein | 97.28 | 257 | BCG_0464c | metal cation transporting P-typ | 35.14 | 1539 | MAP3845 | hypothetical protein | 268 | 100 |
| MAP4_3959 | multifunctional geranylgeranyl pyrophosphate synthet | 394 | Rv3398c | Probable multifunctional geranylger | 32.96 | 359 | Mb3431c | multifunctional dimethylallylt | 32.96 | 359 | MAV_4802 | polyprenyl synthetase | 98.98 | 395 | BCG_3468c | multifunctional geranylgeranyl | 32.96 | 359 | MAP3846 | IdsA | 394 | 100 |
| MAP4_3960 | hypothetical protein | 152 | Rv2431c | PE family protein PE25 | 34.55 | 99 | Mb2457c | PE family protein | 34.55 | 99 | MAV_4801 | hypothetical protein | 98.68 | 152 | BCG_2450c | PE family protein | 34.55 | 99 | MAP0554c | hypothetical protein | 252 | 44.44 |
| MAP4_3961 | hypothetical protein | 89 | Rv3245c | Two component sensory transductic | 42.5 | 567 | Mb3273c | two component sensory trans | 42.5 | 567 | MAV_4800 | hypothetical protein | 94.38 | 89 | BCG_3274c | two component sensory transc | 42.5 | 567 | MAP3847 | hypothetical protein | 89 | 100 |
| MAP4_3962 | hypothetical protein | 340 | Rv2220 | Glutamine synthetase GlnA1 (glutam | 35.19 | 478 | Mb2244 | glutamine synthetase | 35.19 | 478 | MAV_4799 | hypothetical protein | 98.82 | 340 | BCG_2237 | glutamine synthetase glnA1 | 35.19 | 478 | MAP3848 | hypothetical protein | 343 | 99.71 |
| MAP4_3963 | hypothetical protein | 133 | Rv0322 | Probable UDP-glucose 6-dehydroger | 48.39 | 443 | Mb0330 | UDP-glucose 6-dehydrogenas | 48.39 | 443 | MAV_4798 | hypothetical protein | 96.24 | 133 | BCG_0362 | udp-glucose 6-dehydrogenase | 48.39 | 443 | MAP2478 | hypothetical protein | 123 | 40 |
| MAP4_3964 | hypothetical protein | 1026 | Rv3727 | Possible oxidoreductase | 25.8 | 602 | Mb3754 | oxidoreductase | 25.27 | 602 | MAV_4796 | FAD dependent oxidoreductase do | 96.78 | 1019 | BCG_3787 | oxidoreductase | 25.27 | 602 | MAP3849 | hypothetical protein | 1026 | 99.81 |
| MAP4_3965 | putative aldose 1-epimerase family protein | 300 | Rv2070c | Precorrin-6X reductase CobK | 32.88 | 244 | Mb2096c | cobalt-precorrin-6x reductase | 32.88 | 231 | MAV_3731 | phosphatidate cytidylyltransferase | 39.62 | 311 | BCG_2089c | cobalt-precorrin-6x reductase | 32.88 | 231 | MAP3850c | hypothetical protein | 300 | 100 |
| MAP4_3966 | monooxygenase, putative | 393 | Rv0385 | Probable monooxygenase | 79.35 | 390 | Mb0392 | hypothetical protein | 79.35 | 390 | MAV_4795 | oxidoreductase FAD-binding subun | 98.98 | 393 | BCG_0423 | monooxygenase | 79.35 | 390 | MAP3851c | hypothetical protein | 393 | 100 |
| MAP4_3967 | hypothetical protein | 195 | Rv0314c | Possible conserved membrane prote | 51.58 | 220 | Mb0322c | hypothetical protein | 50.53 | 220 | MAV_4794 | hypothetical protein | 95.73 | 164 | BCG_0354c | hypothetical protein | 50.53 | 220 | MAP3852c | hypothetical protein | 195 | 100 |
| MAP4_3968 | endopeptidase ATP binding protein ClpB | 848 | Rv0384c | Probable endopeptidase ATP bindin | 92.57 | 848 | Mb0391c | endopeptidase ATP-binding p | 92.57 | 848 | MAV_4793 | chaperone ClpB | 99.88 | 848 | BCG_0422c | endopeptidase ATP binding pro | 92.57 | 848 | MAP3853 | ClpB | 848 | 100 |
| MAP4_3969 | transposase, IS30 family | 424 | Rv3191c | Probable transposase | 45.17 | 344 | Mb3213c | transposase | 45.17 | 344 | MAV_3355 | PPE family protein | 31.58 | 454 | BCG_3213c | transposase | 45.17 | 344 | MAP1824c | hypothetical protein | 424 | 100 |
| MAP4_3970 | conserved secreted protein | 290 | Rv0383c | Possible conserved secreted protein | 84.83 | 284 | Mb0390c | hypothetical protein | 84.83 | 284 | MAV_4792 | hypothetical protein | 100 | 290 | BCG_0421c | hypothetical protein | 84.83 | 284 | MAP3855 | hypothetical protein | 290 | 100 |
| MAP4_3971 | putative ketoacyl reductase | 257 | Rv1544 | Possible ketoacyl reductase | 40.98 | 267 | Mb1571 | ketoacyl reductase | 40.98 | 267 | MAV_4791 | dehydrogenase | 98.83 | 257 | BCG_1597 | ketoacyl reductase | 40.95 | 231 | MAP3856 | hypothetical protein | 257 | 100 |
| MAP4_3972 | orotate phosphoribosyltransferase PyrE | 179 | Rv0382c | Probable orotate phosphoribosyltra | 90.45 | 179 | Mb0389c | orotate phosphoribosyltransf | 90.45 | 179 | MAV_4790 | orotate phosphoribosyltransferase | 98.88 | 179 | BCG_0420c | orotate phosphoribosyltransfe | 90.45 | 179 | MAP3857 | orotate phosphoribosyltransferase | 179 | 100 |
| MAP4_3973 | hypothetical protein | 303 | Rv0381c | Hypothetical protein | 72.95 | 302 | Mb0388c | hypothetical protein | 72.95 | 302 | MAV_4789 | hypothetical protein | 98.25 | 286 | BCG_0419c | hypothetical protein | 72.95 | 302 | MAP3858 | hypothetical protein | 303 | 100 |
| MAP4_3974 | RNA methyltransferase | 219 | Rv0380c | Possible RNA methyltransferase (RN | 90.16 | 183 | Mb0387c | RNA methyltransferase | 90.16 | 183 | MAV_4788 | spou rRNA methylase | 97.21 | 214 | BCG_0418c | rna methyltransferase | 90.16 | 183 | MAP3859 | hypothetical protein | 219 | 100 |
| MAP4_3975 | putative glycosyl hydrolase | 379 | Rv0365c | hypothetical protein | 84.21 | 376 | Mb0372c | hypothetical protein | 84.21 | 376 | MAV_4787 | hypothetical protein | 98.68 | 379 | BCG_0403c | hypothetical protein | 84.21 | 376 | MAP3860 | hypothetical protein | 396 | 100 |
| MAP4_3976 | Succinyl-CoA:3-ketoacid-coenzyme A transferase Sco | 449 | Rv2503c | Probable succinyl-CoA:3-ketoacid-co | 64 | 218 | Mb2531c | succinyl-CoA:3-ketoacid-coen | 64 | 218 | MAV_4786 | succinyl-CoA:3-ketoacid-coenzyme | 99.78 | 449 | BCG_2523c | succinyl-CoA:3-ketoacid-coenzy | 64 | 218 | MAP3861 | ScoB | 449 | 100 |
| MAP4_3977 | hypothetical protein | 230 | Rv0364 | Possible conserved transmembrane | 81.45 | 227 | Mb0371 | transmembrane protein | 81 | 227 | MAV_4785 | membrane protein DedA family pro | 99.57 | 230 | BCG_0402 | hypothetical protein | 81 | 227 | MAP3862c | hypothetical protein | 230 | 100 |
| MAP4_3978 | hypothetical protein | 293 | Rv0361 | Probable conserved membrane prot | 62.91 | 275 | Mb0368 | hypothetical protein | 62.91 | 275 | MAV_4784 | hypothetical protein | 99.64 | 292 | BCG_0399 | hypothetical protein | 62.91 | 275 | MAP3863c | hypothetical protein | 293 | 100 |
| MAP4_3979 | hypothetical protein | 154 | Rv0360c | hypothetical protein | 85.4 | 145 | Mb0367c | hypothetical protein | 85.4 | 145 | MAV_4783 | hypothetical protein | 98.54 | 137 | BCG_0398c | hypothetical protein | 85.4 | 145 | MAP3864 | hypothetical protein | 154 | 100 |
| MAP4_3980 | putative cation efflux membrane protein | 298 | Rv2025c | hypothetical protein | 28.42 | 332 | Mb2050c | hypothetical protein | 28.42 | 332 | MAV_4782 | cobalt-zinc-cadmium resistance pro | 99.66 | 298 | BCG_2044c | hypothetical protein | 28.42 | 332 | MAP3865c | hypothetical protein | 298 | 100 |
| MAP4_3981 | putative conserved membrane protein | 260 | Rv0359 | Probable conserved integral membr | 79.05 | 259 | Mb0366 | hypothetical protein | 79.45 | 259 | MAV_4781 | peptidase, M50 family protein | 98.85 | 260 | BCG_0397 | integral membrane protein | 79.45 | 259 | MAP3866c | hypothetical protein | 260 | 100 |
| MAP4_3982 | hypothetical protein | 231 | Rv0358 | hypothetical protein | 67.46 | 215 | Mb0365 | hypothetical protein | 67.46 | 215 | MAV_4780 | hypothetical protein | 97.69 | 216 | BCG_0396 | hypothetical protein | 67.46 | 215 | MAP3867c | hypothetical protein | 231 | 100 |
| MAP4_3983 | PE-PGRS family protein | 313 | Rv0754 | PE-PGRS family protein PE_PGRS11 | 63.45 | 584 | Mb0776 | PE-PGRS family protein | 63.45 | 584 | MAV_4778 | pe_pgrs family protein | 98.4 | 313 | BCG_0805 | PE-PGRS family protein | 63.45 | 584 | MAP3868 | hypothetical protein | 313 | 100 |
| MAP4_3984 | adenylosuccinate synthetase PurA | 432 | Rv0357c | Probable adenylosuccinate syntheta | 90.05 | 432 | Mb0364c | adenylosuccinate synthetase | 90.05 | 432 | MAV_4777 | adenylosuccinate synthetase | 99.31 | 432 | BCG_0395c | adenylosuccinate synthetase | 90.05 | 432 | MAP3869 | adenylosuccinate synthetase | 432 | 100 |
| MAP4_3985 | hypothetical protein | 212 | Rv0356c | hypothetical protein | 86.47 | 214 | Mb0363c | hypothetical protein | 86.47 | 214 | MAV_4776 | thioesterase | 100 | 212 | BCG_0394c | hypothetical protein | 86.47 | 214 | MAP3870 | hypothetical protein | 212 | 100 |
| MAP4_3986 | phosphoribosylglycinamide formyltransferase 2PurT | 420 | Rv0389 | Probable phosphoribosylglycinamide | 64.21 | 419 | Mb0395 | phosphoribosylglycinamide fo | 60.84 | 419 | MAV_4775 | phosphoribosylglycinamide formylt | 98.08 | 416 | BCG_0426 | phosphoribosylglycinamide for | 60.84 | 419 | MAP3871 | phosphoribosylglycinamide formyltrans | 420 | 100 |
| MAP4_3987 | hypothetical protein | 146 | Rv0390 | hypothetical protein | 78.57 | 140 | Mb0396 | hypothetical protein | 78.57 | 140 | MAV_4774 | hypothetical protein | 99.32 | 146 | BCG_0427 | hypothetical protein | 78.57 | 140 | MAP3872 | hypothetical protein | 146 | 100 |
| MAP4_3988 | O-acetylhomoserine sulfhydrylase MetZ | 408 | Rv0391 | Probable O-succinylhomoserine sulf | 91.29 | 406 | Mb0397 | O-succinylhomoserine sulfhy | 91.29 | 406 | MAV_4773 | O-succinylhomoserine sulfhydrylas | 99.75 | 408 | BCG_0428 | O-succinylhomoserine sulfhydr | 91.29 | 406 | MAP3873 | O-succinylhomoserine sulfhydrylase | 408 | 100 |
| MAP4_3989 | NADH dehydrogenase NdhA | 480 | Rv0392c | Probable membrane NADH dehydro | 84.25 | 470 | Mb0398c | membrane NADH dehydroge | 84.02 | 470 | MAV_4772 | DoxD family protein/pyridine nucle | 99.57 | 463 | BCG_0429c | membrane NADH dehydrogena | 84.02 | 470 | MAP3874c | hypothetical protein | 480 | 100 |
| MAP4_3990 | putative secreted protein | 206 | Rv0398c | Possible secreted protein | 59.15 | 213 | Mb0404c | hypothetical protein | 59.15 | 213 | MAV_4770 | hypothetical protein | 98.06 | 206 | BCG_0435c | hypothetical protein | 59.15 | 213 | MAP3875c | hypothetical protein | 206 | 100 |
| MAP4_3991 | transcriptional regulator, TetR family | 220 | Rv0238 | Possible transcriptional regulatory p | 34.15 | 204 | Mb0244 | TetR family transcriptional re | 34.15 | 204 | MAV_4769 | TetR family transcriptional regulato | 99.09 | 220 | BCG_0276 | TetR family transcriptional regu | 34.15 | 204 | MAP3876c | hypothetical protein | 220 | 100 |
| MAP4_3992 | acyl-CoA dehydrogenase FadE20 | 382 | Rv2724c | Probable acyl-CoA dehydrogenase F | 56.76 | 386 | Mb2743c | acyl-CoA dehydrogenase | 56.5 | 386 | MAV_4768 | long-chain specific acyl-CoA dehydr | 99.48 | 382 | BCG_2737c | acyl-CoA dehydrogenase fadE2 | 56.76 | 386 | MAP3877c | FadE20_3 | 382 | 100 |
| MAP4_3993 | acyl-CoA dehydrogenase FadE7 | 398 | Rv0400c | Acyl-CoA dehydrogenase FadE7 | 87.31 | 395 | Mb0406c | acyl-CoA dehydrogenase | 87.31 | 395 | MAV_4767 | acyl-CoA dehydrogenase | 99.25 | 398 | BCG_0437c | acyl-CoA dehydrogenase fadE7 | 87.31 | 395 | MAP3878c | FadE7 | 398 | 100 |
| MAP4_3994 | short-chain dehydrogenase | 255 | Rv2857c | Probable short-chain type dehydrog | 38.46 | 258 | Mb2882c | short chain dehydrogenase | 38.46 | 258 | MAV_4766 | short chain dehydrogenase/reducta | 99.19 | 248 | BCG_2879c | short chain dehydrogenase | 38.46 | 258 | MAP3879c | hypothetical protein | 255 | 100 |
| MAP4_3995 | putative conserved membrane protein | 123 | Rv0401 | Probable conserved transmembrane | 70.49 | 123 | Mb0407 | transmembrane protein | 70.49 | 123 | MAV_4765 | hypothetical protein | 99.19 | 123 | BCG_0438 | hypothetical protein | 70.49 | 123 | MAP3880 | hypothetical protein | 123 | 100 |
| MAP4_3996 | putative methyltransferase family protein | 296 | Rv1729c | Possible S-adenosylmethionine-depe | 46.4 | 312 | Mb1758c | hypothetical protein | 46.4 | 312 | MAV_4764 | methyltransferase, putative, family | 98.99 | 296 | BCG_1768c | hypothetical protein | 46.4 | 312 | MAP3881 | hypothetical protein | 296 | 100 |
| MAP4_3997 | putative acetyltransferase | 172 | Rv1604 | Probable inositol-monophosphatase | 32.26 | 270 | Mb3242 | acetyltransferase | 36.67 | 110 | MAV_4763 | acetyltransferase, gnat family prote | 99.42 | 172 | BCG_3243 | acetyltransferase | 36.67 | 110 | MAP3882 | hypothetical protein | 172 | 100 |
| MAP4_3998 | beta-lactamase | 247 | Rv0406c | Beta lactamase like protein | 73.36 | 272 | Mb0414c | beta lactamase like protein | 73.36 | 272 | MAV_4762 | metallo-beta-lactamase | 99.6 | 247 | BCG_0445c | beta-lactamase | 73.36 | 272 | MAP3883c | hypothetical protein | 247 | 100 |
| MAP4_3999 | F420-dependent glucose-6-phosphatedehydrogenase F | 336 | Rv0407 | F420-dependent glucose-6-phospha | 90.48 | 336 | Mb0415 | F420-dependent glucose-6-ph | 90.48 | 336 | MAV_4761 | F420-dependent glucose-6-phosph | 100 | 336 | BCG_0446 | glucose-6-phosphate dehydrog | 90.48 | 336 | MAP3884 | hypothetical protein | 336 | 100 |
| MAP4_4000 | phosphate acetyltransferase Pta | 695 | Rv0408 | Probable phosphate acetyltransfera | 79.59 | 690 | Mb0416 | phosphate acetyltransferase | 79.74 | 690 | MAV_4760 | phosphate acetyltransferase | 99.57 | 695 | BCG_0447 | phosphate acetyltransferase | 79.74 | 690 | MAP3885 | phosphate acetyltransferase | 695 | 100 |
| MAP4_4001 | acetate kinase AckA | 387 | Rv0409 | Probable acetate kinase AckA (aceto | 77.51 | 385 | Mb0417 | acetate kinase | 77.51 | 385 | MAV_4758 | acetate kinase | 98.45 | 387 | BCG_0448 | acetate kinase | 77.51 | 385 | MAP3886 | acetate kinase | 387 | 100 |
| MAP4_4002 | hypothetical protein | 394 | Rv0357c | Probable adenylosuccinate syntheta | 36.84 | 432 | Mb0364c | adenylosuccinate synthetase | 36.84 | 432 | MAV_4759 | hypothetical protein | 98.48 | 394 | BCG_0395c | adenylosuccinate synthetase | 36.84 | 432 | MAP3887c | hypothetical protein | 361 | 100 |
| MAP4_4003 | hypothetical protein | 460 | Rv1795 | ESX conserved component EccD5 ES | 31.43 | 503 | Mb1823 | hypothetical protein | 31.43 | 503 | MAV_4757 | hypothetical protein | 99.57 | 460 | BCG_1827 | hypothetical protein | 31.43 | 503 | MAP3888c | hypothetical protein | 460 | 100 |
| MAP4_4004 | membrane protein, MmpS family | 144 | Rv0677c | Possible conserved membrane prote | 40.71 | 142 | Mb0696c | hypothetical protein | 40.71 | 142 | MAV_4756 | membrane protein | 100 | 136 | BCG_0726c | membrane protein mmpS5 | 40.71 | 142 | MAP3889 | hypothetical protein | 165 | 99.31 |
| MAP4_4005 | membrane protein, MmpL family (mmpL4) | 955 | Rv0450c | Probable conserved transmembrane | 59.77 | 967 | Mb0458c | transmembrane transport pro | 59.66 | 967 | MAV_4755 | MmpL4 protein | 99.79 | 937 | BCG_0489c | transmembrane transport prot | 59.77 | 967 | MAP3890 | hypothetical protein | 955 | 100 |
| MAP4_4006 | Transcriptional regulator, TetR family | 210 | Rv1556 | Possible regulatory protein | 31.15 | 202 | Mb1581 | regulatory protein | 31.15 | 202 | MAV_4754 | TetR family transcriptional regulato | 100 | 210 | BCG_1607 | regulatory protein | 31.15 | 202 | MAP3891 | hypothetical protein | 210 | 100 |
| MAP4_4007 | hypothetical protein | 287 | Rv1073 | hypothetical protein | 54.18 | 283 | Mb1102 | hypothetical protein | 54.18 | 283 | MAV_4752 | hypothetical protein | 99.3 | 287 | BCG_1131 | hypothetical protein | 54.18 | 283 | MAP3892 | hypothetical protein | 303 | 100 |
| MAP4_4008 | serinethreonine protein kinase PknG | 763 | Rv0410c | Serine/threonine-protein kinase Pkn | 85.71 | 750 | Mb0418c | serine/threonine-protein kina | 85.71 | 750 | MAV_4751 | serine/threonine protein kinase | 99.21 | 763 | BCG_0449c | Serine/threonine-protein kinas | 85.71 | 750 | MAP3893c | hypothetical protein | 763 | 100 |
| MAP4_4009 | glutamine-binding lipoprotein GlnH | 326 | Rv0411c | Probable glutamine-binding lipoprot | 86.04 | 328 | Mb0419c | glutamine-binding lipoprotein | 86.04 | 328 | MAV_4750 | extracellular solute-binding protein | 100 | 334 | BCG_0450c | glutamine-binding lipoprotein g | 86.04 | 328 | MAP3894c | GlnH | 309 | 99.68 |
| MAP4_4010 | hypothetical protein | 439 | Rv0412c | Possible conserved membrane prote | 86.33 | 439 | Mb0420c | hypothetical protein | 86.56 | 439 | MAV_4749 | hypothetical protein | 100 | 439 | BCG_0451c | hypothetical protein | 86.56 | 439 | MAP3895c | hypothetical protein | 439 | 100 |
| MAP4_4011 | mutator protein MutT3 | 213 | Rv0413 | Possible mutator protein MutT3 (7,8 | 76.08 | 217 | Mb0421 | 7,8-dihydro-8-oxoguanine-tri | 76.08 | 217 | MAV_4747 | hydrolase, NUDIX family protein | 99.53 | 213 | BCG_0452 | mutator protein MutT3 | 76.08 | 217 | MAP3896 | hypothetical protein | 213 | 100 |
| MAP4_4012 | thiamin-phosphate pyrophosphorylase ThiE | 223 | Rv0414c | Thiamine-phosphate pyrophosphory | 80.8 | 222 | Mb0422c | thiamine-phosphate pyropho | 80.8 | 222 | MAV_4748 | thiamine-phosphate pyrophosphor | 98.65 | 223 | BCG_0453c | thiamine-phosphate pyrophosp | 80.8 | 222 | MAP3897c | thiamine-phosphate pyrophosphorylase | 223 | 100 |
| MAP4_4013 | thiamine biosynthesis oxidoreductase ThiO | 338 | Rv0415 | Possible thiamine biosynthesis oxido | 86.69 | 340 | Mb0423 | thiamine biosynthesis oxidore | 86.39 | 340 | MAV_4746 | glycine oxidase ThiO | 99.41 | 338 | BCG_0454 | thiamine biosynthesis oxidored | 86.69 | 340 | MAP3898 | hypothetical protein | 359 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_4014 | putative sulfur carrier protein ThiS | 65 | Rv0416 | Possible protein ThiS | 69.12 | 68 | Mb0424 | sulfur carrier protein ThiS | 69.12 | 68 | MAV_4745 | sulfur carrier protein ThiS | 100 | 65 | BCG_0455 | sulfur carrier protein ThiS | 69.12 | 68 | MAP3899 | sulfur carrier protein ThiS | 65 | 100 |
| MAP4_4015 | thiamin biosynthesis protein ThiG | 252 | Rv0417 | Probable thiamin biosynthesis prote | 91.27 | 252 | Mb0425 | thiazole synthase | 91.67 | 252 | MAV_4744 | thiazole synthase | 99.6 | 252 | BCG_0456 | thiazole synthase | 91.67 | 252 | MAP3900 | thiazole synthase | 252 | 100 |
| MAP4_4016 | hypothetical protein | 255 | Rv1789 | PPE family protein PPE26 | 39.53 | 393 | Mb1817 | PPE family protein | 39.53 | 393 | MAV_4743 | hypothetical protein | 98.82 | 255 | BCG_1821 | PPE family protein | 39.53 | 393 | MAP3901 | hypothetical protein | 245 | 100 |
| MAP4_4017 | hypothetical protein | 173 | Rv1699 | Probable CTP synthase PyrG | 30 | 586 | Mb1725 | CTP synthetase | 30 | 586 | MAV_4742 | hypothetical protein | 98.84 | 173 | BCG_1737 | CTP synthetase | 30 | 586 | MAP3902c | hypothetical protein | 173 | 100 |
| MAP4_4018 | hypothetical protein | 176 | Rv0929 | Phosphate-transport integral memb | 33.96 | 324 | Mb0952 | phosphate ABC transporter tr | 33.96 | 324 | MAV_4741 | hypothetical protein | 97.16 | 176 | BCG_0981 | phosphate-transport integral m | 33.96 | 324 | MAP3903c | hypothetical protein | 177 | 100 |
| MAP4_4019 | putative interferon-induced transmembrane protein | 110 | Rv0143c | Probable conserved transmembrane | 27.5 | 492 | Mb0211 | transmembrane protein | 33.33 | 367 | MAV_4740 | hypothetical protein | 99.09 | 110 | BCG_0242 | hypothetical protein | 33.33 | 367 | MAP3904 | hypothetical protein | 110 | 100 |
| MAP4_4020 | hypothetical protein | 141 | Rv1616 | hypothetical protein | 32.41 | 132 | Mb1642 | hypothetical protein | 32.41 | 132 | MAV_4739 | hypothetical protein | 100 | 141 | BCG_1654 | hypothetical protein | 32.41 | 132 | MAP3905 | hypothetical protein | 141 | 100 |
| MAP4_4021 | lipoprotein aminopeptidase LpqL | 498 | Rv0418 | Probable lipoprotein aminopeptidas | 80.36 | 500 | Mb0426 | lipoprotein aminopeptidase L | 80.36 | 500 | MAV_4738 | peptidase, M28 family protein | 99.4 | 498 | BCG_0457 | lipoprotein aminopeptidase lpq | 80.36 | 500 | MAP3906 | hypothetical protein | 498 | 99.8 |
| MAP4_4022 | putative lipoprotein aminopeptidase LpqL | 490 | Rv0418 | Probable lipoprotein aminopeptidas | 50.87 | 500 | Mb0426 | lipoprotein aminopeptidase L | 50.87 | 500 | MAV_4737 | peptidase, M28 family protein | 99.18 | 490 | BCG_0457 | lipoprotein aminopeptidase lpq | 50.87 | 500 | MAP3907 | hypothetical protein | 477 | 99.79 |
| MAP4_4023 | lipoprotein peptidase LpqM | 481 | Rv0419 | Possible lipoprotein peptidase LpqM | 77.15 | 498 | Mb0427 | lipoprotein peptidase LpqM | 76.94 | 498 | MAV_4736 | LpqM protein | 98.72 | 471 | BCG_0458 | lipoprotein peptidase lpqM | 76.73 | 498 | MAP3908 | hypothetical protein | 481 | 100 |
| MAP4_4024 | monooxygenase | 291 | Rv1855c | Possible oxidoreductase | 40.86 | 307 | Mb1886c | oxidoreductase | 40.86 | 307 | MAV_4735 | hypothetical protein | 96.56 | 291 | BCG_1891c | oxidoreductase | 40.86 | 307 | MAP3909c | hypothetical protein | 291 | 100 |
| MAP4_4025 | transcriptional regulator, MarR family | 144 | Rv0880 | Possible transcriptional regulatory p | 34.29 | 143 | Mb0904 | MarR family transcriptional re | 34.29 | 143 | MAV_4734 | MarR family transcriptional regulat | 99.31 | 144 | BCG_0932 | MarR family transcriptional reg | 34.29 | 143 | MAP3910c | hypothetical protein | 111 | 99.1 |
| MAP4_4026 | hypothetical protein | 207 | Rv0421c | hypothetical protein | 80.3 | 209 | Mb0429c | hypothetical protein | 80.3 | 209 | MAV_4733 | hypothetical protein | 99.52 | 207 | BCG_0460c | hypothetical protein | 80.3 | 209 | MAP3911c | hypothetical protein | 207 | 100 |
| MAP4_4027 | phosphomethylpyrimidine kinase ThiD | 282 | Rv0422c | Probable phosphomethylpyrimidine | 86.74 | 265 | Mb0430c | phosphomethylpyrimidine kir | 86.74 | 265 | MAV_4732 | phosphomethylpyrimidine kinase | 98.58 | 282 | BCG_0461c | phosphomethylpyrimidine kina | 86.74 | 265 | MAP3912c | phosphomethylpyrimidine kinase | 282 | 100 |
| MAP4_4028 | thiamin biosynthesis protein ThiC | 540 | Rv0423c | Probable thiamine biosynthesis prot | 90.69 | 547 | Mb0431c | thiamine biosynthesis protein | 90.69 | 547 | MAV_4731 | thiamine biosynthesis protein ThiC | 99.81 | 540 | BCG_0462c | thiamine biosynthesis protein T | 90.69 | 547 | MAP3913c | thiamine biosynthesis protein ThiC | 540 | 100 |
| MAP4_4029 | hypothetical protein | 92 | Rv0424c | Hypothetical protein | 80 | 91 | Mb0432c | hypothetical protein | 80 | 91 | MAV_4730 | hypothetical protein | 100 | 92 | BCG_0463c | hypothetical protein | 80 | 91 | MAP3914c | hypothetical protein | 92 | 100 |
| MAP4_4030 | hypothetical protein | 64 | Rv1535 | hypothetical protein | 58.82 | 78 | Mb1562 | hypothetical protein | 58.82 | 78 | MAV_4729 | hypothetical protein | 96.88 | 64 | BCG_1587 | hypothetical protein | 58.82 | 78 | MAP1245 | hypothetical protein | 78 | 57.58 |
| MAP4_4031 | putative transmembrane protein | 149 | Rv0426c | Possible transmembrane protein | 62.42 | 147 | Mb0434c | transmembrane protein | 62.42 | 147 | MAV_4728 | hypothetical protein | 99.28 | 139 | BCG_0465c | hypothetical protein | 62.42 | 147 | MAP3915c | hypothetical protein | 149 | 100 |
| MAP4_4032 | exodeoxyribonuclease III XthA | 272 | Rv0427c | Probable exodeoxyribonuclease III p | 83.4 | 291 | Mb0435c | exodeoxyribonuclease III | 83.4 | 291 | MAV_4727 | exodeoxyribonuclease III | 98.9 | 272 | BCG_0466c | exodeoxyribonuclease III prote | 83.4 | 291 | MAP3916c | hypothetical protein | 272 | 100 |
| MAP4_4033 | hypothetical protein | 265 | Rv0428c | GCN5-related N-acetyltransferase | 54.58 | 302 | Mb0436c | hypothetical protein | 54.9 | 302 | MAV_4726 | hypothetical protein | 94.01 | 267 | BCG_0467c | hypothetical protein | 54.9 | 302 | MAP3917c | hypothetical protein | 278 | 100 |
| MAP4_4034 | peptide deformylase Def | 197 | Rv0429c | Probable polypeptide deformylase D | 87.31 | 197 | Mb0437c | peptide deformylase | 86.8 | 197 | MAV_4725 | peptide deformylase | 97.74 | 177 | BCG_0468c | peptide deformylase | 87.31 | 197 | MAP3918c | peptide deformylase | 197 | 99.49 |
| MAP4_4035 | hypothetical protein | 102 | Rv0430 | hypothetical protein | 97.06 | 102 | Mb0438 | hypothetical protein | 97.06 | 102 | MAV_4724 | hypothetical protein | 100 | 102 | BCG_0469 | hypothetical protein | 97.06 | 102 | MAP3919 | hypothetical protein | 102 | 100 |
| MAP4_4036 | putative tuberculin related peptide | 158 | Rv0431 | Putative tuberculin related peptide | 66.46 | 164 | Mb0439 | tuberculin-like protein | 67.09 | 164 | MAV_4723 | hypothetical protein | 99.3 | 143 | BCG_0470 | tuberculin-like protein | 67.09 | 164 | MAP3920 | hypothetical protein | 158 | 100 |
| MAP4_4037 | periplasmic superoxide dismutase SodC | 227 | Rv0432 | Periplasmic superoxide dismutase [C | 72.89 | 240 | Mb0440 | periplasmic superoxide dismu | 72.89 | 240 | MAV_4722 | superoxide dismutase, Cu-Zn | 99.56 | 227 | BCG_0471 | periplasmic superoxide dismut | 72.89 | 240 | MAP3921 | SodC | 227 | 100 |
| MAP4_4038 | carboxylate-amine ligase | 376 | Rv0433 | hypothetical protein | 87.23 | 376 | Mb0441 | carboxylate-amine ligase | 87.23 | 376 | MAV_4721 | carboxylate-amine ligase | 99.73 | 379 | BCG_0472 | carboxylate-amine ligase | 87.23 | 376 | MAP3922 | carboxylate-amine ligase | 388 | 99.73 |
| MAP4_4039 | ATP-dependent protease La domain family protein | 213 | Rv0434 | hypothetical protein | 66.51 | 217 | Mb0442 | hypothetical protein | 66.98 | 217 | MAV_4720 | ATP-dependent protease La | 99.06 | 213 | BCG_0473 | hypothetical protein | 66.98 | 217 | MAP3923 | hypothetical protein | 213 | 100 |
| MAP4_4040 | oxidoreductase | 340 | Rv1360 | Probable oxidoreductase | 46.23 | 340 | Mb1395 | oxidoreductase | 46.23 | 340 | MAV_4719 | hypothetical protein | 98.53 | 340 | BCG_1422 | oxidoreductase | 46.23 | 340 | MAP3924 | hypothetical protein | 340 | 100 |
| MAP4_4041 | putative enoyl-CoA hydratase | 272 | Rv1070c | Probable enoyl-CoA hydratase EchA | 37.84 | 257 | Mb1099c | enoyl-CoA hydratase | 37.84 | 257 | MAV_4717 | enoyl-CoA hydratase/isomerase | 95.96 | 272 | BCG_1128c | enoyl-CoA hydratase | 37.84 | 257 | MAP3925 | EchA8_2 | 272 | 100 |
| MAP4_4042 | hypothetical protein | 260 | Rv1673c | hypothetical protein | 31.03 | 310 | Mb1700c | hypothetical protein | 31.03 | 310 | MAV_4718 | hypothetical protein | 92.95 | 260 | BCG_1711c | hypothetical protein | 31.03 | 310 | MAP3926c | hypothetical protein | 260 | 100 |
| MAP4_4043 | Transcriptional regulator, TetR family | 198 | Rv0302 | Probable transcriptional regulatory | 35.59 | 210 | Mb0310 | TetR/ACRR family transcriptio | 35.59 | 210 | MAV_4715 | TetR family transcriptional regulato | 97.87 | 188 | BCG_0342 | TetR family transcriptional regu | 35.59 | 210 | MAP3927 | hypothetical protein | 198 | 100 |
| MAP4_4044 | ATPase | 722 | Rv0435c | Putative conserved ATPase | 85.69 | 728 | Mb0443c | ATPase | 85.69 | 728 | MAV_4716 | cell division protein 48 | 99.45 | 722 | BCG_0474c | atpase | 85.69 | 728 | MAP3928c | hypothetical protein | 722 | 100 |
| MAP4_4045 | CDP-diacylglycerol-serineo-phosphatidyl transferase Ps | 287 | Rv0436c | Probable CDP-diacylglycerol--serine | 81.82 | 286 | Mb0444c | CDP-diacylglycerol--serine O- | 81.82 | 286 | MAV_4714 | CDP-diacylglycerol--serine O-phosp | 100 | 287 | BCG_0475c | CDP-diacylglycerol--serine o-ph | 81.82 | 286 | MAP3929c | hypothetical protein | 287 | 100 |
| MAP4_4046 | phosphatidylserine decarboxylase Psd | 240 | Rv0437c | Possible phosphatidylserine decarbo | 79.41 | 231 | Mb0445c | phosphatidylserine decarbox | 79.41 | 231 | MAV_4713 | phosphatidylserine decarboxylase | 99.58 | 240 | BCG_0476c | phosphatidylserine decarboxyl | 79.41 | 231 | MAP3930c | phosphatidylserine decarboxylase | 240 | 100 |
| MAP4_4047 | transporter, major facilitator superfamily protein | 412 | Rv1674c | Probable transcriptional regulatory | 40.54 | 218 | Mb1701c | transcriptional regulator | 40.54 | 218 | MAV_4712 | transporter, major facilitator family | 98.26 | 403 | BCG_1712c | transcriptional regulatory prote | 40.54 | 218 | MAP3931 | hypothetical protein | 412 | 99.76 |
| MAP4_4048 | molybdopterin biosynthesis protein MoeA | 401 | Rv0438c | Probable molybdopterin biosynthesi | 81.19 | 405 | Mb0446c | molybdopterin biosynthesis p | 81.44 | 405 | MAV_4711 | molybdopterin biosynthesis protein | 99 | 404 | BCG_0477c | molybdopterin biosynthesis pr | 81.44 | 405 | MAP3932c | MoaA3 | 401 | 100 |
| MAP4_4049 | dehydrogenasereductase | 312 | Rv0439c | Probable dehydrogenase/reductase | 79.49 | 311 | Mb0447c | short chain dehydrogenase | 79.49 | 311 | MAV_4710 | short chain dehydrogenase | 99.36 | 312 | BCG_0478c | short chain dehydrogenase | 79.49 | 311 | MAP3933c | short chain dehydrogenase | 312 | 100 |
| MAP4_4050 | conserved hypothetical protein, cupin domain-containi | 172 | Rv3471c | hypothetical protein | 26.53 | 177 | Mb3500c | hypothetical protein | 26.26 | 177 | MAV_4709 | cupin domain-containing protein | 100 | 164 | BCG_3536c | hypothetical protein | 26.53 | 177 | MAP3934c | hypothetical protein | 172 | 100 |
| MAP4_4051 | putative peptidase, metallopeptidase family M24 prote | 241 | Rv2535c | Probable cytoplasmic peptidase Pep | 31.29 | 372 | Mb2564c | peptidase PepQ | 31.29 | 372 | MAV_4708 | aminopeptidase | 99.13 | 230 | BCG_2557c | cytoplasmic peptidase pepQ | 31.29 | 372 | MAP3935 | hypothetical protein | 241 | 100 |
| MAP4_4052 | 60 kda chaperonin 2 GroEL2 | 541 | Rv0440 | 60 kDa chaperonin 2 GroEL2 (protei | 95.26 | 540 | Mb0448 | molecular chaperone GroEL | 95.26 | 540 | MAV_4707 | chaperonin GroEL | 99.63 | 541 | BCG_0479 | chaperonin GroEL | 95.26 | 540 | MAP3936 | molecular chaperone GroEL | 541 | 100 |
| MAP4_4053 | hypothetical protein | 266 | Rv3555c | hypothetical protein | 49.63 | 289 | Mb3585c | hypothetical protein | 49.63 | 289 | MAV_4706 | hypothetical protein | 98.87 | 293 | BCG_3619c | hypothetical protein | 49.63 | 289 | MAP3937 | hypothetical protein | 266 | 100 |
| MAP4_4054 | hypothetical protein | 130 | Rv0441c | Hypothetical protein | 67.63 | 142 | Mb0449c | hypothetical protein | 67.63 | 142 | MAV_4705 | hypothetical protein | 99.23 | 130 | BCG_0480c | hypothetical protein | 67.63 | 142 | MAP3938c | hypothetical protein | 130 | 100 |
| MAP4_4055 | PPE family protein | 214 | Rv0442c | PPE family protein PPE10 | 72.22 | 487 | Mb0450c | PPE family protein | 70.93 | 479 | MAV_4704 | PPE family protein | 100 | 214 | BCG_0481c | PPE family protein | 70.93 | 479 | MAP3939c | hypothetical protein | 214 | 100 |
| MAP4_4056 | amidohydrolase family protein | 576 | Rv2913c | Possible D-amino acid aminohydrola | 29.03 | 611 | Mb2937c | D-amino acid aminohydrolase | 29.03 | 611 | MAV_4703 | amidohydrolase | 99.83 | 576 | BCG_2934c | D-amino acid aminohydrolase | 29.03 | 611 | MAP3940c | hypothetical protein | 576 | 100 |
| MAP4_4057 | putative glyoxalase family protein | 121 | Rv0274 | hypothetical protein | 26.97 | 193 | Mb0280 | hypothetical protein | 26.97 | 193 | MAV_4702 | glyoxalase | 98.35 | 121 | BCG_0312 | hypothetical protein | 26.97 | 193 | MAP3941 | hypothetical protein | 121 | 100 |
| MAP4_4058 | hypothetical protein | 171 | Rv0443 | hypothetical protein | 84.52 | 171 | Mb0451 | hypothetical protein | 84.52 | 171 | MAV_4701 | hypothetical protein | 98.25 | 171 | BCG_0482 | hypothetical protein | 84.52 | 171 | MAP3942 | hypothetical protein | 171 | 100 |
| MAP4_4059 | hypothetical protein | 282 | Rv1262c | Hypothetical hit-like protein | 42.31 | 144 | Mb1293c | HIT-like protein | 42.31 | 144 | MAV_4699 | hypothetical protein | 98.58 | 282 | BCG_1321c | HIT family protein | 42.31 | 144 | MAP3943 | hypothetical protein | 264 | 99.62 |
| MAP4_4060 | putative membrane protein, cytochrome c biogenesis | 576 | Rv2874 | Possible integral membrane C-type c | 61.72 | 695 | Mb2899 | integral membrane C-type cy | 61.89 | 695 | MAV_4700 | DipZ protein | 98.61 | 576 | BCG_2896 | integral membrane C-type cyto | 61.89 | 695 | MAP3944c | hypothetical protein | 599 | 99.83 |
| MAP4_4061 | Transcriptional regulator, TetR family | 228 | Rv0452 | Possible transcriptional regulatory p | 78.85 | 236 | Mb0460 | transcriptional regulator | 78.85 | 236 | MAV_4698 | TetR family transcriptional regulato | 99.5 | 200 | BCG_0491 | transcriptional regulatory prote | 78.85 | 236 | MAP3945 | hypothetical protein | 228 | 100 |
| MAP4_4062 | membrane protein, MmpS family | 182 | Rv0451c | Probable conserved membrane prot | 37.58 | 140 | Mb1582 | hypothetical protein | 44.67 | 148 | MAV_4697 | membrane protein | 100 | 182 | BCG_1608 | membrane protein mmpS6 | 44.67 | 148 | MAP3946 | hypothetical protein | 172 | 99.42 |
| MAP4_4063 | transmembrane transport protein MmpL4 | 976 | Rv0450c | Probable conserved transmembrane | 61.48 | 967 | Mb1583 | transmembrane transport pro | 65.51 | 967 | MAV_4696 | MmpL4 protein | 99.9 | 976 | BCG_1609 | transmembrane transport prot | 65.51 | 967 | MAP3947 | hypothetical protein | 976 | 100 |
| MAP4_4064 | hypothetical protein | 150 | Rv0455c | hypothetical protein | 76 | 148 | Mb0463c | hypothetical protein | 76 | 148 | MAV_4695 | hypothetical protein | 99.18 | 122 | BCG_0494c | hypothetical protein | 76 | 148 | MAP3948c | hypothetical protein | 119 | 100 |
| MAP4_4065 | enoyl-CoA hydratase EchA2 | 303 | Rv0456c | enoyl-CoA hydratase EchA2 (enoyl h | 92.69 | 304 | Mb0464c | enoyl-CoA hydratase | 92.69 | 304 | MAV_4694 | enoyl-CoA hydratase | 99.67 | 303 | BCG_0495c | enoyl-CoA hydratase | 92.69 | 304 | MAP3949c | enoyl-CoA hydratase | 303 | 100 |
| MAP4_4066 | hypothetical protein | 102 | Rv3279c | Possible bifunctional protein BirA: bi | 31.25 | 266 | Mb3738c | DNA polymerase III subunit e | 34.15 | 329 | MAV_4693 | hypothetical protein | 99.02 | 102 | BCG_3771c | DNA polymerase III subunit eps | 34.15 | 329 | MAP3950c | hypothetical protein | 102 | 100 |
| MAP4_4067 | peptidase | 679 | Rv0457c | Probable peptidase | 79.34 | 673 | Mb0466c | peptidase | 79.34 | 676 | MAV_0727 | protease 2 | 33.2 | 720 | BCG_0497c | peptidase | 79.34 | 676 | MAP3951c | hypothetical protein | 679 | 100 |
| MAP4_4068 | aldehyde dehydrogenase | 507 | Rv0458 | Probable aldehyde dehydrogenase | 89.35 | 507 | Mb0467 | aldehyde dehydrogenase | 89.35 | 507 | MAV_4691 | eptc-inducible aldehyde dehydroge | 99.61 | 507 | BCG_0498 | aldehyde dehydrogenase | 89.35 | 507 | MAP3952 | hypothetical protein | 507 | 100 |
| MAP4_4069 | hypothetical protein | 160 | Rv0459 | hypothetical protein | 77.4 | 163 | Mb0468 | hypothetical protein | 77.4 | 163 | MAV_4690 | hypothetical protein | 98.75 | 160 | BCG_0499 | hypothetical protein | 77.4 | 163 | MAP3953 | hypothetical protein | 160 | 100 |
| MAP4_4070 | conserved hydrophobic protein | 92 | Rv0460 | Conserved hydrophobic protein | 70.89 | 79 | Mb0469 | hypothetical protein | 70.89 | 79 | MAV_4689 | hypothetical protein | 95.65 | 92 | BCG_0500 | hypothetical protein | 70.89 | 79 | MAP3954 | hypothetical protein | 92 | 100 |
| MAP4_4071 | putative transmembrane protein | 189 | Rv0461 | Probable transmembrane protein | 51.45 | 174 | Mb0470 | hypothetical protein | 51.45 | 174 | MAV_4688 | hypothetical protein | 96.83 | 187 | BCG_0501 | hypothetical protein | 51.45 | 174 | MAP3955 | hypothetical protein | 189 | 100 |
| MAP4_4072 | Dihydrolipoamide dehydrogenase Lpd | 465 | Rv0462 | Dihydrolipoamide dehydrogenase Lp | 89.85 | 464 | Mb0471 | dihydrolipoamide dehydroge | 89.85 | 464 | MAV_4687 | dihydrolipoamide dehydrogenase | 100 | 465 | BCG_0502 | dihydrolipoamide dehydrogena | 89.85 | 464 | MAP3956 | dihydrolipoamide dehydrogenase | 431 | 99.75 |
| MAP4_4073 | putative conserved membrane protein | 93 | Rv0463 | Probable conserved membrane prot | 52.75 | 97 | Mb0472 | hypothetical protein | 52.75 | 97 | MAV_4686 | hypothetical protein | 100 | 93 | BCG_0503 | hypothetical protein | 52.75 | 97 | MAP3957 | hypothetical protein | 93 | 100 |
| MAP4_4074 | hypothetical protein | 185 | Rv0464c | hypothetical protein | 66.85 | 190 | Mb0473c | hypothetical protein | 66.85 | 190 | MAV_4685 | hypothetical protein | 100 | 185 | BCG_0504c | hypothetical protein | 66.85 | 190 | MAP3958c | hypothetical protein | 185 | 100 |
| MAP4_4075 | Transcriptional regulator | 474 | Rv0465c | Probable transcriptional regulatory | 92.18 | 474 | Mb0474c | transcriptional regulator | 91.97 | 474 | MAV_4684 | DNA-binding protein | 100 | 474 | BCG_0505c | transcriptional regulatory prote | 92.18 | 474 | MAP3959c | hypothetical protein | 506 | 99.79 |
| MAP4_4076 | putative acyl-ACP thioesterase | 264 | Rv0466 | hypothetical protein | 88.93 | 264 | Mb0475 | hypothetical protein | 88.93 | 264 | MAV_4683 | acyl-ACP thioesterase | 99.61 | 258 | BCG_0506 | hypothetical protein | 88.93 | 264 | MAP3960 | hypothetical protein | 264 | 100 |
| MAP4_4077 | Isocitrate lyase Icl | 430 | Rv0467 | Isocitrate lyase Icl (isocitrase) (isocit | 92.74 | 428 | Mb0476 | isocitrate lyase | 92.74 | 428 | MAV_4682 | isocitrate lyase | 99.77 | 428 | BCG_0507 | isocitrate lyase icl | 92.74 | 428 | MAP3961 | isocitrate lyase | 430 | 100 |
| MAP4_4078 | 3-hydroxybutyryl-CoA dehydrogenase FadB2 | 287 | Rv0468 | 3-hydroxybutyryl-CoA dehydrogenas | 90.94 | 286 | Mb0477 | 3-hydroxybutyryl-CoA dehydr | 90.94 | 286 | MAV_4681 | 3-hydroxybutyryl-CoA dehydrogena | 99.65 | 297 | BCG_0508 | 3-hydroxybutyryl-CoA dehydro | 90.94 | 286 | MAP3962 | 3-hydroxybutyryl-CoA dehydrogenase | 287 | 100 |
| MAP4_4079 | mycolic acid synthase UmaA | 286 | Rv0469 | Possible mycolic acid synthase UmaA | 82.52 | 286 | Mb0478 | mycolic acid synthase | 82.52 | 286 | MAV_4680 | methoxy mycolic acid synthase 1 | 99.65 | 289 | BCG_0509 | mycolic acid synthase umaA1 | 82.52 | 286 | MAP3963 | UmaA1 | 286 | 100 |
| MAP4_4080 | mycolic acid synthase PcaA | 288 | Rv0470c | Mycolic acid synthase PcaA (cyclopr | 82.93 | 287 | Mb0479c | mycolic acid synthase PcaA | 82.93 | 287 | MAV_4679 | cyclopropane-fatty-acyl-phospholip | 99.3 | 286 | BCG_0510c | mycolic acid synthase PcaA | 82.93 | 287 | MAP3964c | UmaA2 | 288 | 100 |
| MAP4_4081 | Transcriptional regulator, TetR family | 235 | Rv0472c | Probable transcriptional regulatory | 87.34 | 234 | Mb0482c | TetR family transcriptional re | 87.34 | 234 | MAV_4678 | TetR family transcriptional regulato | 100 | 224 | BCG_0513c | TetR family transcriptional regu | 86.9 | 234 | MAP3965c | hypothetical protein | 235 | 100 |
| MAP4_4082 | hypothetical protein | 456 | Rv0473 | Possible conserved transmembrane | 87.53 | 456 | Mb0483 | transmembrane protein | 87.53 | 456 | MAV_4677 | hypothetical protein | 98.19 | 436 | BCG_0514 | hypothetical protein | 87.53 | 456 | MAP3966 | hypothetical protein | 456 | 100 |
| MAP4_4083 | Transcriptional regulator | 138 | Rv0474 | Probable transcriptional regulatory | 86.67 | 140 | Mb0484 | transcriptional regulator | 86.67 | 140 | MAV_4676 | XRE family transcriptional regulator | 100 | 138 | BCG_0515 | transcriptional regulatory prote | 86.67 | 140 | MAP3967 | hypothetical protein | 138 | 100 |
| MAP4_4084 | iron-regulated heparin binding hemagglutinin HbhA | 195 | Rv0475 | Iron-regulated heparin binding hem | 88.05 | 199 | Mb0485 | heparin binding hemagglutini | 88.05 | 199 | MAV_4675 | heparin binding hemagglutinin hbh | 99.38 | 205 | BCG_0516 | Heparin binding hemagglutinin | 88.05 | 199 | MAP3968 | hypothetical protein | 195 | 100 |
| MAP4_4085 | hypothetical protein | 87 | Rv0476 | Possible conserved transmembrane | 86.49 | 87 | Mb0486 | transmembrane protein | 86.49 | 87 | MAV_4674 | hypothetical protein | 100 | 87 | BCG_0517 | hypothetical protein | 86.49 | 87 | MAP3969 | hypothetical protein | 87 | 100 |
| MAP4_4086 | putative conserved secreted protein | 141 | Rv0477 | Possible conserved secreted protein | 68.03 | 148 | Mb0487 | hypothetical protein | 68.03 | 148 | MAV_4673 | hypothetical protein | 97.87 | 141 | BCG_0518 | hypothetical protein | 68.03 | 148 | MAP3970 | hypothetical protein | 141 | 100 |
| MAP4_4087 | Deoxyribose-phosphate aldolase DeoC | 223 | Rv0478 | Probable deoxyribose-phosphate ald | 82.27 | 224 | Mb0488 | deoxyribose-phosphate aldol | 82.27 | 224 | MAV_4672 | deoxyribose-phosphate aldolase | 98.65 | 223 | BCG_0519 | deoxyribose-phosphate aldolas | 82.27 | 224 | MAP3971 | deoxyribose-phosphate aldolase | 223 | 100 |
| MAP4_4088 | putative conserved membrane protein | 352 | Rv0479c | Probable conserved membrane prot | 60.56 | 348 | Mb0489c | hypothetical protein | 60.56 | 348 | MAV_4671 | hypothetical protein | 99.15 | 352 | BCG_0520c | hypothetical protein | 60.56 | 348 | MAP3972c | hypothetical protein | 352 | 100 |
| MAP4_4089 | amidohydrolase | 274 | Rv0480c | Possible amidohydrolase | 77.5 | 280 | Mb0490c | hypothetical protein | 77.5 | 311 | MAV_4670 | carbon-nitrogen hydrolase | 99.27 | 274 | BCG_0521c | hypothetical protein | 77.5 | 311 | MAP3973c | hypothetical protein | 274 | 100 |
| MAP4_4090 | hypothetical protein | 174 | Rv0481c | Hypothetical protein | 66.47 | 174 | Mb0491c | hypothetical protein | 66.47 | 174 | MAV_3993 | hypothetical protein | 39.08 | 168 | BCG_0522c | hypothetical protein | 66.47 | 174 | MAP3974c | hypothetical protein | 174 | 100 |
| MAP4_4091 | UDP-N-acetylenolpyruvoylglucosamine reductase Mur | 372 | Rv0482 | Probable UDP-N-acetylenolpyruvoyl | 74.2 | 369 | Mb0492 | UDP-N-acetylenolpyruvoylglu | 74.2 | 369 | MAV_4668 | UDP-N-acetylenolpyruvoylglucosam | 98.92 | 372 | BCG_0523 | UDP-N-acetylenolpyruvoylgluc | 74.2 | 369 | MAP3975 | UDP-N-acetylenolpyruvoylglucosamine | 372 | 100 |
| MAP4_4092 | putative lipoprotein LprQ | 446 | Rv0483 | Probable conserved lipoprotein LprQ | 78.35 | 451 | Mb0493 | lipoprotein LprQ | 78.35 | 451 | MAV_4666 | ErfK/YbiS/YcfS/YnhG family protein | 99.77 | 443 | BCG_0524 | lipoprotein lprQ | 78.35 | 451 | MAP3976 | hypothetical protein | 446 | 100 |
| MAP4_4093 | short-chain type oxidoreductase | 249 | Rv0484c | Probable short-chain type oxidoredu | 88.11 | 251 | Mb0494c | short-chain type oxidoreduct | 88.52 | 251 | MAV_4667 | oxidoreductase | 99.6 | 249 | BCG_0525c | short-chain type oxidoreductas | 88.52 | 251 | MAP3977c | hypothetical protein | 249 | 100 |
| MAP4_4094 | transcriptional regulatory protein | 428 | Rv0485 | Possible transcriptional regulatory p | 82.51 | 438 | Mb0495 | transcriptional regulator | 82.51 | 438 | MAV_4665 | ROK family protein | 100 | 428 | BCG_0526 | transcriptional regulatory prote | 82.51 | 438 | MAP3978 | hypothetical protein | 428 | 100 |
| MAP4_4095 | mannosyltransferase | 441 | Rv0486 | Glycosyltransferase MshA | 88.35 | 480 | Mb0496 | mannosyltransferase | 88.35 | 480 | MAV_4664 | hypothetical protein | 98.82 | 424 | BCG_0527 | mannosyltransferase | 88.35 | 480 | MAP3979 | hypothetical protein | 441 | 100 |
| MAP4_4096 | hypothetical protein | 169 | Rv0487 | hypothetical protein | 78.26 | 183 | Mb0497 | hypothetical protein | 78.26 | 183 | MAV_4663 | hypothetical protein | 100 | 169 | BCG_0528 | hypothetical protein | 78.26 | 183 | MAP3980 | hypothetical protein | 169 | 100 |
| MAP4_4097 | phosphoglycerate mutase 1 GpmA | 249 | Rv0489 | Probable phosphoglycerate mutase | 90.17 | 249 | Mb0499 | phosphoglyceromutase | 90.17 | 249 | MAV_4662 | phosphoglyceromutase | 99.2 | 249 | BCG_0530 | phosphoglyceromutase | 90.17 | 249 | MAP3981 | phosphoglyceromutase | 249 | 100 |
| MAP4_4098 | two component sensor histidine kinase SenX3 | 409 | Rv0490 | Putative two component sensor hist | 83.66 | 410 | Mb0500 | two component sensor histid | 83.66 | 410 | MAV_4661 | hisitidine protein kinase SenX3 | 99.02 | 407 | BCG_0531 | two component sensor histidin | 83.41 | 410 | MAP3982 | SenX3 | 409 | 100 |
| MAP4_4099 | two component sensory transduction proteinRegX3 | 227 | Rv0491 | Two component sensory transductio | 99.12 | 227 | Mb0501 | two component sensory trans | 99.12 | 227 | MAV_4660 | DNA-binding response regulator | 100 | 227 | BCG_0532 | two component sensory transd | 98.68 | 227 | MAP3983 | RegX3 | 227 | 100 |
| MAP4_4100 | putative hydrolase, NUDIX family protein | 166 | Rv3908 | Possible mutator protein MutT4 | 30.09 | 248 | Mb3938 | hypothetical protein | 30.09 | 248 | MAV_4659 | hydrolase, nudix family protein, pu | 99.4 | 166 | BCG_3965 | hypothetical protein | 30.09 | 248 | MAP3984c | hypothetical protein | 166 | 100 |
| MAP4_4101 | hypothetical protein | 314 | Rv0493c | hypothetical protein | 72.78 | 329 | Mb0504c | hypothetical protein | 73.1 | 329 | MAV_4658 | hypothetical protein | 99.04 | 314 | BCG_0535c | hypothetical protein | 73.1 | 329 | MAP3985c | hypothetical protein | 314 | 100 |
| MAP4_4102 | hypothetical protein | 267 | Rv0495c | hypothetical protein | 89.14 | 296 | Mb0506c | hypothetical protein | 89.14 | 296 | MAV_4657 | hypothetical protein | 99.63 | 267 | BCG_0537c | hypothetical protein | 89.14 | 296 | MAP3986c | hypothetical protein | 267 | 100 |
| MAP4_4103 | PpxGppA phosphatase | 338 | Rv0496 | hypothetical protein | 86.59 | 328 | Mb0507 | hypothetical protein | 86.59 | 328 | MAV_4656 | Ppx/GppA phosphatase | 100 | 338 | BCG_0538 | hypothetical protein | 86.59 | 328 | MAP3987 | hypothetical protein | 338 | 100 |
| MAP4_4104 | hypothetical protein | 322 | Rv0497 | Probable conserved transmembrane | 58.13 | 310 | Mb0508 | transmembrane protein | 58.13 | 310 | MAV_4655 | hypothetical protein | 99.69 | 322 | BCG_0539 | hypothetical protein | 58.13 | 310 | MAP3988 | hypothetical protein | 322 | 100 |
| MAP4_4105 | hypothetical protein | 280 | Rv0498 | hypothetical protein | 92.14 | 280 | Mb0509 | hypothetical protein | 92.14 | 280 | MAV_4654 | hypothetical protein | 99.64 | 280 | BCG_0540 | hypothetical protein | 92.14 | 280 | MAP3989 | hypothetical protein | 280 | 100 |
| MAP4_4106 | thioesterase-like superfamily protein | 280 | Rv0499 | hypothetical protein | 75.17 | 291 | Mb0510 | hypothetical protein | 75.17 | 291 | MAV_4653 | hypothetical protein | 98.93 | 280 | BCG_0541 | hypothetical protein | 75.17 | 291 | MAP3990 | hypothetical protein | 280 | 100 |
| MAP4_4107 | Pyrroline-5-carboxylate reductase ProC | 295 | Rv0500 | Probable pyrroline-5-carboxylate re | 81.02 | 295 | Mb0511 | pyrroline-5-carboxylate redu | 81.36 | 295 | MAV_4652 | pyrroline-5-carboxylate reductase | 98.64 | 295 | BCG_0542 | pyrroline-5-carboxylate reduct | 81.36 | 295 | MAP3991 | pyrroline-5-carboxylate reductase | 298 | 100 |
| MAP4_4108 | hypothetical protein | 85 | Rv0500A | hypothetical protein | 83.53 | 78 | Mb0512 | hypothetical protein | 83.53 | 78 | MAV_4651 | hypothetical protein | 100 | 45 | BCG_0543 | hypothetical protein | 83.53 | 78 | MAP3992 | hypothetical protein | 85 | 100 |
| MAP4_4109 | UDP-glucose 4-epimerase GalE1 | 375 | Rv0501 | Possible UDP-glucose 4-epimerase G | 89.89 | 376 | Mb0513 | UDP-glucose 4-epimerase | 89.89 | 376 | MAV_4649 | NAD dependent epimerase/dehydr | 100 | 375 | BCG_0544 | udp-glucose 4-epimerase galE2 | 89.89 | 376 | MAP3993 | GalE1 | 375 | 100 |
| MAP4_4110 | putative acyltransferase family protein | 354 | Rv0502 | hypothetical protein | 91.29 | 358 | Mb0514 | hypothetical protein | 91.29 | 358 | MAV_4648 | acyltransferase | 99.72 | 354 | BCG_0545 | hypothetical protein | 91.29 | 358 | MAP3994 | hypothetical protein | 354 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_4111 | cyclopropane-fatty-acyl-phospholipid synthase2, C ma | 299 | Rv0503c | Cyclopropane-fatty-acyl-phospholipi | 78.22 | 302 | Mb0515c | cyclopropane-fatty-acyl-phos | 78.22 | 302 | MAV_4647 | cyclopropane-fatty-acyl-phospholip | 100 | 299 | BCG_0546c | cyclopropane-fatty-acyl-phospl | 78.22 | 302 | MAP3995c | CmaA2 | 299 | 99.67 |
| MAP4_4112 | hypothetical protein | 174 | Rv0504c | hypothetical protein | 84.34 | 166 | Mb0516c | hypothetical protein | 84.34 | 166 | MAV_4646 | hypothetical protein | 100 | 174 | BCG_0547c | hypothetical protein | 84.34 | 166 | MAP3996c | hypothetical protein | 174 | 100 |
| MAP4_4113 | phosphoserine phosphatase SerB | 303 | Rv0505c | Possible phosphoserine phosphatas | 85.06 | 373 | Mb0517c | phosphoserine phosphatase | 85.06 | 373 | MAV_4645 | HAD-superfamily protein subfamily | 99.34 | 303 | BCG_0548c | phosphoserine phosphatase se | 85.06 | 373 | MAP3997c | hypothetical protein | 303 | 100 |
| MAP4_4114 | hypothetical protein | 209 | Rv0667 | DNA-directed RNA polymerase (beta | 30.51 | 1172 | Mb0686 | DNA-directed RNA polymeras | 30.51 | 1172 | MAV_2417 | hypothetical protein | 40 | 51 | BCG_0716 | DNA-directed RNA polymerase | 30.51 | 1172 | MAP0136 | hypothetical protein | 140 | 38.46 |
| MAP4_4115 | hypothetical protein | 261 | Rv1018c | Probable UDP-N-acetylglucosamine | 27.66 | 495 | Mb1046c | bifunctional N-acetylglucosan | 27.08 | 495 | MAV_3817 | hypothetical protein | 45.45 | 238 | BCG_1075c | bifunctional N-acetylglucosami | 27.66 | 495 | MAP3008c | hypothetical protein | 238 | 45.45 |
| MAP4_4116 | hypothetical protein | 220 | Rv0343 | Isoniazid inductible gene protein Ini | 24.68 | 493 | Mb0350 | isoniazid inductible gene prot | 24.68 | 493 | MAV_2417 | hypothetical protein | 40 | 51 | BCG_0382 | isoniazid inductible gene prote | 24.68 | 493 | MAP0912c | AccD2 | 531 | 27.78 |
| MAP4_4119 | Esat-6 like protein EsxE | 90 | Rv3904c | Putative ESAT-6 like protein EsxE (hy | 72.22 | 90 | Mb3934c | hypothetical protein | 71.11 | 90 | MAV_4643 | hypothetical protein | 98.89 | 96 | BCG_3961c | ESAT-6 like protein 12 esxE | 71.11 | 90 | MAP3999c | hypothetical protein | 90 | 100 |
| MAP4_4120 | Esat-6 like protein EsxF | 102 | Rv3905c | Putative ESAT-6 like protein EsxF (hy | 67.33 | 103 | Mb3935c | hypothetical protein | 72.73 | 57 | MAV_4642 | hypothetical protein | 100 | 102 | BCG_3962c | ESAT-6 like protein 13 esxF | 72.73 | 57 | MAP4000c | hypothetical protein | 113 | 100 |
| MAP4_4121 | hypothetical protein | 89 | Rv0508 | hypothetical protein | 72.29 | 97 | Mb0520 | hypothetical protein | 72.29 | 97 | MAV_4641 | hypothetical protein | 97.75 | 89 | BCG_0551 | hypothetical protein | 72.29 | 97 | MAP4001 | hypothetical protein | 89 | 100 |
| MAP4_4122 | glutamyl-tRNA reductase HemA | 459 | Rv0509 | Probable glutamyl-tRNA reductase H | 86.5 | 468 | Mb0521 | glutamyl-tRNA reductase | 86.5 | 468 | MAV_4640 | glutamyl-tRNA reductase | 100 | 459 | BCG_0552 | glutamyl-tRNA reductase | 86.5 | 468 | MAP4002 | glutamyl-tRNA reductase | 459 | 100 |
| MAP4_4123 | porphobilinogen deaminase HemC | 315 | Rv0510 | Probable porphobilinogen deaminas | 90.61 | 309 | Mb0523 | porphobilinogen deaminase | 90.61 | 309 | MAV_4639 | porphobilinogen deaminase | 99.68 | 315 | BCG_0553 | porphobilinogen deaminase | 90.61 | 309 | MAP4003 | porphobilinogen deaminase | 315 | 100 |
| MAP4_4124 | uroporphyrinogen-III C-methyltransferase HemD | 552 | Rv0511 | Probable uroporphyrin-III C-methylt | 87.59 | 565 | Mb0524 | uroporphyrin-III C-methyltran | 87.59 | 565 | MAV_4638 | uroporphyrinogen-III synthase | 98.88 | 537 | BCG_0554 | uroporphyrin-III c-methyltrans | 87.59 | 565 | MAP4004 | hypothetical protein | 552 | 100 |
| MAP4_4125 | delta-aminolevulinic acid dehydratase HemB | 326 | Rv0512 | Probable delta-aminolevulinic acid d | 91.38 | 329 | Mb0525 | delta-aminolevulinic acid deh | 91.08 | 329 | MAV_4637 | delta-aminolevulinic acid dehydrata | 99.32 | 295 | BCG_0555 | delta-aminolevulinic acid dehy | 91.08 | 329 | MAP4005 | delta-aminolevulinic acid dehydratase | 326 | 100 |
| MAP4_4126 | hypothetical protein | 186 | Rv0513 | Possible conserved transmembrane | 70.88 | 182 | Mb0526 | transmembrane protein | 70.88 | 182 | MAV_4636 | hypothetical protein | 99.38 | 161 | BCG_0556 | hypothetical protein | 70.88 | 182 | MAP4006 | hypothetical protein | 198 | 99.46 |
| MAP4_4127 | hypothetical protein | 86 | Rv0514 | Possible transmembrane protein | 66.67 | 99 | Mb0527 | transmembrane protein | 66.67 | 99 | MAV_4634 | transmembrane protein | 100 | 86 | BCG_0557 | hypothetical protein | 66.67 | 99 | MAP0286 | hypothetical protein | 86 | 41.18 |
| MAP4_4128 | putative anti-anti-sigma factor | 146 | Rv0516c | Possible anti-anti-sigma factor | 53.85 | 158 | Mb0529c | hypothetical protein | 53.85 | 158 | MAV_4635 | STAS domain-containing protein | 99.32 | 146 | BCG_0559c | hypothetical protein | 53.85 | 158 | MAP4007c | hypothetical protein | 146 | 100 |
| MAP4_4129 | membrane acyltransferase | 437 | Rv0517 | Possible membrane acyltransferase | 76.89 | 436 | Mb0530 | membrane acyltransferase | 76.89 | 436 | MAV_4633 | acyltransferase, putative | 99.27 | 412 | BCG_0560 | membrane acyltransferase | 76.89 | 436 | MAP4008 | hypothetical protein | 437 | 100 |
| MAP4_4130 | hypothetical protein | 229 | Rv0518 | Possible exported protein | 69.13 | 231 | Mb0531 | hypothetical protein | 69.13 | 231 | MAV_4632 | hypothetical protein | 100 | 229 | BCG_0561 | hypothetical protein | 69.13 | 231 | MAP4009 | hypothetical protein | 245 | 99.56 |
| MAP4_4131 | hypothetical protein | 38 | Rv1795 | ESX conserved component EccD5 ES | 38.64 | 503 | Mb1823 | hypothetical protein | 38.64 | 503 | MAV_4631 | hypothetical protein | 100 | 38 | BCG_1827 | hypothetical protein | 38.64 | 503 | MAP2924 | NicT | 410 | 32.43 |
| MAP4_4132 | putative acyltransferase | 720 | Rv1565c | hypothetical protein | 29.59 | 729 | Mb1592c | hypothetical protein | 29.59 | 729 | MAV_4630 | acyltransferase domain-containing | 99.01 | 706 | BCG_1618c | hypothetical protein | 29.59 | 729 | MAP4010c | hypothetical protein | 720 | 100 |
| MAP4_4133 | hypothetical protein | 317 | Rv0519c | Possible conserved membrane prote | 75.09 | 300 | Mb0532c | hypothetical protein | 75.09 | 300 | MAV_4629 | esterase | 100 | 276 | BCG_0562c | hypothetical protein | 75.09 | 300 | MAP4011c | hypothetical protein | 317 | 100 |
| MAP4_4134 | hypothetical protein | 89 | Rv2411c | hypothetical protein | 39.29 | 551 | Mb2434c | hypothetical protein | 39.29 | 551 | | | | | BCG_2427c | hypothetical protein | 39.29 | 551 | MAP4012c | hypothetical protein | 89 | 100 |
| MAP4_4135 | putative alkanesulfonate monooxygenase | 643 | Rv0132c | Putative F420-dependent glucose-6- | 26.35 | 360 | Mb0137c | F420-dependent glucose-6-ph | 26.35 | 360 | MAV_4628 | alkanesulfonate monoxygenase | 96.28 | 381 | BCG_0166c | F420-dependent glucose-6-pho | 26.35 | 360 | MAP4013 | hypothetical protein | 643 | 100 |
| MAP4_4138 | 2-dehydropantoate 2-reductase | 305 | Rv2691 | TRK system potassium uptake prote | 35.82 | 227 | Mb2603 | 2-dehydropantoate 2-reducta | 25.48 | 275 | MAV_4625 | 2-dehydropantoate 2-reductase | 99.34 | 305 | BCG_2704 | TRK system potassium uptake | 35.82 | 227 | MAP4016c | hypothetical protein | 305 | 100 |
| MAP4_4139 | putative mandelate racemasemuconatelactonizing enz | 393 | Rv0553 | Probable muconate cycloisomerase | 31.89 | 326 | Mb0568 | O-succinylbenzoate synthase | 31.89 | 326 | MAV_4624 | mandelate racemase/muconate lac | 99.49 | 393 | BCG_0598 | O-succinylbenzoate synthase | 31.89 | 326 | MAP4017c | hypothetical protein | 394 | 99.75 |
| MAP4_4140 | hypothetical protein | 131 | Rv0523c | hypothetical protein | 76.74 | 131 | Mb0536c | hypothetical protein | 76.74 | 131 | MAV_4623 | hypothetical protein | 100 | 142 | BCG_0566c | hypothetical protein | 76.74 | 131 | MAP4018c | hypothetical protein | 142 | 100 |
| MAP4_4141 | hypothetical protein | 114 | Rv1161 | Respiratory nitrate reductase (alpha | 44.44 | 1232 | Mb1193 | respiratory nitrate reductase | 44.44 | 1232 | MAV_4622 | hypothetical protein | 97.37 | 114 | BCG_1223 | respiratory nitrate reductase (a | 44.44 | 1232 | MAP4019 | hypothetical protein | 115 | 100 |
| MAP4_4142 | glutamate-1-semialdehyde aminotransferase HemL | 445 | Rv0524 | Probable glutamate-1-semialdehyde | 82.92 | 462 | Mb0537 | glutamate-1-semialdehyde ar | 82.92 | 462 | MAV_4621 | glutamate-1-semialdehyde aminotr | 99.33 | 445 | BCG_0567 | glutamate-1-semialdehyde ami | 82.92 | 462 | MAP4020 | glutamate-1-semialdehyde aminotransf | 445 | 100 |
| MAP4_4143 | phosphoglycerate mutase family protein | 202 | Rv0525 | hypothetical protein | 84.58 | 202 | Mb0538 | hypothetical protein | 84.58 | 202 | MAV_4620 | phosphoglycerate mutase | 100 | 202 | BCG_0568 | hypothetical protein | 84.58 | 202 | MAP4021 | hypothetical protein | 202 | 100 |
| MAP4_4144 | thioredoxin | 197 | Rv0526 | Possible thioredoxin protein (thiol-d | 82.23 | 216 | Mb0539 | thioredoxin protein | 82.23 | 216 | MAV_4619 | hypothetical protein | 100 | 197 | BCG_0569 | thioredoxin protein | 82.23 | 216 | MAP4022 | hypothetical protein | 197 | 100 |
| MAP4_4145 | cytochrome C biogenesis protein CcdA | 259 | Rv0527 | Possible cytochrome C-type biogene | 88.03 | 259 | Mb0540 | cytochrome C-type biogenesi | 88.03 | 259 | MAV_4618 | cytochrome C biogenesis protein tr | 100 | 259 | BCG_0570 | cytochrome c-type biogenesis | 88.03 | 259 | MAP4023 | CcsA | 259 | 100 |
| MAP4_4146 | hypothetical protein | 546 | Rv0528 | Probable conserved transmembrane | 83.04 | 529 | Mb0541 | transmembrane protein | 83.04 | 529 | MAV_4617 | hypothetical protein | 99.45 | 546 | BCG_0571 | hypothetical protein | 83.04 | 529 | MAP4024 | hypothetical protein | 546 | 100 |
| MAP4_4147 | cytochrome C biogenesis protein CcsA | 325 | Rv0529 | Possible cytochrome C-type biogene | 84 | 324 | Mb0542 | cytochrome C-type biogenesi | 84 | 324 | MAV_4616 | cytochrome C-type biogenesis prot | 99.69 | 325 | BCG_0572 | cytochrome c-type biogenesis | 84 | 324 | MAP4025 | CcsB | 325 | 100 |
| MAP4_4148 | hypothetical protein | 434 | Rv0530 | hypothetical protein | 66.97 | 405 | Mb0543 | hypothetical protein | 66.97 | 405 | MAV_4615 | hypothetical protein | 99.08 | 432 | BCG_0573 | hypothetical protein | 66.97 | 405 | MAP4026 | hypothetical protein | 434 | 100 |
| MAP4_4149 | hypothetical protein | 53 | Rv0530A | hypothetical protein | 86.84 | 53 | Mb1878 | hypothetical protein | 21.28 | 140 | MAV_4614 | hypothetical protein | 100 | 53 | BCG_1883 | hypothetical protein | 21.28 | 140 | MAP0924 | hypothetical protein | 302 | 75 |
| MAP4_4150 | hypothetical protein | 108 | Rv0531 | Possible conserved membrane prote | 66.67 | 105 | Mb0544 | hypothetical protein | 66.67 | 105 | MAV_4613 | hypothetical protein | 100 | 108 | BCG_0574 | hypothetical protein | 66.67 | 105 | MAP4027 | hypothetical protein | 110 | 99.07 |
| MAP4_4151 | 3-oxoacyl-ACP synthase IIIFabH | 335 | Rv0533c | 3-oxoacyl-[acyl-carrier-protein] synt | 77.01 | 335 | Mb0547c | 3-oxoacyl-ACP synthase | 77.01 | 335 | MAV_4612 | 3-oxoacyl-(acyl carrier protein) synt | 99.1 | 335 | BCG_0577c | 3-oxoacyl-ACP synthase | 77.01 | 335 | MAP4028c | 3-oxoacyl-ACP synthase III | 335 | 100 |
| MAP4_4152 | 1,4-dihydroxy-2-naphthoateoctaprenyltransferase Men | 290 | Rv0534c | 1,4-dihydroxy-2-naphthoate octapre | 82.76 | 292 | Mb0548c | 1,4-dihydroxy-2-naphthoate c | 82.76 | 292 | MAV_4611 | 1,4-dihydroxy-2-naphthoate octapr | 98.28 | 290 | BCG_0578c | 1,4-dihydroxy-2-naphthoate oc | 82.76 | 292 | MAP4029c | 1,4-dihydroxy-2-naphthoate octaprenyl | 290 | 100 |
| MAP4_4153 | 5'-methylthioadenosine phosphorylase Pnp | 260 | Rv0535 | Probable 5'-methylthioadenosine ph | 77.65 | 264 | Mb0549 | 5'-methylthioadenosine phos | 77.65 | 264 | MAV_4610 | 5'-methylthioadenosine phosphory | 97.35 | 264 | BCG_0579 | 5'-methylthioadenosine phospl | 77.65 | 264 | MAP4030 | 5'-methylthioadenosine phosphorylase | 260 | 100 |
| MAP4_4156 | hypothetical protein | 575 | Rv0537c | Probable integral membrane protein | 56.03 | 477 | Mb0551c | hypothetical protein | 56.03 | 477 | MAV_4608 | hypothetical protein | 98.61 | 575 | BCG_0581c | integral membrane protein | 56.03 | 477 | MAP4033c | hypothetical protein | 575 | 100 |
| MAP4_4157 | hypothetical protein | 559 | Rv0538 | Possible conserved membrane prote | 54.18 | 548 | Mb0552 | hypothetical protein | 53.7 | 548 | MAV_4606 | hypothetical protein | 96.48 | 556 | BCG_0582 | hypothetical protein | 53.7 | 548 | MAP4034 | hypothetical protein | 559 | 100 |
| MAP4_4158 | dolichyl-phosphate sugar synthase | 220 | Rv0539 | Probable dolichyl-phosphate sugar s | 88.1 | 210 | Mb0553 | dolichyl-phosphate sugar syn | 88.1 | 210 | MAV_4605 | glycosyltransferase | 99.09 | 220 | BCG_0583 | dolichyl-phosphate sugar synth | 88.1 | 210 | MAP4035 | hypothetical protein | 220 | 100 |
| MAP4_4159 | hypothetical protein | 218 | Rv0540 | hypothetical protein | 76.5 | 220 | Mb0554 | hypothetical protein | 76.5 | 220 | MAV_4604 | hypothetical protein | 97.71 | 218 | BCG_0584 | hypothetical protein | 76.5 | 220 | MAP4036 | hypothetical protein | 218 | 100 |
| MAP4_4160 | hypothetical protein | 458 | Rv0541c | Probable conserved integral membr | 77.29 | 449 | Mb0555c | hypothetical protein | 77.51 | 449 | MAV_4603 | integral membrane protein | 97.7 | 450 | BCG_0585c | integral membrane protein | 77.51 | 449 | MAP4037c | hypothetical protein | 458 | 100 |
| MAP4_4161 | O-succinylbenzoic acid--CoA ligase MenE | 363 | Rv0542c | Possible O-succinylbenzoic acid--Co | 77.6 | 362 | Mb0556c | O-succinylbenzoic acid--CoA l | 77.6 | 362 | MAV_4602 | O-succinylbenzoic acid--CoA ligase | 98.62 | 363 | BCG_0586c | O-succinylbenzoic acid--CoA lig | 77.6 | 362 | MAP4038c | O-succinylbenzoic acid--CoA ligase | 363 | 100 |
| MAP4_4162 | hypothetical protein | 100 | Rv0543c | hypothetical protein | 76.09 | 100 | Mb0557c | hypothetical protein | 76.09 | 100 | MAV_4601 | hypothetical protein | 98.77 | 81 | BCG_0587c | hypothetical protein | 76.09 | 100 | MAP4039c | hypothetical protein | 100 | 100 |
| MAP4_4163 | transmembrane protein | 102 | Rv0544c | Possible conserved transmembrane | 59.6 | 92 | Mb0558c | transmembrane protein | 59.6 | 92 | MAV_4600 | hypothetical protein | 98.04 | 102 | BCG_0588c | hypothetical protein | 59.6 | 92 | MAP4040c | hypothetical protein | 102 | 100 |
| MAP4_4164 | low affinity inorganic phosphate transporter membran | 413 | Rv0545c | Probable low-affinity inorganic phos | 83.64 | 417 | Mb0559c | inorganic phosphate transpor | 83.91 | 417 | MAV_4599 | phosphate transporter | 100 | 413 | BCG_0589c | low-affinity inorganic phosphat | 83.91 | 417 | MAP4041c | hypothetical protein | 422 | 99.76 |
| MAP4_4165 | hypothetical protein | 135 | Rv0546c | hypothetical protein | 83.59 | 128 | Mb0560c | hypothetical protein | 83.59 | 128 | MAV_4598 | hypothetical protein | 100 | 135 | BCG_0590c | hypothetical protein | 83.59 | 128 | MAP4042c | hypothetical protein | 135 | 100 |
| MAP4_4166 | oxidoreductase | 298 | Rv0547c | Possible oxidoreductase | 75.43 | 294 | Mb0561c | short chain dehydrogenase | 75.43 | 294 | MAV_4597 | short chain dehydrogenase | 98.99 | 298 | BCG_0591c | short chain dehydrogenase | 75.43 | 294 | MAP4043c | short chain dehydrogenase | 298 | 100 |
| MAP4_4167 | naphthoate synthase MenB | 300 | Rv0548c | Naphthoate synthase MenB (dihydro | 92.67 | 314 | Mb0562c | naphthoate synthase | 92.67 | 314 | MAV_4596 | naphthoate synthase | 99.3 | 287 | BCG_0592c | naphthoate synthase | 92.67 | 314 | MAP4044c | naphthoate synthase | 300 | 100 |
| MAP4_4168 | hypothetical protein | 151 | Rv1598c | hypothetical protein | 37.74 | 136 | Mb1624c | hypothetical protein | 37.74 | 136 | MAV_4595 | cell entry (mce) related family prot | 100 | 151 | BCG_1636c | hypothetical protein | 37.74 | 136 | MAP0168c | hypothetical protein | 146 | 62.76 |
| MAP4_4169 | putative oxidoreductase, aldo-keto reductase family pr | 306 | Rv2298 | hypothetical protein | 26.89 | 323 | Mb2320 | hypothetical protein | 26.89 | 323 | MAV_4594 | oxidoreductase YdbC | 98.69 | 306 | BCG_2314 | hypothetical protein | 26.89 | 323 | MAP4046c | hypothetical protein | 306 | 100 |
| MAP4_4170 | Transcriptional regulator, TetR family | 179 | Rv0067c | Possible transcriptional regulatory p | 34.72 | 189 | Mb0068c | TetR family transcriptional re | 34.72 | 189 | MAV_4593 | TetR family transcriptional regulato | 98.88 | 179 | BCG_0098c | TetR family transcriptional regu | 34.72 | 189 | MAP4047 | hypothetical protein | 209 | 99.44 |
| MAP4_4171 | fatty-acid-CoA ligase FadD8 | 533 | Rv0551c | Probable fatty-acid-CoA ligase FadD | 83.4 | 571 | Mb0566c | acyl-CoA synthetase | 83.4 | 571 | MAV_4592 | acyl-CoA synthetase | 99.81 | 533 | BCG_0596c | acyl-CoA synthetase | 83.4 | 571 | MAP4048c | acyl-CoA synthetase | 533 | 100 |
| MAP4_4172 | amidohydrolase family protein | 536 | Rv0552 | hypothetical protein | 79.14 | 534 | Mb0567 | hypothetical protein | 79.14 | 534 | MAV_4591 | amidohydrolase | 99.07 | 536 | BCG_0597 | hypothetical protein | 78.95 | 534 | MAP4049 | hypothetical protein | 574 | 99.81 |
| MAP4_4173 | muconate cycloisomerase MenC | 326 | Rv0553 | Probable muconate cycloisomerase | 81.29 | 326 | Mb0568 | O-succinylbenzoate synthase | 81.29 | 326 | MAV_4590 | O-succinylbenzoate synthase | 99.08 | 326 | BCG_0598 | O-succinylbenzoate synthase | 81.29 | 326 | MAP4050 | O-succinylbenzoate synthase | 326 | 100 |
| MAP4_4174 | non-heme peroxidase BpoC | 261 | Rv0554 | Possible peroxidase BpoC (non-haen | 81.32 | 262 | Mb0569 | peroxidase BpoC | 81.32 | 262 | MAV_4589 | alpha/beta hydrolase | 99.23 | 261 | BCG_0599 | peroxidase bpoC | 81.32 | 262 | MAP4051 | BpoC_2 | 261 | 100 |
| MAP4_4175 | bifunctional menaquinone biosynthesis protein MenD | 545 | Rv0555 | Probable bifunctional menaquinone | 88.45 | 554 | Mb0570 | 2-succinyl-5-enolpyruvyl-6-hy | 88.45 | 554 | MAV_4588 | 2-succinyl-5-enolpyruvyl-6-hydroxy | 100 | 545 | BCG_0600 | 2-succinyl-5-enolpyruvyl-6-hyd | 88.45 | 554 | MAP4052 | 2-succinyl-5-enolpyruvyl-6-hydroxy-3- c | 545 | 100 |
| MAP4_4176 | hypothetical protein | 174 | Rv0556 | Probable conserved transmembrane | 81.44 | 171 | Mb0571 | transmembrane protein | 82.04 | 171 | MAV_4587 | hypothetical protein | 98.8 | 167 | BCG_0601 | hypothetical protein | 82.04 | 171 | MAP4053 | hypothetical protein | 174 | 100 |
| MAP4_4177 | mannosyltransferase PimB | 384 | Rv0557 | Mannosyltransferase MgtA | 86.34 | 378 | Mb0572 | mannosyltransferase | 86.34 | 378 | MAV_4586 | glycosyl transferase | 99.74 | 384 | BCG_0602 | mannosyltransferase | 86.34 | 378 | MAP4054 | hypothetical protein | 384 | 100 |
| MAP4_4178 | ubiquinonemenaquinone biosynthesismethyl transfera | 261 | Rv0558 | Probable ubiquinone/menaquinone | 89.04 | 234 | Mb0573 | ubiquinone/menaquinone bio | 89.04 | 234 | MAV_4584 | ubiquinone/menaquinone biosynth | 99.6 | 247 | BCG_0603 | ubiquinone/menaquinone bios | 89.04 | 234 | MAP4055 | ubiquinone/menaquinone biosynthesis | 230 | 99.57 |
| MAP4_4179 | putative conserved secreted protein | 130 | Rv0559c | Possible conserved secreted protein | 54.69 | 112 | Mb0574c | hypothetical protein | 54.69 | 112 | MAV_4583 | hypothetical protein | 100 | 134 | BCG_0604c | hypothetical protein | 54.69 | 112 | MAP4056c | hypothetical protein | 130 | 100 |
| MAP4_4180 | putative oxidoreductase | 412 | Rv0561c | Possible oxidoreductase | 80.84 | 408 | Mb0576c | oxidoreductase | 80.84 | 408 | MAV_4582 | FAD dependent oxidoreductase, pu | 98.54 | 414 | BCG_0606c | oxidoreductase | 80.84 | 408 | MAP4057c | hypothetical protein | 412 | 100 |
| MAP4_4181 | polyprenyl-diphosphate synthase GrcC1 | 335 | Rv0562 | Probable polyprenyl-diphosphate sy | 78.81 | 335 | Mb0577 | polyprenyl synthetase | 78.81 | 335 | MAV_4581 | polyprenyl synthetase | 98.77 | 325 | BCG_0607 | polyprenyl-diphosphate syntha | 78.81 | 335 | MAP4058 | GrcC1 | 335 | 100 |
| MAP4_4182 | protease transmembrane heat shock protein HtpX | 287 | Rv0563 | Probable protease transmembrane | 91.23 | 286 | Mb0578 | heat shock protein HtpX | 91.23 | 286 | MAV_4580 | heat shock protein HtpX | 100 | 287 | BCG_0608 | heat shock protein HtpX | 91.23 | 286 | MAP4059 | heat shock protein HtpX | 287 | 100 |
| MAP4_4183 | putative transcriptional regulator | 86 | Rv2515c | hypothetical protein | 38 | 415 | Mb2544c | hypothetical protein | 38 | 415 | MAV_4579 | transcriptional regulator | 100 | 86 | BCG_2536c | hypothetical protein | 38 | 415 | MAP1477c | hypothetical protein | 224 | 40 |
| MAP4_4184 | putative transmembrane sulfate family protein | 511 | Rv3273 | Probable transmembrane carbonic a | 59.55 | 764 | Mb3301 | transmembrane carbonic anh | 59.55 | 764 | MAV_4578 | carbonate dehydratase | 100 | 511 | BCG_3302 | transmembrane carbonic anhy | 59.55 | 764 | MAP4060c | hypothetical protein | 511 | 100 |
| MAP4_4185 | glycerol-3-phosphate dehydrogenase GpdA1 | 332 | Rv0564c | Probable glycerol-3-phosphate dehy | 90.32 | 341 | Mb0579c | NAD(P)H-dependent glycerol- | 90.32 | 341 | MAV_4577 | NAD(P)H-dependent glycerol-3-pho | 97.07 | 341 | BCG_0609c | NAD(P)H-dependent glycerol-3 | 90.32 | 341 | MAP4061c | NAD(P)H-dependent glycerol-3-phosph | 332 | 100 |
| MAP4_4186 | monooxygenase, flavin-binding family | 506 | Rv0565c | Probable monooxygenase | 79.32 | 486 | Mb0580c | monooxygenase | 79.32 | 486 | MAV_4576 | monooxygenase, flavin-binding fam | 100 | 506 | BCG_0610c | monooxygenase | 79.32 | 486 | MAP4062c | hypothetical protein | 506 | 100 |
| MAP4_4187 | putative nucleotide-binding protein | 163 | Rv0566c | hypothetical protein | 92.02 | 163 | Mb0581c | nucleotide-binding protein | 92.02 | 163 | MAV_4575 | nucleotide-binding protein | 98.77 | 163 | BCG_0611c | nucleotide-binding protein | 92.02 | 163 | MAP4063c | nucleotide-binding protein | 163 | 100 |
| MAP4_4188 | putative methyltransferase | 313 | Rv3787c | hypothetical protein | 59.86 | 308 | Mb3816c | hypothetical protein | 59.86 | 308 | MAV_4573 | methyltransferase | 97.44 | 313 | BCG_3849c | hypothetical protein | 59.86 | 308 | MAP4064c | hypothetical protein | 313 | 100 |
| MAP4_4189 | putative divalent cation-transport membrane protein, | 453 | Rv0924c | Divalent cation-transport integral m | 26.52 | 428 | Mb0948c | manganese transport protein | 26.85 | 684 | MAV_4571 | metal ion transporter, NRAMP fam | 99.77 | 432 | BCG_0976c | manganese transport protein N | 26.22 | 428 | MAP4065 | hypothetical protein | 453 | 100 |
| MAP4_4190 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_4191 | hypothetical protein | 438 | Rv1078 | Probable proline-rich antigen homol | 28.42 | 240 | Mb1107 | hypothetical protein | 28.42 | 240 | MAV_4570 | hypothetical protein | 96.96 | 409 | BCG_1136 | hypothetical protein | 28.42 | 240 | MAP4067c | hypothetical protein | 438 | 100 |
| MAP4_4192 | cytochrome P450 | 409 | Rv1880c | Probable cytochrome P450 140 Cyp | 35 | 438 | Mb1912c | cytochrome p450 140 CYP14 | 35 | 438 | MAV_4569 | cytochrome P450 superfamily prot | 98.78 | 409 | BCG_1917c | cytochrome p450 140 CYP140 | 35 | 438 | MAP4068c | hypothetical protein | 409 | 100 |
| MAP4_4193 | hypothetical protein | 292 | Rv1832 | Probable glycine dehydrogenase Gc | 32.93 | 941 | Mb1863 | glycine dehydrogenase | 34.15 | 941 | MAV_4568 | hypothetical protein | 99.3 | 284 | BCG_1867 | glycine dehydrogenase | 34.15 | 941 | MAP4069c | hypothetical protein | 292 | 100 |
| MAP4_4194 | putative hydrolase, alphabeta hydrolase fold protein | 289 | Rv2715 | Possible hydrolase | 44.37 | 341 | Mb2734 | hydrolase | 44.37 | 341 | MAV_4567 | dihydrolipoyllysine-residue acetyltr | 98.62 | 289 | BCG_2728 | hydrolase | 44.37 | 341 | MAP2832 | hypothetical protein | 343 | 44.91 |
| MAP4_4195 | hypothetical protein | 697 | Rv3671c | Membrane-associated serine protea | 29.17 | 397 | Mb3695c | membrane-associated serine | 29.17 | 397 | MAV_4566 | hypothetical protein | 94.91 | 727 | BCG_3729c | membrane-associated serine p | 29.17 | 397 | MAP4070c | hypothetical protein | 697 | 100 |
| MAP4_4196 | galactose-1-phosphate uridylyltransferase GalT | 365 | Rv0618 | Probable galactose-1-phosphate uri | 76.32 | 231 | Mb0635 | galactose-1-phosphate uridyl | 77.32 | 394 | MAV_4565 | galactose-1-phosphate uridylyltran | 98.9 | 369 | BCG_0665 | galactose-1-phosphate uridylyl | 77.6 | 394 | MAP4071 | hypothetical protein | 365 | 100 |
| MAP4_4197 | galactokinase GalK | 363 | Rv0620 | Probable galactokinase GalK (galact | 70.52 | 363 | Mb0636 | galactokinase | 70.44 | 363 | MAV_4564 | galactokinase | 97.8 | 363 | BCG_0666 | galactokinase | 70.44 | 363 | MAP4072 | galactokinase | 363 | 100 |
| MAP4_4199 | putative transcription antitermination regulatory prote | 230 | Rv2820c | Hypothetical protein | 40 | 302 | Mb2844c | hypothetical protein | 40 | 302 | MAV_4562 | ANTAR domain-containing protein | 100 | 230 | BCG_2839c | hypothetical protein | 40 | 302 | MAP4074 | hypothetical protein | 207 | 99.52 |
| MAP4_4200 | putative lipoprotein LpqN | 225 | Rv0583c | Probable conserved lipoprotein Lpq | 60.79 | 228 | Mb0598c | lipoprotein LpqN | 60.79 | 228 | MAV_4561 | LpqN protein | 95.11 | 219 | BCG_0628c | lipoprotein lpqN | 60.79 | 228 | MAP4075c | hypothetical protein | 225 | 100 |
| MAP4_4201 | putative exported protein, glycosylhydrolase family pro | 878 | Rv0584 | Possible conserved exported protein | 72.35 | 877 | Mb0599 | hypothetical protein | 72.23 | 877 | MAV_4560 | alpha-1,2-mannosidase | 98.52 | 878 | BCG_0629 | hypothetical protein | 72.23 | 877 | MAP4076 | hypothetical protein | 878 | 100 |
| MAP4_4202 | hypothetical protein | 791 | Rv0585c | Probable conserved integral membr | 78.49 | 795 | Mb0600c | hypothetical protein | 78.36 | 795 | MAV_4559 | hypothetical protein | 99.24 | 791 | BCG_0630c | integral membrane protein | 78.36 | 795 | MAP4077c | hypothetical protein | 791 | 99.87 |
| MAP4_4203 | putative methyltransferase family protein | 320 | Rv3767c | Possible S-adenosylmethionine-depe | 61.54 | 314 | Mb3793c | hypothetical protein | 61.54 | 314 | MAV_4558 | methyltransferase, putative, family | 98.75 | 320 | BCG_3826c | hypothetical protein | 61.54 | 314 | MAP4078 | hypothetical protein | 320 | 100 |
| MAP4_4205 | hypothetical protein | 87 | Rv1960c | Possible antitoxin ParD1 | 83.13 | 83 | Mb1995c | hypothetical protein | 83.13 | 83 | MAV_4555 | addiction module antidote protein, | 97.7 | 122 | BCG_1999c | hypothetical protein | 83.13 | 83 | MAP4080c | hypothetical protein | 87 | 100 |
| MAP4_4206 | Transcriptional regulator, GntR family | 236 | Rv0586 | Probable transcriptional regulatory | 67.81 | 240 | Mb0601 | GntR family transcriptional re | 67.81 | 240 | MAV_1821 | GntR family transcriptional regulato | 29.11 | 246 | BCG_0631 | GntR family transcriptional reg | 67.81 | 240 | MAP4081 | hypothetical protein | 236 | 100 |
| MAP4_4207 | putative membrane protein YrbE2A | 265 | Rv0587 | Conserved hypothetical integral mer | 90.57 | 265 | Mb0602 | hypothetical protein | 90.57 | 265 | MAV_4553 | hypothetical protein | 99.62 | 260 | BCG_0632 | integral membrane protein Yrb | 90.57 | 265 | MAP4082 | hypothetical protein | 265 | 100 |
| MAP4_4208 | putative membrane protein YrbE2B | 292 | Rv0588 | Conserved hypothetical integral mer | 92.36 | 295 | Mb0603 | hypothetical protein | 92.36 | 295 | MAV_4552 | hypothetical protein | 99.66 | 292 | BCG_0633 | integral membrane protein Yrb | 92.36 | 295 | MAP4083 | hypothetical protein | 292 | 100 |
| MAP4_4209 | MCE-family protein Mce2A | 404 | Rv0589 | Mce-family protein Mce2A | 82.67 | 404 | Mb0604 | MCE-family protein MCE2A | 82.43 | 404 | MAV_4551 | virulence factor Mce | 99.5 | 404 | BCG_0634 | mce-family protein mce2A | 82.43 | 404 | MAP4084 | Mce2 | 380 | 98.65 |
| MAP4_4210 | MCE-family protein Mce2B | 343 | Rv0170 | Mce-family protein Mce1B | 63.29 | 346 | Mb0605 | MCE-family protein MCE2B | 80.17 | 343 | MAV_4550 | virulence factor Mce | 99.42 | 343 | BCG_0635 | mce-family protein mce2B | 80.17 | 343 | MAP4085 | hypothetical protein | 343 | 100 |
| MAP4_4211 | mce family protein Mce2C | 480 | Rv0591 | Mce-family protein Mce2C | 76.4 | 481 | Mb0606 | MCE-family protein MCE2C | 76.6 | 481 | MAV_4549 | mce-family protein mce2c | 98.96 | 480 | BCG_0636 | mce-family protein mce2C | 76.6 | 481 | MAP4086 | hypothetical protein | 484 | 100 |
| MAP4_4212 | mce family protein Mce2D | 499 | Rv0592 | Mce-family protein Mce2D | 82.78 | 508 | Mb0607 | hypothetical protein | 82.69 | 478 | MAV_4548 | virulence factor Mce | 99.6 | 499 | BCG_0637 | mce-family protein mce2Da | 83.01 | 516 | MAP4087 | hypothetical protein | 499 | 99.8 |
| MAP4_4213 | MCE-family lipoprotein LprL | 379 | Rv0593 | Possible Mce-family lipoprotein LprL | 77.25 | 402 | Mb0179 | MCE-family lipoprotein LprK | 64.8 | 390 | MAV_4547 | virulence factor Mce | 98.68 | 392 | BCG_0639 | mce family lipoprotein LprL | 77.25 | 402 | MAP4088 | hypothetical protein | 379 | 100 |
| MAP4_4214 | MCE-family lipoprotein Mce2F | 512 | Rv0594 | Mce-family protein Mce2F | 80.27 | 516 | Mb0610 | MCE-family protein MCE2F | 80.27 | 516 | MAV_4546 | mce-family protein mce2f | 99.02 | 508 | BCG_0640 | mce-family protein mce2F | 80.27 | 516 | MAP4089 | hypothetical protein | 512 | 100 |
| MAP4_4215 | hypothetical protein | 233 | Rv0625c | Probable conserved transmembrane | 78.48 | 246 | Mb0641c | transmembrane protein | 78.48 | 246 | MAV_4545 | hypothetical protein | 98.28 | 233 | BCG_0671c | hypothetical protein | 78.48 | 246 | MAP4090c | hypothetical protein | 233 | 100 |

# Table S1 continued

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_4216 | exodeoxyribonuclease V alpha chain RecD | 574 | Rv0629c | Probable exonuclease V (alpha chair | 71.76 | 575 | Mb0645c | exonuclease V subunit alpha | 71.58 | 575 | MAV_4544 | exodeoxyribonuclease V, alpha sub | 99.12 | 570 | BCG_0675c | exonuclease V (alpha chain) re | 71.58 | 575 | MAP4091c | hypothetical protein | 574 | 100 |
| MAP4_4219 | exonuclease V gamma chain RecC | 1096 | Rv0631c | Probable exonuclease V (gamma cha | 70.67 | 1097 | Mb0648c | exonuclease V subunit gamm | 70.49 | 1097 | MAV_4542 | exodeoxyribonuclease V, gamma su | 98.36 | 1096 | BCG_0678c | exonuclease V (gamma chain) r | 70.58 | 1097 | MAP4094c | RecC | 1096 | 100 |
| MAP4_4220 | methoxy mycolic acid synthase MmaA2 | 288 | Rv0644c | Methoxy mycolic acid synthase 2 Mr | 74.65 | 287 | Mb0663c | methoxy mycolic acid synthas | 74.31 | 287 | MAV_4541 | cyclopropane-fatty-acyl-phospholip | 100 | 288 | BCG_0693c | methoxy mycolic acid synthase | 74.31 | 287 | MAP4095c | hypothetical protein | 288 | 100 |
| MAP4_4221 | putative nitroreductase family protein | 171 | Rv0306 | Putative oxidoreductase | 24.62 | 223 | Mb0314 | oxidoreductase | 24.62 | 223 | MAV_4540 | nitroreductase | 98.83 | 171 | BCG_0346 | oxidoreductase | 24.62 | 223 | MAP4096 | hypothetical protein | 171 | 100 |
| MAP4_4222 | putative methyltransferase | 257 | Rv2952 | Possible methyltransferase (methyla | 30.52 | 270 | Mb2976 | methyltransferase | 30.52 | 270 | MAV_4539 | methyltransferase small domain-co | 98.39 | 249 | BCG_2973 | methyltransferase | 30.52 | 270 | MAP4097 | hypothetical protein | 257 | 100 |
| MAP4_4223 | putative cyanate hydratase | 151 | Rv3627c | hypothetical protein | 34.29 | 461 | Mb3651c | hypothetical protein | 34.29 | 461 | MAV_4538 | cyanate hydratase | 100 | 155 | BCG_3685c | hypothetical protein | 34.29 | 461 | MAP4098 | cyanate hydratase | 151 | 100 |
| MAP4_4224 | putative phospholipase, patatin family protein | 339 | Rv2037c | Conserved transmembrane protein | 39.94 | 324 | Mb2063c | transmembrane protein | 40.25 | 324 | MAV_4537 | phospholipase, patatin family prote | 99.12 | 340 | BCG_2056c | hypothetical protein | 40.25 | 324 | MAP4099 | hypothetical protein | 339 | 100 |
| MAP4_4225 | hypothetical protein | 159 | Rv2493 | Possible antitoxin VapB38 | 45 | 73 | Mb2521 | hypothetical protein | 45 | 73 | MAV_4536 | hypothetical protein | 98.11 | 159 | BCG_2513 | hypothetical protein | 45 | 73 | MAP4100c | hypothetical protein | 159 | 100 |
| MAP4_4226 | Molybdopterin oxidoreductase | 788 | Rv0197 | Possible oxidoreductase | 25.27 | 762 | Mb0203 | oxidoreductase | 25.27 | 748 | MAV_4535 | nitrate reductase NarB | 97.84 | 788 | BCG_0234 | oxidoreductase | 25.27 | 748 | MAP4101c | hypothetical protein | 608 | 99.84 |
| MAP4_4227 | enoyl-CoA hydratase EchA3 | 231 | Rv0632c | Probable enoyl-CoA hydratase EchA | 86.15 | 231 | Mb0649c | enoyl-CoA hydratase | 86.15 | 231 | MAV_4534 | enoyl-CoA hydratase | 99.13 | 231 | BCG_0679c | enoyl-CoA hydratase | 85.71 | 231 | MAP4102c | EchA3 | 430 | 100 |
| MAP4_4228 | hypothetical protein | 280 | Rv0633c | Possible exported protein | 76.89 | 279 | Mb0650c | hypothetical protein | 75.76 | 276 | MAV_4533 | hypothetical protein | 100 | 277 | BCG_0680c | hypothetical protein | 75.76 | 276 | MAP4103c | hypothetical protein | 280 | 100 |
| MAP4_4229 | glyoxalase II | 237 | Rv0634c | Possible glyoxalase II (hydroxyacylgl | 88.61 | 237 | Mb0651c | glyoxalase II | 88.61 | 237 | MAV_4532 | metallo-beta-lactamase | 99.16 | 237 | BCG_0681c | glyoxalase II | 88.61 | 237 | MAP4104c | hypothetical protein | 237 | 100 |
| MAP4_4230 | hypothetical protein | 76 | Rv0634A | hypothetical protein | 56.58 | 83 | Mb0652 | hypothetical protein | 56.58 | 83 | MAV_4531 | hypothetical protein | 100 | 68 | BCG_0682 | hypothetical protein | 56.58 | 83 | MAP4105 | hypothetical protein | 76 | 100 |
| MAP4_4231 | 50S ribosomal protein L33 | 55 | Rv0634B | 50S ribosomal protein L33 RpmG2 | 98.18 | 55 | Mb0653 | 50S ribosomal protein L33 | 98.18 | 55 | MAV_4528 | ribosomal protein L33 | 97.67 | 43 | BCG_0683 | 50S ribosomal protein L33 | 98.18 | 55 | MAP4106 | 50S ribosomal protein L33 | 55 | 100 |
| MAP4_4232 | (3R)-hydroxyacyl-ACP dehydratase subunit HadA | 159 | Rv0635 | (3R)-hydroxyacyl-ACP dehydratase s | 82.39 | 158 | Mb0654 | (3R)-hydroxyacyl-ACP dehydr | 82.39 | 158 | MAV_4527 | (3R)-hydroxyacyl-ACP dehydratase | 100 | 159 | BCG_0684 | (3R)-hydroxyacyl-ACP dehydrat | 82.39 | 158 | MAP4107 | (3R)-hydroxyacyl-ACP dehydratase subu | 159 | 100 |
| MAP4_4233 | (3R)-hydroxyacyl-ACP dehydratase subunit HadB | 142 | Rv0636 | (3R)-hydroxyacyl-ACP dehydratase s | 93.66 | 142 | Mb0655 | (3R)-hydroxyacyl-ACP dehydr | 92.96 | 142 | MAV_4526 | (3R)-hydroxyacyl-ACP dehydratase | 99.25 | 134 | BCG_0685 | (3R)-hydroxyacyl-ACP dehydrat | 92.96 | 142 | MAP4108 | (3R)-hydroxyacyl-ACP dehydratase subu | 142 | 100 |
| MAP4_4234 | (3R)-hydroxyacyl-ACP dehydratase subunit HadC | 167 | Rv0637 | (3R)-hydroxyacyl-ACP dehydratase s | 79.64 | 166 | Mb0656 | (3R)-hydroxyacyl-ACP dehydr | 79.64 | 166 | MAV_4525 | (3R)-hydroxyacyl-ACP dehydratase | 100 | 167 | BCG_0686 | (3R)-hydroxyacyl-ACP dehydrat | 79.64 | 166 | MAP4109 | (3R)-hydroxyacyl-ACP dehydratase subu | 167 | 100 |
| MAP4_4235 | preprotein translocase subunit SecE | 147 | Rv0638 | Probable preprotein translocase Sec | 63.58 | 161 | Mb0657 | preprotein translocase subun | 63.58 | 161 | MAV_4523 | preprotein translocase subunit Sec | 99.32 | 147 | BCG_0687 | preprotein translocase subunit | 63.58 | 161 | MAP4110 | preprotein translocase subunit SecE | 147 | 100 |
| MAP4_4236 | Transcription antitermination protein NusG | 256 | Rv0639 | Probable transcription antiterminati | 85.94 | 238 | Mb0658 | transcription antitermination | 85.94 | 238 | MAV_4522 | transcription antitermination prote | 100 | 256 | BCG_0688 | transcription antitermination p | 85.94 | 238 | MAP4111 | transcription antitermination protein N | 256 | 100 |
| MAP4_4237 | 50S ribosomal protein L11 | 142 | Rv0640 | 50S ribosomal protein L11 RplK | 92.96 | 142 | Mb0659 | 50S ribosomal protein L11 | 92.96 | 142 | MAV_4521 | 50S ribosomal protein L11 | 100 | 142 | BCG_0689 | 50S ribosomal protein L11 | 92.96 | 142 | MAP4112 | 50S ribosomal protein L11 | 142 | 100 |
| MAP4_4238 | 50S ribosomal protein L1 | 235 | Rv0641 | 50S ribosomal protein L1 RplA | 93.99 | 235 | Mb0660 | 50S ribosomal protein L1 | 93.56 | 235 | MAV_4520 | 50S ribosomal protein L1 | 100 | 235 | BCG_0690 | 50S ribosomal protein L1 | 93.56 | 235 | MAP4113 | 50S ribosomal protein L1 | 235 | 100 |
| MAP4_4239 | RNA polymerase sigma-70 factor, ECF subfamily | 420 | Rv1189 | Possible alternative RNA polymerase | 28.57 | 290 | Mb1221 | RNA polymerase sigma factor | 28.57 | 290 | MAV_4519 | RNA polymerase ECF-subfamily pro | 98.33 | 420 | BCG_1251 | RNA polymerase sigma factor S | 28.57 | 401 | MAP4114c | hypothetical protein | 420 | 100 |
| MAP4_4240 | hypothetical protein | 232 | Rv1216c | Probable conserved integral membra | 38.46 | 224 | Mb1248c | hypothetical protein | 38.46 | 224 | MAV_4518 | DGPF domain-containing protein | 99.14 | 232 | BCG_1276c | integral membrane protein | 38.46 | 224 | MAP4115c | hypothetical protein | 226 | 99.56 |
| MAP4_4241 | methoxy mycolic acid synthase MmaA4 | 298 | Rv0642c | Methoxy mycolic acid synthase 4 Mr | 89.26 | 301 | Mb0661c | methoxy mycolic acid synthas | 88.93 | 301 | MAV_4517 | cyclopropane-fatty-acyl-phospholip | 99.66 | 298 | BCG_0691c | methoxy mycolic acid synthase | 88.93 | 301 | MAP4116c | hypothetical protein | 298 | 100 |
| MAP4_4242 | methoxy mycolic acid synthase MmaA1 | 286 | Rv0645c | Methoxy mycolic acid synthase 1 Mr | 73.08 | 286 | Mb0664c | methoxy mycolic acid synthas | 73.08 | 286 | MAV_4516 | methoxy mycolic acid synthase 1 | 99.65 | 286 | BCG_0694c | methoxy mycolic acid synthase | 73.08 | 286 | MAP4117c | hypothetical protein | 286 | 100 |
| MAP4_4243 | lipaseesterase LipG | 302 | Rv0646c | Probable lipase/esterase LipG | 78 | 301 | Mb0665c | lipase/esterase | 78 | 301 | MAV_4515 | alpha/beta hydrolase | 99.34 | 302 | BCG_0695c | lipase/esterase lipG | 78 | 301 | MAP4118c | hypothetical protein | 302 | 100 |
| MAP4_4244 | conserved hypothetical protein, ABC1 family protein | 452 | Rv0647c | hypothetical protein | 91.05 | 488 | Mb0666c | hypothetical protein | 91.05 | 488 | MAV_4514 | ABC transporter | 99.77 | 444 | BCG_0696c | hypothetical protein | 91.05 | 488 | MAP4119c | hypothetical protein | 452 | 100 |
| MAP4_4245 | hypothetical protein | 201 | Rv3910 | Probable conserved transmembrane | 35.19 | 1184 | Mb3940 | transmembrane protein | 35.19 | 1184 | MAV_4513 | hypothetical protein | 98.45 | 194 | BCG_3967 | hypothetical protein | 35.19 | 1184 | MAP4120c | hypothetical protein | 201 | 100 |
| MAP4_4246 | alpha-mannosidase | 1394 | Rv0648 | Alpha-mannosidase | 74.51 | 1215 | Mb0667 | alpha-mannosidase | 74.35 | 1215 | MAV_4512 | alpha-mannosidase | 98.71 | 1394 | BCG_0697 | alpha-mannosidase | 74.48 | 1398 | MAP4121 | hypothetical protein | 1407 | 100 |
| MAP4_4247 | malonyl CoA-ACP transacylase FabD2 | 205 | Rv0649 | Possible malonyl CoA-acyl carrier pr | 77.96 | 224 | Mb0668 | malonyl CoA-ACP transacylas | 77.96 | 224 | MAV_4511 | FabD2 protein | 98.54 | 205 | BCG_0698 | malonyl CoA-ACP transacylase | 77.96 | 224 | MAP4122 | FabD2 | 205 | 100 |
| MAP4_4248 | sugar kinase | 306 | Rv0650 | Possible sugar kinase | 73.18 | 302 | Mb0669 | sugar kinase | 73.18 | 302 | MAV_4510 | sugar kinase | 99.35 | 306 | BCG_0699 | sugar kinase | 73.18 | 302 | MAP4123 | hypothetical protein | 306 | 100 |
| MAP4_4249 | hypothetical protein | 150 | Rv1145 | Probable conserved transmembrane | 38.46 | 303 | Mb1177 | transmembrane transport pr | 38.46 | 781 | MAV_4509 | hypothetical protein | 99.33 | 150 | BCG_1207 | transmembrane transport prot | 38.46 | 781 | MAP4124 | hypothetical protein | 150 | 100 |
| MAP4_4250 | 50S ribosomal protein L10 RplJ | 196 | Rv0651 | 50S ribosomal protein L10 RplJ | 92.53 | 178 | Mb0670 | 50S ribosomal protein L10 | 92.53 | 178 | MAV_4508 | 50S ribosomal protein L10 | 98.47 | 196 | BCG_0700 | 50S ribosomal protein L10 | 92.53 | 178 | MAP4125 | 50S ribosomal protein L10 | 196 | 100 |
| MAP4_4251 | 50S ribosomal protein L7L12 RplL | 130 | Rv0652 | 50S ribosomal protein L7/L12 RplL (S | 93.08 | 130 | Mb0671 | 50S ribosomal protein L7/L12 | 93.08 | 130 | MAV_4507 | 50S ribosomal protein L7/L12 | 100 | 130 | BCG_0701 | 50S ribosomal protein L7/L12 | 93.08 | 130 | MAP4126 | 50S ribosomal protein L7/L12 | 130 | 100 |
| MAP4_4252 | Transcriptional regulator, TetR family | 251 | Rv0653c | Possible transcriptional regulatory p | 75.46 | 231 | Mb0672c | TetR family transcriptional re | 75.46 | 231 | MAV_4506 | TetR family transcriptional regulato | 98.24 | 227 | BCG_0702c | TetR family transcriptional regu | 75.46 | 231 | MAP4127c | hypothetical protein | 251 | 100 |
| MAP4_4253 | dioxygenase | 483 | Rv0654 | Probable dioxygenase | 75.31 | 501 | Mb0673 | dioxygenase | 75.31 | 501 | MAV_4505 | Sim14 protein | 98.34 | 501 | BCG_0703 | dioxygenase | 75.31 | 501 | MAP4128 | hypothetical protein | 483 | 100 |
| MAP4_4254 | ribonucleotide-transport ATP-binding protein ABC tran | 336 | Rv0655 | Possible ribonucleotide-transport AT | 91.94 | 359 | Mb0674 | ribonucleotide ABC transport | 91.94 | 359 | MAV_4504 | ABC transporter ATP-binding prote | 100 | 336 | BCG_0704 | ribonucleotide-transport ATP-b | 91.94 | 359 | MAP4129 | hypothetical protein | 336 | 100 |
| MAP4_4255 | DNA-directed RNA polymerase beta chain RpoB | 1175 | Rv0667 | DNA-directed RNA polymerase (beta | 93.94 | 1172 | Mb0686 | DNA-directed RNA polymeras | 93.94 | 1172 | MAV_4503 | DNA-directed RNA polymerase sub | 99.91 | 1144 | BCG_0716 | DNA-directed RNA polymerase | 93.94 | 1172 | MAP4130 | DNA-directed RNA polymerase subunit | 1198 | 99.91 |
| MAP4_4256 | DNA-directed RNA polymerase beta chain RpoC | 1316 | Rv0668 | DNA-directed RNA polymerase (beta | 97.49 | 1316 | Mb0687 | DNA-directed RNA polymeras | 97.49 | 1316 | MAV_4502 | DNA-directed RNA polymerase sub | 99.77 | 1316 | BCG_0717 | DNA-directed RNA polymerase | 97.42 | 1316 | MAP4131 | DNA-directed RNA polymerase subunit | 1316 | 100 |
| MAP4_4257 | endonuclease IV End | 251 | Rv0670 | Probable endonuclease IV End (endo | 81.75 | 252 | Mb0689 | endonuclease IV | 81.75 | 252 | MAV_4501 | endonuclease IV | 98.8 | 325 | BCG_0719 | endonuclease IV | 81.75 | 252 | MAP4132 | endonuclease IV | 251 | 100 |
| MAP4_4258 | acyl-CoA dehydrogenase FadE8 | 532 | Rv0672 | Probable acyl-CoA dehydrogenase F | 90.6 | 542 | Mb0691 | acyl-CoA dehydrogenase | 90.6 | 542 | MAV_4500 | acyl-CoA dehydrogenase | 99.62 | 542 | BCG_0721 | acyl-CoA dehydrogenase fadE8 | 90.6 | 542 | MAP4133 | FadE8 | 532 | 100 |
| MAP4_4259 | enoyl-CoA hydratase EchA4 | 312 | Rv0673 | Possible enoyl-CoA hydratase EchA4 | 92.31 | 312 | Mb0692 | enoyl-CoA hydratase | 92.31 | 312 | MAV_4499 | enoyl-CoA hydratase | 99.68 | 312 | BCG_0722 | enoyl-CoA hydratase | 92.31 | 312 | MAP4134 | enoyl-CoA hydratase | 312 | 100 |
| MAP4_4260 | conserved hypothetical protein, PaaX-like protein famil | 239 | Rv0674 | hypothetical protein | 75.43 | 240 | Mb0693 | hypothetical protein | 75.43 | 240 | MAV_4498 | hypothetical protein | 98.74 | 239 | BCG_0723 | hypothetical protein | 75.43 | 240 | MAP4135 | hypothetical protein | 239 | 100 |
| MAP4_4261 | enoyl-CoA hydratase EchA5 | 255 | Rv0675 | Probable enoyl-CoA hydratase EchA | 87.4 | 263 | Mb0694 | enoyl-CoA hydratase | 87.4 | 263 | MAV_4497 | enoyl-CoA hydratase | 100 | 255 | BCG_0724 | enoyl-CoA hydratase | 87.4 | 263 | MAP4136 | enoyl-CoA hydratase | 255 | 100 |
| MAP4_4262 | conserved threonine rich protein | 161 | Rv0679c | Conserved threonine rich protein | 65.31 | 165 | Mb0698c | hypothetical protein | 65.31 | 165 | MAV_4496 | hypothetical protein | 99.31 | 144 | BCG_0728c | hypothetical protein | 65.31 | 165 | MAP4137c | hypothetical protein | 161 | 100 |
| MAP4_4263 | hypothetical protein | 125 | Rv0680c | Probable conserved transmembrane | 66.67 | 124 | Mb0699c | transmembrane protein | 66.67 | 124 | MAV_4495 | hypothetical protein | 100 | 125 | BCG_0729c | hypothetical protein | 66.67 | 124 | MAP4138c | hypothetical protein | 125 | 100 |
| MAP4_4264 | Transcriptional regulator, TetR family | 210 | Rv0681 | Probable transcriptional regulatory | 93.68 | 196 | Mb0700 | TetR family transcriptional re | 93.68 | 196 | MAV_4494 | TetR family transcriptional regulato | 100 | 210 | BCG_0730 | TetR family transcriptional regu | 93.68 | 196 | MAP4139 | hypothetical protein | 210 | 100 |
| MAP4_4265 | 30S ribosomal protein S12 RpsL | 124 | Rv0682 | 30S ribosomal protein S12 RpsL | 99.19 | 124 | Mb0701 | 30S ribosomal protein S12 | 99.19 | 124 | MAV_4492 | 30S ribosomal protein S12 | 100 | 124 | BCG_0731 | 30S ribosomal protein S12 | 99.19 | 124 | MAP4140 | 30S ribosomal protein S12 | 124 | 100 |
| MAP4_4266 | 30S ribosomal protein S7 RpsG | 156 | Rv0683 | 30S ribosomal protein S7 RpsG | 96.79 | 156 | Mb0702 | 30S ribosomal protein S7 | 96.79 | 156 | MAV_4491 | 30S ribosomal protein S7 | 100 | 156 | BCG_0732 | 30S ribosomal protein S7 | 96.79 | 156 | MAP4141 | 30S ribosomal protein S7 | 156 | 100 |
| MAP4_4267 | Translation elongation factor G FusA1 | 701 | Rv0684 | Probable elongation factor G FusA1 | 91.16 | 701 | Mb0703 | elongation factor G | 91.16 | 701 | MAV_4490 | elongation factor G | 100 | 701 | BCG_0733 | elongation factor G | 91.16 | 701 | MAP4142 | elongation factor G | 701 | 100 |
| MAP4_4268 | iron-regulated elongation factor tu Tuf | 396 | Rv0685 | Probable iron-regulated elongation f | 96.97 | 396 | Mb0704 | elongation factor Tu | 96.97 | 396 | MAV_4489 | elongation factor Tu | 100 | 396 | BCG_0734 | elongation factor Tu | 96.97 | 396 | MAP4143 | elongation factor Tu | 396 | 100 |
| MAP4_4269 | PE family protein | 205 | Rv0872c | PE-PGRS family protein PE_PGRS15 | 62.38 | 606 | Mb0896c | PE-PGRS family protein | 62.38 | 608 | MAV_1346 | PE family protein | 45.74 | 278 | BCG_0924c | PE-PGRS family protein | 62.38 | 609 | MAP4144 | hypothetical protein | 205 | 100 |
| MAP4_4270 | hypothetical protein | 282 | Rv0686 | Probable membrane protein | 74.47 | 265 | Mb0705 | hypothetical protein | 74.11 | 265 | MAV_4487 | hypothetical protein | 99.29 | 282 | BCG_0735 | hypothetical protein | 74.11 | 265 | MAP4145 | hypothetical protein | 282 | 100 |
| MAP4_4271 | short-chain type dehydrogenasereductase FabG | 275 | Rv0687 | Probable short-chain type dehydrog | 81.09 | 275 | Mb0706 | 3-ketoacyl-ACP reductase | 81.09 | 275 | MAV_4486 | short chain dehydrogenase | 99.64 | 275 | BCG_0736 | 3-ketoacyl-ACP reductase | 81.09 | 275 | MAP4146 | 3-ketoacyl-ACP reductase | 275 | 100 |
| MAP4_4272 | ferredoxin reductase | 398 | Rv0688 | Putative ferredoxin reductase | 82.26 | 406 | Mb0707 | ferredoxin reductase | 82.26 | 406 | MAV_4485 | ferredoxin reductase | 98.99 | 398 | BCG_0737 | ferredoxin reductase | 82.26 | 406 | MAP4147 | hypothetical protein | 398 | 100 |
| MAP4_4273 | inositol-monophosphatase | 275 | Rv1604 | Probable inositol-monophosphatase | 33.61 | 270 | Mb1630 | inositol-monophosphatase | 33.2 | 270 | MAV_4484 | inositol monophosphatase | 99.64 | 275 | BCG_1642 | inositol-monophosphatase imp | 33.2 | 270 | MAP4148c | hypothetical protein | 275 | 100 |
| MAP4_4274 | oxidoreductase, aldoketo reductase family protein | 286 | Rv2971 | Probable oxidoreductase | 66.91 | 282 | Mb2996 | oxidoreductase | 66.91 | 282 | MAV_4483 | 2,5-diketo-D-gluconic acid reductas | 98.95 | 286 | BCG_2993 | oxidoreductase | 66.91 | 282 | MAP4149 | hypothetical protein | 286 | 100 |
| MAP4_4275 | hypothetical protein | 347 | Rv0690c | hypothetical protein | 68.41 | 349 | Mb0709c | hypothetical protein | 68.41 | 349 | MAV_4482 | hypothetical protein | 99.14 | 347 | BCG_0739c | hypothetical protein | 68.41 | 349 | MAP4150c | hypothetical protein | 347 | 100 |
| MAP4_4276 | Transcriptional regulator, TetR family | 197 | Rv0691c | Probable transcriptional regulatory | 79.29 | 198 | Mb0710c | transcriptional regulator | 79.29 | 198 | MAV_4481 | TetR family transcriptional regulato | 100 | 197 | BCG_0740c | transcriptional regulatory prote | 79.29 | 198 | MAP4151c | hypothetical protein | 210 | 100 |
| MAP4_4277 | hypothetical protein | 52 | Rv0691A | Mycofactocin precursor protein | 79.31 | 62 | Mb1866c | hypothetical protein | 29.03 | 628 | MAV_4480 | hypothetical protein | 100 | 52 | BCG_1870c | hypothetical protein | 29.03 | 628 | | | | |
| MAP4_4278 | hypothetical protein | 109 | Rv0692 | hypothetical protein | 82.24 | 109 | Mb0711 | hypothetical protein | 82.24 | 109 | MAV_4479 | hypothetical protein | 99.03 | 103 | BCG_0741 | hypothetical protein | 82.24 | 109 | MAP4152 | hypothetical protein | 109 | 100 |
| MAP4_4279 | coenzyme PQQ synthesis protein E PqqE | 404 | Rv0693 | Probable coenzyme PQQ synthesis p | 87.78 | 391 | Mb0712 | coenzyme PQQ synthesis prot | 87.78 | 391 | MAV_4478 | radical SAM domain-containing pro | 99.5 | 404 | BCG_0742 | coenzyme PQQ synthesis prote | 87.78 | 391 | MAP4153 | PqqE | 404 | 100 |
| MAP4_4280 | L-lactate dehydrogenase LldD1 | 394 | Rv0694 | Possible L-lactate dehydrogenase (cy | 89 | 396 | Mb0713 | L-lactate dehydrogenase (cyto | 89 | 396 | MAV_4477 | FMN-dependent dehydrogenase | 99.49 | 394 | BCG_0743 | L-lactate dehydrogenase (cytoc | 89 | 396 | MAP4154 | LldD1 | 394 | 100 |
| MAP4_4281 | putative creatinine amidohydrolase | 243 | Rv0695 | hypothetical protein | 75.6 | 251 | Mb0714 | hypothetical protein | 75.6 | 251 | MAV_4476 | creatininase subfamily protein | 98.77 | 243 | BCG_0744 | hypothetical protein | 75.6 | 251 | MAP4155 | hypothetical protein | 243 | 100 |
| MAP4_4282 | membrane sugar transferase | 472 | Rv0696 | Probable membrane sugar transfera | 82.48 | 470 | Mb0715 | membrane sugar transferase | 82.48 | 470 | MAV_4475 | membrane sugar transferase | 99.79 | 472 | BCG_0745 | membrane sugar transferase | 82.48 | 470 | MAP4157 | hypothetical protein | 250 | 99.6 |
| MAP4_4283 | dehydrogenase | 479 | Rv0697 | Probable dehydrogenase | 72.65 | 479 | Mb0716 | dehydrogenase | 72.65 | 479 | MAV_4474 | FAD dependent oxidoreductase, pu | 97.7 | 479 | BCG_0746 | dehydrogenase | 72.65 | 479 | MAP4158 | hypothetical protein | 479 | 100 |
| MAP4_4284 | Transcriptional regulator, TetR family | 181 | Rv1556 | Possible regulatory protein | 45.28 | 202 | Mb1581 | regulatory protein | 45.28 | 202 | MAV_4473 | hypothetical protein | 99.45 | 181 | BCG_1607 | regulatory protein | 45.28 | 202 | MAP4159 | hypothetical protein | 181 | 100 |
| MAP4_4285 | 30S ribosomal protein S10 RpsJ | 101 | Rv0700 | 30S ribosomal protein S10 RpsJ (tran | 99.01 | 101 | Mb0720 | 30S ribosomal protein S10 | 99.01 | 101 | MAV_4472 | 30S ribosomal protein S10 | 100 | 101 | BCG_0750 | 30S ribosomal protein S10 | 99.01 | 101 | MAP4160 | 30S ribosomal protein S10 | 101 | 100 |
| MAP4_4286 | 50S ribosomal protein L3 | 217 | Rv0701 | 50S ribosomal protein L3 RplC | 94.01 | 217 | Mb0721 | 50S ribosomal protein L3 | 94.01 | 217 | MAV_4471 | 50S ribosomal protein L3 | 100 | 217 | BCG_0751 | 50S ribosomal protein L3 | 94.01 | 217 | MAP4161 | 50S ribosomal protein L3 | 217 | 100 |
| MAP4_4287 | 50S ribosomal protein L4 | 217 | Rv0702 | 50S ribosomal protein L4 RplD | 93.02 | 223 | Mb0722 | 50S ribosomal protein L4 | 93.02 | 223 | MAV_4470 | 50S ribosomal protein L4 | 99.54 | 217 | BCG_0752 | 50S ribosomal protein L4 | 93.02 | 223 | MAP4162 | 50S ribosomal protein L4 | 217 | 100 |
| MAP4_4288 | 50S ribosomal protein L23 | 100 | Rv0703 | 50S ribosomal protein L23 RplW | 91 | 100 | Mb0723 | 50S ribosomal protein L23 | 91 | 100 | MAV_4469 | 50S ribosomal protein L23 | 100 | 100 | BCG_0753 | 50S ribosomal protein L23 | 91 | 100 | MAP4163 | 50S ribosomal protein L23 | 100 | 100 |
| MAP4_4289 | 50S ribosomal protein L2 | 280 | Rv0704 | 50S ribosomal protein L2 RplB | 93.93 | 280 | Mb0724 | 50S ribosomal protein L2 | 93.93 | 280 | MAV_4468 | 50S ribosomal protein L2 | 99.64 | 280 | BCG_0754 | 50S ribosomal protein L2 | 93.93 | 280 | MAP4164 | 50S ribosomal protein L2 | 280 | 100 |
| MAP4_4290 | 30S ribosomal protein S19 | 93 | Rv0705 | 30S ribosomal protein S19 RpsS | 95.7 | 93 | Mb0725 | 30S ribosomal protein S19 | 95.7 | 93 | MAV_4467 | 30S ribosomal protein S19 | 100 | 93 | BCG_0755 | 30S ribosomal protein S19 | 95.7 | 93 | MAP4165 | 30S ribosomal protein S19 | 93 | 100 |
| MAP4_4291 | 50S ribosomal protein L22 | 180 | Rv0706 | 50S ribosomal protein L22 RplV | 78.42 | 197 | Mb0726 | 50S ribosomal protein L22 | 78.42 | 197 | MAV_4466 | 50S ribosomal protein L22 | 99.44 | 180 | BCG_0756 | 50S ribosomal protein L22 | 78.42 | 197 | MAP4166 | 50S ribosomal protein L22 | 180 | 100 |
| MAP4_4292 | 30S ribosomal protein S3 | 280 | Rv0707 | 30S ribosomal protein S3 RpsC | 96.85 | 274 | Mb0727 | 30S ribosomal protein S3 | 96.85 | 274 | MAV_4465 | 30S ribosomal protein S3 | 99.29 | 280 | BCG_0757 | 30S ribosomal protein S3 | 96.85 | 274 | MAP4167 | 30S ribosomal protein S3 | 280 | 100 |
| MAP4_4293 | 50S ribosomal protein L16 | 138 | Rv0708 | 50S ribosomal protein L16 RplP | 94.93 | 138 | Mb0728 | 50S ribosomal protein L16 | 94.93 | 138 | MAV_4464 | 50S ribosomal protein L16 | 100 | 138 | BCG_0758 | 50S ribosomal protein L16 | 94.93 | 138 | MAP4168 | 50S ribosomal protein L16 | 138 | 100 |
| MAP4_4294 | 50S ribosomal protein L29 | 77 | Rv0709 | 50S ribosomal protein L29 RpmC | 92.21 | 77 | Mb0729 | 50S ribosomal protein L29 | 92.21 | 77 | MAV_4463 | 50S ribosomal protein L29 | 100 | 77 | BCG_0759 | 50S ribosomal protein L29 | 92.21 | 77 | MAP4169 | 50S ribosomal protein L29 | 77 | 100 |
| MAP4_4295 | 30S ribosomal protein S17 | 117 | Rv0710 | 30S ribosomal protein S17 RpsQ | 89.58 | 136 | Mb0730 | 30S ribosomal protein S17 | 89.58 | 136 | MAV_4462 | 30S ribosomal protein S17 | 100 | 116 | BCG_0760 | 30S ribosomal protein S17 | 89.58 | 136 | MAP4170 | 30S ribosomal protein S17 | 117 | 100 |
| MAP4_4296 | arylsulfatase AtsA | 789 | Rv0711 | Possible arylsulfatase AtsA (aryl-sulf | 87.8 | 787 | Mb0732 | arylsulfatase | 87.58 | 636 | MAV_4461 | arylsulfatase | 99.87 | 789 | BCG_0761 | arylsulfatase atsA | 87.68 | 787 | MAP4171 | AtsA | 789 | 100 |
| MAP4_4297 | periplasmic phosphate-binding lipoprotein PstS3 | 374 | Rv0928 | Periplasmic phosphate-binding lipop | 63.39 | 370 | Mb0951 | periplasmic phosphate-bindir | 63.39 | 370 | MAV_4460 | phosphate ABC transporter phosph | 99.73 | 375 | BCG_0980 | periplasmic phosphate-binding | 63.39 | 370 | MAP4172c | PhoS2_3 | 374 | 100 |
| MAP4_4298 | hypothetical protein | 313 | Rv0713 | Probable conserved transmembrane | 59.74 | 313 | Mb0734 | transmembrane protein | 59.74 | 313 | MAV_4459 | hypothetical protein | 99.04 | 313 | BCG_0763 | hypothetical protein | 59.74 | 313 | MAP4173 | hypothetical protein | 313 | 100 |
| MAP4_4299 | putative sulfatase modifying factor 1 enzyme | 296 | Rv0712 | hypothetical protein | 81.02 | 299 | Mb0733 | hypothetical protein | 81.02 | 299 | MAV_4458 | sulfatase-modifying factor 1 | 99.32 | 296 | BCG_0762 | hypothetical protein | 81.02 | 299 | MAP4174 | hypothetical protein | 296 | 100 |
| MAP4_4300 | putative conserved membrane protein | 306 | Rv0713 | Probable conserved transmembrane | 58.61 | 313 | Mb0734 | transmembrane protein | 58.61 | 313 | MAV_4457 | hypothetical protein | 99.32 | 295 | BCG_0763 | hypothetical protein | 58.61 | 313 | MAP4175 | hypothetical protein | 306 | 100 |
| MAP4_4301 | 13E12 repeat family protein | 500 | Rv0336 | Conserved 13E12 repeat family prot | 68.3 | 503 | Mb0343 | hypothetical protein | 68.3 | 503 | MAV_4456 | hypothetical protein | 98.2 | 500 | BCG_0375 | hypothetical protein | 68.3 | 503 | MAP4176 | hypothetical protein | 500 | 100 |
| MAP4_4302 | 50S ribosomal protein L14 | 122 | Rv0714 | 50S ribosomal protein L14 RplN | 100 | 122 | Mb0735 | 50S ribosomal protein L14 | 100 | 122 | MAV_4455 | 50S ribosomal protein L14 | 100 | 122 | BCG_0764 | 50S ribosomal protein L14 | 100 | 122 | MAP4177 | 50S ribosomal protein L14 | 122 | 100 |
| MAP4_4303 | 50S ribosomal protein L24 | 105 | Rv0715 | 50S ribosomal protein L24 RplX | 91.43 | 105 | Mb0736 | 50S ribosomal protein L24 | 91.43 | 105 | MAV_4454 | 50S ribosomal protein L24 | 100 | 105 | BCG_0765 | 50S ribosomal protein L24 | 91.43 | 105 | MAP4178 | 50S ribosomal protein L24 | 105 | 100 |
| MAP4_4304 | 50S ribosomal protein L5 | 187 | Rv0716 | 50S ribosomal protein L5 RplE | 90.91 | 187 | Mb0737 | 50S ribosomal protein L5 | 90.91 | 187 | MAV_4453 | 50S ribosomal protein L5 | 98.93 | 187 | BCG_0766 | 50S ribosomal protein L5 | 90.91 | 187 | MAP4179 | 50S ribosomal protein L5 | 187 | 100 |
| MAP4_4305 | 30S ribosomal protein S14 | 61 | Rv0717 | 30S ribosomal protein S14 RpsN1 | 91.8 | 61 | Mb0738 | 30S ribosomal protein S14 | 91.8 | 61 | MAV_4452 | 30S ribosomal protein S14 | 100 | 61 | BCG_0767 | 30S ribosomal protein S14 | 91.8 | 61 | MAP4180 | 30S ribosomal protein S14 | 61 | 100 |
| MAP4_4306 | 30S ribosomal protein S8 | 132 | Rv0718 | 30S ribosomal protein S8 RpsH | 97.73 | 132 | Mb0739 | 30S ribosomal protein S8 | 97.73 | 132 | MAV_4451 | 30S ribosomal protein S8 | 100 | 130 | BCG_0768 | 30S ribosomal protein S8 | 97.73 | 132 | MAP4181 | 30S ribosomal protein S8 | 132 | 100 |
| MAP4_4307 | 50S ribosomal protein L6 | 179 | Rv0719 | 50S ribosomal protein L6 RplF | 93.3 | 179 | Mb0740 | 50S ribosomal protein L6 | 93.3 | 179 | MAV_4450 | 50S ribosomal protein L6 | 100 | 179 | BCG_0769 | 50S ribosomal protein L6 | 93.3 | 179 | MAP4182 | 50S ribosomal protein L6 | 179 | 100 |
| MAP4_4308 | 50S ribosomal protein L18 | 135 | Rv0720 | 50S ribosomal protein L18 RplR | 87.7 | 122 | Mb0741 | 50S ribosomal protein L18 | 87.7 | 122 | MAV_4449 | 50S ribosomal protein L18 | 99.18 | 122 | BCG_0770 | 50S ribosomal protein L18 | 87.7 | 122 | MAP4183 | 50S ribosomal protein L18 | 135 | 100 |
| MAP4_4309 | 30S ribosomal protein S5 | 224 | Rv0721 | 30S ribosomal protein S5 RpsE | 88.84 | 220 | Mb0742 | 30S ribosomal protein S5 | 88.84 | 220 | MAV_4448 | 30S ribosomal protein S5 | 100 | 225 | BCG_0771 | 30S ribosomal protein S5 | 88.84 | 220 | MAP4184 | 30S ribosomal protein S5 | 224 | 100 |
| MAP4_4310 | 50S ribosomal protein L30 | 71 | Rv0722 | 50S ribosomal protein L30 RpmD | 85.29 | 65 | Mb0743 | 50S ribosomal protein L30 | 85.29 | 65 | MAV_4447 | 50S ribosomal protein L30 | 100 | 71 | BCG_0772 | 50S ribosomal protein L30 | 85.29 | 65 | MAP4185 | 50S ribosomal protein L30 | 71 | 100 |
| MAP4_4311 | 50S ribosomal protein L15 | 146 | Rv0723 | 50S ribosomal protein L15 RplO | 89.73 | 146 | Mb0744 | 50S ribosomal protein L15 | 90.41 | 146 | MAV_4446 | 50S ribosomal protein L15 | 100 | 146 | BCG_0773 | 50S ribosomal protein L15 | 90.41 | 146 | MAP4186 | 50S ribosomal protein L15 | 146 | 100 |
| MAP4_4312 | putative monooxygenase, luciferase-like monooxygena | 308 | Rv1936 | Possible monooxygenase | 27.84 | 369 | Mb1971 | monooxygenase | 27.84 | 369 | MAV_4445 | hypothetical protein | 99.03 | 308 | BCG_1975 | monooxygenase | 27.84 | 369 | MAP4187c | hypothetical protein | 308 | 100 |
| MAP4_4313 | putative endopeptidase IV SppA | 595 | Rv0724 | Possible protease IV SppA (endopep | 75.33 | 623 | Mb0745 | endopeptidase IV | 75.33 | 623 | MAV_4443 | signal peptide peptidase SppA, 67K | 99.66 | 595 | BCG_0774 | protease IV sppA (endopeptida | 75.33 | 623 | MAP4188 | hypothetical protein | 595 | 100 |
| MAP4_4314 | putative methyltransferase | 304 | Rv1729c | Possible S-adenosylmethionine-depe | 69.64 | 312 | Mb1758c | hypothetical protein | 69.64 | 312 | MAV_4444 | methyltransferase, putative, family | 99.01 | 304 | BCG_1768c | hypothetical protein | 69.64 | 312 | MAP4189c | hypothetical protein | 304 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_4315 | putative methyltransferase | 306 | Rv0830 | Possible S-adenosylmethionine-depe | 55.89 | 301 | Mb0853 | hypothetical protein | 55.89 | 301 | MAV_4442 | methyltransferase, putative, family | 99.02 | 306 | BCG_0883 | hypothetical protein | 55.89 | 301 | MAP4190c | hypothetical protein | 306 | 100 |
| MAP4_4316 | putative methyltransferase | 314 | Rv0726c | Possible S-adenosylmethionine-depe | 66.67 | 367 | Mb0747c | hypothetical protein | 66.67 | 367 | MAV_4441 | methyltransferase | 99.36 | 314 | BCG_0776c | hypothetical protein | 66.67 | 367 | MAP4191c | hypothetical protein | 356 | 100 |
| MAP4_4317 | alcohol dehydrogenase Adh | 410 | Rv1895 | Possible dehydrogenase | 28.14 | 384 | Mb2283 | zinc-dependent alcohol dehy | 25.36 | 361 | MAV_4440 | zinc-binding dehydrogenase | 99.76 | 410 | BCG_2277 | zinc-dependent alcohol dehydr | 25.36 | 361 | MAP4192 | Adh | 410 | 100 |
| MAP4_4318 | L-fuculose phosphate aldolase FucA | 217 | Rv0727c | Possible L-fuculose phosphate aldola | 82.03 | 218 | Mb0748c | L-fuculose phosphate aldolas | 82.49 | 218 | MAV_4439 | L-fuculose-phosphate aldolase | 98.62 | 217 | BCG_0777c | L-fuculose phosphate aldolase | 82.49 | 218 | MAP4193c | L-fuculose-phosphate aldolase | 217 | 100 |
| MAP4_4319 | D-3-phosphoglycerate dehydrogenase SerA2 | 327 | Rv0728c | Possible D-3-phosphoglycerate dehy | 82.15 | 326 | Mb0749c | D-3-phosphoglycerate dehydr | 82.46 | 326 | MAV_4438 | 2-hydroxyacid dehydrogenase | 97.25 | 326 | BCG_0778c | D-3-phosphoglycerate dehydro | 82.46 | 326 | MAP4194c | hypothetical protein | 327 | 100 |
| MAP4_4320 | putative xylulose kinase XylB | 451 | Rv0729 | Possible D-xylulose kinase XylB (xylu | 71.78 | 448 | Mb0750 | D-xylulose kinase XylB | 72.01 | 448 | MAV_4437 | carbohydrate kinase, FGGY family p | 99.78 | 451 | BCG_0779 | d-xylulose kinase xylB | 71.78 | 448 | MAP4195 | hypothetical protein | 451 | 100 |
| MAP4_4321 | hypothetical protein | 221 | Rv0730 | GCN5-related N-acetyltransferase | 81.6 | 242 | Mb0751 | hypothetical protein | 81.6 | 242 | MAV_4436 | hypothetical protein | 100 | 221 | BCG_0780 | hypothetical protein | 81.6 | 242 | MAP4196 | hypothetical protein | 221 | 100 |
| MAP4_4322 | putative methyltransferase | 303 | Rv0830 | Possible S-adenosylmethionine-depe | 54.61 | 301 | Mb0853 | hypothetical protein | 54.61 | 301 | MAV_4435 | methyltransferase, putative, family | 99.67 | 303 | BCG_0883 | hypothetical protein | 54.61 | 301 | MAP4197c | hypothetical protein | 303 | 100 |
| MAP4_4323 | preprotein translocase subunit SecY | 441 | Rv0732 | Probable preprotein translocase Sec | 94.56 | 441 | Mb0753 | preprotein translocase subun | 94.56 | 441 | MAV_4434 | preprotein translocase subunit Sec | 99.77 | 453 | BCG_0782 | preprotein translocase subunit | 94.56 | 441 | MAP4198 | preprotein translocase subunit SecY | 441 | 100 |
| MAP4_4324 | adenylate kinase Adk | 181 | Rv0733 | Adenylate kinase Adk (ATP-AMP tra | 87.29 | 181 | Mb0754 | adenylate kinase | 87.29 | 181 | MAV_4433 | adenylate kinase | 99.45 | 181 | BCG_0783 | adenylate kinase | 87.29 | 181 | MAP4199 | adenylate kinase | 181 | 100 |
| MAP4_4325 | methionine aminopeptidase MapA | 266 | Rv0734 | Methionine aminopeptidase MapA ( | 86.09 | 266 | Mb0755 | methionine aminopeptidase | 86.09 | 266 | MAV_4432 | methionine aminopeptidase | 98.12 | 266 | BCG_0784 | methionine aminopeptidase | 86.09 | 266 | MAP4200 | methionine aminopeptidase | 266 | 100 |
| MAP4_4326 | RNA polymerase sigma factor SigL | 181 | Rv0735 | Probable alternative RNA polymeras | 88.95 | 177 | Mb0756 | RNA polymerase sigma factor | 88.95 | 177 | MAV_4431 | RNA polymerase sigma factor SigL | 99.44 | 178 | BCG_0785 | RNA polymerase sigma factor S | 88.95 | 177 | MAP4201 | RNA polymerase sigma factor SigL | 181 | 100 |
| MAP4_4327 | putative conserved membrane protein | 236 | Rv0736 | Anti-sigma factor RslA | 69.32 | 250 | Mb0757 | hypothetical protein | 69.32 | 250 | MAV_4430 | hypothetical protein | 100 | 239 | BCG_0786 | hypothetical protein | 69.32 | 250 | MAP4202 | hypothetical protein | 236 | 100 |
| MAP4_4328 | putative oxidoreductase | 413 | Rv0575c | Possible oxidoreductase | 27.96 | 388 | Mb0590c | hypothetical protein | 27.96 | 378 | MAV_4429 | FAD binding domain-containing pro | 98.06 | 413 | BCG_0620c | hypothetical protein | 27.96 | 378 | MAP4203 | hypothetical protein | 413 | 100 |
| MAP4_4329 | putative transmembrane protein | 197 | Rv1888c | Possible transmembrane protein | 56.62 | 186 | Mb1920c | transmembrane protein | 49.06 | 239 | MAV_4428 | hypothetical protein | 96.81 | 188 | BCG_1925c | hypothetical protein | 49.06 | 239 | MAP4204 | hypothetical protein | 197 | 100 |
| MAP4_4330 | putative methyltransferase, type 11 family protein | 208 | Rv1147 | hypothetical protein | 38.76 | 216 | Mb1178 | hypothetical protein | 38.76 | 216 | MAV_4426 | methyltransferase, UbiE/COQ5 fam | 98.08 | 208 | BCG_1208 | hypothetical protein | 38.76 | 216 | MAP4205 | hypothetical protein | 208 | 100 |
| MAP4_4331 | putative ABC transporter permease family protein | 832 | Rv0987 | Probable adhesion component trans | 26.18 | 855 | Mb1014 | adhesion component transpo | 25.14 | 431 | MAV_4427 | efflux ABC transporter permease | 97.8 | 817 | BCG_1042 | adhesion component transport | 25.94 | 855 | MAP4206c | hypothetical protein | 832 | 100 |
| MAP4_4332 | putative ABC transporter ATP-binding protein | 231 | Rv2564 | Probable glutamine-transport ATP-b | 46.19 | 330 | Mb2593 | glutamine-transport ATP-bind | 46.19 | 330 | MAV_4425 | ABC transporter ATPase | 98.27 | 231 | BCG_2586 | glutamine-transport ATP-bindi | 46.19 | 330 | MAP4207c | hypothetical protein | 231 | 100 |
| MAP4_4333 | putative thiaminepyrophosphate-dependent enzyme | 601 | Rv3003c | Acetolactate synthase (large subunit | 26.67 | 618 | Mb3028c | acetolactate synthase 1 catal | 26.67 | 618 | MAV_4424 | acetolactate synthase | 98.46 | 583 | BCG_3025c | acetolactate synthase 1 catalyt | 26.67 | 618 | MAP4208 | hypothetical protein | 601 | 100 |
| MAP4_4334 | hypothetical protein | 215 | Rv1512 | Probable nucleotide-sugar epimeras | 22.67 | 322 | Mb2384 | amidase | 29.59 | 484 | MAV_4423 | hypothetical protein | 100 | 215 | BCG_2377 | amidase | 29.59 | 484 | MAP4209 | hypothetical protein | 215 | 100 |
| MAP4_4335 | putative 3-oxoacyl-ACPsynthase III | 341 | Rv0533c | 3-oxoacyl-[acyl-carrier-protein] synt | 23.08 | 335 | Mb0547c | 3-oxoacyl-ACP synthase | 23.08 | 335 | MAV_4422 | 3-oxoacyl-ACP synthase III | 98.83 | 341 | BCG_0577c | 3-oxoacyl-ACP synthase | 23.08 | 335 | MAP4210 | hypothetical protein | 341 | 100 |
| MAP4_4336 | putative aminotransferase | 352 | Rv3772 | Probable histidinol-phosphate amin | 36.39 | 353 | Mb3800 | aminotransferase | 36.39 | 353 | MAV_4421 | histidinol-phosphate aminotransfer | 99.15 | 352 | BCG_3833 | aminotransferase | 36.39 | 353 | MAP4211 | hypothetical protein | 352 | 100 |
| MAP4_4337 | Transcriptional regulator, MarR family | 168 | Rv0737 | Possible transcriptional regulatory p | 88.2 | 165 | Mb0758 | transcriptional regulator | 88.2 | 165 | MAV_4420 | MarR family transcriptional regulat | 98.81 | 168 | BCG_0787 | transcriptional regulatory prote | 88.2 | 165 | MAP4212 | hypothetical protein | 168 | 100 |
| MAP4_4338 | 3-hydroxyisobutyrate dehydrogenase MmsB | 295 | Rv0751c | Probable 3-hydroxyisobutyrate dehy | 81.12 | 294 | Mb0773c | 3-hydroxyisobutyrate dehydr | 81.12 | 294 | MAV_4419 | 3-hydroxyisobutyrate dehydrogena | 99.31 | 291 | BCG_0802c | 3-hydroxyisobutyrate dehydrog | 80.77 | 294 | MAP4213c | hypothetical protein | 295 | 100 |
| MAP4_4339 | acyl-CoA dehydrogenase FadE9 | 386 | Rv0752c | Probable acyl-CoA dehydrogenase F | 88.43 | 390 | Mb0774c | acyl-CoA dehydrogenase | 88.43 | 390 | MAV_4418 | acyl-CoA dehydrogenase member 8 | 99.74 | 386 | BCG_0803c | acyl-CoA dehydrogenase fadE9 | 88.43 | 390 | MAP4214c | FadE9 | 386 | 100 |
| MAP4_4340 | methylmalonate-semialdehyde dehydrogenase MmsA | 506 | Rv0753c | Probable methylmalonate-semialde | 91.75 | 510 | Mb0775c | methylmalonate-semialdehyd | 91.55 | 510 | MAV_4417 | methylmalonate-semialdehyde deh | 99.8 | 506 | BCG_0804c | methylmalonate-semialdehyde | 91.75 | 510 | MAP4215c | hypothetical protein | 506 | 100 |
| MAP4_4341 | hypothetical protein | 474 | Rv2000 | hypothetical protein | 62.58 | 537 | Mb2023 | hypothetical protein | 62.58 | 537 | MAV_4416 | hypothetical protein | 98.73 | 474 | BCG_2017 | hypothetical protein | 62.58 | 537 | MAP4216 | hypothetical protein | 474 | 100 |
| MAP4_4342 | putative RNA polymerase sigma factor | 179 | Rv0735 | Probable alternative RNA polymeras | 30.32 | 177 | Mb0756 | RNA polymerase sigma factor | 30.32 | 177 | MAV_4415 | RNA polymerase sigma factor, sigm | 98.88 | 179 | BCG_0785 | RNA polymerase sigma factor S | 30.32 | 177 | MAP4217 | hypothetical protein | 179 | 100 |
| MAP4_4343 | Rieske (2Fe-2S) domain-containing protein | 235 | Rv0496 | hypothetical protein | 33.06 | 328 | Mb0507 | hypothetical protein | 33.06 | 328 | MAV_4414 | Rieske (2Fe-2S) domain-containing | 100 | 235 | BCG_0538 | hypothetical protein | 33.06 | 328 | MAP4218 | hypothetical protein | 235 | 100 |
| MAP4_4344 | hypothetical protein | 130 | Rv3811 | hypothetical protein | 37.14 | 539 | Mb3841 | hypothetical protein | 37.14 | 539 | MAV_4413 | copper binding proteins, plastocyan | 98.46 | 130 | BCG_3873 | hypothetical protein | 37.14 | 539 | MAP4219 | hypothetical protein | 130 | 100 |
| MAP4_4345 | hypothetical protein | 306 | Rv0805 | Class III cyclic nucleotide phosphodie | 24.35 | 318 | Mb0828 | hypothetical protein | 24.35 | 318 | MAV_4412 | metallophosphoesterase | 99.02 | 306 | BCG_0857 | hypothetical protein | 24.35 | 318 | MAP4220 | hypothetical protein | 306 | 100 |
| MAP4_4346 | putative acyltransferase | 362 | Rv0111 | Possible transmembrane acyltransfe | 44.23 | 685 | Mb0115 | transmembrane acyltransfera | 44.23 | 685 | MAV_4410 | AtfA_1 | 99.45 | 362 | BCG_0144 | acyltransferase | 44.23 | 685 | MAP4221c | hypothetical protein | 441 | 100 |
| MAP4_4347 | putative acyltransferase AtfA_1 | 381 | Rv0517 | Possible membrane acyltransferase | 30.77 | 436 | Mb0530 | membrane acyltransferase | 30.77 | 436 | MAV_4409 | acyltransferase | 99.74 | 381 | BCG_0560 | membrane acyltransferase | 30.77 | 436 | MAP4222c | AtfA_1 | 381 | 100 |
| MAP4_4348 | putative acyltransferase | 374 | Rv0111 | Possible transmembrane acyltransfe | 42.62 | 685 | Mb0115 | transmembrane acyltransfera | 42.62 | 685 | MAV_4408 | acyltransferase | 100 | 374 | BCG_0144 | acyltransferase | 42.62 | 685 | MAP4223c | AtfA_2 | 374 | 100 |
| MAP4_4349 | dTDP-4-dehydrorhamnose 3,5-epimerase RmlC | 201 | Rv3465 | dTDP-4-dehydrorhamnose 3,5-epim | 82.65 | 202 | Mb3494 | dTDP-4-dehydrorhamnose 3,5 | 82.65 | 202 | MAV_4407 | dTDP-4-dehydrorhamnose 3,5-epin | 99 | 201 | BCG_3530 | dTDP-4-dehydrorhamnose 3,5- | 82.65 | 202 | MAP4224c | RmlC | 201 | 100 |
| MAP4_4350 | dTDP-glucose 4,6-dehydratase rmlB | 331 | Rv3464 | dTDP-glucose 4,6-dehydratase RmlB | 92.45 | 331 | Mb3493 | dTDP-glucose 4,6-dehydratas | 92.45 | 331 | MAV_4406 | dTDP-glucose 4,6-dehydratase | 100 | 331 | BCG_3529 | dTDP-glucose 4,6-dehydratase | 92.45 | 331 | MAP4225c | RmlB | 331 | 100 |
| MAP4_4351 | hypothetical protein | 288 | Rv3463 | hypothetical protein | 64.98 | 285 | Mb3492 | hypothetical protein | 64.98 | 285 | MAV_4405 | hypothetical protein | 99.31 | 288 | BCG_3528 | hypothetical protein | 64.98 | 285 | MAP4226c | hypothetical protein | 288 | 100 |
| MAP4_4352 | hypothetical protein | 282 | Rv3463 | hypothetical protein | 82.86 | 285 | Mb3492 | hypothetical protein | 82.86 | 285 | MAV_4404 | hypothetical protein | 98.94 | 282 | BCG_3528 | hypothetical protein | 82.86 | 285 | MAP4227c | hypothetical protein | 282 | 100 |
| MAP4_4353 | translation initiation factor 1 | 73 | Rv3462c | Probable translation initiation factor | 100 | 73 | Mb3491c | translation initiation factor IF | 100 | 73 | MAV_4403 | translation initiation factor IF-1 | 100 | 73 | BCG_3527c | translation initiation factor IF-1 | 100 | 73 | MAP4228 | translation initiation factor IF-1 | 73 | 100 |
| MAP4_4354 | 50S ribosomal protein L36 | 37 | Rv3461c | 50S ribosomal protein L36 RpmJ | 97.3 | 37 | Mb3490c | 50S ribosomal protein L36 | 97.3 | 37 | MAV_4402 | 50S ribosomal protein L36 | 100 | 37 | BCG_3526c | 50S ribosomal protein L36 | 97.3 | 37 | MAP4229 | 50S ribosomal protein L36 | 37 | 100 |
| MAP4_4355 | 30S ribosomal protein S13 RpsM | 124 | Rv3460c | 30S ribosomal protein S13 RpsM | 94.35 | 124 | Mb3489c | 30S ribosomal protein S13 | 94.35 | 124 | MAV_4401 | 30S ribosomal protein S13 | 100 | 110 | BCG_3525c | 30S ribosomal protein S13 | 94.35 | 124 | MAP4230 | 30S ribosomal protein S13 | 124 | 100 |
| MAP4_4356 | 30S ribosomal protein S11 RpsK | 138 | Rv3459c | 30S ribosomal protein S11 RpsK | 94.96 | 139 | Mb3488c | 30S ribosomal protein S11 | 94.24 | 139 | MAV_4400 | 30S ribosomal protein S11 | 100 | 138 | BCG_3524c | 30S ribosomal protein S11 | 94.24 | 139 | MAP4231 | 30S ribosomal protein S11 | 138 | 100 |
| MAP4_4357 | 30S ribosomal protein S4 RpsD | 201 | Rv3458c | 30S ribosomal protein S4 RpsD | 93.03 | 201 | Mb3487c | 30S ribosomal protein S4 | 93.03 | 201 | MAV_4399 | 30S ribosomal protein S4 | 100 | 201 | BCG_3523c | 30S ribosomal protein S4 | 93.03 | 201 | MAP4232 | 30S ribosomal protein S4 | 201 | 100 |
| MAP4_4358 | DNA-directed RNA polymerase alpha subunit | 347 | Rv3457c | Probable DNA-directed RNA polyme | 96.83 | 347 | Mb3486c | DNA-directed RNA polymeras | 96.83 | 347 | MAV_4398 | DNA-directed RNA polymerase sub | 100 | 347 | BCG_3522c | DNA-directed RNA polymerase | 96.83 | 347 | MAP4233 | DNA-directed RNA polymerase subunit | 347 | 100 |
| MAP4_4359 | 50S ribosomal protein L17 RplQ | 186 | Rv3456c | 50S ribosomal protein L17 RplQ | 92.74 | 180 | Mb3485c | 50S ribosomal protein L17 | 92.74 | 180 | MAV_4397 | 50S ribosomal protein L17 | 98.39 | 186 | BCG_3521c | 50S ribosomal protein L17 | 92.74 | 180 | MAP4234 | 50S ribosomal protein L17 | 186 | 100 |
| MAP4_4360 | tRNA pseudouridine synthase A | 251 | Rv3455c | Probable tRNA pseudouridine synth | 83.2 | 256 | Mb3484c | tRNA pseudouridine synthase | 83.2 | 297 | MAV_4395 | tRNA pseudouridine synthase A | 99.6 | 251 | BCG_3520c | tRNA pseudouridine synthase A | 83.2 | 256 | MAP4235 | tRNA pseudouridine synthase A | 251 | 100 |
| MAP4_4361 | putative cutinase precursor Cut4 | 211 | Rv3452 | Probable cutinase precursor Cut4 | 77.37 | 226 | Mb3482 | cutinase | 77.37 | 226 | MAV_4396 | cutinase | 99.03 | 206 | BCG_3518 | cutinase precursor cut4 | 77.37 | 226 | MAP4236c | hypothetical protein | 211 | 100 |
| MAP4_4362 | putative cutinase precursor Cut3 | 289 | Rv3451 | Probable cutinase precursor Cut3 | 63.79 | 262 | Mb3481 | cutinase | 63.79 | 262 | MAV_4394 | serine esterase, cutinase | 99.65 | 289 | BCG_3517 | cutinase precursor cut3 | 62.95 | 261 | MAP4237c | hypothetical protein | 289 | 100 |
| MAP4_4363 | putative conserved membrane protein | 453 | Rv3450c | ESX conserved component EccB4 ES | 58.3 | 470 | Mb3480c | hypothetical protein | 58.3 | 470 | MAV_4392 | hypothetical protein | 97.59 | 457 | BCG_3516c | hypothetical protein | 58.3 | 470 | MAP4238 | hypothetical protein | 477 | 99.78 |
| MAP4_4364 | putative membrane-anchored mycosin MycP4 | 432 | Rv3449 | Probable membrane-anchored myc | 68.57 | 455 | Mb3479 | secreted serine protease | 68.57 | 455 | MAV_4393 | peptidase | 96.74 | 429 | BCG_3515 | serine protease | 68.57 | 455 | MAP4239c | hypothetical protein | 432 | 100 |
| MAP4_4365 | putative conserved membrane protein | 452 | Rv3448 | ESX conserved component EccD4 ES | 47 | 467 | Mb3478 | hypothetical protein | 46.78 | 467 | MAV_4391 | hypothetical protein | 96.9 | 453 | BCG_3514 | integral membrane protein | 47 | 467 | MAP4240c | hypothetical protein | 452 | 100 |
| MAP4_4366 | putative conserved membrane protein | 1214 | Rv3447c | ESX conserved component EccC4 ES | 62.63 | 1236 | Mb3477c | hypothetical protein | 62.55 | 1236 | MAV_4390 | ftsk/SpoIIIE family protein | 98.31 | 1197 | BCG_3513c | hypothetical protein | 62.63 | 1236 | MAP4241 | hypothetical protein | 1214 | 100 |
| MAP4_4367 | hypothetical protein | 405 | Rv3446c | Hypothetical alanine and valine rich | 56.31 | 404 | Mb3476c | hypothetical protein | 56.31 | 404 | MAV_4389 | hypothetical protein | 97.34 | 376 | BCG_3512c | hypothetical protein | 56.31 | 404 | MAP4242 | hypothetical protein | 405 | 100 |
| MAP4_4368 | ESAT-6 like protein EsxU | 105 | Rv3445c | ESAT-6 like protein EsxU | 80 | 105 | Mb3475c | hypothetical protein | 79.05 | 125 | MAV_4388 | hypothetical protein | 94.95 | 99 | BCG_3511c | hypothetical protein | 79.05 | 125 | MAP4243 | hypothetical protein | 105 | 100 |
| MAP4_4369 | ESAT-6 like protein EsxT | 98 | Rv3444c | Putative ESAT-6 like protein EsxT | 77.32 | 100 | Mb3474c | hypothetical protein | 77.32 | 100 | MAV_4387 | hypothetical protein | 100 | 98 | BCG_3510c | hypothetical protein | 77.32 | 100 | MAP4244 | hypothetical protein | 98 | 100 |
| MAP4_4370 | 50S ribosomal protein L13 RplM | 147 | Rv3443c | 50S ribosomal protein L13 RplM | 88.44 | 147 | Mb3473c | 50S ribosomal protein L13 | 88.44 | 147 | MAV_4386 | 50S ribosomal protein L13 | 100 | 147 | BCG_3509c | 50S ribosomal protein L13 | 88.44 | 147 | MAP4245 | 50S ribosomal protein L13 | 147 | 100 |
| MAP4_4371 | 30S ribosomal protein S9 RpsI | 166 | Rv3442c | 30S ribosomal protein S9 RpsI | 90.91 | 151 | Mb3472c | 30S ribosomal protein S9 | 90.91 | 151 | MAV_4385 | 30S ribosomal protein S9 | 98.19 | 166 | BCG_3508c | 30S ribosomal protein S9 | 90.91 | 151 | MAP4246 | 30S ribosomal protein S9 | 166 | 100 |
| MAP4_4372 | phospho-sugar mutase MrsA | 444 | Rv3441c | Probable phospho-sugar mutase / M | 86.16 | 448 | Mb3471c | phosphoglucosamine mutase | 86.16 | 448 | MAV_4384 | phosphoglucosamine mutase | 99.55 | 444 | BCG_3507c | phosphoglucosamine mutase | 86.16 | 448 | MAP4247 | phosphoglucosamine mutase | 444 | 100 |
| MAP4_4373 | hypothetical protein | 109 | Rv3440c | Hypothetical protein | 57.84 | 103 | Mb3470c | hypothetical protein | 57.84 | 103 | MAV_4383 | hypothetical protein | 100 | 109 | BCG_3506c | hypothetical protein | 57.84 | 103 | MAP4248 | hypothetical protein | 109 | 100 |
| MAP4_4374 | conserved alanine and proline rich protein | 461 | Rv3439c | Conserved hypothetical alanine and | 60.54 | 467 | Mb3469c | hypothetical protein | 60.54 | 467 | MAV_4382 | hypothetical protein | 91.28 | 488 | BCG_3505c | hypothetical protein | 60.54 | 467 | MAP4249 | hypothetical protein | 461 | 100 |
| MAP4_4375 | putative coenzyme F420-dependent oxidoreductase | 346 | Rv3520c | Possible coenzyme F420-dependent | 41.54 | 347 | Mb3550c | coenzyme F420-dependent o | 41.54 | 347 | MAV_4381 | oxidoreductase | 99.13 | 346 | BCG_3584c | coenzyme F420-dependent oxi | 41.54 | 347 | MAP4250c | hypothetical protein | 347 | 100 |
| MAP4_4376 | hypothetical protein | 279 | Rv3438 | hypothetical protein | 78.57 | 280 | Mb3468 | hypothetical protein | 78.57 | 280 | MAV_4380 | hypothetical protein | 97.49 | 279 | BCG_3504 | hypothetical protein | 78.57 | 280 | MAP4251c | hypothetical protein | 279 | 100 |
| MAP4_4377 | hypothetical protein | 89 | Rv1535 | hypothetical protein | 44.87 | 78 | Mb1562 | hypothetical protein | 44.87 | 78 | MAV_4379 | hypothetical protein | 95.31 | 64 | BCG_1587 | hypothetical protein | 44.87 | 78 | MAP4252c | hypothetical protein | 89 | 100 |
| MAP4_4378 | glucosamine-fructose-6-phosphate aminotransferase G | 624 | Rv3436c | Probable glucosamine--fructose-6-p | 90.24 | 624 | Mb3466c | glucosamine--fructose-6-phos | 90.24 | 624 | MAV_4377 | glucosamine--fructose-6-phosphate | 99.84 | 624 | BCG_3502c | glucosamine--fructose-6-phosp | 90.24 | 624 | MAP4253 | glucosamine--fructose-6-phosphate am | 624 | 100 |
| MAP4_4379 | putative conserved membrane protein | 299 | Rv3435c | Probable conserved transmembrane | 51.87 | 284 | Mb3465c | transmembrane protein | 51.87 | 284 | MAV_4376 | hypothetical protein | 100 | 295 | BCG_3501c | hypothetical protein | 51.87 | 284 | MAP4254 | hypothetical protein | 299 | 100 |
| MAP4_4380 | putative conserved membrane protein | 243 | Rv3434c | Possible conserved transmembrane | 75.65 | 237 | Mb3464c | transmembrane protein | 75.22 | 237 | MAV_4375 | hypothetical protein | 99.15 | 234 | BCG_3500c | hypothetical protein | 75.65 | 237 | MAP4255 | hypothetical protein | 243 | 100 |
| MAP4_4381 | putative carbohydrate kinase | 473 | Rv3433c | hypothetical protein | 88.16 | 473 | Mb3463c | hypothetical protein | 88.37 | 473 | MAV_4374 | carbohydrate kinase | 99.58 | 473 | BCG_3499c | hypothetical protein | 87.53 | 472 | MAP4256 | hypothetical protein | 473 | 100 |
| MAP4_4382 | glutamate decarboxylase | 463 | Rv3432c | Probable glutamate decarboxylase G | 87.42 | 460 | Mb3462c | glutamate decarboxylase | 87.42 | 460 | MAV_4373 | glutamate decarboxylase | 98.49 | 459 | BCG_3498c | glutamate decarboxylase gadB | 87.42 | 460 | MAP4257 | GadB | 463 | 100 |
| MAP4_4383 | alanine racemase | 391 | Rv3423c | Alanine racemase Alr | 82.9 | 408 | Mb3457c | alanine racemase | 82.9 | 408 | MAV_4372 | alanine racemase | 99.23 | 388 | BCG_3493c | alanine racemase | 82.9 | 408 | MAP4258 | alanine racemase | 391 | 100 |
| MAP4_4384 | putative hydrolase, alphabeta hydrolase family protein | 349 | Rv3171c | Possible non-heme haloperoxidase H | 29.51 | 299 | Mb3196c | non-Heme haloperoxidase Hp | 29.33 | 299 | MAV_4371 | alpha/beta hydrolase | 99.71 | 349 | BCG_3195c | non-heme haloperoxidase hpx | 29.33 | 299 | MAP4259 | hypothetical protein | 334 | 100 |
| MAP4_4385 | hypothetical protein | 159 | Rv3422c | hypothetical protein | 76.51 | 168 | Mb3456c | hypothetical protein | 76.51 | 168 | MAV_4370 | hypothetical protein | 100 | 159 | BCG_3492c | hypothetical protein | 76.51 | 168 | MAP4260 | hypothetical protein | 159 | 100 |
| MAP4_4386 | hypothetical protein | 208 | Rv3421c | hypothetical protein | 80.1 | 211 | Mb3455c | hypothetical protein | 80.1 | 211 | MAV_4369 | peptidase M22, glycoprotease | 98.56 | 208 | BCG_3491c | hypothetical protein | 80.1 | 211 | MAP4261 | hypothetical protein | 208 | 100 |
| MAP4_4387 | ribosomal-protein-alanine acetyltransferase RimI | 156 | Rv3420c | Ribosomal-protein-alanine acetyltra | 81.17 | 158 | Mb3454c | ribosomal-protein-alanine ac | 81.17 | 158 | MAV_4368 | ribosomal-protein-alanine acetyltra | 100 | 156 | BCG_3490c | ribosomal-protein-alanine acet | 81.17 | 158 | MAP4262 | hypothetical protein | 156 | 100 |
| MAP4_4388 | O-sialoglycoprotein endopeptidase Gcp | 341 | Rv3419c | Probable O-sialoglycoprotein endop | 86.59 | 344 | Mb3453c | DNA-binding/iron metallopro | 86.59 | 344 | MAV_4367 | DNA-binding/iron metalloprotein/A | 100 | 341 | BCG_3489c | DNA-binding/iron metalloprote | 86.59 | 344 | MAP4263 | DNA-binding/iron metalloprotein/AP en | 341 | 100 |
| MAP4_4389 | 10 kda chaperonin GroES | 100 | Rv3418c | 10 kDa chaperonin GroES (protein C | 97 | 100 | Mb3452c | co-chaperonin GroES | 97 | 100 | MAV_4366 | co-chaperonin GroES | 100 | 100 | BCG_3488c | co-chaperonin GroES | 97 | 100 | MAP4264 | molecular chaperone GroES | 100 | 100 |
| MAP4_4390 | 60 kda chaperonin 1 GroEL | 538 | Rv3417c | 60 kDa chaperonin 1 GroEL1 (protei | 84.82 | 539 | Mb3451c | molecular chaperone GroEL | 84.82 | 539 | MAV_4365 | chaperonin GroEL | 99.81 | 538 | BCG_3487c | chaperonin GroEL | 84.82 | 539 | MAP4265 | molecular chaperone GroEL | 538 | 100 |
| MAP4_4391 | putative conserved membrane protein | 508 | Rv3645 | Probable conserved transmembrane | 37.15 | 549 | Mb3669 | transmembrane protein | 37.15 | 549 | MAV_0518 | adenylate cyclase, family protein 3 | 36.11 | 534 | BCG_3703 | hypothetical protein | 37.15 | 549 | MAP4266 | hypothetical protein | 508 | 100 |
| MAP4_4392 | hypothetical protein | 120 | Rv2061c | hypothetical protein | 39.13 | 134 | Mb2087c | hypothetical protein | 39.13 | 134 | MAV_5301 | thioredoxin-disulfide reductase | 35 | 366 | BCG_2080c | hypothetical protein | 39.13 | 134 | MAP4267 | hypothetical protein | 120 | 100 |
| MAP4_4393 | putative transcriptional regulator | 102 | Rv2021c | Transcriptional regulatory protein | 48.96 | 101 | Mb2044c | hypothetical protein | 48.96 | 101 | MAV_0348 | XRE family transcriptional regulator | 42.5 | 474 | BCG_2038c | hypothetical protein | 48.96 | 101 | MAP4268c | hypothetical protein | 102 | 100 |
| MAP4_4394 | hypothetical protein | 134 | Rv2022c | hypothetical protein | 51.38 | 201 | Mb2045c | hypothetical protein | 51.38 | 201 | MAV_2156 | P450 heme-thiolate protein | 33.96 | 437 | BCG_2039c | hypothetical protein | 51.38 | 201 | MAP4269c | hypothetical protein | 134 | 100 |
| MAP4_4395 | hypothetical protein | 230 | Rv3482c | Probable conserved membrane prot | 50 | 260 | Mb3512c | hypothetical protein | 50 | 260 | MAV_3061 | hypothetical protein | 57.14 | 221 | BCG_3546c | hypothetical protein | 50 | 496 | MAP4270 | hypothetical protein | 230 | 100 |
| MAP4_4396 | putative oxidoreductase | 399 | Rv1751 | Probable oxidoreductase | 47.63 | 460 | Mb1780 | hypothetical protein | 47.38 | 460 | MAV_4364 | hypothetical protein | 99.48 | 384 | BCG_1790 | hypothetical protein | 47.63 | 460 | MAP4271 | hypothetical protein | 399 | 100 |
| MAP4_4397 | periplasmic superoxide dismutase SodC | 254 | Rv0432 | Periplasmic superoxide dismutase [C | 52.6 | 240 | Mb0440 | periplasmic superoxide dismu | 52.6 | 240 | MAV_4362 | superoxide dismutase, Cu-Zn | 99.61 | 254 | BCG_0471 | periplasmic superoxide dismut | 52.6 | 240 | MAP4272c | hypothetical protein | 254 | 100 |
| MAP4_4398 | transcriptional regulator whib-like WhiB3 | 102 | Rv3416 | Transcriptional regulatory protein W | 90.2 | 102 | Mb3450 | transcriptional regulator Whi | 90.2 | 102 | MAV_4361 | transcription factor WhiB | 98.81 | 84 | BCG_3486 | transcriptional regulatory prote | 90.2 | 102 | MAP4273c | WhiB3 | 102 | 100 |
| MAP4_4399 | hypothetical protein | 276 | Rv3415c | hypothetical protein | 70.48 | 275 | Mb3449c | hypothetical protein | 70.48 | 275 | MAV_4360 | hypothetical protein | 98.55 | 276 | BCG_3485c | hypothetical protein | 70.48 | 275 | MAP4274 | hypothetical protein | 276 | 100 |
| MAP4_4400 | RNA polymerase sigma factor SigD | 198 | Rv3414c | Probable alternative RNA polymeras | 88.89 | 212 | Mb3448c | RNA polymerase sigma factor | 88.89 | 212 | MAV_4359 | RNA polymerase sigma factor SigD | 100 | 192 | BCG_3484c | RNA polymerase sigma factor S | 88.89 | 212 | MAP4275 | RNA polymerase sigma factor SigD | 198 | 100 |
| MAP4_4401 | putative alanine and proline rich protein | 266 | Rv3413c | Unknown alanine and proline rich pr | 58.79 | 299 | Mb3447c | hypothetical protein | 58.79 | 299 | MAV_4358 | hypothetical protein | 99.25 | 266 | BCG_3483c | hypothetical protein | 58.79 | 299 | MAP4276 | hypothetical protein | 266 | 100 |
| MAP4_4402 | hypothetical protein | 137 | Rv3412 | hypothetical protein | 94.85 | 136 | Mb3446 | hypothetical protein | 94.85 | 136 | MAV_4357 | hypothetical protein | 100 | 137 | BCG_3482 | hypothetical protein | 94.85 | 136 | MAP4277c | hypothetical protein | 137 | 100 |
| MAP4_4403 | inosine-5-monophosphate dehydrogenase GuaB2 | 531 | Rv3411c | Probable inosine-5'-monophosphate | 93.97 | 529 | Mb3445c | inosine 5'-monophosphate de | 93.97 | 529 | MAV_4356 | inosine 5'-monophosphate dehydro | 100 | 531 | BCG_3481c | inosine 5'-monophosphate deh | 93.97 | 529 | MAP4278 | inosine 5'-monophosphate dehydrogen | 531 | 100 |
| MAP4_4404 | inosine-5-monophosphate dehydrogenase GuaB3 | 375 | Rv3410c | Probable inosine-5'-monophosphate | 92.51 | 375 | Mb3444c | inosine 5-monophosphate de | 92.51 | 375 | MAV_4355 | inosine 5-monophosphate dehydro | 98.42 | 379 | BCG_3480c | inosine 5-monophosphate deh | 92.51 | 375 | MAP4279 | inosine 5-monophosphate dehydrogena | 375 | 100 |
| MAP4_4406 | transposase, IS900 | 406 | Rv0797 | Putative transposase for insertion se | 28.61 | 364 | Mb3360 | transposase | 28.35 | 570 | MAV_1059 | transposase | 29.01 | 350 | BCG_3397 | transposase fusion protein | 28.35 | 570 | MAP0034 | hypothetical protein | 406 | 100 |
| MAP4_4407 | short-chain type dehydrogenasereductase | 273 | Rv0687 | Probable short-chain type dehydrog | 43.12 | 275 | Mb0706 | 3-ketoacyl-ACP reductase | 43.12 | 275 | MAV_5244 | cholesterol oxidase | 98.9 | 273 | BCG_0736 | 3-ketoacyl-ACP reductase | 43.12 | 275 | MAP4282 | hypothetical protein | 273 | 100 |
| MAP4_4408 | hypothetical protein | 70 | Rv0092 | Cation transporter P-type ATPase a C | 34.38 | 761 | Mb0106c | cation-transporter P-type ATP | 38.71 | 752 | MAV_5245 | hypothetical protein | 98.57 | 70 | BCG_0136c | cation-transporter P-type atpa | 38.71 | 752 | MAP4283 | hypothetical protein | 70 | 100 |
| MAP4_4409 | cation transporter P-type ATPase A | 742 | Rv0092 | Cation transporter P-type ATPase a C | 47.69 | 761 | Mb0095 | cation transporter P-type ATP | 47.69 | 761 | MAV_5246 | copper-translocating P-type ATPase | 96.19 | 762 | BCG_0125 | cation transporter p-type atpa | 47.69 | 761 | MAP4284 | CtpA | 742 | 100 |
| MAP4_4410 | putative conserved membrane protein | 469 | Rv1639c | hypothetical protein | 55.56 | 489 | Mb1666c | hypothetical protein | 55.56 | 489 | MAV_3129 | esterase | 59.51 | 467 | BCG_1678c | hypothetical protein | 55.56 | 489 | MAP4285 | hypothetical protein | 500 | 99.79 |
| MAP4_4411 | putative polysaccharide deacetylase | 283 | Rv1096 | Possible glycosyl hydrolase | 27.84 | 291 | Mb1126 | glycosyl hydrolase | 27.84 | 291 | MAV_5248 | polysaccharide deacetylase | 100 | 269 | BCG_1156 | glycosyl hydrolase | 27.84 | 291 | MAP4286 | hypothetical protein | 283 | 100 |
| MAP4_4412 | Transcriptional regulator, MarR family | 151 | Rv0042c | Possible transcriptional regulatory p | 37.1 | 208 | Mb0043c | MarR family transcriptional re | 37.1 | 208 | MAV_5249 | MarR family transcriptional regulat | 97.12 | 139 | BCG_0073c | transcriptional regulatory prote | 37.1 | 208 | MAP4287c | hypothetical protein | 151 | 100 |

# Table S1 continued

| | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP4_4413 | lipoprotein LpqP | 323 | Rv0671 | Possible conserved lipoprotein LpqP | 49.84 | 280 | Mb0690 | lipoprotein LpqP | 49.84 | 280 | MAV_5250 | LpqP protein | 97.77 | 314 | BCG_0720 | lipoprotein lpqP | 49.84 | 280 | MAP4288 | hypothetical protein | 323 | 100 |
| MAP4_4414 | putative secretory lipase | 436 | Rv1592c | hypothetical protein | 27.48 | 446 | Mb1618c | hypothetical protein | 27.48 | 446 | MAV_5251 | secretory lipase | 99.31 | 436 | BCG_1630c | hypothetical protein | 27.48 | 446 | MAP4289 | hypothetical protein | 436 | 100 |
| MAP4_4415 | Transcriptional regulator, TetR family | 186 | Rv0775 | hypothetical protein | 24.78 | 207 | Mb0798 | hypothetical protein | 24.78 | 207 | MAV_5252 | hypothetical protein | 100 | 186 | BCG_0827 | hypothetical protein | 24.78 | 207 | MAP4290 | hypothetical protein | 186 | 100 |
| MAP4_4416 | Transcriptional regulator, TetR family | 202 | Rv0078 | Probable transcriptional regulatory | 86.07 | 201 | Mb0080 | transcriptional regulator | 85.57 | 201 | MAV_5253 | TetR family transcriptional regulato | 100 | 202 | BCG_0109 | transcriptional regulatory prote | 85.57 | 201 | MAP4291c | hypothetical protein | 202 | 100 |
| MAP4_4417 | putative oxidoreductase | 276 | Rv0077c | Probable oxidoreductase | 79.71 | 276 | Mb0079c | oxidoreductase | 79.71 | 276 | MAV_5254 | hydrolase, alpha/beta hydrolase fa | 99.64 | 276 | BCG_0108c | oxidoreductase | 79.71 | 276 | MAP4292 | hypothetical protein | 276 | 100 |
| MAP4_4418 | short-chain type dehydrogenasereductase | 253 | Rv3549c | Probable short-chain type dehydrog | 35.22 | 259 | Mb3579c | short chain dehydrogenase | 35.22 | 259 | MAV_5255 | NAD dependent epimerase/dehydr | 99.6 | 253 | BCG_3613c | short chain dehydrogenase | 35.22 | 259 | MAP4293 | hypothetical protein | 253 | 100 |
| MAP4_4419 | fatty-acid-CoA ligase FadD1 | 546 | Rv1750c | Possible fatty-acid-CoA ligase FadD1 | 80.42 | 532 | Mb1779c | acyl-CoA synthetase | 80.42 | 532 | MAV_5257 | acyl-CoA synthetase | 98.72 | 546 | BCG_1789c | acyl-CoA synthetase | 80.42 | 532 | MAP4294 | acyl-CoA synthetase | 546 | 100 |
| MAP4_4420 | hypothetical protein | 216 | Rv1176c | hypothetical protein | 29.11 | 189 | Mb1209c | hypothetical protein | 29.11 | 189 | MAV_5256 | hypothetical protein | 98.61 | 216 | BCG_1239c | hypothetical protein | 29.11 | 189 | MAP4295c | hypothetical protein | 216 | 100 |
| MAP4_4421 | hypothetical protein | 143 | Rv3542c | hypothetical protein | 32.67 | 311 | Mb3572c | hypothetical protein | 32.67 | 311 | MAV_5258 | hypothetical protein | 97.9 | 143 | BCG_3606c | hypothetical protein | 32.67 | 311 | MAP4296c | hypothetical protein | 143 | 100 |
| MAP4_4422 | hypothetical protein | 388 | Rv3540c | Probable lipid transfer protein or ke | 30.96 | 386 | Mb3570c | lipid-transfer protein | 30.96 | 386 | MAV_5259 | hypothetical protein | 98.97 | 388 | BCG_3604c | lipid-transfer protein | 30.96 | 386 | MAP4297c | hypothetical protein | 388 | 100 |
| MAP4_4423 | hypothetical protein | 109 | Rv0275c | Possible transcriptional regulatory p | 40.74 | 241 | Mb0281c | TetR family transcriptional re | 40.74 | 241 | MAV_5260 | hypothetical protein | 98.17 | 109 | BCG_0313c | TetR family transcriptional regu | 40.74 | 241 | MAP0788c | aminotransferase | 393 | 47.37 |
| MAP4_4424 | putative CoA-transferase family III protein | 776 | Rv1866 | hypothetical protein | 27.33 | 778 | Mb1897 | hypothetical protein | 27.2 | 778 | MAV_5261 | caib/baif family protein | 97.94 | 776 | BCG_1902 | hypothetical protein | 27.2 | 778 | MAP4298c | hypothetical protein | 776 | 100 |
| MAP4_4425 | putative amidohydrolase | 451 | Rv3510c | hypothetical protein | 25.47 | 278 | Mb3540c | hypothetical protein | 25.47 | 278 | MAV_5262 | amidohydrolase | 99.11 | 457 | BCG_3574c | hypothetical protein | 25.47 | 278 | MAP4299c | hypothetical protein | 451 | 100 |
| MAP4_4426 | putative transcriptional regulator, LacI family protein | 334 | Rv0328 | Possible transcriptional regulatory p | 36 | 200 | Mb0335 | TetR/AcrR family transcriptio | 36 | 200 | MAV_5263 | LacI family transcriptional regulato | 99.4 | 334 | BCG_0367 | TetR family transcriptional regu | 36 | 200 | MAP4300 | hypothetical protein | 334 | 100 |
| MAP4_4427 | hypothetical protein | 137 | Rv3542c | hypothetical protein | 30.47 | 311 | Mb3572c | hypothetical protein | 30.47 | 311 | MAV_5264 | acyl dehydratase | 98.54 | 137 | BCG_3606c | hypothetical protein | 30.47 | 311 | MAP4301c | hypothetical protein | 137 | 100 |
| MAP4_4428 | hypothetical protein | 402 | Rv3540c | Probable lipid transfer protein or ke | 29.44 | 386 | Mb3570c | lipid-transfer protein | 29.44 | 386 | MAV_5265 | nonspecific lipid-transfer protein | 99.5 | 404 | BCG_3604c | lipid-transfer protein | 29.44 | 386 | MAP4302c | hypothetical protein | 402 | 99 |
| MAP4_4429 | putative acyl-CoA dehydrogenase | 678 | Rv0271c | Probable acyl-CoA dehydrogenase F | 37.64 | 731 | Mb0277c | acyl-CoA dehydrogenase | 37.64 | 731 | MAV_0587 | acyl-CoA dehydrogenase | 40.18 | 707 | BCG_0309c | acyl-CoA dehydrogenase fadE6 | 37.64 | 731 | MAP4303c | hypothetical protein | 678 | 100 |
| MAP4_4430 | Transcriptional regulator, TetR family | 226 | Rv1556 | Possible regulatory protein | 38.78 | 202 | Mb1581 | regulatory protein | 38.78 | 202 | MAV_5267 | TetR family transcriptional regulato | 100 | 194 | BCG_1607 | regulatory protein | 38.78 | 202 | MAP4304 | hypothetical protein | 226 | 100 |
| MAP4_4431 | hypothetical protein | 365 | Rv3531c | Hypothetical protein | 26.98 | 375 | Mb3561c | hypothetical protein | 26.98 | 375 | MAV_5268 | hypothetical protein | 98.9 | 365 | BCG_3595c | hypothetical protein | 26.98 | 375 | MAP4305 | hypothetical protein | 306 | 100 |
| MAP4_4432 | hypothetical protein | 390 | Rv3529c | hypothetical protein | 32.1 | 384 | Mb3559c | hypothetical protein | 32.1 | 384 | MAV_5269 | hypothetical protein | 99.49 | 390 | BCG_3593c | hypothetical protein | 32.1 | 384 | MAP4306 | hypothetical protein | 390 | 100 |
| MAP4_4433 | hypothetical protein | 355 | Rv3071 | hypothetical protein | 55.04 | 369 | Mb3098 | hypothetical protein | 55.04 | 369 | MAV_5270 | hypothetical protein | 98.59 | 355 | BCG_3096 | hypothetical protein | 55.04 | 369 | MAP4307 | hypothetical protein | 355 | 100 |
| MAP4_4434 | fructose-bisphosphate aldolase | 297 | Rv1084 | hypothetical protein | 30.56 | 673 | Mb1113 | hypothetical protein | 30.56 | 673 | MAV_5271 | fructose-1,6-bisphosphate aldolase | 99.66 | 297 | BCG_1142 | hypothetical protein | 30.56 | 673 | MAP4308c | fructose-1,6-bisphosphate aldolase | 309 | 100 |
| MAP4_4435 | anti-anti-sigma factor | 125 | Rv3687c | Anti-anti-sigma factor RsfB (anti-sig | 44 | 122 | Mb3712c | hypothetical protein | 45.45 | 81 | MAV_5272 | anti-anti-sigma factor | 99.2 | 125 | BCG_3746c | hypothetical protein | 45.45 | 81 | MAP4309 | hypothetical protein | 110 | 99.09 |
| MAP4_4436 | putative aminoglycoside phosphotransferase | 361 | Rv3168 | Putative aminoglycoside phosphotra | 27.37 | 378 | Mb3193 | hypothetical protein | 27.37 | 378 | MAV_5273 | phosphotransferase enzyme family | 98.89 | 361 | BCG_3192 | hypothetical protein | 27.37 | 378 | MAP4310c | hypothetical protein | 361 | 100 |
| MAP4_4437 | hypothetical protein | 378 | Rv3169 | hypothetical protein | 28.03 | 374 | Mb3194 | hypothetical protein | 28.03 | 374 | MAV_5274 | hypothetical protein | 98.41 | 378 | BCG_3193 | hypothetical protein | 28.03 | 374 | MAP4311c | hypothetical protein | 391 | 100 |
| MAP4_4438 | Transcriptional regulator, TetR family | 206 | Rv0472c | Probable transcriptional regulatory | 27.21 | 234 | Mb0482c | TetR family transcriptional re | 27.21 | 234 | MAV_5275 | TetR family transcriptional regulato | 99.51 | 206 | BCG_0513c | TetR family transcriptional regu | 24.74 | 234 | MAP4312 | hypothetical protein | 206 | 100 |
| MAP4_4439 | putative phosphotransferase enzyme family protein | 374 | Rv3197 | Probable conserved ATP-binding pro | 55.56 | 447 | Mb3220 | ABC transporter ATP-binding | 55.56 | 447 | MAV_5276 | phosphotransferase enzyme family | 99.2 | 378 | BCG_3220 | ABC transporter ATP-binding p | 55.56 | 447 | MAP4313 | hypothetical protein | 374 | 100 |
| MAP4_4440 | putative amidohydrolase family protein | 588 | Rv2913c | Possible D-amino acid aminohydrola | 27.52 | 611 | Mb2937c | D-amino acid aminohydrolase | 27.52 | 611 | MAV_5277 | amidohydrolase | 99.49 | 588 | BCG_2934c | D-amino acid aminohydrolase | 27.52 | 611 | MAP4314 | hypothetical protein | 588 | 100 |
| MAP4_4441 | putative dioxygenase, Rieske (2Fe-2S) domain-containi | 448 | Rv3161c | Possible dioxygenase | 34.78 | 382 | Mb3186c | dioxygenase | 34.3 | 382 | MAV_5278 | Rieske (2Fe-2S) domain-containing | 98.21 | 448 | BCG_3185c | dioxygenase | 34.3 | 382 | MAP4315 | hypothetical protein | 448 | 100 |
| MAP4_4442 | hypothetical protein | 126 | Rv0076c | Probable membrane protein | 50 | 129 | Mb0078c | hypothetical protein | 50 | 129 | MAV_5279 | hypothetical protein | 100 | 74 | BCG_0107c | hypothetical protein | 50 | 129 | MAP4316 | hypothetical protein | 126 | 100 |
| MAP4_4443 | two-component system response regulator | 218 | Rv3133c | Two component transcriptional regu | 36.71 | 217 | Mb3157c | two component transcription | 36.71 | 217 | MAV_5280 | two-component system response r | 98.62 | 218 | BCG_3156c | two component transcriptional | 36.71 | 217 | MAP4317c | hypothetical protein | 218 | 100 |
| MAP4_4444 | putative two-component histidine kinase | 406 | Rv0845 | Possible two component sensor kina | 25.65 | 425 | Mb0868 | two component sensor kinase | 25.54 | 425 | MAV_5281 | histidine kinase domain-containing | 98.77 | 406 | BCG_0897 | two component sensor kinase | 25.54 | 425 | MAP4318c | hypothetical protein | 406 | 100 |
| MAP4_4445 | hypothetical protein | 126 | Rv1138c | Possible oxidoreductase | 39.22 | 338 | Mb1170c | oxidoreductase | 39.22 | 338 | MAV_5282 | hypothetical protein | 100 | 126 | BCG_1200c | oxidoreductase | 39.22 | 338 | MAP4319 | hypothetical protein | 126 | 100 |
| MAP4_4446 | transmembrane transport protein, MmpL family | 952 | Rv0450c | Probable conserved transmembrane | 35.53 | 967 | Mb1787 | transmembrane transport pro | 47.78 | 945 | MAV_5284 | membrane protein, MmpL family p | 98.32 | 952 | BCG_1797 | transmembrane transport prot | 47.78 | 945 | MAP4320 | hypothetical protein | 952 | 100 |
| MAP4_4447 | hypothetical protein | 1403 | Rv3894c | ESX conserved component EccC2 ES | 88.13 | 1396 | Mb3924c | hypothetical protein | 89.7 | 833 | MAV_2932 | ftsk/SpoIIIE family protein | 30.62 | 1375 | BCG_3951c | hypothetical protein | 89.7 | 833 | MAP4321c | hypothetical protein | 1403 | 99.93 |
| MAP4_4450 | hypothetical protein | 288 | Rv3896c | hypothetical protein | 64.73 | 302 | Mb3926c | hypothetical protein | 59.67 | 288 | MAV_5286 | transglycosylase | 96.88 | 288 | BCG_3953c | hypothetical protein | 59.67 | 288 | MAP4324c | hypothetical protein | 288 | 100 |
| MAP4_4451 | hypothetical protein | 306 | Rv2083 | hypothetical protein | 53.82 | 314 | Mb3927c | hypothetical protein | 56.35 | 329 | MAV_5287 | hypothetical protein | 100 | 306 | BCG_3954c | hypothetical protein | 56.35 | 329 | MAP4325c | hypothetical protein | 306 | 100 |
| MAP4_4452 | hypothetical protein | 719 | Rv3899c | hypothetical protein | 64.69 | 410 | Mb3928c | hypothetical protein | 73.61 | 293 | MAV_5288 | hypothetical protein | 98.28 | 419 | BCG_3955c | hypothetical protein | 73.61 | 293 | MAP4326c | hypothetical protein | 719 | 100 |
| MAP4_4453 | hypothetical protein | 181 | Rv3901c | Possible membrane protein | 58.75 | 149 | Mb3931c | hypothetical protein | 58.75 | 149 | MAV_5290 | hypothetical protein | 35.08 | 217 | BCG_3958c | hypothetical protein | 58.23 | 131 | MAP4327c | hypothetical protein | 181 | 100 |
| MAP4_4454 | hypothetical protein | 188 | Rv3901c | Possible membrane protein | 43.36 | 149 | Mb3931c | hypothetical protein | 43.36 | 149 | MAV_5290 | hypothetical protein | 74.87 | 217 | BCG_3958c | hypothetical protein | 51.22 | 131 | MAP4328c | hypothetical protein | 188 | 100 |
| MAP4_4455 | hypothetical protein | 109 | Rv2078 | hypothetical protein | 56.31 | 104 | Mb2104 | hypothetical protein | 56.31 | 104 | MAV_5291 | hypothetical protein | 94.44 | 72 | BCG_2097 | hypothetical protein | 56.31 | 104 | MAP4329c | hypothetical protein | 109 | 100 |
| MAP4_4456 | hypothetical protein | 655 | Rv2079 | hypothetical protein | 51.96 | 656 | Mb2105 | hypothetical protein | 52.1 | 656 | MAV_5292 | hypothetical protein | 96.64 | 655 | BCG_2098 | hypothetical protein | 52.1 | 656 | MAP4330c | hypothetical protein | 655 | 100 |
| MAP4_4457 | hypothetical protein | 169 | Rv3906c | hypothetical protein | 75.74 | 169 | Mb3936c | hypothetical protein | 75.74 | 169 | MAV_5293 | hypothetical protein | 99.41 | 169 | BCG_3963c | hypothetical protein | 75.74 | 169 | MAP4331c | hypothetical protein | 169 | 100 |
| MAP4_4458 | poly(A) polymerase | 480 | Rv3907c | Probable poly(A) polymerase PcnA ( | 87.06 | 480 | Mb3937c | poly(A) polymerase | 87.06 | 480 | MAV_5294 | tRNA adenylyltransferase | 99.17 | 480 | BCG_3964c | poly(A) polymerase | 87.06 | 480 | MAP4332c | PcnA | 480 | 100 |
| MAP4_4459 | hypothetical protein | 542 | Rv2079 | hypothetical protein | 55.09 | 656 | Mb2105 | hypothetical protein | 55.09 | 656 | MAV_5295 | hypothetical protein | 94.41 | 455 | BCG_2098 | hypothetical protein | 55.09 | 656 | MAP4333 | hypothetical protein | 542 | 100 |
| MAP4_4460 | putative hydrolase, NUDIX domain protein | 249 | Rv3908 | Possible mutator protein MutT4 | 81.03 | 248 | Mb3938 | hypothetical protein | 81.03 | 248 | MAV_5296 | MutT/nudix family protein | 100 | 249 | BCG_3965 | hypothetical protein | 81.03 | 248 | MAP4334 | hypothetical protein | 249 | 100 |
| MAP4_4461 | hypothetical protein | 800 | Rv3909 | hypothetical protein | 76.43 | 802 | Mb3939 | hypothetical protein | 76.43 | 802 | MAV_1814 | acyl-CoA dehydrogenase | 33.33 | 382 | BCG_3966 | hypothetical protein | 76.3 | 802 | MAP4335 | hypothetical protein | 800 | 100 |
| MAP4_4462 | hypothetical protein | 1188 | Rv3910 | Probable conserved transmembrane | 77.01 | 1184 | Mb3940 | transmembrane protein | 77.01 | 1184 | MAV_5298 | virulence factor mvin family protei | 99.16 | 1211 | BCG_3967 | hypothetical protein | 77.01 | 1184 | MAP4336 | hypothetical protein | 1188 | 99.92 |
| MAP4_4463 | RNA polymerase sigma factor SigM | 195 | Rv3911 | Possible alternative RNA polymerase | 83.44 | 222 | Mb3941 | RNA polymerase sigma factor | 82.16 | 196 | MAV_5299 | RNA polymerase sigma factor SigM | 100 | 195 | BCG_0016 | RNA polymerase sigma factor S | 82.7 | 196 | MAP4337 | RNA polymerase sigma factor SigM | 195 | 100 |
| MAP4_4464 | putative alanine rich protein | 232 | Rv3912 | Hypothetical alanine rich protein | 54.12 | 254 | Mb3943 | hypothetical protein | 54.12 | 254 | MAV_5300 | hypothetical protein | 91.34 | 254 | BCG_0018 | hypothetical protein | 54.12 | 254 | MAP4338 | hypothetical protein | 232 | 100 |
| MAP4_4465 | thioredoxin reductase | 336 | Rv3913 | Probable thioredoxin reductase TrxE | 80.99 | 335 | Mb3944 | thioredoxin reductase | 80.99 | 335 | MAV_5301 | thioredoxin-disulfide reductase | 99.7 | 366 | BCG_0019 | thioredoxin reductase trxB2 (T | 80.99 | 335 | MAP4339 | hypothetical protein | 336 | 100 |
| MAP4_4466 | thioredoxin | 117 | Rv3914 | Thioredoxin TrxC (TRX) (MPT46) | 88.03 | 116 | Mb3945 | thioredoxin | 88.03 | 116 | MAV_5302 | thioredoxin | 99.15 | 117 | BCG_0020 | thioredoxin trxC (TRX) (MPT46) | 88.03 | 116 | MAP4340 | TrxC | 117 | 100 |
| MAP4_4467 | putative peptidoglycan hydrolase | 406 | Rv3915 | Probable peptidoglycan hydrolase | 90.39 | 406 | Mb3946 | hydrolase | 90.39 | 406 | MAV_5303 | N-acetylmuramoyl-L-alanine amida | 100 | 406 | BCG_0021 | hydrolase | 90.39 | 406 | MAP4341 | CwlM | 406 | 100 |
| MAP4_4468 | hypothetical protein | 250 | Rv3916c | hypothetical protein | 83.06 | 244 | Mb3947c | hypothetical protein | 83.06 | 244 | MAV_5304 | hypothetical protein | 100 | 243 | BCG_0022c | hypothetical protein | 83.06 | 244 | MAP4342c | hypothetical protein | 250 | 100 |
| MAP4_4469 | chromosome partitioning protein ParB | 328 | Rv3917c | Probable chromosome partitioning | 84.89 | 344 | Mb3948c | chromosome partitioning pro | 84.89 | 344 | MAV_5306 | ParB-like partition proteins | 100 | 328 | BCG_0023c | chromosome partitioning prote | 84.89 | 344 | MAP4343c | hypothetical protein | 328 | 100 |
| MAP4_4470 | chromosome partitioning protein ParA | 367 | Rv3918c | Probable chromosome partitioning | 82.49 | 347 | Mb3949c | chromosome partitioning pro | 82.49 | 347 | MAV_5307 | CobQ/CobB/MinD/ParA nucleotide | 94.82 | 365 | BCG_0024c | chromosome partitioning prote | 82.49 | 347 | MAP4344c | hypothetical protein | 367 | 100 |
| MAP4_4471 | glucose-inhibited division protein B Gid | 248 | Rv3919c | Probable glucose-inhibited division | 73.27 | 224 | Mb3950c | 16S rRNA methyltransferase | 73.27 | 224 | MAV_5308 | 16S rRNA methyltransferase GidB | 97.55 | 245 | BCG_0025c | 16S rRNA methyltransferase Gi | 73.27 | 224 | MAP4345c | 16S rRNA methyltransferase GidB | 248 | 100 |
| MAP4_4472 | single-stranded nucleic acid binding R3H domain-conta | 183 | Rv3920c | Conserved protein similar to jag pro | 85.03 | 187 | Mb3951c | hypothetical protein | 84.49 | 187 | MAV_5309 | R3H domain-containing protein | 100 | 183 | BCG_0026c | hypothetical protein | 84.49 | 187 | MAP4346c | hypothetical protein | 195 | 100 |
| MAP4_4473 | putative conserved membrane protein | 353 | Rv3921c | Probable conserved transmembrane | 82.79 | 366 | Mb3952c | inner membrane protein tran | 82.79 | 366 | MAV_5310 | inner membrane protein translocas | 99.43 | 350 | BCG_0027c | preprotein translocase subunit | 82.51 | 366 | MAP4347c | inner membrane protein translocase co | 353 | 100 |
| MAP4_4474 | hemolysin | 115 | Rv3922c | Possible hemolysin | 64.29 | 120 | Mb3953c | hypothetical protein | 64.29 | 120 | MAV_5311 | hypothetical protein | 99.13 | 115 | BCG_0028c | hypothetical protein | 64.29 | 120 | MAP4348c | hypothetical protein | 115 | 100 |
| MAP4_4475 | ribonuclease P protein component RnpA | 119 | Rv3923c | Ribonuclease P protein component | 59.5 | 125 | Mb3954c | ribonuclease P | 60.33 | 116 | MAV_5312 | ribonuclease P | 95.76 | 119 | BCG_0029c | ribonuclease P | 59.5 | 125 | MAP4349c | ribonuclease P | 119 | 100 |
| MAP4_4476 | 50S ribosomal protein L34 | 47 | Rv3924c | 50S ribosomal protein L34 RpmH | 91.49 | 47 | Mb3955c | 50S ribosomal protein L34 | 91.49 | 47 | MAV_5313 | 50S ribosomal protein L34 | 100 | 47 | BCG_0030c | 50S ribosomal protein L34 | 91.49 | 47 | MAP4350c | 50S ribosomal protein L34 | 47 | 100 |
| | | | | | | | | | | | | | | | | | | | MAP0124 | hypothetical protein | 236 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP0998c | hypothetical protein | 216 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1075c | hypothetical protein | 88 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1088 | hypothetical protein | 171 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1229 | hypothetical protein | 398 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1265 | hypothetical protein | 219 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1278 | hypothetical protein | 370 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1420 | hypothetical protein | 6384 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1818c | hypothetical protein | 67 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2186c | hypothetical protein | 142 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2193 | hypothetical protein | 378 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2248c | hypothetical protein | 331 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2425c | hypothetical protein | 147 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2505 | hypothetical protein | 203 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2511 | hypothetical protein | 346 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2678c | hypothetical protein | 91 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP3050c | hypothetical protein | 115 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP3421c | hypothetical protein | 135 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP3629c | hypothetical protein | 94 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP1346 | Conserved hypothetical protein | 962 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2133 | Membrane protein | 1485 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2187c | Proline rich protein precursor | 1083 | No identitity |
| | | | | | | | | | | | | | | | | | | | MAP2827c | iron dependent repressor, IdeR | 570 | No identitity |
| | | | | | | | | | | | | | | | | | | | | | | |
| | | Average | | | **62.70349** | | | | **62.50775** | | | | **94.13585** | | | | **62.49926** | | | | | **98.15136** |
| | | Range | | | **19.28 100.00** | | | | **20.69 100.00** | | | | **23.19 100.00** | | | | **20 100** | | | | | **23.53 100.00** |
| | | Variance | | | **538.7261** | | | | **540.8841** | | | | **276.9931** | | | | **540.9068** | | | | | **105.8526** |

# Table S2

**Table S2. Characteristics of bovine repository serum samples**

| Sample No. | IDEXX Serum ELISA result | IDEXX Serum ELISA OD | IDEXX Serum ELISA SP ratio | araChek ELISA ELISA result | araChek ELISA ELISA OD | Milk-Archive ELISA result | Milk-Archive ELISA OD | Milk-Archive ELISA SP ratio | EYM Fecal culture Result | Avg CFU/g | MGIT Fecal Cultu Result | IGIT Fecal Cultu Days to + | IGIT Fecal Cultu AF stain | IGIT Fecal Cultu PCR confirm | rek Fecal Cultur Result | rek Fecal Cultur Days to + | rek Fecal Cultur AF stain | rek Fecal Cultur PCR confirm | TacMan Fecal PC Result | T TacMan Fecal PCR CT value 1 | tracore Fecal P Result | etracore Fecal PCR CT value 1 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0010 | Positive | 2.836 | 2.498 | Positive | 3.8185 | Positive | 2.149 | 2.562 | Positive | 87.5 | Positive | 19 | Positive | Yes | Heavy | 20 | Positive | Yes | Heavy | 25.18 | Heavy | 26.41 |
| 0020 | Positive | 2.625 | 2.55 | Positive | 3.2085 | Positive | 1.847 | 2.309 | Positive | 12.25 | Positive | 27 | Positive | Yes | Heavy | 20 | Positive | Yes | Heavy | 27.23 | Light | 31.99 |
| 0058 | Positive | 1.8 | 1.559 | Positive | 1.0445 | Positive | 0.939 | 1.193 | Positive | 125 | Positive | 20 | Positive | Yes | Heavy | 21 | Positive | Yes | Heavy | 24.61 | Heavy | 27.86 |
| 0074 | Positive | 1.997 | 1.842 | Positive | 0.6705 | Positive | 0.7 | 0.751 | Positive | 8.75 | Positive | 31 | Positive | Yes | Moderate | 28 | Positive | Yes | Heavy | 29.70 | Light | 29.85 |
| 0304 | Positive | 2.789 | 2.75 | Positive | 2.437 | Susp | 0.29 | 0.307 | Positive | 200 | Positive | 19 | Positive | Yes | Heavy | 18 | Positive | Yes | Heavy | 23.08 | Heavy | 25.95 |
| 0392 | Positive | 1.482 | 1.355 | Positive | 0.8305 | Positive | 0.732 | 0.788 | Positive | 3.75 | Positive | 30 | Positive | Yes | Light | 30 | Positive | Yes | Heavy | 26.59 | Moderate | 29.22 |
| 0420 | Positive | 2.569 | 2.136 | Positive | 1.613 | Positive | 1.629 | 1.824 | Positive | 87.5 | Positive | 20 | Positive | Yes | Heavy | 17 | Positive | Yes | Heavy | 22.68 | Moderate | 28.47 |
| 0467 | Positive | 1.718 | 1.578 | Positive | 1.0575 | Positive | 0.406 | 0.413 | Positive | 2.25 | Positive | 30 | Positive | Yes | Moderate | 28 | Positive | Yes | Heavy | 28.45 | Low positive | 31.16 |
| 0522 | Positive | 2.457 | 2.48 | Positive | 2.691 |  |  |  | Positive | 300 | Positive | 15 | Positive | Yes | Heavy | 15 | Positive | Yes | Heavy | 19.08 | Heavy | 23.38 |
| 0627 | Positive | 1.714 | 1.482 | Positive | 0.6115 | Positive | 1.157 | 1.485 | Positive | 32.5 | Positive | 23 | Positive | Yes | Light | 32 | Positive | Yes | Heavy | 27.32 | Light | 30.63 |
| 0684 | Positive | 2.789 | 2.263 | Positive | 2.11 | Positive | 1.844 | 2.409 | Positive | 300 | Positive | 19 | Positive | Yes | Heavy | 16 | Positive | Yes | Heavy | 22.81 | Heavy | 25.70 |
| 0714 | Positive | 2.833 | 2.868 | Positive | 3.2825 | Positive | 2.103 | 2.654 | Positive | 0.5 | Positive | 26 | Positive | Yes | Moderate | 23 | Positive | Yes | Heavy | 28.56 | Light | 34.57 |
| 0722 | Positive | 1.968 | 1.585 | Positive | 0.8975 | Positive | 1.332 | 1.72 | Positive | 87.5 | Positive | 23 | Positive | Yes | Heavy | 21 | Positive | Yes | Heavy | 23.83 | Heavy | 26.90 |
| 0771 | Positive | 0.698 | 0.721 | Positive | 0.3595 | Neg. | 0.206 | 0.197 | Positive | 13.5 | Positive | 27 | Positive | Yes | Moderate | 28 | Positive | Yes | Heavy | 27.85 | Light | 30.80 |
| 0787 | Positive | 2.296 | 2 | Positive | 1.047 | Positive | 1.448 | 1.876 | Positive | 300 | Positive | 15 | Positive | Yes | Heavy | 20 | Positive | Yes | Heavy | 19.42 | Heavy | 19.96 |
| 0936 | Positive | 1.649 | 1.437 | Positive | 0.5145 | Positive | 0.688 | 0.777 | Positive | 1 | Positive | 29 | Positive | Yes | Light | 30 | Positive | Yes | Heavy | 30.72 | Light | 34.64 |
| 0951 | Positive | 2.232 | 1.803 | Positive | 0.491 | Positive | 1.218 | 1.567 | Positive | 300 | Positive | 17 | Positive | Yes | Heavy | 17 | Positive | Yes | Heavy | 20.07 | Heavy | 21.35 |
| 0999 | Positive | 2.965 | 2.682 | Positive | 2.7175 | Positive | 2.307 | 2.606 | Positive | 20.25 | Positive | 26 | Positive | Yes | Moderate | 25 | Positive | Yes | Heavy | 25.68 | Moderate | 29.65 |
| 1005 | Positive | 2.333 | 2.469 | Positive | 1.2785 | Positive | 1.207 | 1.51 | Positive | 87.5 | Positive | 24 | Positive | Yes | Heavy | 21 | Positive | Yes | Heavy | 25.41 | Heavy | 26.17 |
| 1037 | Positive | 2.13 | 2.366 | Positive | 1.319 | Positive | 1.249 | 1.487 | Positive | 300 | Positive | 15 | Positive | Yes | Heavy | 18 | Positive | Yes | Heavy | 23.22 | Heavy | 25.09 |
| 1094 | Positive | 2.274 | 2.207 | Positive | 1.279 | Positive | 1.358 | 1.678 | Positive | 87.5 | Positive | 10 | Positive | Yes | Light | 32 | Positive | Yes | Heavy | 20.02 | Heavy | 25.94 |
| 1206 | Positive | 2.162 | 2.261 | Positive | 0.4745 | Positive | 1.194 | 1.418 | Positive | 300 | Positive | 14 | Positive | Yes | Heavy | 7 | Positive | Yes | Heavy | 17.48 | Heavy | 20.96 |
| 1261 | Positive | 2.383 | 2.445 | Positive | 1.9275 | Positive | 2.189 | 2.744 | Positive | 87.5 | Positive | 16 | Positive | Yes | Heavy | 21 | Positive | Yes | Heavy | 20.45 | Heavy | 23.84 |
| 1264 | Positive | 1.431 | 2.133 | Positive | 0.6905 | Positive | 0.937 | 1.156 | Positive | 18.5 | Positive | 27 | Positive | Yes | Moderate | 23 | Positive | Yes | Heavy | 29.22 | Light | 32.83 |
| 1297 | Positive | 1.912 | 1.951 | Positive | 0.758 | Positive | 0.486 | 0.557 | Positive | 0.75 | Positive | 33 | Positive | Yes | Moderate | 24 | Positive | Yes | Heavy | 30.37 | Light | 33.41 |
| 1330 | Positive | 1.376 | 2.177 | Positive | 0.917 | Positive | 1.298 | 1.636 | Positive | 300 | Positive | 17 | Positive | Yes | Light | 35 | Positive | Yes | Heavy | 23.11 | Heavy | 25.85 |
| 1342 | Positive | 1.641 | 1.579 | Positive | 0.5175 | Positive | 0.368 | 0.435 | Positive | 187.5 | Positive | 21 | Positive | Yes | Moderate | 23 | Positive | Yes | Heavy | 23.53 | Heavy | 27.41 |
| 1415 | Positive | 1.915 | 1.995 | Positive | 1.4285 | Positive | 0.849 | 0.99 | Positive | 150 | Positive | 23 | Positive | Yes | Moderate | 24 | Positive | Yes | Heavy | 23.29 | Heavy | 25.65 |
| 1674 | Positive | 1.386 | 2.111 | Positive | 1.1095 | Positive | 1.175 | 1.473 | Positive | 300 | Positive | 19 | Positive | Yes | Heavy | 19 | Positive | Yes | Heavy | 22.98 | Moderate | 29.10 |
| 1690 | Positive | 2.343 | 2.999 | Positive | 1.718 | Positive | 1.83 | 2.391 | Positive | 87.5 | Positive | 20 | Positive | Yes | Heavy | 16 | Positive | Yes | Heavy | 27.02 | Moderate | 29.37 |
| 1712 | Positive | 2.805 | 3.134 | Positive | 2.455 | Positive | 2.045 | 2.603 | Positive | 300 | Positive | 16 | Positive | Yes | Heavy | 13 | Positive | Yes | Heavy | 22.64 | Heavy | 25.12 |
| 1718 | Positive | 2.007 | 2.257 | Positive | 0.761 | Positive | 1.123 | 1.33 | Positive | 87.5 | Positive | 23 | Positive | Yes | Heavy | 16 | Positive | Yes | Heavy | 25.14 | Heavy | 27.33 |
| 1746 | Positive | 2.449 | 2.57 | Positive | 1.802 | Positive | 0.986 | 1.16 | Positive | 0.75 | Positive | 35 | Positive | Yes | Light | 29 | Positive | Yes | Moderate | 31.08 | Light | 33.59 |
| 1998 | Positive | 2.731 | 2.9 | Positive | 2.566 | Positive | 1.403 | 1.766 | Positive | 19.75 | Positive | 31 | Positive | Yes | Moderate | 22 | Positive | Yes | Heavy | 24.01 | Heavy | 26.60 |
| 2234 | Positive | 1.655 | 2.064 | Positive | 1.467 | Positive | 1.396 | 1.806 | Positive | 87.5 | Positive | 27 | Positive | Yes | Heavy | 20 | Positive | Yes | Heavy | 29.14 | Moderate | 29.79 |
| 2298 | Positive | 2.443 | 3.304 | Positive | 3.0455 | Positive | 1.065 | 1.398 | Positive | 300 | Positive | 14 | Positive | Yes | Heavy | 17 | Positive | Yes | Heavy | 22.01 | Heavy | 24.78 |
| 2356 | Positive | 1.988 | 2.464 | Positive | 1.719 | Positive | 1.469 | 1.905 | Positive | 300 | Positive | 16 | Positive | Yes | Heavy | 17 | Positive | Yes | Heavy | 25.76 | Moderate | 28.21 |
| 2490 | Positive | 1.381 | 1.924 | Positive | 1.8705 | Positive | 0.366 | 0.434 | Positive | 100 | Positive | 20 | Positive | Yes | Heavy | 16 | Positive | Yes | Heavy | 25.92 | Moderate | 29.38 |
| 2574 | Positive | 1.16 | 1.528 | Positive | 0.4315 | Positive | 0.759 | 0.977 | Positive | 300 | Positive | 17 | Positive | Yes | Light | 35 | Positive | Yes | Heavy | 25.01 | Heavy | 27.07 |
| 2783 | Positive | 1.518 | 1.824 | Positive | 1.483 | Positive | 1.087 | 1.392 | Positive | 11.25 | Positive | 27 | Positive | Yes | Moderate | 22 | Positive | Yes | Heavy | 30.53 | Light | 34.05 |
| 2800 | Positive | 2.405 | 2.995 | Positive | 2.467 | Positive | 2.433 | 3.201 | Positive | 125 | Positive | 16 | Positive | Yes | Heavy | 16 | Positive | Yes | Heavy | 25.75 | Heavy | 27.46 |
| 2954 | Positive | 1.615 | 1.989 | Positive | 1.468 | Positive | 0.941 | 1.195 | Positive | 6.5 | Positive | 27 | Positive | Yes | Heavy | 21 | Positive | Yes | Moderate | 31.98 | Light | 33.60 |
| 1057 | Neg. | 0.054 | 0.009 | Neg. | 0.063 | Neg. | 0.063 | 0.016 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1081 | Neg. | 0.053 | 0.005 | Neg. | 0.0525 | Neg. | 0.065 | 0.017 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1153 | Neg. | 0.055 | 0.011 | Neg. | 0.054 | Neg. | 0.112 | 0.079 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1224 | Neg. | 0.052 | 0.003 | Neg. | 0.0555 | Neg. | 0.058 | 0.007 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1294 | Neg. | 0.048 | -0.007 | Neg. | 0.0505 | Neg. | 0.057 | 0.007 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1301 | Neg. | 0.058 | 0.003 | Neg. | 0.055 | Neg. | 0.066 | 0.019 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1348 | Neg. | 0.059 | 0.006 | Neg. | 0.057 | Neg. | 0.059 | 0.01 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1365 | Neg. | 0.053 | -0.005 | Neg. | 0.054 | Neg. | 0.05 | 0.003 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1372 | Neg. | 0.055 | 0.008 | Neg. | 0.0575 | Neg. | 0.057 | -0.008 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1380 | Neg. | 0.06 | 0.008 | Neg. | 0.054 | Neg. | 0.073 | 0.031 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1395 | Neg. | 0.055 | 0.007 | Neg. | 0.054 | Neg. | 0.098 | 0.065 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1420 | Neg. | 0.052 | 0.005 | Neg. | 0.0555 | Neg. | 0.06 | 0.013 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1465 | Neg. | 0.057 | 0.007 | Neg. | 0.058 | Neg. | 0.057 | 0.007 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1476 | Neg. | 0.056 | 0.009 | Neg. | 0.0545 | Neg. | 0.076 | 0.018 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1497 | Neg. | 0.056 | 0.005 | Neg. | 0.0535 | Neg. | 0.058 | 0.009 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1579 | Neg. | 0.057 | 0.002 | Neg. | 0.0575 | Neg. | 0.06 | 0.014 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1591 | Neg. | 0.051 | -0.002 | Neg. | 0.052 | Neg. | 0.061 | 0.013 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1630 | Neg. | 0.057 | 0.009 | Neg. | 0.056 | Neg. | 0.059 | 0.009 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1634 | Neg. | 0.052 | 0.005 | Neg. | 0.05 | Neg. | 0.059 | 0.009 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1643 | Neg. | 0.056 | 0 | Neg. | 0.053 | Neg. | 0.063 | 0.015 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1671 | Neg. | 0.061 | 0.01 | Neg. | 0.0535 | Neg. | 0.059 | 0.01 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1724 | Neg. | 0.053 | 0.004 | Neg. | 0.053 | Neg. | 0.053 | 0.007 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1762 | Neg. | 0.055 | 0.01 | Neg. | 0.0575 | Neg. | 0.062 | 0.014 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1775 | Neg. | 0.048 | 0 | Neg. | 0.0655 | Neg. | 0.053 | 0.003 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1803 | Neg. | 0.058 | 0.004 | Neg. | 0.058 | Neg. | 0.059 | 0.01 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1833 | Neg. | 0.056 | 0.009 | Neg. | 0.0585 | Neg. | 0.055 | 0.003 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1910 | Neg. | 0.053 | -0.005 | Neg. | 0.0535 | Neg. | 0.057 | 0.006 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1938 | Neg. | 0.056 | 0 | Neg. | 0.053 | Neg. | 0.061 | 0.013 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1959 | Neg. | 0.053 | 0.006 | Neg. | 0.053 | Neg. | 0.061 | 0.013 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |
| 1970 | Neg. | 0.055 | 0.01 | Neg. | 0.053 | Neg. | 0.1 | 0.049 | Neg. | 0 | Neg. |  | Neg. |  | Neg. |  | Neg. |  | Neg. | Undetermined | Neg. | Undetermined |

# Table S3

**Table S3. Univariate statistical comparisons of responses between clinical and subclinical cows on 729 seroreactive Mtb proteins**

| Rank[a] | Mtb Gene ID | Map Homolog | % Identity | Description | Spot ID | T Test P-value | T Test BH P-value | AUC | Rank-Sum P-value | Rank Sum BH P-value | Mean all infected[b] | Mean Subclinical | 95% CI Minimum | 95% CI Maximum | Median Subclinical | Mean Clinical | 95% CI Minimum | 95% CI Maximum | Median Clinical |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Rv1860 | MAP1569 | 78 | Alanine and proline rich secreted protein Apa (fibronectin atta | Rv1860.1477 | 4.39E-02 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 14.5 | 13.0 | 12.0 | 14.0 | 13.1 | 15.3 | 15.1 | 15.5 | 15.3 |
| 2 | Rv2878c | MAP2942c | 78 | Soluble secreted antigen Mpt53 precursor | Rv2878c.3783 | 2.25E-03 | 4.10E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 13.7 | 11.7 | 11.0 | 12.4 | 11.7 | 14.8 | 14.3 | 15.2 | 15.0 |
| 3 | Rv3879c | MAP2472 | 50 | ESX-1 secretion-associated protein EspK Alanine and proline ric | Rv3879c.4124 | 3.04E-01 | 7.74E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 14.7 | 14.9 | 14.5 | 15.2 | 15.0 | 14.6 | 14.5 | 14.8 | 14.6 |
| 4 | Rv3043c | MAP3091c | 93 | Probable cytochrome C oxidase polypeptide I CtaD (cytochrom | Rv3043c.1478 | 5.97E-01 | 9.20E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 14.5 | 14.4 | 14.2 | 14.7 | 14.4 | 14.5 | 14.2 | 14.8 | 14.4 |
| 5 | Rv2672 | MAP2792 | 78 | Possible secreted protease | Rv2672.1481 | 9.61E-01 | 9.82E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 14.4 | 14.4 | 13.5 | 15.4 | 14.6 | 14.4 | 13.8 | 14.9 | 14.5 |
| 6 | Rv3515c | MAP0550 | 90 | Fatty-acid-CoA ligase FadD19 (fatty-acid-CoA synthetase) (fatty | Rv3515c.3817 | 7.86E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 14.3 | 14.4 | 14.0 | 14.7 | 14.3 | 14.3 | 13.9 | 14.7 | 14.4 |
| 7 | Rv0954 | MAP0900 | 55 | Probable conserved transmembrane protein | Rv0954.2404 | 9.25E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 14.2 | 14.2 | 13.7 | 14.6 | 14.1 | 14.2 | 13.7 | 14.7 | 14.4 |
| 8 | Rv0479c | MAP3972c | 59 | Probable conserved membrane protein | Rv0479c.381 | 9.54E-01 | 9.82E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 14.2 | 14.2 | 13.7 | 14.6 | 14.3 | 14.1 | 13.8 | 14.5 | 14.2 |
| 9 | Rv3614c | MAP2306 | 43 | ESX-1 secretion-associated protein EspD | Rv3614c.3831 | 4.37E-01 | 8.38E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 14.1 | 14.0 | 13.9 | 14.1 | 14.0 | 14.1 | 13.8 | 14.4 | 14.0 |
| 10 | Rv0338c | MAP3831c | 77 | Probable iron-sulfur-binding reductase | Rv0338c.1240 | 7.76E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 14.0 | 14.1 | 13.8 | 14.4 | 14.0 | 14.0 | 13.6 | 14.4 | 14.2 |
| 11 | Rv2495c | MAP2307c | 73 | Probable branched-chain keto acid dehydrogenase E2 compon | Rv2495c.1480 | 7.37E-01 | 9.57E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.9 | 13.9 | 13.6 | 14.2 | 13.9 | 14.0 | 13.6 | 14.3 | 14.0 |
| 12 | Rv3692 | MAP0359c | 88 | Probable methanol dehydrogenase transcriptional regulatory p | Rv3692.2526 | 9.31E-01 | 9.82E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 14.0 | 14.0 | 13.5 | 14.5 | 13.7 | 14.0 | 13.7 | 14.3 | 13.9 |
| 13 | Rv3766 | MAP1313c | 29 | Hypothetical protein | Rv3766.4196 | 2.77E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.7 | 13.4 | 13.3 | 13.5 | 13.4 | 13.9 | 13.6 | 14.3 | 13.9 |
| 14 | Rv0396 | MAP0294c | 46 | Hypothetical protein | Rv0396.2720 | 3.31E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.5 | 12.9 | 12.6 | 13.2 | 12.7 | 13.9 | 13.2 | 14.5 | 13.5 |
| 15 | Rv0171 | MAP3606 | 79 | Mce-family protein Mce1C | Rv0171.3238 | 9.14E-01 | 9.81E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.9 | 13.9 | 13.2 | 14.6 | 13.9 | 13.9 | 13.3 | 14.4 | 14.0 |
| 16 | Rv0040c | MAP0047c | 78 | Secreted proline rich protein Mtc28 (proline rich 28 kDa antige | Rv0040c.1188 | 3.21E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.3 | 12.2 | 11.4 | 13.0 | 12.1 | 13.8 | 13.2 | 14.5 | 14.0 |
| 17 | Rv2995c | MAP3032c | 88 | Probable 3-isopropylmalate dehydrogenase LeuB (beta-IPM de | Rv2995c.3959 | 7.87E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.8 | 13.9 | 13.3 | 14.4 | 13.9 | 13.8 | 13.3 | 14.2 | 13.9 |
| 18 | Rv1166 | MAP2615c | 83 | Probable conserved lipoprotein LpqW | Rv1166.2863 | 6.43E-01 | 9.33E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.7 | 13.6 | 13.2 | 14.1 | 13.5 | 13.8 | 13.5 | 14.0 | 13.8 |
| 19 | Rv1004c | MAP0210c | 54 | Probable membrane protein | Rv1004c.613 | 3.81E-01 | 8.35E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.9 | 14.1 | 13.6 | 14.7 | 14.0 | 13.7 | 13.1 | 14.4 | 13.6 |
| 20 | Rv0388c | MAP1515 | 64 | PPE family protein PPE9 | Rv0388c.3900 | 1.74E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.6 | 13.4 | 13.0 | 13.7 | 13.3 | 13.7 | 13.4 | 14.0 | 13.6 |
| 21 | Rv1343c | MAP2418 | 82 | Probable conserved lipoprotein LprD | Rv1343c.938 | 7.36E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.5 | 13.0 | 12.9 | 13.1 | 13.1 | 13.7 | 13.1 | 14.3 | 13.7 |
| 22 | Rv3267 | MAP0191c | 82 | Conserved protein (CPSA-related protein) | Rv3267.821 | 1.38E-02 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 13.6 | 13.3 | 13.1 | 13.4 | 13.3 | 13.7 | 13.5 | 13.9 | 13.6 |
| 23 | Rv2435c | MAP1279c | 65 | Hypothetical protein | Rv2435c-sB.56 | 2.45E-01 | 7.49E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 13.9 | 14.3 | 13.6 | 15.1 | 14.0 | 13.7 | 13.3 | 14.1 | 13.6 |
| 24 | Rv1323 | MAP2436c | 91 | Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA | Rv1323.2958 | 9.76E-02 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.5 | 13.1 | 13.0 | 13.3 | 13.2 | 13.7 | 13.1 | 14.3 | 13.7 |
| 25 | Rv3587c | MAP0471 | 87 | Probable conserved membrane protein | Rv3587c.3848 | 8.33E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.5 | 13.3 | 13.1 | 13.4 | 13.3 | 13.7 | 13.3 | 14.0 | 13.8 |
| 26 | Rv3920c | MAP4346c | 93 | Conserved protein similar to jag protein | Rv3920c.1872 | 6.00E-01 | 9.20E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.6 | 13.5 | 13.3 | 13.8 | 13.5 | 13.7 | 13.3 | 14.0 | 13.6 |
| 27 | Rv3757c | MAP0146 | 74 | Possible osmoprotectant (glycine betaine/carnitine/choline/L-p | Rv3757c.3907 | 1.07E-01 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.5 | 13.1 | 12.8 | 13.5 | 13.0 | 13.7 | 13.3 | 14.0 | 13.8 |
| 28 | Rv0442c | MAP3939c | 72 | PPE family protein PPE10 | Rv0442c.3421 | 8.90E-03 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.4 | 12.8 | 12.6 | 12.9 | 12.7 | 13.7 | 13.2 | 14.1 | 13.7 |
| 29 | Rv2056c | MAP3768c | 80 | 30S ribosomal protein S14 RpsN2 | Rv2056c.2133 | 3.01E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.3 | 12.6 | 12.1 | 13.1 | 12.5 | 13.7 | 13.3 | 14.0 | 13.7 |
| 30 | Rv0809 | MAP0366 | 90 | Probable phosphoribosylformylglycinamidine CYCLO-ligase Pur | Rv0809.350 | 2.34E-01 | 7.42E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 13.7 | 13.9 | 13.6 | 14.2 | 14.0 | 13.6 | 13.4 | 13.8 | 13.6 |
| 31 | Rv0313 | MAP3018 | 31 | hypothetical protein | Rv0313.3534 | 1.52E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.5 | 13.2 | 12.8 | 13.5 | 13.3 | 13.6 | 13.2 | 14.0 | 13.4 |
| 32 | Rv3494c | MAP0569 | 86 | Mce-family protein Mce4F | Rv3494c.2372 | 3.33E-01 | 8.11E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 13.7 | 14.0 | 13.3 | 14.7 | 13.9 | 13.6 | 13.4 | 13.8 | 13.6 |
| 33 | Rv3347c | MAP2121c | 61 | Hypothetical protein | Rv3347c-sB.11 | 7.17E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.4 | 13.2 | 13.0 | 13.4 | 13.2 | 13.6 | 13.2 | 13.9 | 13.6 |
| 34 | Rv1363c | MAP0751c | 60 | Possible membrane protein | Rv1363c.3934 | 1.41E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.5 | 13.3 | 13.1 | 13.5 | 13.4 | 13.6 | 13.4 | 13.8 | 13.5 |
| 35 | Rv3245c | MAP3359c | 88 | Two component sensory transduction histidine kinase MtrB | Rv3245c.3141 | 9.17E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.4 | 12.9 | 12.5 | 13.4 | 12.8 | 13.6 | 13.2 | 14.0 | 13.5 |
| 36 | Rv2914c | MAP1332 | 52 | Probable transmembrane serine/threonine-protein kinase I Pkı | Rv2914c.829 | 1.60E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.4 | 13.1 | 12.6 | 13.5 | 13.2 | 13.6 | 13.3 | 13.8 | 13.6 |
| 37 | Rv0553 | MAP1382c | 82 | Probable muconate cycloisomerase MenC (cis,cis-muconate la | Rv0553.2813 | 3.83E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.3 | 12.8 | 12.7 | 12.9 | 12.8 | 13.6 | 13.0 | 14.1 | 13.7 |
| 38 | Rv1368 | MAP1138c | 30 | Probable conserved lipoprotein LprF | Rv1368.4131 | 4.05E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.4 | 13.2 | 12.4 | 13.9 | 13.0 | 13.6 | 13.3 | 13.8 | 13.7 |
| 39 | Rv3029c | MAP3061c | 92 | Probable electron transfer flavoprotein (beta-subunit) FixA (be | Rv3029c.1343 | 4.58E-01 | 8.44E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.6 | 13.7 | 13.5 | 13.9 | 13.7 | 13.6 | 13.3 | 13.8 | 13.4 |
| 40 | Rv1968 | MAP2114c | 47 | Mce-family protein Mce3C | Rv1968.1514 | 2.16E-03 | 4.10E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 13.4 | 13.0 | 13.0 | 13.1 | 13.0 | 13.6 | 13.4 | 13.7 | 13.5 |
| 41 | Rv2207 | MAP1948 | 83 | Probable nicotinate-nucleotide-dimethylbenzimidazol phospho | Rv2207.503 | 2.88E-01 | 7.74E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.6 | 13.8 | 13.7 | 14.0 | 13.9 | 13.5 | 13.1 | 14.0 | 13.6 |
| 42 | Rv2436 | MAP0299c | 70 | Ribokinase RbsK | Rv2436.1059 | 6.37E-01 | 9.31E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.5 | 13.4 | 13.2 | 13.6 | 13.3 | 13.5 | 13.2 | 13.9 | 13.6 |
| 43 | Rv1718 | MAP0381 | 33 | hypothetical protein | Rv1718.1922 | 7.39E-01 | 9.57E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.6 | 13.6 | 13.2 | 14.0 | 13.7 | 13.5 | 13.2 | 13.8 | 13.5 |
| 44 | Rv2835c | MAP1809c | 33 | Probable Sn-glycerol-3-phosphate transport integral membran | Rv2835c.764 | 4.68E-02 | 6.27E-01 | 0.81 | 1.95E-01 | 8.76E-01 | 13.3 | 13.0 | 12.8 | 13.2 | 13.0 | 13.5 | 13.2 | 13.9 | 13.6 |
| 45 | Rv3539 | MAP3939c | 60 | PPE family protein PPE63 | Rv3539.636 | 1.26E-01 | 6.73E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.4 | 13.0 | 12.9 | 13.2 | 13.0 | 13.5 | 13.0 | 14.0 | 13.5 |
| 46 | Rv2176 | MAP1914 | 73 | Probable transmembrane serine/threonine-protein kinase L Pk | Rv2176.3992 | 1.58E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.4 | 13.2 | 13.0 | 13.4 | 13.2 | 13.5 | 13.2 | 13.8 | 13.5 |
| 47 | Rv0621 | MAP2026 | 56 | Possible membrane protein | Rv0621.2227 | 2.57E-01 | 7.62E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.4 | 13.1 | 12.8 | 13.5 | 13.2 | 13.5 | 13.1 | 13.9 | 13.4 |
| 48 | Rv3811 | MAP0209c | 77 | hypothetical protein | Rv3811.839 | 4.51E-02 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 13.2 | 12.7 | 12.3 | 13.1 | 12.9 | 13.5 | 13.2 | 13.7 | 13.4 |
| 49 | Rv3413c | MAP4276 | 59 | Unknown alanine and proline rich protein | Rv3413c.2208 | 2.87E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.3 | 12.9 | 12.0 | 13.7 | 12.6 | 13.5 | 13.3 | 13.7 | 13.4 |
| 50 | Rv1217c | MAP2561 | 76 | Probable tetronasin-transport integral membrane protein ABC | Rv1217c.2562 | 3.79E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.3 | 13.0 | 12.8 | 13.3 | 13.1 | 13.5 | 13.3 | 13.6 | 13.5 |
| 51 | Rv2500c | MAP2312c | 90 | Possible acyl-CoA dehydrogenase FadE19 (MMGC) | Rv2500c.640 | 7.28E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.3 | 13.0 | 12.9 | 13.1 | 13.0 | 13.5 | 13.1 | 13.9 | 13.4 |
| 52 | Rv3005c | MAP2663c | 70 | hypothetical protein | Rv3005c.2773 | 4.27E-01 | 8.35E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.4 | 13.2 | 12.9 | 13.6 | 13.2 | 13.5 | 13.0 | 13.9 | 13.5 |
| 53 | Rv3604c | MAP0454 | 54 | Probable conserved transmembrane protein rich in alanine and | Rv3604c.3266 | 3.88E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.3 | 13.0 | 12.8 | 13.1 | 12.9 | 13.5 | 13.1 | 13.8 | 13.5 |
| 54 | Rv2423 | MAP1673c | 58 | Hypothetical protein | Rv2423.781 | 1.12E-01 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.3 | 12.9 | 12.5 | 13.2 | 12.9 | 13.4 | 12.9 | 14.0 | 13.5 |
| 55 | Rv1272c | MAP2500 | 79 | Probable drugs-transport transmembrane ATP-binding protein | Rv1272c.3435 | 5.28E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.4 | 13.2 | 12.6 | 13.8 | 13.2 | 13.4 | 13.2 | 13.7 | 13.4 |
| 56 | Rv2903c | MAP2971c | 72 | Probable signal peptidase I LepB (SPASE I) (leader peptidase I) | Rv2903c.1924 | 2.64E-01 | 7.62E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 13.5 | 13.7 | 13.5 | 13.9 | 13.7 | 13.4 | 13.1 | 13.8 | 13.3 |
| 57 | Rv1634 | MAP1336 | 69 | Possible drug efflux membrane protein | Rv1634.234 | 3.00E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.3 | 12.9 | 12.2 | 13.7 | 13.2 | 13.4 | 13.2 | 13.7 | 13.4 |
| 58 | Rv0914c | MAP2897c | 29 | Possible lipid carrier protein or keto acyl-CoA thiolase | Rv0914c.519 | 2.25E-01 | 7.31E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 13.6 | 13.9 | 13.6 | 14.1 | 13.8 | 13.4 | 12.9 | 14.0 | 13.5 |
| 59 | Rv2984 | MAP3022 | 86 | Polyphosphate kinase PPK (polyphosphoric acid kinase) (ATP-p | Rv2984.2576 | 7.92E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.5 | 13.5 | 13.1 | 13.9 | 13.7 | 13.4 | 13.0 | 13.9 | 13.5 |
| 60 | Rv0167 | MAP3602 | 93 | Conserved integral membrane protein YrbE1A | Rv0167.2782 | 5.55E-01 | 8.97E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.4 | 13.3 | 13.0 | 13.5 | 13.2 | 13.4 | 13.0 | 13.9 | 13.4 |
| 61 | Rv3033 | MAP3596c | 40 | hypothetical protein | Rv3033.3805 | 6.27E-01 | 9.31E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.5 | 13.6 | 13.0 | 14.3 | 13.5 | 13.4 | 13.1 | 13.8 | 13.5 |
| 62 | Rv1346 | MAP1553c | 82 | Acyl-CoA dehydrogenase MbtN | Rv1346.4114 | 3.56E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.2 | 12.7 | 12.3 | 13.1 | 12.8 | 13.4 | 13.2 | 13.6 | 13.5 |
| 63 | Rv1326c | MAP2434 | 89 | 1,4-alpha-glucan branching enzyme GlgB (glycogen branching e | Rv1326c.2859 | 5.47E-01 | 8.97E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.6 | 13.8 | 12.7 | 15.0 | 13.3 | 13.4 | 13.0 | 13.8 | 13.3 |
| 64 | Rv1836c | MAP1548c | 69 | hypothetical protein | Rv1836c.366 | 3.71E-01 | 8.32E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.5 | 13.7 | 13.4 | 13.9 | 13.6 | 13.4 | 13.0 | 13.8 | 13.3 |
| 65 | Rv2700 | MAP2817 | 82 | Possible conserved secreted alanine rich protein | Rv2700.4380 | 5.12E-01 | 8.89E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.4 | 13.2 | 13.0 | 13.4 | 13.3 | 13.4 | 12.9 | 13.9 | 13.4 |
| 66 | Rv2450c | MAP2273c | 87 | Probable resuscitation-promoting factor RpfE | Rv2450c.2067 | 5.16E-01 | 8.89E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.3 | 13.1 | 12.5 | 13.7 | 13.4 | 13.4 | 13.0 | 13.8 | 13.4 |
| 67 | Rv3869 | MAP3779 | 34 | ESX conserved component EccB1 ESX-1 type VII secretion syste | Rv3869.3550 | 2.54E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.2 | 12.7 | 12.4 | 13.0 | 12.8 | 13.4 | 13.1 | 13.7 | 13.6 |
| 68 | Rv1295 | MAP2467c | 90 | Threonine synthase ThrC (ts) | Rv1295.497 | 8.60E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.4 | 13.4 | 12.9 | 13.8 | 13.5 | 13.4 | 13.1 | 13.7 | 13.3 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 69 | Rv3330 | MAP3448 | 82 | Probable penicillin-binding protein DacB1 (D-alanyl-D-alanine c | Rv3330.29 | 3.60E-01 | 8.25E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.5 | 13.7 | 13.4 | 14.0 | 13.7 | 13.4 | 13.0 | 13.8 | 13.4 |
| 70 | Rv3148 | MAP3204 | 90 | Probable NADH dehydrogenase I (chain D) NuoD (NADH-ubiqui | Rv3148.2829 | 2.51E-01 | 7.60E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.3 | 13.1 | 12.9 | 13.4 | 13.2 | 13.4 | 13.1 | 13.7 | 13.3 |
| 71 | Rv3289c | MAP3409c | 67 | Possible transmembrane protein | Rv3289c.2424 | 1.59E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.3 | 13.0 | 12.7 | 13.3 | 12.8 | 13.4 | 13.0 | 13.8 | 13.4 |
| 72 | Rv3279c | MAP3397c | 70 | Possible bifunctional protein BirA: biotin operon repressor + bi | Rv3279c.1921 | 2.41E-01 | 7.47E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.3 | 13.0 | 12.8 | 13.1 | 13.0 | 13.4 | 12.8 | 14.0 | 13.5 |
| 73 | Rv0550c | MAP3394c | 39 | Possible antitoxin VapB3 | Rv0550c.3862 | 5.09E-01 | 8.89E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.4 | 13.5 | 13.2 | 13.9 | 13.4 | 13.4 | 13.1 | 13.7 | 13.5 |
| 74 | Rv3505 | MAP2588 | 85 | Probable acyl-CoA dehydrogenase FadE27 | Rv3505.3530 | 2.34E-01 | 7.42E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.3 | 13.0 | 13.0 | 13.1 | 13.1 | 13.4 | 12.9 | 13.8 | 13.5 |
| 75 | Rv1171 | MAP2612c | 67 | hypothetical protein | Rv1171.4179 | 2.73E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.3 | 13.2 | 13.1 | 13.2 | 13.2 | 13.4 | 13.0 | 13.7 | 13.4 |
| 76 | Rv2846c | MAP1868c | 88 | Possible integral membrane efflux protein EfpA | Rv2846c.2862 | 2.07E-01 | 7.15E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.2 | 12.9 | 12.7 | 13.2 | 12.9 | 13.4 | 12.8 | 13.9 | 13.3 |
| 77 | Rv1963c | MAP0116 | 30 | Probable transcriptional repressor (probably TetR-family) Mce3 | Rv1963c.813 | 8.46E-01 | 9.70E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.4 | 13.4 | 12.9 | 14.0 | 13.2 | 13.4 | 12.9 | 13.9 | 13.4 |
| 78 | Rv3483c | MAP2522 | 32 | Possible exported protein | Rv3483c.4483 | 9.42E-01 | 9.82E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.4 | 13.4 | 13.0 | 13.8 | 13.2 | 13.4 | 12.8 | 13.9 | 13.2 |
| 79 | Rv2345 | MAP2133 | 70 | hypothetical protein | Rv2345.1147 | 9.74E-01 | 9.89E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.4 | 13.4 | 13.0 | 13.8 | 13.2 | 13.4 | 13.0 | 13.7 | 13.4 |
| 80 | Rv1145 | MAP4124 | 79 | Probable conserved transmembrane transport protein MmpL1 | Rv1145.1926 | 2.46E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.1 | 12.6 | 12.3 | 12.9 | 12.7 | 13.4 | 13.0 | 13.7 | 13.4 |
| 81 | Rv2051c | MAP1799c | 69 | hypothetical protein | Rv2051c-sB.85 | 2.82E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.1 | 12.7 | 12.5 | 13.0 | 12.8 | 13.4 | 13.0 | 13.7 | 13.5 |
| 82 | Rv1733c | MAP1301 | 29 | Probable conserved transmembrane protein | Rv1733c.3513 | 5.01E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.2 | 12.8 | 12.5 | 13.1 | 12.8 | 13.3 | 13.1 | 13.6 | 13.4 |
| 83 | Rv0362 | MAP2500 | 25 | Possible Mg2+ transport transmembrane protein MgtE | Rv0362.3418 | 6.61E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.2 | 12.8 | 12.5 | 13.0 | 12.6 | 13.3 | 12.9 | 13.8 | 13.3 |
| 84 | Rv1068c | MAP4144 | 48 | PE-PGRS family protein PE_PGRS20 | Rv1068c.528 | 7.75E-01 | 9.65E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.3 | 13.2 | 12.3 | 14.1 | 12.9 | 13.3 | 13.1 | 13.6 | 13.3 |
| 85 | Rv0234c | MAP3673c | 86 | Succinate-semialdehyde dehydrogenase [NADP+] dependent (S | Rv0234c.831 | 4.36E-01 | 8.38E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.2 | 12.9 | 12.1 | 13.7 | 13.3 | 13.3 | 13.0 | 13.6 | 13.5 |
| 86 | Rv1234 | MAP2549c | 91 | Probable transmembrane protein | Rv1234.1292 | 8.90E-01 | 9.77E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.3 | 13.3 | 12.8 | 13.8 | 13.5 | 13.3 | 13.0 | 13.7 | 13.4 |
| 87 | Rv0341 | MAP2079 | 25 | Isoniazid inductible gene protein IniB | Rv0341.1403 | 1.24E-01 | 6.73E-01 | 0.11 | 9.52E-02 | 7.98E-01 | 13.5 | 13.8 | 13.4 | 14.2 | 13.8 | 13.3 | 13.1 | 13.6 | 13.2 |
| 88 | Rv0931c | MAP3387c | 67 | Transmembrane serine/threonine-protein kinase D PknD (prot | Rv0931c.4303 | 8.36E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.3 | 13.3 | 13.1 | 13.5 | 13.3 | 13.3 | 13.0 | 13.7 | 13.3 |
| 89 | Rv0227c | MAP3666c | 80 | Probable conserved membrane protein | Rv0227c.2110 | 3.40E-01 | 8.15E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 13.0 | 12.8 | 13.3 | 13.0 | 13.3 | 12.9 | 13.8 | 13.2 |
| 90 | Rv1918c | MAP3939c | 58 | PPE family protein PPE35 | Rv1918c.367 | 1.84E-01 | 6.88E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 13.1 | 13.0 | 13.1 | 13.1 | 13.3 | 13.0 | 13.6 | 13.4 |
| 91 | Rv2192c | MAP1931c | 85 | Probable anthranilate phosphoribosyltransferase TrpD | Rv2192c.4133 | 7.29E-01 | 9.56E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.4 | 13.4 | 12.9 | 14.0 | 13.3 | 13.3 | 13.0 | 13.6 | 13.4 |
| 92 | Rv0187 | MAP3627 | 74 | Probable O-methyltransferase | Rv0187.620 | 8.68E-02 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.1 | 12.8 | 12.6 | 13.0 | 12.9 | 13.3 | 12.9 | 13.8 | 13.2 |
| 93 | Rv3150 | MAP0738c | 90 | Probable NADH dehydrogenase I (chain F) NuoF (NADH-ubiquin | Rv3150.517 | 8.41E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.3 | 13.2 | 12.9 | 13.6 | 13.3 | 13.3 | 12.7 | 13.9 | 13.3 |
| 94 | Rv0583c | MAP4075c | 62 | Probable conserved lipoprotein LpqN | Rv0583c.1889 | 6.85E-01 | 9.46E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 13.1 | 12.3 | 13.9 | 12.7 | 13.3 | 13.1 | 13.5 | 13.3 |
| 95 | Rv0391 | MAP0282c | 91 | Probable O-succinylhomoserine sulfhydrylase MetZ (OSH sulfh | Rv0391.524 | 3.41E-01 | 8.15E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 12.9 | 12.6 | 13.3 | 12.8 | 13.3 | 12.7 | 13.9 | 13.6 |
| 96 | Rv0912 | MAP0846 | 74 | Probable conserved transmembrane protein | Rv0912.939 | 1.36E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.2 | 12.9 | 12.8 | 13.1 | 13.0 | 13.3 | 12.9 | 13.7 | 13.4 |
| 97 | Rv3747 | MAP2626 | 35 | hypothetical protein | Rv3747.1852 | 2.56E-01 | 7.62E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.6 | 11.8 | 13.3 | 12.4 | 13.3 | 12.4 | 14.2 | 13.1 |
| 98 | Rv0191 | MAP0963c | 76 | Probable conserved integral membrane protein | Rv0191.236 | 1.01E-01 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.1 | 12.6 | 12.1 | 13.1 | 12.5 | 13.3 | 12.9 | 13.6 | 13.3 |
| 99 | Rv3271c | MAP2784 | 29 | Probable conserved integral membrane protein | Rv3271c.3333 | 4.38E-01 | 8.38E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 13.0 | 12.7 | 13.4 | 13.2 | 13.3 | 12.8 | 13.8 | 13.2 |
| 100 | Rv2996c | MAP0129 | 89 | Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH) | Rv2996c.4596 | 6.01E-01 | 9.20E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.2 | 13.1 | 12.7 | 13.5 | 13.3 | 13.3 | 12.9 | 13.6 | 13.4 |
| 101 | Rv0684 | MAP4142 | 91 | Probable elongation factor G FusA1 (EF-G) | Rv0684.552 | 8.96E-01 | 9.77E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.3 | 13.2 | 12.4 | 14.1 | 13.0 | 13.3 | 13.0 | 13.6 | 13.4 |
| 102 | Rv1539 | MAP1250 | 81 | Probable lipoprotein signal peptidase LspA | Rv1539.3910 | 4.94E-01 | 8.80E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.2 | 13.0 | 12.5 | 13.4 | 13.1 | 13.3 | 12.6 | 14.0 | 13.0 |
| 103 | Rv3507 | MAP4144 | 55 | PE-PGRS family protein PE_PGRS53 | Rv3507-s1.258 | 4.19E-01 | 8.35E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.4 | 13.5 | 13.3 | 13.8 | 13.6 | 13.3 | 12.7 | 13.8 | 13.1 |
| 104 | Rv0014c | MAP0016c | 86 | Transmembrane serine/threonine-protein kinase B PknB (prote | Rv0014c.4591 | 8.73E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.3 | 13.4 | 12.4 | 14.3 | 12.9 | 13.3 | 12.9 | 13.6 | 13.3 |
| 105 | Rv0400c | MAP3878c | 87 | Acyl-CoA dehydrogenase FadE7 | Rv0400c.357 | 5.66E-01 | 9.02E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.2 | 13.2 | 13.0 | 13.4 | 13.1 | 13.3 | 13.0 | 13.6 | 13.3 |
| 106 | Rv1435c | MAP3811 | 56 | Probable conserved proline, glycine, valine-rich secreted prote | Rv1435c.3507 | 7.08E-01 | 9.54E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.2 | 13.2 | 12.9 | 13.5 | 13.1 | 13.3 | 13.0 | 13.6 | 13.2 |
| 107 | Rv0072 | MAP2126 | 46 | Probable glutamine-transport transmembrane protein ABC tra | Rv0072.3666 | 4.46E-01 | 8.42E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 13.3 | 13.5 | 13.2 | 13.8 | 13.4 | 13.3 | 12.9 | 13.7 | 13.2 |
| 108 | Rv0217c | MAP1735 | 73 | Possible esterase LipW | Rv0217c.4238 | 1.13E-01 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.2 | 13.0 | 12.8 | 13.1 | 12.9 | 13.3 | 13.0 | 13.5 | 13.4 |
| 109 | Rv3794 | MAP0229c | 82 | Integral membrane indolylacetylinositol arabinosyltransferase | Rv3794.84 | 3.05E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.6 | 12.3 | 12.9 | 12.7 | 13.3 | 12.9 | 13.6 | 13.3 |
| 110 | Rv2552c | MAP1080 | 82 | Probable shikimate 5-dehydrogenase AroE (5-dehydroshikimat | Rv2552c.4523 | 5.56E-01 | 8.97E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.2 | 13.1 | 12.7 | 13.4 | 13.2 | 13.3 | 12.8 | 13.8 | 13.3 |
| 111 | Rv1592c | MAP1286c | 79 | hypothetical protein | Rv1592c.806 | 2.10E-01 | 7.15E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.1 | 12.8 | 12.5 | 13.2 | 12.8 | 13.3 | 12.8 | 13.7 | 13.2 |
| 112 | Rv2264c | MAP0254c | 62 | hypothetical protein | Rv2264c.570 | 8.80E-01 | 9.73E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.2 | 13.2 | 12.4 | 14.0 | 13.3 | 13.3 | 12.9 | 13.6 | 13.4 |
| 113 | Rv1672c | MAP2534c | 26 | Probable conserved integral membrane transport protein | Rv1672c.511 | 3.05E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 12.7 | 12.0 | 13.4 | 12.8 | 13.3 | 12.7 | 13.8 | 13.3 |
| 114 | Rv0777 | MAP0611 | 88 | Probable adenylosuccinate lyase PurB (adenylosuccinase) (ASL) | Rv0777.812 | 1.10E-01 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.1 | 12.8 | 12.7 | 12.9 | 12.8 | 13.3 | 12.8 | 13.7 | 13.4 |
| 115 | Rv2782c | MAP2890c | 84 | Probable zinc protease PepR | Rv2782c.4274 | 3.98E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.1 | 12.8 | 12.7 | 12.8 | 12.8 | 13.3 | 12.9 | 13.6 | 13.4 |
| 116 | Rv3023c | MAP3759 | 46 | Probable transposase | Rv3023c.2838 | 5.79E-01 | 9.08E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.2 | 12.9 | 12.1 | 13.8 | 12.7 | 13.3 | 12.9 | 13.6 | 13.4 |
| 117 | Rv2446c | MAP2269c | 80 | Probable conserved integral membrane protein | Rv2446c.4373 | 6.82E-01 | 9.46E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 13.2 | 12.8 | 13.5 | 13.3 | 13.3 | 12.9 | 13.6 | 13.2 |
| 118 | Rv3573c | MAP0492 | 81 | Probable acyl-CoA dehydrogenase FadE34 | Rv3573c.661 | 3.04E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 12.9 | 12.6 | 13.2 | 12.8 | 13.3 | 12.8 | 13.7 | 13.3 |
| 119 | Rv1679 | MAP1085 | 28 | Possible acyl-CoA dehydrogenase FadE16 | Rv1679.934 | 4.80E-01 | 8.69E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.2 | 13.1 | 12.8 | 13.4 | 13.0 | 13.2 | 13.0 | 13.5 | 13.3 |
| 120 | Rv1305 | MAP2456c | 90 | Probable ATP synthase C chain AtpE (lipid-binding protein) (dic | Rv1305.3794 | 7.61E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.5 | 11.9 | 13.0 | 12.6 | 13.2 | 12.8 | 13.6 | 13.4 |
| 121 | Rv2048c | MAP0931 | 81 | Polyketide synthase Pks12 | Rv2048c-s4.28 | 1.52E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.1 | 12.8 | 12.4 | 13.2 | 12.9 | 13.2 | 13.0 | 13.5 | 13.3 |
| 122 | Rv3115 | MAP3759c | 46 | Probable transposase | Rv3115.3127 | 2.65E-01 | 7.62E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.1 | 12.7 | 12.1 | 13.4 | 12.6 | 13.2 | 12.9 | 13.6 | 13.4 |
| 123 | Rv3008 | MAP2446c | 38 | Hypothetical protein | Rv3008.4209 | 1.15E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.1 | 12.8 | 12.6 | 13.1 | 12.8 | 13.2 | 12.9 | 13.5 | 13.4 |
| 124 | Rv1925 | MAP1647 | 75 | Probable acyl-CoA ligase FadD31 (acyl-CoA synthetase) (acyl-Co | Rv1925.4129 | 7.07E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.5 | 12.1 | 13.0 | 12.4 | 13.2 | 12.9 | 13.5 | 13.4 |
| 125 | Rv1449c | MAP1178c | 87 | Transketolase Tkt (TK) | Rv1449c.1124 | 9.99E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.4 | 11.7 | 13.0 | 12.4 | 13.2 | 12.9 | 13.6 | 13.3 |
| 126 | Rv0330c | MAP3575 | 35 | Hypothetical protein | Rv0330c.167 | 1.31E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.5 | 11.9 | 13.1 | 12.7 | 13.2 | 12.9 | 13.6 | 13.2 |
| 127 | Rv3553 | MAP0513c | 88 | Possible oxidoreductase | Rv3553.782 | 8.70E-02 | 6.48E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.0 | 12.6 | 12.1 | 13.0 | 12.5 | 13.2 | 12.9 | 13.5 | 13.3 |
| 128 | Rv1223 | MAP2555c | 82 | Probable serine protease HtrA (DEGP protein) | Rv1223.3729 | 2.78E-01 | 7.74E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.1 | 12.9 | 12.7 | 13.2 | 13.0 | 13.2 | 12.9 | 13.6 | 13.3 |
| 129 | Rv2750 | MAP0711c | 77 | Probable dehydrogenase | Rv2750.471 | 8.48E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.2 | 13.1 | 12.5 | 13.7 | 13.1 | 13.2 | 12.8 | 13.6 | 13.2 |
| 130 | Rv1015c | MAP0979c | 85 | 50S ribosomal protein L25 RplY | Rv1015c.1025 | 8.54E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.7 | 12.7 | 12.8 | 12.7 | 13.2 | 12.8 | 13.7 | 13.0 |
| 131 | Rv0810c | MAP0640c | 77 | hypothetical protein | Rv0810c.383 | 3.32E-01 | 8.11E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 12.8 | 12.3 | 13.3 | 12.9 | 13.2 | 12.7 | 13.7 | 13.1 |
| 132 | Rv2463 | MAP2283 | 83 | Probable esterase/lipase LipP | Rv2463.351 | 5.75E-01 | 9.06E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.2 | 13.1 | 13.0 | 13.2 | 13.1 | 13.2 | 12.9 | 13.5 | 13.3 |
| 133 | Rv3602c | MAP0456 | 82 | Pantoate--beta-alanine ligase PanC (pantothenate synthetase) | Rv3602c.3271 | 1.81E-01 | 6.88E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.7 | 12.1 | 13.2 | 12.9 | 13.2 | 12.9 | 13.5 | 13.3 |
| 134 | Rv2587c | MAP1043 | 87 | Probable protein-export membrane protein SecD | Rv2587c.1979 | 8.60E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.2 | 13.3 | 12.2 | 14.5 | 13.6 | 13.2 | 12.6 | 13.8 | 13.2 |
| 135 | Rv3762c | MAP0262 | 79 | Possible hydrolase | Rv3762c.4308 | 4.48E-01 | 8.42E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 13.0 | 12.8 | 13.2 | 12.9 | 13.2 | 12.8 | 13.6 | 13.2 |
| 136 | Rv2563 | MAP0606 | 36 | Probable glutamine-transport transmembrane protein ABC tra | Rv2563.3672 | 5.21E-01 | 8.93E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.1 | 12.8 | 12.1 | 13.6 | 12.7 | 13.2 | 12.5 | 13.9 | 13.2 |
| 137 | Rv2756c | MAP3279 | 23 | Possible type I restriction/modification system DNA methylase | Rv2756c.1128 | 1.04E-01 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.7 | 12.4 | 13.1 | 12.9 | 13.2 | 13.0 | 13.4 | 13.3 |
| 138 | Rv2081c | MAP2394 | 32 | Conserved transmembrane protein | Rv2081c.3607 | 3.98E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 13.0 | 12.7 | 13.3 | 12.8 | 13.2 | 12.8 | 13.5 | 13.1 |
| 139 | Rv3366 | MAP3474 | 84 | Probable tRNA/rRNA methylase SpoU (tRNA/rRNA methyltrans | Rv3366.1007 | 1.27E-01 | 6.73E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.0 | 12.7 | 12.3 | 13.1 | 12.8 | 13.2 | 13.0 | 13.4 | 13.1 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 140 | Rv2164c | MAP1904c | 77 | Probable conserved proline rich membrane protein | Rv2164c.3850 | 6.00E-01 | 9.20E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.3 | 13.4 | 12.7 | 14.1 | 13.3 | 13.2 | 13.0 | 13.4 | 13.1 |
| 141 | Rv2487c | MAP4144 | 60 | PE-PGRS family protein PE_PGRS42 | Rv2487c.83 | 8.16E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.2 | 13.3 | 12.6 | 14.0 | 13.2 | 13.2 | 12.8 | 13.6 | 13.0 |
| 142 | Rv1293 | MAP0986c | 86 | Diaminopimelate decarboxylase LysA (DAP decarboxylase) | Rv1293.4278 | 1.44E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.1 | 12.8 | 12.6 | 13.0 | 12.7 | 13.2 | 12.8 | 13.6 | 13.2 |
| 143 | Rv1364c | MAP0130 | 76 | Possible sigma factor regulatory protein | Rv1364c.834 | 3.84E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.1 | 12.9 | 12.5 | 13.3 | 13.0 | 13.2 | 12.8 | 13.6 | 13.4 |
| 144 | Rv2100 | MAP4176 | 43 | hypothetical protein | Rv2100.1189 | 3.38E-01 | 8.15E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 12.8 | 12.4 | 13.2 | 12.9 | 13.2 | 12.6 | 13.8 | 13.0 |
| 145 | Rv1047 | MAP3759c | 46 | Probable transposase | Rv1047.4283 | 7.32E-01 | 9.56E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.1 | 13.0 | 12.1 | 13.9 | 12.9 | 13.2 | 12.8 | 13.5 | 13.3 |
| 146 | Rv3566c | MAP0501 | 68 | Arylamine N-acetyltransferase Nat (arylamine acetylase) | Rv3566c.374 | 6.07E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.8 | 12.5 | 13.0 | 12.8 | 13.2 | 12.9 | 13.4 | 13.2 |
| 147 | Rv2685 | MAP3793 | 71 | Probable arsenic-transport integral membrane protein ArsB1 | Rv2685.1093 | 1.94E-01 | 6.98E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.7 | 12.2 | 13.2 | 12.5 | 13.2 | 12.7 | 13.7 | 13.3 |
| 148 | Rv0364 | MAP0370 | 84 | Possible conserved transmembrane protein | Rv0364.1883 | 6.58E-01 | 9.36E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.2 | 13.1 | 12.9 | 13.2 | 13.1 | 13.2 | 12.8 | 13.5 | 13.1 |
| 149 | Rv3307 | MAP3429 | 82 | Probable purine nucleoside phosphorylase DeoD (inosine phos | Rv3307.3656 | 1.16E-01 | 6.48E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 13.3 | 13.6 | 13.4 | 13.9 | 13.5 | 13.2 | 12.8 | 13.6 | 13.1 |
| 150 | Rv3090 | MAP0462 | 38 | Unknown alanine and valine rich protein | Rv3090.479 | 6.31E-01 | 9.31E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.1 | 13.0 | 12.3 | 13.6 | 13.2 | 13.2 | 12.8 | 13.6 | 13.2 |
| 151 | Rv2962c | MAP2851c | 30 | Possible glycosyl transferase | Rv2962c.3128 | 1.08E-02 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 12.9 | 12.3 | 12.0 | 12.7 | 12.4 | 13.2 | 12.9 | 13.4 | 13.3 |
| 152 | Rv3629c | MAP0434 | 75 | Probable conserved integral membrane protein | Rv3629c.2527 | 2.36E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 13.0 | 12.7 | 12.5 | 12.9 | 12.7 | 13.2 | 12.9 | 13.4 | 13.1 |
| 153 | Rv3525c | MAP0540 | 83 | Possible siderophore-binding protein | Rv3525c.3315 | 3.04E-01 | 7.74E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.1 | 12.9 | 12.8 | 13.0 | 13.0 | 13.2 | 12.8 | 13.6 | 13.1 |
| 154 | Rv2286c | MAP2286c | 30 | hypothetical protein | Rv2286c.4202 | 7.66E-01 | 9.65E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 13.0 | 12.0 | 14.0 | 12.6 | 13.2 | 12.6 | 13.7 | 13.0 |
| 155 | Rv1254 | MAP0616c | 79 | Probable acyltransferase | Rv1254.1090 | 3.09E-01 | 7.75E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.1 | 12.9 | 12.7 | 13.1 | 12.8 | 13.2 | 12.7 | 13.6 | 13.3 |
| 156 | Rv0899 | MAP1680c | 33 | Outer membrane protein A OmpA | Rv0899.1537 | 8.14E-01 | 9.65E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.2 | 13.3 | 12.3 | 14.4 | 13.8 | 13.2 | 12.7 | 13.7 | 13.3 |
| 157 | Rv3502c | MAP0561 | 82 | Probable short-chain type dehydrogenase/reductase Possible 1 | Rv3502c.1062 | 3.32E-01 | 8.11E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.2 | 13.4 | 13.3 | 13.4 | 13.4 | 13.2 | 12.8 | 13.5 | 13.2 |
| 158 | Rv2064 | MAP1810 | 74 | Precorrin-3B synthase CobG | Rv2064.3844 | 2.25E-01 | 7.31E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.1 | 12.9 | 12.6 | 13.1 | 13.0 | 13.2 | 12.8 | 13.5 | 13.1 |
| 159 | Rv2292c | MAP3661c | 30 | Hypothetical protein | Rv2292c.1541 | 8.00E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.1 | 13.1 | 12.6 | 13.5 | 13.3 | 13.2 | 12.9 | 13.5 | 13.1 |
| 160 | Rv0304 | MAP0210c | 37 | hypothetical protein | Rv0304-s1.34 | 7.74E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.2 | 13.3 | 12.7 | 13.8 | 13.0 | 13.2 | 12.8 | 13.5 | 13.3 |
| 161 | Rv2262c | MAP3280c | 27 | hypothetical protein | Rv2262c.4370 | 4.46E-01 | 8.42E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.1 | 12.9 | 12.4 | 13.3 | 13.0 | 13.2 | 12.6 | 13.7 | 13.4 |
| 162 | Rv1031 | MAP0227c | 46 | Probable potassium-transporting ATPase C chain KdpC (potassi | Rv1031.1005 | 3.54E-01 | 8.22E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.8 | 12.4 | 13.3 | 12.8 | 13.2 | 12.8 | 13.5 | 13.3 |
| 163 | Rv0872c | MAP4144 | 62 | PE-PGRS family protein PE_PGRS15 | Rv0872c.1408 | 4.05E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 13.0 | 12.6 | 12.4 | 12.9 | 12.7 | 13.2 | 12.8 | 13.5 | 13.2 |
| 164 | Rv1493 | MAP0673 | 91 | Probable methylmalonyl-CoA mutase large subunit MutB (MCM | Rv1493.3443 | 7.15E-01 | 9.56E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.1 | 13.1 | 13.0 | 13.1 | 13.1 | 13.1 | 12.8 | 13.5 | 13.1 |
| 165 | Rv0258c | MAP3704c | 84 | hypothetical protein | Rv0258c.3897 | 2.46E-01 | 7.49E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.0 | 12.7 | 12.1 | 13.2 | 12.5 | 13.1 | 12.7 | 13.6 | 13.2 |
| 166 | Rv0730 | MAP4196 | 81 | GCN5-related N-acetyltransferase | Rv0730.4213 | 2.39E-01 | 7.47E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.7 | 12.2 | 13.1 | 12.4 | 13.1 | 12.6 | 13.7 | 13.3 |
| 167 | Rv0085 | MAP1526 | 37 | Possible hydrogenase HycP | Rv0085.165 | 5.24E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.0 | 12.6 | 12.3 | 12.9 | 12.6 | 13.1 | 12.8 | 13.5 | 13.3 |
| 168 | Rv0383c | MAP3855 | 85 | Possible conserved secreted protein | Rv0383c.663 | 1.12E-01 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.6 | 12.1 | 13.0 | 12.4 | 13.1 | 12.8 | 13.5 | 13.3 |
| 169 | Rv1630 | MAP1325 | 97 | 30S ribosomal protein S1 RpsA | Rv1630.3839 | 2.07E-01 | 7.15E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.7 | 12.3 | 13.2 | 12.9 | 13.1 | 12.9 | 13.4 | 13.2 |
| 170 | Rv1779c | MAP1493c | 56 | Possible integral membrane protein | Rv1779c.2853 | 1.23E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.4 | 12.2 | 12.6 | 12.4 | 13.1 | 12.8 | 13.5 | 13.2 |
| 171 | Rv3293 | MAP3413 | 80 | Probable piperideine-6-carboxilic acid dehydrogenase Pcd (pip | Rv3293.3133 | 1.96E-01 | 6.98E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.8 | 12.6 | 13.1 | 12.9 | 13.1 | 12.8 | 13.4 | 13.1 |
| 172 | Rv3344c | No hit | 0 | PE-PGRS family protein PE_PGRS49 | Rv3344c.3521 | 4.23E-01 | 8.35E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.3 | 13.6 | 12.7 | 14.4 | 13.8 | 13.1 | 12.9 | 13.4 | 13.1 |
| 173 | Rv2818c | MAP0893 | 30 | Hypothetical protein | Rv2818c.3561 | 6.66E-02 | 6.48E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.9 | 12.8 | 12.9 | 12.9 | 13.1 | 12.9 | 13.3 | 13.3 |
| 174 | Rv1469 | MAP3384 | 32 | Hypothetical protein | Rv1469-m2.85 | 2.17E-01 | 7.29E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.8 | 12.0 | 10.8 | 13.3 | 11.7 | 13.1 | 12.6 | 13.7 | 13.0 |
| 175 | Rv0878c | MAP3939c | 55 | PPE family protein PPE13 | Rv0878c.2251 | 9.74E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.8 | 12.1 | 11.4 | 12.9 | 12.4 | 13.1 | 12.7 | 13.6 | 13.2 |
| 176 | Rv1515c | MAP3643c | 26 | hypothetical protein | Rv1515c.2786 | 9.16E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.1 | 13.1 | 12.9 | 13.3 | 13.0 | 13.1 | 12.8 | 13.5 | 13.1 |
| 177 | Rv3802c | MAP0218 | 76 | Probable conserved membrane protein | Rv3802c.86 | 3.75E-01 | 8.34E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.0 | 12.7 | 12.3 | 13.2 | 13.0 | 13.1 | 12.5 | 13.8 | 13.0 |
| 178 | Rv0831c | MAP2559 | 27 | hypothetical protein | Rv0831c.2975 | 2.60E-01 | 7.62E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.0 | 12.7 | 12.5 | 13.0 | 12.8 | 13.1 | 12.5 | 13.7 | 12.9 |
| 179 | Rv1174c | MAP1143c | 62 | Low molecular weight T-cell antigen TB8.4 | Rv1174c.2915 | 1.06E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 11.5 | 10.5 | 12.5 | 11.8 | 13.1 | 11.7 | 14.5 | 13.6 |
| 180 | Rv2080 | MAP2417c | 32 | Lipoprotein LppJ | Rv2080.2745 | 7.32E-01 | 9.56E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.1 | 13.2 | 12.9 | 13.5 | 13.2 | 13.1 | 12.8 | 13.5 | 13.0 |
| 181 | Rv0625c | MAP4090c | 78 | Probable conserved transmembrane protein | Rv0625c.456 | 3.88E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.7 | 12.1 | 13.4 | 13.0 | 13.1 | 12.8 | 13.5 | 13.1 |
| 182 | Rv1509 | MAP3459 | 27 | Hypothetical protein | Rv1509.2791 | 8.82E-02 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.0 | 12.7 | 12.5 | 12.9 | 12.8 | 13.1 | 12.7 | 13.5 | 13.3 |
| 183 | Rv3355c | MAP3462c | 78 | Probable integral membrane protein | Rv3355c.398 | 1.20E-01 | 6.66E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.6 | 12.2 | 13.0 | 12.7 | 13.1 | 12.7 | 13.5 | 13.3 |
| 184 | Rv3333c | MAP3461 | 29 | Hypothetical proline rich protein | Rv3333c.1182 | 8.99E-01 | 9.78E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.1 | 13.1 | 12.8 | 13.3 | 13.1 | 13.1 | 12.6 | 13.6 | 13.2 |
| 185 | Rv2880c | MAP2943c | 88 | hypothetical protein | Rv2880c.1628 | 1.33E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 13.0 | 12.6 | 12.3 | 13.0 | 12.7 | 13.1 | 12.7 | 13.5 | 13.2 |
| 186 | Rv2682c | MAP2803c | 88 | Probable 1-deoxy-D-xylulose 5-phosphate synthase Dxs1 (1-de | Rv2682c.3441 | 1.62E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.0 | 12.8 | 12.6 | 13.0 | 12.8 | 13.1 | 12.8 | 13.4 | 13.2 |
| 187 | Rv2935 | MAP2230c | 37 | Phenolpthiocerol synthesis type-I polyketide synthase PpsE | Rv2935-s3.56 | 5.40E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.8 | 12.0 | 13.6 | 13.1 | 13.1 | 12.6 | 13.6 | 13.2 |
| 188 | Rv1227c | MAP2102c | 44 | Probable transmembrane protein | Rv1227c.425 | 2.09E-01 | 7.15E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.5 | 12.0 | 13.1 | 12.8 | 13.1 | 12.5 | 13.7 | 13.1 |
| 189 | Rv0155 | MAP3572 | 89 | Probable NAD(P) transhydrogenase (subunit alpha) PntAa [first | Rv0155.2816 | 1.93E-02 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 12.9 | 12.5 | 12.2 | 12.8 | 12.6 | 13.1 | 12.9 | 13.3 | 13.1 |
| 190 | Rv0588 | MAP4083 | 92 | Conserved hypothetical integral membrane protein YrbE2B | Rv0588.184 | 1.55E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.7 | 12.2 | 13.1 | 12.8 | 13.1 | 12.8 | 13.4 | 13.1 |
| 191 | Rv1728c | MAP2475 | 65 | hypothetical protein | Rv1728c.3933 | 3.96E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.8 | 12.2 | 13.3 | 12.8 | 13.1 | 12.8 | 13.4 | 13.1 |
| 192 | Rv1705c | MAP1506 | 45 | PPE family protein PPE22 | Rv1705c.3108 | 4.87E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.4 | 12.2 | 12.6 | 12.5 | 13.1 | 12.5 | 13.6 | 13.0 |
| 193 | Rv3578 | MAP0484c | 76 | Possible arsenical pump integral membrane protein ArsB2 | Rv3578.1103 | 4.96E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.6 | 12.3 | 12.9 | 12.6 | 13.1 | 12.8 | 13.4 | 13.2 |
| 194 | Rv0389 | MAP2259 | 64 | Probable phosphoribosylglycinamide formyltransferase 2 PurT | Rv0389.237 | 5.96E-01 | 9.20E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.9 | 12.3 | 13.5 | 13.1 | 13.1 | 12.6 | 13.6 | 13.0 |
| 195 | Rv3864 | MAP2079 | 33 | ESX-1 secretion-associated protein EspE | Rv3864.4115 | 4.28E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.8 | 12.3 | 13.3 | 12.9 | 13.1 | 12.6 | 13.6 | 13.0 |
| 196 | Rv3009c | MAP3042c | 91 | Probable glutamyl-tRNA(GLN) amidotransferase (subunit B) Ga | Rv3009c.1704 | 6.16E-01 | 9.31E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.2 | 13.4 | 12.4 | 14.5 | 13.0 | 13.1 | 12.5 | 13.7 | 12.8 |
| 197 | Rv0589 | MAP4084 | 83 | Mce-family protein Mce2A | Rv0589.2664 | 1.11E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.5 | 12.1 | 12.9 | 12.4 | 13.1 | 12.7 | 13.5 | 13.1 |
| 198 | Rv1682 | MAP2622 | 34 | Probable coiled-coil structural protein | Rv1682.4245 | 5.70E-02 | 6.39E-01 | 0.11 | 9.52E-02 | 7.98E-01 | 13.3 | 13.8 | 13.4 | 14.2 | 13.8 | 13.1 | 12.7 | 13.5 | 13.1 |
| 199 | Rv2982c | MAP3020c | 84 | Probable glycerol-3-phosphate dehydrogenase [NAD(P)+] GpdA | Rv2982c.496 | 9.42E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.2 | 11.6 | 12.9 | 12.5 | 13.1 | 12.6 | 13.6 | 13.2 |
| 200 | Rv1551 | MAP0705 | 86 | Possible acyltransferase PlsB1 | Rv1551.3724 | 6.83E-01 | 9.46E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.1 | 13.0 | 12.8 | 13.2 | 13.0 | 13.1 | 12.8 | 13.3 | 13.1 |
| 201 | Rv3495c | MAP0568 | 82 | Possible Mce-family lipoprotein LprN (Mce-family lipoprotein M | Rv3495c.3692 | 8.29E-01 | 9.70E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.1 | 13.1 | 12.8 | 13.5 | 13.0 | 13.1 | 12.8 | 13.4 | 13.1 |
| 202 | Rv1964 | MAP2117c | 56 | Conserved hypothetical integral membrane protein YrbE3A | Rv1964.2499 | 7.96E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.1 | 13.0 | 12.7 | 13.3 | 13.0 | 13.1 | 12.8 | 13.4 | 13.2 |
| 203 | Rv1662 | MAP3191 | 58 | Probable polyketide synthase Pks8 | Rv1662-s3.34 | 2.39E-01 | 7.47E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.9 | 12.6 | 12.0 | 13.2 | 12.5 | 13.1 | 12.8 | 13.4 | 13.2 |
| 204 | Rv3498c | MAP0565 | 83 | Mce-family protein Mce4B | Rv3498c.2668 | 1.76E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.6 | 12.2 | 12.9 | 12.4 | 13.1 | 12.5 | 13.7 | 13.2 |
| 205 | Rv1802 | MAP1519 | 50 | PPE family protein PPE30 | Rv1802.1503 | 9.96E-01 | 9.98E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.1 | 13.1 | 12.6 | 13.6 | 13.3 | 13.1 | 12.6 | 13.5 | 13.0 |
| 206 | Rv0017c | MAP0020c | 85 | Probable cell division protein RodA | Rv0017c.341 | 5.32E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.9 | 12.8 | 13.1 | 12.9 | 13.1 | 12.6 | 13.5 | 13.2 |
| 207 | Rv2088 | MAP3259 | 48 | Transmembrane serine/threonine-protein kinase J PknJ (protei | Rv2088.4298 | 3.73E-01 | 8.34E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 13.2 | 13.4 | 12.9 | 13.8 | 13.6 | 13.1 | 12.7 | 13.4 | 13.2 |
| 208 | Rv0505c | MAP3997c | 85 | Possible phosphoserine phosphatase SerB1 (PSP) (O-phosphos | Rv0505c.3100 | 1.05E-01 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.9 | 12.5 | 12.0 | 12.9 | 12.3 | 13.1 | 12.7 | 13.4 | 13.1 |
| 209 | Rv2746c | MAP2857c | 74 | Probable PGP synthase PgsA3 (CDP-diacylglycerol--glycerol-3-p | Rv2746c.2180 | 2.12E-01 | 7.15E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.5 | 11.9 | 13.1 | 12.8 | 13.1 | 12.6 | 13.5 | 13.2 |
| 210 | Rv1795 | MAP1510 | 79 | ESX conserved component EccD5 ESX-5 type VII secretion syste | Rv1795.2565 | 9.96E-02 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.7 | 12.5 | 12.9 | 12.6 | 13.1 | 12.7 | 13.4 | 13.3 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 211 | Rv1554 | MAP2117c | 32 | Probable fumarate reductase [membrane anchor subunit] Frd | Rv1554.3515 | 1.43E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 13.0 | 12.7 | 12.5 | 12.9 | 12.8 | 13.1 | 12.7 | 13.4 | 13.3 |
| 212 | Rv3163c | MAP3217c | 80 | Possible conserved secreted protein | Rv3163c.3116 | 2.66E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.5 | 12.3 | 12.7 | 12.5 | 13.1 | 12.7 | 13.4 | 13.1 |
| 213 | Rv1228 | MAP4253 | 30 | Probable lipoprotein LpqX | Rv1228.721 | 1.25E-01 | 6.73E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 12.8 | 12.3 | 11.6 | 12.9 | 12.5 | 13.1 | 12.8 | 13.3 | 13.2 |
| 214 | Rv1208 | MAP2569c | 82 | Probable glucosyl-3-phosphoglycerate synthase GpgS | Rv1208.789 | 5.15E-01 | 8.89E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 13.0 | 12.9 | 12.6 | 13.2 | 13.0 | 13.1 | 12.7 | 13.4 | 13.1 |
| 215 | Rv1689 | MAP1396 | 87 | Probable tyrosyl-tRNA synthase TyrS (TYRRS) | Rv1689.3405 | 7.87E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.8 | 12.4 | 12.0 | 12.9 | 12.4 | 13.1 | 12.7 | 13.4 | 13.2 |
| 216 | Rv1637c | MAP0174 | 81 | hypothetical protein | Rv1637c.3655 | 3.96E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.9 | 12.7 | 13.1 | 12.8 | 13.1 | 12.8 | 13.3 | 13.1 |
| 217 | Rv2335 | MAP2042c | 78 | Probable serine acetyltransferase CysE (sat) | Rv2335.444 | 3.94E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.7 | 12.0 | 13.3 | 13.0 | 13.1 | 12.6 | 13.5 | 13.0 |
| 218 | Rv1072 | MAP1019 | 86 | Probable conserved transmembrane protein | Rv1072.4218 | 2.59E-01 | 7.62E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.6 | 12.1 | 13.0 | 12.5 | 13.1 | 12.4 | 13.7 | 13.0 |
| 219 | Rv1796 | MAP1511 | 73 | Hypothetical protein | Rv1796.281 | 4.40E-01 | 8.41E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.2 | 13.4 | 12.9 | 13.9 | 13.1 | 13.1 | 12.5 | 13.6 | 13.1 |
| 220 | Rv3145 | MAP3201 | 82 | Probable NADH dehydrogenase I (chain A) NuoA (NADH-ubiqui | Rv3145.118 | 5.49E-02 | 6.35E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.8 | 12.3 | 11.8 | 12.7 | 12.5 | 13.1 | 12.8 | 13.3 | 13.1 |
| 221 | Rv2783c | MAP2891c | 90 | Bifunctional protein polyribonucleotide nucleotidyltransferase | Rv2783c.4130 | 1.48E-01 | 6.83E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.9 | 12.6 | 12.3 | 13.0 | 12.5 | 13.1 | 12.7 | 13.4 | 13.0 |
| 222 | Rv3881c | MAP1144c | 24 | Secreted ESX-1 substrate protein B, EspB. Conserved alanine a | Rv3881c.3206 | 4.11E-01 | 8.35E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.2 | 13.4 | 12.8 | 13.9 | 13.2 | 13.1 | 12.6 | 13.5 | 13.1 |
| 223 | Rv2398c | MAP2211c | 86 | Probable sulfate-transport integral membrane protein ABC tra | Rv2398c.182 | 7.09E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.8 | 12.3 | 11.9 | 12.8 | 12.3 | 13.1 | 12.6 | 13.5 | 13.0 |
| 224 | Rv3878 | MAP3837c | 47 | ESX-1 secretion-associated protein EspJ Conserved alanine rich | Rv3878.1247 | 8.69E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.0 | 13.0 | 12.5 | 13.5 | 12.9 | 13.1 | 12.7 | 13.4 | 13.2 |
| 225 | Rv1861 | MAP1570 | 57 | Probable conserved transmembrane protein | Rv1861.2093 | 5.47E-01 | 8.97E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.0 | 12.8 | 12.2 | 13.4 | 13.0 | 13.1 | 12.5 | 13.6 | 13.1 |
| 226 | Rv2156c | MAP2540c | 90 | Probable phospho-N-acetylmuramoyl-pentappeptidetransfera | Rv2156c.3393 | 6.93E-01 | 9.51E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.0 | 12.9 | 12.8 | 13.1 | 13.0 | 13.1 | 12.6 | 13.5 | 13.1 |
| 227 | Rv2414c | MAP1299 | 33 | hypothetical protein | Rv2414c.4306 | 4.99E-02 | 6.27E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.6 | 12.5 | 12.7 | 12.6 | 13.0 | 12.7 | 13.4 | 13.2 |
| 228 | Rv2046 | MAP1781 | 57 | Probable lipoprotein LppI | Rv2046.1899 | 7.16E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.4 | 12.0 | 12.8 | 12.5 | 13.0 | 12.6 | 13.5 | 13.1 |
| 229 | Rv3155 | MAP3211 | 95 | Probable NADH dehydrogenase I (chain K) NuoK (NADH-ubiqui | Rv3155.4162 | 7.65E-02 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.7 | 12.6 | 12.8 | 12.7 | 13.0 | 12.7 | 13.4 | 13.1 |
| 230 | Rv0025 | MAP0037 | 58 | hypothetical protein | Rv0025.3865 | 5.24E-01 | 8.93E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.1 | 13.2 | 12.9 | 13.6 | 13.1 | 13.0 | 12.7 | 13.4 | 13.0 |
| 231 | Rv3042c | MAP0343 | 84 | Probable phosphoserine phosphatase SerB2 (PSP) (O-phospho | Rv3042c.2837 | 1.83E-01 | 6.88E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.7 | 12.4 | 12.9 | 12.8 | 13.0 | 12.6 | 13.5 | 13.3 |
| 232 | Rv2740 | MAP1602c | 65 | Epoxide hydrolase | Rv2740.650 | 3.91E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.8 | 12.5 | 13.2 | 12.9 | 13.0 | 12.7 | 13.4 | 13.1 |
| 233 | Rv0650 | MAP4123 | 72 | Possible sugar kinase | Rv0650.3365 | 3.85E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.9 | 12.5 | 12.3 | 12.7 | 12.5 | 13.0 | 12.7 | 13.4 | 13.1 |
| 234 | Rv2048c | MAP0931 | 81 | Polyketide synthase Pks12 | Rv2048c-s5.57 | 8.21E-01 | 9.68E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.0 | 13.0 | 12.6 | 13.4 | 12.9 | 13.0 | 12.7 | 13.4 | 13.1 |
| 235 | Rv2330c | MAP2103c | 73 | Probable lipoprotein LppP | Rv2330c.914 | 4.15E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.9 | 12.6 | 13.1 | 12.8 | 13.0 | 12.7 | 13.3 | 13.2 |
| 236 | Rv2048c | MAP0931 | 81 | Polyketide synthase Pks12 | Rv2048c-s6.8 | 1.13E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.5 | 12.1 | 12.9 | 12.6 | 13.0 | 12.6 | 13.4 | 13.0 |
| 237 | Rv0314c | MAP3802c | 54 | Possible conserved membrane protein | Rv0314c.454 | 6.56E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.6 | 12.4 | 12.9 | 12.7 | 13.0 | 12.8 | 13.3 | 13.1 |
| 238 | Rv2709 | MAP2825 | 69 | Probable conserved transmembrane protein | Rv2709.361 | 4.11E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.8 | 12.4 | 13.2 | 12.8 | 13.0 | 12.7 | 13.4 | 13.1 |
| 239 | Rv2458 | MAP2279 | 76 | Probable homocysteine S-methyltransferase MmuM (S-methyl | Rv2458.3371 | 2.06E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.5 | 12.3 | 12.7 | 12.5 | 13.0 | 12.8 | 13.3 | 13.1 |
| 240 | Rv2958c | MAP2851c | 34 | Possible glycosyl transferase | Rv2958c.3689 | 7.41E-01 | 9.57E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.1 | 13.1 | 12.8 | 13.4 | 13.0 | 13.0 | 12.5 | 13.6 | 13.0 |
| 241 | Rv3313c | MAP3438c | 84 | Probable adenosine deaminase Add (adenosine aminohydrola | Rv3313c.3388 | 4.63E-01 | 8.48E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 13.0 | 12.9 | 12.8 | 13.0 | 12.9 | 13.0 | 12.7 | 13.3 | 13.1 |
| 242 | Rv0125 | MAP3527 | 71 | Probable serine protease PepA (serine proteinase) (MTB32A) | Rv0125.3792 | 1.27E-01 | 6.73E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.8 | 12.4 | 12.0 | 12.9 | 12.5 | 13.0 | 12.6 | 13.5 | 12.9 |
| 243 | Rv0170 | MAP3605 | 78 | Mce-family protein Mce1B | Rv0170.2951 | 1.76E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.5 | 12.2 | 12.9 | 12.5 | 13.0 | 12.5 | 13.6 | 13.0 |
| 244 | Rv1987 | MAP1706 | 74 | Possible chitinase | Rv1987.1806 | 3.70E-01 | 8.32E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.6 | 12.0 | 13.3 | 12.9 | 13.0 | 12.7 | 13.4 | 13.1 |
| 245 | Rv0493c | MAP3985c | 73 | hypothetical protein | Rv0493c.790 | 1.66E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.6 | 12.1 | 13.0 | 12.7 | 13.0 | 12.7 | 13.4 | 13.0 |
| 246 | Rv3221c | MAP3322c | 92 | Biotinylated protein TB7.3 | Rv3221c.3803 | 2.42E-01 | 7.47E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.5 | 11.9 | 13.1 | 12.4 | 13.0 | 12.7 | 13.3 | 13.0 |
| 247 | Rv3828c | MAP2620c | 39 | Possible resolvase | Rv3828c.3796 | 4.67E-01 | 8.54E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.6 | 11.7 | 13.5 | 12.6 | 13.0 | 12.8 | 13.3 | 13.0 |
| 248 | Rv2701c | MAP2818c | 74 | Inositol-1-monophosphatase SuhB | Rv2701c.469 | 9.11E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.0 | 13.0 | 12.8 | 13.2 | 12.9 | 13.0 | 12.7 | 13.3 | 13.1 |
| 249 | Rv0996 | MAP0927 | 64 | Probable conserved transmembrane protein | Rv0996.959 | 5.03E-01 | 8.85E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.8 | 12.7 | 12.9 | 12.8 | 13.0 | 12.4 | 13.7 | 13.1 |
| 250 | Rv2506 | MAP0666c | 80 | Probable transcriptional regulatory protein (probably TetR-fam | Rv2506.742 | 6.60E-01 | 9.36E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.1 | 13.2 | 12.7 | 13.6 | 12.9 | 13.0 | 12.7 | 13.3 | 13.0 |
| 251 | Rv1777 | MAP0009 | 65 | Probable cytochrome P450 144 Cyp144 | Rv1777.3809 | 5.23E-01 | 8.93E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 13.1 | 13.4 | 12.6 | 14.2 | 13.1 | 13.0 | 12.4 | 13.6 | 13.2 |
| 252 | Rv3201c | MAP3300c | 77 | hypothetical protein | Rv3201c.2594 | 6.39E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.5 | 12.3 | 12.7 | 12.6 | 13.0 | 12.6 | 13.4 | 13.1 |
| 253 | Rv0244c | MAP3694c | 91 | hypothetical protein | Rv0244c.280 | 3.56E-01 | 8.22E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 13.1 | 13.3 | 13.0 | 13.7 | 13.3 | 13.0 | 12.5 | 13.6 | 12.8 |
| 254 | Rv0032 | MAP1275 | 36 | Possible 8-amino-7-oxononanoate synthase BioF2 (AONS) (8-a | Rv0032.1125 | 1.34E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.8 | 12.4 | 11.9 | 12.9 | 12.5 | 13.0 | 12.7 | 13.3 | 13.0 |
| 255 | Rv3486 | MAP1775 | 24 | hypothetical protein | Rv3486.133 | 3.25E-01 | 8.04E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.6 | 11.9 | 13.2 | 12.8 | 13.0 | 12.7 | 13.3 | 13.0 |
| 256 | Rv0767c | MAP0601c | 76 | hypothetical protein | Rv0767c.3337 | 1.52E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.7 | 12.4 | 13.0 | 12.8 | 13.0 | 12.8 | 13.3 | 13.0 |
| 257 | Rv0433 | MAP3922 | 87 | hypothetical protein | Rv0433.1077 | 3.22E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.5 | 12.3 | 12.7 | 12.4 | 13.0 | 12.7 | 13.3 | 13.1 |
| 258 | Rv1488 | MAP1214 | 93 | Possible exported conserved protein | Rv1488.1185 | 3.49E-01 | 8.22E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.5 | 11.6 | 13.3 | 12.7 | 13.0 | 12.5 | 13.5 | 13.2 |
| 259 | Rv0228 | MAP3667 | 80 | Probable integral membrane acyltransferase | Rv0228.3987 | 8.69E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.0 | 13.0 | 12.7 | 13.4 | 12.9 | 13.0 | 12.7 | 13.3 | 13.1 |
| 260 | Rv2316 | MAP2090 | 85 | Probable sugar-transport integral membrane protein ABC tran | Rv2316.180 | 2.95E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.6 | 12.1 | 13.1 | 12.5 | 13.0 | 12.5 | 13.6 | 12.9 |
| 261 | Rv0108c | MAP3499c | 83 | Hypothetical protein | Rv0108c.384 | 7.64E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.9 | 12.6 | 12.4 | 12.8 | 12.6 | 13.0 | 12.6 | 13.4 | 13.1 |
| 262 | Rv2768c | MAP1003c | 51 | PPE family protein PPE43 | Rv2768c.929 | 6.29E-01 | 9.31E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.0 | 12.9 | 12.7 | 13.1 | 12.8 | 13.0 | 12.6 | 13.4 | 12.9 |
| 263 | Rv0426c | MAP3915c | 65 | Possible transmembrane protein | Rv0426c.2070 | 7.82E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.0 | 13.0 | 12.9 | 13.2 | 13.1 | 13.0 | 12.8 | 13.2 | 13.1 |
| 264 | Rv1239c | MAP2542 | 78 | Possible magnesium and cobalt transport transmembrane prot | Rv1239c.3394 | 8.84E-01 | 9.73E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.0 | 12.9 | 12.5 | 13.4 | 12.9 | 13.0 | 12.6 | 13.4 | 13.0 |
| 265 | Rv3350c | MAP2047 | 62 | PPE family protein PPE56 | Rv3350c-s5.2 | 1.40E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.7 | 12.6 | 12.7 | 12.7 | 13.0 | 12.6 | 13.3 | 12.8 |
| 266 | Rv1395 | MAP0223c | 35 | Transcriptional regulatory protein | Rv1395.3671 | 1.47E-01 | 6.83E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.9 | 12.6 | 12.6 | 12.7 | 12.6 | 13.0 | 12.6 | 13.4 | 13.1 |
| 267 | Rv0953c | MAP0899c | 88 | Possible oxidoreductase | Rv0953c.1045 | 8.16E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.0 | 12.9 | 12.6 | 13.3 | 12.9 | 13.0 | 12.8 | 13.2 | 13.0 |
| 268 | Rv1437 | MAP1165 | 82 | Probable phosphoglycerate kinase Pgk | Rv1437.808 | 8.39E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.4 | 11.9 | 12.8 | 12.3 | 13.0 | 12.6 | 13.4 | 12.9 |
| 269 | Rv2843 | MAP2911 | 73 | Probable conserved transmembrane alanine rich protein | Rv2843.368 | 4.80E-01 | 8.69E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.7 | 12.2 | 13.3 | 12.8 | 13.0 | 12.7 | 13.3 | 13.1 |
| 270 | Rv0178 | MAP3613 | 60 | Probable conserved Mce associated membrane protein | Rv0178.1783 | 8.06E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.0 | 13.1 | 12.5 | 13.7 | 12.8 | 13.0 | 12.3 | 13.6 | 12.7 |
| 271 | Rv3603c | MAP0455 | 88 | Conserved hypothetical alanine and leucine rich protein | Rv3603c.481 | 7.17E-01 | 9.56E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.9 | 12.7 | 11.7 | 13.8 | 12.7 | 13.0 | 12.4 | 13.5 | 13.0 |
| 272 | Rv0729 | MAP4195 | 72 | Possible D-xylulose kinase XylB (xylulokinase) (xylulose kinase) | Rv0729.3995 | 2.33E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.5 | 12.3 | 12.6 | 12.5 | 13.0 | 12.7 | 13.3 | 13.1 |
| 273 | Rv0817c | MAP0291 | 71 | Probable conserved exported protein | Rv0817c.4426 | 7.10E-01 | 9.54E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.9 | 12.5 | 13.2 | 13.0 | 13.0 | 12.6 | 13.3 | 13.1 |
| 274 | Rv1971 | MAP0765 | 56 | Mce-family protein Mce3F | Rv1971.3526 | 9.44E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 13.0 | 13.0 | 12.3 | 13.7 | 12.9 | 13.0 | 12.6 | 13.3 | 13.1 |
| 275 | Rv3538 | MAP0529c | 85 | Probable dehydrogenase Possible 2-enoyl acyl-CoA hydratase | Rv3538.757 | 8.94E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.9 | 12.7 | 12.5 | 12.9 | 12.8 | 13.0 | 12.7 | 13.2 | 13.0 |
| 276 | Rv1431 | MAP1162 | 75 | hypothetical protein | Rv1431.4009 | 1.65E-01 | 6.83E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.7 | 12.6 | 12.7 | 12.7 | 13.0 | 12.6 | 13.3 | 13.0 |
| 277 | Rv3433c | MAP4256 | 88 | hypothetical protein | Rv3433c.3715 | 2.83E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.9 | 12.7 | 12.3 | 13.0 | 12.6 | 13.0 | 12.6 | 13.3 | 13.1 |
| 278 | Rv1787 | MAP1505 | 52 | PPE family protein PPE25 | Rv1787.639 | 1.10E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.3 | 11.8 | 12.7 | 12.5 | 13.0 | 12.3 | 13.6 | 12.9 |
| 279 | Rv3796 | MAP2220 | 26 | hypothetical protein | Rv3796.499 | 6.85E-01 | 9.46E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.8 | 12.0 | 13.5 | 13.1 | 13.0 | 12.5 | 13.4 | 13.0 |
| 280 | Rv2447c | MAP2270c | 85 | Probable folylpolyglutamate synthase protein FolC (folylpoly-g | Rv2447c.3138 | 4.25E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.8 | 12.5 | 13.1 | 12.7 | 13.0 | 12.7 | 13.3 | 12.8 |
| 281 | Rv0304 | MAP0210c | 37 | hypothetical protein | Rv0304-s2.14 | 9.93E-01 | 9.98E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 13.0 | 13.0 | 12.7 | 13.2 | 13.1 | 13.0 | 12.6 | 13.3 | 13.0 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 282 | Rv1199c | MAP3759c | 47 | Possible transposase | Rv1199c.2543 | 7.83E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.9 | 12.8 | 12.2 | 13.5 | 12.6 | 13.0 | 12.6 | 13.3 | 13.1 |
| 283 | Rv0344c | MAP0258 | 70 | Probable lipoprotein LpqJ | Rv0344c.3612 | 4.62E-01 | 8.48E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.7 | 12.1 | 13.3 | 12.6 | 13.0 | 12.6 | 13.3 | 13.1 |
| 284 | Rv3209 | MAP3310 | 57 | hypothetical protein | Rv3209-m2.37 | 7.98E-01 | 9.65E-01 | 0.67 | 5.17E-01 | 9.11E-01 | 12.9 | 12.9 | 12.3 | 13.4 | 12.6 | 13.0 | 12.8 | 13.2 | 12.9 |
| 285 | Rv2186c | MAP1924c | 84 | hypothetical protein | Rv2186c.4112 | 1.28E-01 | 6.73E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.5 | 12.1 | 12.9 | 12.6 | 13.0 | 12.6 | 13.3 | 13.2 |
| 286 | Rv0597c | MAP3780 | 44 | hypothetical protein | Rv0597c.1681 | 9.18E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 13.0 | 13.0 | 11.8 | 14.2 | 12.7 | 13.0 | 12.4 | 13.6 | 13.0 |
| 287 | Rv1683 | MAP1389 | 84 | Possible bifunctional enzyme; long-chain acyl-CoA synthase an | Rv1683.1139 | 4.70E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.8 | 12.5 | 12.3 | 12.7 | 12.5 | 13.0 | 12.6 | 13.3 | 12.9 |
| 288 | Rv0425c | MAP3845 | 38 | Possible metal cation transporting P-type ATPase CtpH | Rv0425c-s2.25 | 2.62E-01 | 7.62E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 13.0 | 13.2 | 13.0 | 13.4 | 13.3 | 13.0 | 12.6 | 13.3 | 13.0 |
| 289 | Rv2280 | MAP1073 | 35 | Probable dehydrogenase | Rv2280.3412 | 1.66E-01 | 6.83E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 13.2 | 13.6 | 13.0 | 14.3 | 13.8 | 13.0 | 12.5 | 13.4 | 13.1 |
| 290 | Rv1774 | MAP0081 | 29 | Probable oxidoreductase | Rv1774.1095 | 2.41E-01 | 7.47E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 12.2 | 13.0 | 12.5 | 12.9 | 12.6 | 13.2 | 12.9 |
| 291 | Rv3859c | MAP0172 | 92 | Probable ferredoxin-dependent glutamate synthase [NADPH] ( | Rv3859c-s2.11 | 1.96E-01 | 6.98E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.4 | 11.7 | 13.0 | 12.7 | 12.9 | 12.6 | 13.3 | 13.0 |
| 292 | Rv0594 | MAP1476c | 80 | Mce-family protein Mce2F | Rv0594.1787 | 5.47E-01 | 8.97E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.6 | 12.0 | 13.3 | 12.7 | 12.9 | 12.3 | 13.6 | 12.8 |
| 293 | Rv3884c | MAP0167 | 88 | ESX conserved component EccA2 ESX-2 type VII secretion syste | Rv3884c.830 | 1.98E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 12.7 | 12.3 | 12.2 | 12.5 | 12.3 | 12.9 | 12.6 | 13.3 | 12.9 |
| 294 | Rv2491 | MAP0541c | 32 | hypothetical protein | Rv2491.3631 | 8.44E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.9 | 12.9 | 12.7 | 13.1 | 12.9 | 12.9 | 12.6 | 13.3 | 13.0 |
| 295 | Rv3061c | MAP3238 | 84 | Probable acyl-CoA dehydrogenase FadE22 | Rv3061c.3835 | 1.51E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.8 | 12.4 | 11.9 | 12.8 | 12.6 | 12.9 | 12.5 | 13.4 | 13.2 |
| 296 | Rv2133c | MAP1878c | 79 | hypothetical protein | Rv2133c.4420 | 4.99E-01 | 8.80E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.7 | 12.7 | 12.8 | 12.7 | 12.9 | 12.4 | 13.5 | 13.1 |
| 297 | Rv1680 | MAP1807c | 24 | Hypothetical protein | Rv1680.4524 | 6.04E-01 | 9.22E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 13.0 | 13.1 | 12.7 | 13.4 | 13.1 | 12.9 | 12.6 | 13.3 | 13.0 |
| 298 | Rv0256c | MAP2595 | 66 | PPE family protein PPE2 | Rv0256c.1816 | 7.00E-01 | 9.51E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 13.0 | 13.2 | 12.4 | 14.0 | 13.4 | 12.9 | 12.2 | 13.6 | 12.9 |
| 299 | Rv0948c | MAP0892c | 72 | Chorismate mutase | Rv0948c.2718 | 6.56E-01 | 9.36E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.9 | 12.8 | 12.5 | 13.1 | 12.7 | 12.9 | 12.6 | 13.3 | 13.0 |
| 300 | Rv3166c | MAP3220c | 61 | hypothetical protein | Rv3166c.2806 | 6.72E-01 | 9.46E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.7 | 12.0 | 13.5 | 12.5 | 12.9 | 12.5 | 13.4 | 12.8 |
| 301 | Rv1616 | MAP1309 | 63 | hypothetical protein | Rv1616.986 | 3.41E-01 | 8.15E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.7 | 12.3 | 13.0 | 12.6 | 12.9 | 12.6 | 13.3 | 12.9 |
| 302 | Rv1391 | MAP1125 | 90 | Probable DNA/pantothenate metabolism flavoprotein homolo | Rv1391.231 | 5.18E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.3 | 12.0 | 12.7 | 12.5 | 12.9 | 12.6 | 13.3 | 13.0 |
| 303 | Rv3379c | MAP2803c | 49 | Probable 1-deoxy-D-xylulose 5-phosphate synthase Dxs2 (1-de | Rv3379c.255 | 1.68E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.2 | 11.4 | 12.9 | 12.5 | 12.9 | 12.6 | 13.3 | 13.0 |
| 304 | Rv0293c | MAP3789c | 77 | hypothetical protein | Rv0293c.4570 | 4.17E-01 | 8.35E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.9 | 12.7 | 12.4 | 12.9 | 12.8 | 12.9 | 12.4 | 13.4 | 12.9 |
| 305 | Rv0901 | MAP2837c | 36 | Possible conserved exported or membrane protein | Rv0901.3321 | 1.79E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.3 | 12.1 | 12.5 | 12.2 | 12.9 | 12.6 | 13.3 | 13.0 |
| 306 | Rv0725c | MAP4189c | 78 | hypothetical protein | Rv0725c.769 | 9.74E-02 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.4 | 12.0 | 12.7 | 12.3 | 12.9 | 12.5 | 13.4 | 13.0 |
| 307 | Rv1908c | MAP1668c | 71 | Catalase-peroxidase-peroxynitritase T KatG | Rv1908c.611 | 8.95E-01 | 9.77E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.9 | 12.9 | 12.5 | 13.2 | 12.9 | 12.9 | 12.5 | 13.3 | 12.7 |
| 308 | Rv0209 | MAP3644 | 60 | Hypothetical protein | Rv0209.214 | 4.18E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 11.9 | 13.2 | 12.4 | 12.9 | 12.6 | 13.3 | 13.0 |
| 309 | Rv0932c | MAP3388c | 81 | Periplasmic phosphate-binding lipoprotein PstS2 (PBP-2) (PstS | Rv0932c.356 | 1.50E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.4 | 12.0 | 12.8 | 12.5 | 12.9 | 12.4 | 13.4 | 12.9 |
| 310 | Rv1400c | MAP1128c | 77 | Probable lipase LipH | Rv1400c.3384 | 5.90E-01 | 9.16E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.8 | 12.4 | 13.1 | 12.7 | 12.9 | 12.5 | 13.3 | 13.0 |
| 311 | Rv2771c | MAP2876c | 84 | hypothetical protein | Rv2771c.717 | 1.89E-01 | 6.94E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.2 | 11.5 | 12.9 | 12.4 | 12.9 | 12.6 | 13.2 | 13.1 |
| 312 | Rv1290c | MAP1726c | 34 | hypothetical protein | Rv1290c.1705 | 6.25E-03 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 12.5 | 11.7 | 11.5 | 11.9 | 11.7 | 12.9 | 12.4 | 13.5 | 12.8 |
| 313 | Rv0755c | MAP3939c | 61 | PPE family protein PPE12 | Rv0755c.1996 | 8.73E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.9 | 13.0 | 11.9 | 14.1 | 12.5 | 12.9 | 12.4 | 13.4 | 13.0 |
| 314 | Rv3721c | MAP0322c | 78 | DNA polymerase III (subunit gamma/tau) DnaZ/X | Rv3721c.2274 | 3.94E-01 | 8.35E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 13.0 | 13.1 | 12.9 | 13.2 | 13.0 | 12.9 | 12.6 | 13.2 | 12.8 |
| 315 | Rv0534c | MAP4029c | 84 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase MenA (DH | Rv0534c.3947 | 4.71E-01 | 8.58E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.9 | 12.7 | 12.6 | 12.9 | 12.7 | 12.9 | 12.5 | 13.3 | 13.1 |
| 316 | Rv0010c | MAP0012c | 72 | Probable conserved membrane protein | Rv0010c.2359 | 2.65E-01 | 7.62E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 12.4 | 12.8 | 12.7 | 12.9 | 12.5 | 13.3 | 13.1 |
| 317 | Rv2680 | MAP2801 | 83 | hypothetical protein | Rv2680.1030 | 9.42E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.9 | 12.9 | 12.7 | 13.2 | 12.9 | 12.9 | 12.6 | 13.2 | 12.9 |
| 318 | Rv1022 | MAP0989 | 84 | Probable conserved lipoprotein LpqU | Rv1022.2762 | 1.01E-01 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.8 | 12.5 | 12.2 | 12.7 | 12.5 | 12.9 | 12.5 | 13.3 | 12.9 |
| 319 | Rv0355c | MAP0554c | 63 | PPE family protein PPE8 | Rv0355c-s5.86 | 6.23E-01 | 9.31E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.0 | 13.3 | 12.6 | 12.9 | 12.5 | 13.3 | 12.9 |
| 320 | Rv3626c | MAP0437 | 77 | hypothetical protein | Rv3626c.4250 | 3.04E-01 | 7.74E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 13.1 | 13.4 | 12.7 | 14.2 | 13.1 | 12.9 | 12.4 | 13.4 | 13.0 |
| 321 | Rv3446c | MAP4242 | 57 | Hypothetical alanine and valine rich protein | Rv3446c.229 | 8.44E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.8 | 12.7 | 13.0 | 12.8 | 12.9 | 12.5 | 13.3 | 13.0 |
| 322 | Rv2575 | MAP1060c | 77 | Possible conserved membrane glycine rich protein | Rv2575.3080 | 6.27E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.4 | 12.1 | 12.7 | 12.4 | 12.9 | 12.6 | 13.2 | 12.9 |
| 323 | Rv2048c | MAP0931 | 81 | Polyketide synthase Pks12 | Rv2048c-s1.40 | 5.10E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.4 | 12.2 | 12.6 | 12.4 | 12.9 | 12.5 | 13.3 | 13.1 |
| 324 | Rv0680c | MAP4138c | 67 | Probable conserved transmembrane protein | Rv0680c.3801 | 1.71E-01 | 6.83E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.4 | 12.0 | 12.9 | 12.5 | 12.9 | 12.6 | 13.2 | 13.0 |
| 325 | Rv0071 | MAP2313c | 28 | Possible maturase | Rv0071.4206 | 5.95E-01 | 9.20E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.2 | 13.2 | 12.8 | 12.9 | 12.5 | 13.3 | 12.9 |
| 326 | Rv0102 | MAP2297c | 51 | hypothetical protein | Rv0102.3750 | 3.51E-01 | 8.22E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.6 | 12.3 | 13.0 | 12.4 | 12.9 | 12.5 | 13.3 | 13.0 |
| 327 | Rv1258c | MAP2516 | 71 | Probable conserved integral membrane transport protein | Rv1258c.815 | 1.68E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.3 | 11.8 | 12.9 | 12.5 | 12.9 | 12.5 | 13.3 | 12.7 |
| 328 | Rv1083 | MAP2707c | 64 | hypothetical protein | Rv1083.2376 | 6.47E-01 | 9.34E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.9 | 13.1 | 12.5 | 13.6 | 12.9 | 12.9 | 12.5 | 13.3 | 12.9 |
| 329 | Rv1502 | MAP0692c | 30 | Hypothetical protein | Rv1502.3081 | 8.17E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.4 | 12.1 | 12.7 | 12.4 | 12.9 | 12.5 | 13.2 | 12.9 |
| 330 | Rv1780 | MAP1494 | 89 | hypothetical protein | Rv1780.2456 | 4.94E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.3 | 12.3 | 12.4 | 12.3 | 12.9 | 12.5 | 13.3 | 12.8 |
| 331 | Rv0900 | MAP3452c | 27 | Possible membrane protein | Rv0900.2984 | 1.88E-01 | 6.94E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.8 | 12.5 | 12.2 | 12.9 | 12.5 | 12.9 | 12.6 | 13.2 | 12.8 |
| 332 | Rv0312 | MAP3800 | 70 | Conserved hypothetical proline and threonine rich protein | Rv0312.1119 | 9.13E-03 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.5 | 12.3 | 12.6 | 12.5 | 12.9 | 12.7 | 13.1 | 12.9 |
| 333 | Rv1283c | MAP2488 | 85 | Probable oligopeptide-transport integral membrane protein A | Rv1283c.4258 | 1.24E-01 | 6.73E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.3 | 11.8 | 12.8 | 12.1 | 12.9 | 12.6 | 13.2 | 13.0 |
| 334 | Rv0044c | MAP0054c | 83 | Possible oxidoreductase | Rv0044c.755 | 4.56E-01 | 8.44E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.7 | 12.6 | 12.9 | 12.8 | 12.9 | 12.6 | 13.2 | 12.9 |
| 335 | Rv3308 | MAP3430 | 74 | Probable phosphomannomutase PmmB (phosphomannose mu | Rv3308.2278 | 1.10E-01 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.5 | 12.5 | 12.6 | 12.5 | 12.9 | 12.5 | 13.2 | 12.8 |
| 336 | Rv3343c | MAP2253 | 60 | PPE family protein PPE54 | Rv3343c-s4.46 | 8.01E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.8 | 12.4 | 13.2 | 12.9 | 12.9 | 12.5 | 13.3 | 13.1 |
| 337 | Rv2415c | MAP2226c | 69 | hypothetical protein | Rv2415c.3948 | 1.58E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.8 | 12.6 | 12.4 | 12.8 | 12.7 | 12.9 | 12.6 | 13.2 | 12.9 |
| 338 | Rv2048c | MAP0931 | 81 | Polyketide synthase Pks12 | Rv2048c-s3.46 | 1.45E-01 | 6.83E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 12.5 | 12.6 | 12.6 | 12.9 | 12.5 | 13.2 | 13.0 |
| 339 | Rv3630 | MAP0433c | 80 | Probable conserved integral membrane protein | Rv3630.3117 | 9.07E-01 | 9.81E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.9 | 12.8 | 12.5 | 13.2 | 12.8 | 12.9 | 12.4 | 13.3 | 13.1 |
| 340 | Rv3003c | MAP2636 | 92 | Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid | Rv3003c.541 | 5.73E-01 | 9.06E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.7 | 12.2 | 13.2 | 12.6 | 12.9 | 12.5 | 13.3 | 12.7 |
| 341 | Rv1686c | MAP1392c | 88 | Probable conserved integral membrane protein ABC transport | Rv1686c.3224 | 6.15E-01 | 9.31E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.8 | 12.8 | 12.7 | 12.9 | 12.7 | 12.9 | 12.5 | 13.2 | 12.8 |
| 342 | Rv0161 | MAP3578 | 81 | Possible oxidoreductase | Rv0161.3411 | 3.46E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.7 | 12.4 | 12.3 | 12.6 | 12.4 | 12.9 | 12.6 | 13.2 | 12.9 |
| 343 | Rv0093c | MAP1814 | 42 | Probable conserved membrane protein | Rv0093c.85 | 5.04E-01 | 8.85E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.4 | 13.0 | 12.8 | 12.9 | 12.5 | 13.2 | 12.8 |
| 344 | Rv3470c | MAP3038c | 27 | Probable acetolactate synthase (large subunit) IlvB2 (AHAS) (a | Rv3470c.1984 | 2.77E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.6 | 12.1 | 11.9 | 12.4 | 12.1 | 12.9 | 12.4 | 13.3 | 13.0 |
| 345 | Rv0305c | MAP3939c | 57 | PPE family protein PPE6 | Rv0305c.1428 | 6.49E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.3 | 12.0 | 12.5 | 12.1 | 12.9 | 12.4 | 13.3 | 13.1 |
| 346 | Rv1663 | MAP1370 | 63 | Probable polyketide synthase Pks17 | Rv1663.4588 | 9.51E-01 | 9.82E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.9 | 12.8 | 12.1 | 13.6 | 13.2 | 12.9 | 12.5 | 13.2 | 13.0 |
| 347 | Rv1142c | MAP2389c | 72 | Probable enoyl-CoA hydratase EchA10 (enoyl hydrase) (unsatu | Rv1142c.3229 | 3.47E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 12.7 | 12.3 | 12.0 | 12.6 | 12.2 | 12.9 | 12.6 | 13.1 | 12.8 |
| 348 | Rv3894c | MAP4321c | 88 | ESX conserved component EccC2 ESX-2 type VII secretion syste | Rv3894c-s1.34 | 5.59E-01 | 8.97E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.2 | 13.2 | 12.8 | 12.9 | 12.5 | 13.2 | 12.9 |
| 349 | Rv1486c | MAP1212c | 78 | hypothetical protein | Rv1486c.2492 | 9.29E-01 | 9.82E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.9 | 12.9 | 12.5 | 13.3 | 12.8 | 12.9 | 12.6 | 13.2 | 13.0 |
| 350 | Rv1184c | MAP2234 | 46 | Possible exported protein | Rv1184c.4081 | 9.79E-01 | 9.90E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.9 | 12.9 | 12.4 | 13.3 | 12.7 | 12.9 | 12.5 | 13.2 | 12.9 |
| 351 | Rv1468c | MAP4144 | 66 | PE-PGRS family protein PE_PGRS29 | Rv1468c.3967 | 2.61E-01 | 7.62E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.4 | 12.0 | 12.8 | 12.5 | 12.9 | 12.2 | 13.5 | 12.9 |
| 352 | Rv1257c | MAP2517 | 87 | Probable oxidoreductase | Rv1257c.1105 | 8.62E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.8 | 12.3 | 13.3 | 12.8 | 12.9 | 12.5 | 13.2 | 13.0 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 353 | Rv2597 | MAP1035c | 72 | Probable membrane protein | Rv2597.1525 | 3.66E-01 | 8.32E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.6 | 12.3 | 12.9 | 12.5 | 12.9 | 12.5 | 13.2 | 12.9 |
| 354 | Rv2538c | MAP1093 | 90 | 3-dehydroquinate synthase AroB | Rv2538c.3966 | 2.68E-01 | 7.65E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 12.4 | 12.8 | 12.5 | 12.9 | 12.5 | 13.2 | 12.8 |
| 355 | Rv3368c | MAP0746 | 80 | Possible oxidoreductase | Rv3368c.447 | 2.61E-01 | 7.62E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.6 | 12.3 | 12.8 | 12.7 | 12.9 | 12.5 | 13.2 | 13.0 |
| 356 | Rv2193 | MAP0773 | 93 | Probable cytochrome C oxidase (subunit III) CtaE | Rv2193.4085 | 1.62E-01 | 6.83E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.3 | 11.7 | 12.8 | 12.3 | 12.8 | 12.6 | 13.1 | 12.9 |
| 357 | Rv3723 | MAP0324 | 84 | Probable conserved transmembrane protein | Rv3723.922 | 3.05E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.3 | 11.6 | 13.1 | 12.6 | 12.8 | 12.5 | 13.2 | 12.8 |
| 358 | Rv0658c | MAP2640c | 26 | Probable conserved integral membrane protein | Rv0658c.2183 | 1.27E-01 | 6.73E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.1 | 11.7 | 12.6 | 12.0 | 12.8 | 12.2 | 13.5 | 12.9 |
| 359 | Rv0304c | MAP0210c | 35 | PPE family protein PPE5 | Rv0304c.2592 | 1.88E-01 | 6.94E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.5 | 12.3 | 12.7 | 12.5 | 12.8 | 12.5 | 13.2 | 13.0 |
| 360 | Rv2997 | MAP2158 | 81 | Possible alanine rich dehydrogenase | Rv2997.1108 | 7.70E-02 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.1 | 11.7 | 12.6 | 12.3 | 12.8 | 12.3 | 13.3 | 12.9 |
| 361 | Rv1521 | MAP3752 | 63 | Probable fatty-acid-AMP ligase FadD25 (fatty-acid-AMP synthe | Rv1521.343 | 7.14E-01 | 9.56E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.7 | 12.3 | 13.2 | 12.9 | 12.8 | 12.4 | 13.3 | 13.0 |
| 362 | Rv2693c | MAP2810c | 69 | Probable conserved integral membrane alanine and leucine ric | Rv2693c.1888 | 4.95E-01 | 8.80E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 12.2 | 13.0 | 12.5 | 12.8 | 12.3 | 13.4 | 13.0 |
| 363 | Rv1405c | MAP0251c | 75 | Putative methyltransferase | Rv1405c.4235 | 8.95E-01 | 9.77E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.8 | 12.8 | 12.3 | 13.3 | 12.8 | 12.8 | 12.6 | 13.1 | 12.8 |
| 364 | Rv3824c | MAP2231 | 53 | Conserved polyketide synthase associated protein PapA1 | Rv3824c.548 | 1.95E-01 | 6.98E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.3 | 11.7 | 12.8 | 12.3 | 12.8 | 12.3 | 13.4 | 12.7 |
| 365 | Rv1568 | MAP1274 | 82 | Adenosylmethionine-8-amino-7-oxononanoate aminotransfera | Rv1568.3690 | 4.30E-01 | 8.35E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 12.9 | 13.0 | 12.8 | 13.2 | 13.1 | 12.8 | 12.4 | 13.2 | 12.8 |
| 366 | Rv3732 | MAP1715 | 27 | hypothetical protein | Rv3732.3503 | 3.31E-01 | 8.11E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.6 | 12.3 | 12.9 | 12.6 | 12.8 | 12.6 | 13.1 | 12.8 |
| 367 | Rv2921c | MAP2989c | 80 | Probable cell division protein FtsY (SRP receptor) (signal recogr | Rv2921c.2821 | 8.75E-02 | 6.48E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 13.1 | 13.6 | 13.1 | 14.2 | 13.4 | 12.8 | 12.4 | 13.3 | 12.9 |
| 368 | Rv3103c | MAP3173c | 64 | Hypothetical proline-rich protein | Rv3103c.418 | 6.24E-01 | 9.31E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.7 | 12.6 | 12.9 | 12.7 | 12.8 | 12.5 | 13.2 | 12.9 |
| 369 | Rv2243 | MAP1996 | 86 | Malonyl CoA-acyl carrier protein transacylase FabD (malonyl C | Rv2243.2793 | 6.47E-01 | 9.34E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.6 | 12.0 | 13.3 | 12.6 | 12.8 | 12.5 | 13.2 | 12.9 |
| 370 | Rv1924c | MAP1715 | 34 | hypothetical protein | Rv1924c.2719 | 7.64E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.8 | 12.7 | 12.9 | 12.7 | 12.8 | 12.4 | 13.3 | 12.9 |
| 371 | Rv0694 | MAP1635c | 89 | Possible L-lactate dehydrogenase (cytochrome) LldD1 | Rv0694.1670 | 3.09E-01 | 7.75E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.4 | 11.8 | 13.0 | 12.3 | 12.8 | 12.3 | 13.4 | 13.0 |
| 372 | Rv3563 | MAP0504c | 78 | Probable acyl-CoA dehydrogenase FadE32 | Rv3563.2080 | 9.80E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.5 | 11.9 | 11.3 | 12.6 | 12.0 | 12.8 | 12.4 | 13.2 | 12.8 |
| 373 | Rv2977c | MAP3017c | 79 | Probable thiamine-monophosphate kinase ThiL (thiamine-phos | Rv2977c.1369 | 6.84E-01 | 9.46E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.8 | 12.8 | 12.6 | 12.9 | 12.7 | 12.8 | 12.6 | 13.1 | 12.7 |
| 374 | Rv2213 | MAP1953 | 83 | Probable aminopeptidase PepB | Rv2213.2566 | 1.01E-01 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.6 | 12.3 | 11.8 | 12.7 | 12.4 | 12.8 | 12.6 | 13.0 | 12.9 |
| 375 | Rv1216c | MAP2562 | 65 | Probable conserved integral membrane protein | Rv1216c.154 | 5.15E-01 | 8.89E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.6 | 12.2 | 13.1 | 12.6 | 12.8 | 12.7 | 13.0 | 12.8 |
| 376 | Rv0562 | MAP4058 | 79 | Probable polyprenyl-diphosphate synthase GrcC1 (polyprenyl | Rv0562.213 | 9.48E-01 | 9.82E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.8 | 12.8 | 12.7 | 13.0 | 12.9 | 12.8 | 12.6 | 13.1 | 12.7 |
| 377 | Rv1898 | MAP1624 | 88 | hypothetical protein | Rv1898.399 | 3.10E-01 | 7.75E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.5 | 12.2 | 12.7 | 12.6 | 12.8 | 12.3 | 13.4 | 12.9 |
| 378 | Rv3038c | MAP3086c | 84 | hypothetical protein | Rv3038c.2229 | 2.66E-01 | 7.62E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.4 | 12.0 | 12.8 | 12.5 | 12.8 | 12.3 | 13.3 | 13.0 |
| 379 | Rv2471 | MAP0695 | 79 | Probable alpha-glucosidase AglA (maltase) (glucoinvertase) (gl | Rv2471.4585 | 4.34E-01 | 8.36E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.4 | 12.9 | 12.6 | 12.8 | 12.5 | 13.1 | 12.7 |
| 380 | Rv3018c | MAP3737 | 69 | PPE family protein PPE46 | Rv3018c.4387 | 3.94E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.3 | 11.5 | 13.2 | 12.3 | 12.8 | 12.3 | 13.4 | 12.9 |
| 381 | Rv0601c | MAP1101 | 43 | Two component sensor kinase [first part] | Rv0601c.3609 | 3.48E-01 | 8.22E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.5 | 12.1 | 12.9 | 12.7 | 12.8 | 12.5 | 13.2 | 12.9 |
| 382 | Rv3669 | MAP0405c | 79 | Probable conserved transmembrane protein | Rv3669.999 | 6.99E-02 | 6.48E-01 | 0.11 | 9.52E-02 | 7.98E-01 | 13.0 | 13.4 | 13.1 | 13.7 | 13.3 | 12.8 | 12.4 | 13.2 | 12.8 |
| 383 | Rv0959 | MAP0906 | 90 | hypothetical protein | Rv0959.2569 | 2.65E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.4 | 12.3 | 12.5 | 12.4 | 12.8 | 12.6 | 13.1 | 12.8 |
| 384 | Rv2588c | MAP1042 | 85 | Probable conserved membrane protein secretion factor YajC | Rv2588c.2708 | 1.65E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.4 | 12.0 | 12.7 | 12.3 | 12.8 | 12.4 | 13.2 | 12.6 |
| 385 | Rv3743c | MAP3384 | 35 | Probable cation transporter P-type ATPase CtpJ | Rv3743c.3725 | 4.27E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.6 | 12.4 | 12.8 | 12.5 | 12.8 | 12.4 | 13.2 | 12.9 |
| 386 | Rv1146 | MAP2324c | 83 | Probable conserved transmembrane transport protein MmpL1 | Rv1146.1968 | 4.51E-01 | 8.44E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.6 | 12.1 | 13.0 | 12.5 | 12.8 | 12.4 | 13.2 | 13.0 |
| 387 | Rv2149c | MAP1893c | 84 | Conserved protein YfiH | Rv2149c.1902 | 1.83E-01 | 6.88E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.6 | 12.2 | 11.6 | 12.8 | 12.3 | 12.8 | 12.4 | 13.2 | 12.9 |
| 388 | Rv0354c | MAP0542c | 29 | PPE family protein PPE7 | Rv0354c.1862 | 4.03E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.8 | 12.7 | 12.6 | 12.8 | 12.7 | 12.8 | 12.5 | 13.1 | 12.8 |
| 389 | Rv0869c | MAP0807c | 88 | Probable molybdenum cofactor biosynthesis protein A2 MoaA | Rv0869c.1948 | 5.54E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.7 | 12.4 | 12.9 | 12.6 | 12.8 | 12.5 | 13.1 | 12.9 |
| 390 | Rv3031 | MAP3063 | 86 | hypothetical protein | Rv3031.838 | 8.63E-01 | 9.70E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.8 | 12.9 | 12.3 | 13.5 | 12.8 | 12.8 | 12.3 | 13.3 | 12.9 |
| 391 | Rv1183 | MAP2232 | 57 | hypothetical protein | Rv1183-sB.31 | 7.06E-02 | 6.48E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.5 | 11.8 | 11.4 | 12.2 | 11.9 | 12.8 | 12.0 | 13.6 | 12.8 |
| 392 | Rv2416c | MAP2325 | 35 | Enhanced intracellular survival protein Eis,GCN5-related N-ace | Rv2416c.1674 | 1.14E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.3 | 12.0 | 12.6 | 12.4 | 12.8 | 12.4 | 13.2 | 13.0 |
| 393 | Rv1302 | MAP2459c | 94 | Probable undecapaprenyl-phosphate alpha-N-acetylglucosami | Rv1302.2258 | 2.93E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.6 | 12.4 | 12.7 | 12.6 | 12.8 | 12.4 | 13.2 | 12.9 |
| 394 | Rv1487 | MAP1213 | 81 | hypothetical protein | Rv1487.1285 | 7.42E-01 | 9.57E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.8 | 12.9 | 12.4 | 13.4 | 12.9 | 12.8 | 12.4 | 13.2 | 12.8 |
| 395 | Rv0769 | MAP0350 | 81 | Probable dehydrogenase/reductase | Rv0769.4214 | 8.11E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.8 | 12.9 | 12.1 | 13.8 | 12.5 | 12.8 | 12.5 | 13.1 | 13.0 |
| 396 | Rv3273 | MAP0127 | 60 | Probable transmembrane carbonic anhydrase (carbonate dehy | Rv3273.2287 | 9.99E-01 | 9.99E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.8 | 12.8 | 12.5 | 13.1 | 12.8 | 12.8 | 12.4 | 13.2 | 12.7 |
| 397 | Rv2721c | MAP0904 | 60 | hypothetical protein | Rv2721c.4328 | 5.05E-01 | 8.86E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.9 | 13.0 | 12.5 | 13.5 | 13.0 | 12.8 | 12.5 | 13.1 | 12.9 |
| 398 | Rv1442 | MAP1424c | 22 | Probable biotin sulfoxide reductase BisC (BDS reductase) (BSO | Rv1442.258 | 1.78E-01 | 6.85E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.7 | 12.5 | 12.3 | 12.8 | 12.6 | 12.8 | 12.5 | 13.1 | 12.9 |
| 399 | Rv0497 | MAP3988 | 60 | Probable conserved transmembrane protein | Rv0497.1242 | 5.44E-01 | 8.97E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.9 | 13.1 | 12.3 | 14.0 | 13.5 | 12.8 | 12.5 | 13.1 | 12.9 |
| 400 | Rv3892c | MAP0158 | 70 | PPE family protein PPE69 | Rv3892c.3820 | 8.32E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.8 | 12.7 | 12.0 | 13.4 | 12.7 | 12.8 | 12.3 | 13.3 | 12.8 |
| 401 | Rv2098c | MAP4144 | 64 | hypothetical protein | Rv2098c.4098 | 3.08E-01 | 7.75E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.9 | 13.1 | 12.7 | 13.6 | 12.9 | 12.8 | 12.4 | 13.2 | 12.8 |
| 402 | Rv3438 | MAP4251c | 79 | hypothetical protein | Rv3438.1536 | 4.24E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.5 | 11.8 | 13.1 | 12.8 | 12.8 | 12.6 | 13.0 | 12.8 |
| 403 | Rv0018c | MAP0021c | 77 | Phosphoserine/threonine phosphatase PstP | Rv0018c.2949 | 1.79E-01 | 6.88E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.6 | 12.3 | 11.9 | 12.8 | 12.4 | 12.8 | 12.6 | 13.0 | 12.7 |
| 404 | Rv0843 | MAP0688 | 44 | Probable dehydrogenase | Rv0843.2236 | 6.38E-01 | 9.31E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 12.3 | 13.0 | 12.7 | 12.8 | 12.4 | 13.2 | 12.7 |
| 405 | Rv3001c | MAP3036c | 88 | Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-aci | Rv3001c.1658 | 5.46E-01 | 8.97E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.4 | 12.9 | 12.8 | 12.8 | 12.6 | 13.0 | 12.8 |
| 406 | Rv1808 | MAP0966c | 60 | PPE family protein PPE32 | Rv1808.1797 | 2.21E-01 | 7.31E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.1 | 11.3 | 12.8 | 12.3 | 12.8 | 12.1 | 13.5 | 12.6 |
| 407 | Rv2594c | MAP1036 | 83 | Probable crossover junction endodeoxyribonuclease RuvC (hol | Rv2594c.1589 | 2.45E-01 | 7.49E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.6 | 12.4 | 11.9 | 12.9 | 12.6 | 12.8 | 12.5 | 13.1 | 12.9 |
| 408 | Rv0628c | MAP0638 | 26 | hypothetical protein | Rv0628c.801 | 1.42E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.5 | 12.0 | 11.3 | 12.7 | 12.2 | 12.8 | 12.4 | 13.2 | 12.8 |
| 409 | Rv0215c | MAP3651c | 87 | Probable acyl-CoA dehydrogenase FadE3 | Rv0215c.1795 | 3.02E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.2 | 11.5 | 12.9 | 12.5 | 12.8 | 12.0 | 13.6 | 12.7 |
| 410 | Rv1902c | MAP1423 | 87 | Probable sialic acid-transport integral membrane protein NanT | Rv1902c.2532 | 2.12E-01 | 7.15E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.4 | 12.0 | 12.7 | 12.3 | 12.8 | 12.3 | 13.2 | 12.9 |
| 411 | Rv1591 | MAP0283c | 64 | Probable transmembrane protein | Rv1591.3832 | 3.51E-01 | 8.22E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 12.9 | 13.0 | 12.7 | 13.4 | 12.9 | 12.8 | 12.4 | 13.1 | 12.6 |
| 412 | Rv0045c | MAP0055c | 78 | Possible hydrolase | Rv0045c.4526 | 5.42E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.7 | 12.3 | 13.0 | 12.5 | 12.8 | 12.6 | 13.0 | 12.7 |
| 413 | Rv1801 | MAP0853 | 49 | PPE family protein PPE29 | Rv1801.902 | 4.28E-01 | 8.35E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.7 | 12.5 | 12.2 | 12.9 | 12.5 | 12.8 | 12.3 | 13.3 | 12.7 |
| 414 | Rv1791 | MAP1507 | 87 | PE family protein PE19 | Rv1791.1491 | 6.18E-01 | 9.31E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.7 | 12.5 | 11.5 | 13.5 | 12.7 | 12.8 | 12.4 | 13.1 | 12.8 |
| 415 | Rv1555 | MAP3033c | 30 | Probable fumarate reductase [membrane anchor subunit] Frd | Rv1555.4376 | 6.61E-01 | 9.36E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.8 | 12.7 | 12.5 | 12.9 | 12.8 | 12.8 | 12.5 | 13.0 | 12.9 |
| 416 | Rv0770 | MAP0604 | 69 | Probable dehydrogenase/reductase | Rv0770.473 | 6.35E-01 | 9.31E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.7 | 12.3 | 13.0 | 12.8 | 12.8 | 12.4 | 13.1 | 12.8 |
| 417 | Rv2695 | MAP2812 | 76 | Conserved hypothetical alanine rich protein | Rv2695.3634 | 1.95E-01 | 6.98E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.7 | 12.4 | 12.1 | 12.8 | 12.6 | 12.8 | 12.4 | 13.1 | 12.8 |
| 418 | Rv1856c | MAP1564c | 80 | Possible oxidoreductase | Rv1856c.4490 | 8.30E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.8 | 12.7 | 12.4 | 13.1 | 12.6 | 12.8 | 12.4 | 13.2 | 13.0 |
| 419 | Rv1441c | MAP4144 | 55 | PE-PGRS family protein PE_PGRS26 | Rv1441c.248 | 8.09E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.8 | 12.9 | 12.2 | 13.6 | 12.8 | 12.8 | 12.3 | 13.2 | 12.6 |
| 420 | Rv1753c | MAP3939c | 59 | PPE family protein PPE24 | Rv1753c.4608 | 1.52E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.3 | 12.1 | 12.5 | 12.3 | 12.8 | 12.2 | 13.3 | 12.7 |
| 421 | Rv0422c | MAP3912c | 87 | Probable phosphomethylpyrimidine kinase ThiD (HMP-phosph | Rv0422c.3071 | 8.65E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.8 | 12.7 | 12.3 | 13.1 | 12.5 | 12.8 | 12.5 | 13.1 | 12.9 |
| 422 | Rv1600 | MAP1294 | 86 | Probable histidinol-phosphate aminotransferase HisC1 | Rv1600.2246 | 7.02E-01 | 9.51E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.5 | 12.8 | 12.7 | 12.8 | 12.3 | 13.3 | 12.7 |
| 423 | Rv2702 | MAP2819 | 83 | Polyphosphate glucokinase PpgK (polyphosphate-glucose phos | Rv2702.1337 | 1.42E-01 | 6.83E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 12.9 | 13.1 | 12.9 | 13.3 | 13.1 | 12.8 | 12.4 | 13.1 | 12.6 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 424 | Rv3546 | MAP0521c | 86 | Probable acetyl-CoA acetyltransferase FadA5 (acetoacetyl-CoA | Rv3546.1224 | 5.56E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.4 | 11.6 | 13.3 | 12.4 | 12.8 | 12.4 | 13.2 | 12.9 |
| 425 | Rv2608 | MAP1761c | 60 | PPE family protein PPE42 | Rv2608.1505 | 4.11E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.4 | 11.6 | 13.1 | 12.3 | 12.8 | 12.4 | 13.2 | 12.7 |
| 426 | Rv0799c | MAP0631c | 80 | hypothetical protein | Rv0799c.502 | 6.20E-01 | 9.31E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.8 | 12.9 | 12.7 | 13.1 | 13.0 | 12.8 | 12.3 | 13.2 | 12.5 |
| 427 | Rv1806 | MAP1507 | 57 | PE family protein PE20 | Rv1806.1780 | 8.06E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 11.7 | 13.6 | 12.7 | 12.8 | 12.4 | 13.1 | 12.9 |
| 428 | Rv1536 | MAP1246 | 88 | Isoleucyl-tRNA synthetase IleS | Rv1536.4030 | 1.38E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.2 | 11.9 | 12.4 | 12.2 | 12.8 | 12.1 | 13.4 | 13.0 |
| 429 | Rv0591 | MAP4086 | 76 | Mce-family protein Mce2C | Rv0591.925 | 8.39E-01 | 9.70E-01 | 0.47 | 1.00E+00 | 1.00E+00 | 12.8 | 12.9 | 11.5 | 14.4 | 12.2 | 12.8 | 12.2 | 13.3 | 13.0 |
| 430 | Rv1110 | MAP2684c | 90 | Probable LYTB-related protein LytB2 | Rv1110.791 | 4.89E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.5 | 11.9 | 11.5 | 12.4 | 11.8 | 12.8 | 12.2 | 13.3 | 12.6 |
| 431 | Rv3489 | MAP4147 | 39 | hypothetical protein | Rv3489.2111 | 4.47E-01 | 8.42E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.4 | 11.7 | 13.1 | 12.5 | 12.8 | 12.4 | 13.2 | 12.9 |
| 432 | Rv1108c | MAP2686 | 86 | Probable exodeoxyribonuclease VII (large subunit) XseA (exonu | Rv1108c.4572 | 8.44E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.8 | 12.8 | 12.4 | 13.3 | 12.6 | 12.8 | 12.4 | 13.1 | 12.8 |
| 433 | Rv0075 | MAP2055 | 39 | Probable aminotransferase | Rv0075.1091 | 1.02E-01 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.2 | 12.0 | 12.5 | 12.2 | 12.8 | 12.3 | 13.2 | 12.8 |
| 434 | Rv2510c | MAP2319c | 73 | hypothetical protein | Rv2510c.1411 | 9.52E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.8 | 12.7 | 12.4 | 13.1 | 12.6 | 12.8 | 12.4 | 13.1 | 12.9 |
| 435 | Rv2380c | MAP2172c | 65 | Peptide synthetase MbtE (peptide synthase) | Rv2380c-s2.37 | 4.82E-01 | 8.70E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.5 | 11.9 | 13.1 | 12.3 | 12.8 | 12.4 | 13.1 | 12.9 |
| 436 | Rv3838c | MAP0193 | 81 | Prephenate dehydratase PheA | Rv3838c.1650 | 9.71E-01 | 9.88E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.8 | 12.8 | 12.1 | 13.4 | 12.5 | 12.8 | 12.4 | 13.1 | 12.9 |
| 437 | Rv0982 | MAP0734 | 84 | Two component sensor kinase MprB | Rv0982.2571 | 2.50E-01 | 7.58E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.7 | 12.6 | 12.7 | 12.7 | 12.8 | 12.6 | 12.9 | 12.7 |
| 438 | Rv1727 | MAP0250 | 35 | hypothetical protein | Rv1727.433 | 8.44E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.0 | 13.4 | 12.7 | 12.8 | 12.4 | 13.1 | 12.9 |
| 439 | Rv3343c | MAP2253 | 60 | PPE family protein PPE54 | Rv3343c-s2.85 | 3.05E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.3 | 11.7 | 12.9 | 12.2 | 12.8 | 12.4 | 13.1 | 12.8 |
| 440 | Rv1311 | MAP2450c | 89 | Probable ATP synthase epsilon chain AtpC | Rv1311.3506 | 9.41E-01 | 9.82E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.8 | 12.8 | 12.2 | 13.4 | 12.7 | 12.8 | 12.5 | 13.0 | 12.8 |
| 441 | Rv0929 | MAP0652 | 83 | Phosphate-transport integral membrane ABC transporter PstC | Rv0929.57 | 9.99E-01 | 9.99E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.8 | 12.7 | 12.3 | 13.2 | 12.6 | 12.8 | 12.2 | 13.3 | 12.9 |
| 442 | Rv1896c | MAP1622c | 75 | hypothetical protein | Rv1896c.186 | 6.85E-01 | 9.46E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 12.0 | 13.2 | 12.8 | 12.7 | 12.3 | 13.2 | 12.7 |
| 443 | Rv1115 | MAP2675c | 84 | Possible exported protein | Rv1115.1601 | 6.43E-01 | 9.33E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.8 | 12.9 | 12.3 | 13.6 | 13.2 | 12.7 | 12.3 | 13.1 | 12.8 |
| 444 | Rv0480c | MAP3973c | 78 | Possible amidohydrolase | Rv0480c.2490 | 6.20E-01 | 9.31E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.6 | 12.3 | 12.9 | 12.6 | 12.7 | 12.4 | 13.1 | 12.9 |
| 445 | Rv2131c | MAP0389 | 78 | Monophosphatase CysQ | Rv2131c.1048 | 5.78E-01 | 9.08E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 12.5 | 12.7 | 12.6 | 12.7 | 12.4 | 13.1 | 12.6 |
| 446 | Rv2151c | MAP1927c | 30 | Possible cell division protein FtsQ | Rv2151c.3669 | 8.01E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.8 | 12.8 | 12.4 | 13.2 | 12.8 | 12.7 | 12.5 | 13.0 | 12.8 |
| 447 | Rv3867 | MAP0040 | 29 | ESX-1 secretion-associated protein EspH | Rv3867.3542 | 8.69E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.7 | 12.6 | 11.2 | 14.0 | 12.1 | 12.7 | 12.3 | 13.2 | 13.0 |
| 448 | Rv2605c | MAP1729c | 87 | Probable acyl-CoA thioesterase II TesB2 (TEII) | Rv2605c.178 | 6.76E-01 | 9.46E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.7 | 12.7 | 12.4 | 12.9 | 12.6 | 12.7 | 12.5 | 13.0 | 12.7 |
| 449 | Rv1508c | MAP0286 | 48 | Probable membrane protein | Rv1508c.3142 | 3.62E-02 | 6.27E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.5 | 12.0 | 11.7 | 12.2 | 11.9 | 12.7 | 12.2 | 13.3 | 12.8 |
| 450 | Rv2870c | MAP2940c | 84 | Probable 1-deoxy-D-xylulose 5-phosphate reductoisomerase D | Rv2870c.525 | 5.51E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.5 | 11.9 | 13.1 | 12.6 | 12.7 | 12.3 | 13.2 | 12.8 |
| 451 | Rv0515 | MAP4176 | 68 | Conserved 13E12 repeat family protein | Rv0515.4305 | 4.56E-01 | 8.44E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.6 | 12.3 | 12.9 | 12.6 | 12.7 | 12.5 | 13.0 | 12.8 |
| 452 | Rv0461 | MAP3955 | 65 | Probable transmembrane protein | Rv0461.4182 | 9.53E-01 | 9.82E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.8 | 12.2 | 13.3 | 12.6 | 12.7 | 12.3 | 13.1 | 12.9 |
| 453 | Rv3116 | MAP3306c | 57 | Probable molybdenum cofactor biosynthesis protein MoeB2 (M | Rv3116.4139 | 2.98E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.3 | 11.7 | 12.9 | 12.2 | 12.7 | 12.3 | 13.2 | 12.6 |
| 454 | Rv2139 | MAP1883 | 81 | Probable dihydroorotate dehydrogenase PyrD | Rv2139.3682 | 9.49E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.8 | 12.2 | 13.4 | 12.6 | 12.7 | 12.2 | 13.3 | 12.6 |
| 455 | Rv0509 | MAP4002 | 85 | hypothetical protein | Rv0509-sA.20 | 4.98E-01 | 8.80E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.7 | 12.5 | 12.0 | 13.0 | 12.4 | 12.7 | 12.3 | 13.1 | 12.7 |
| 456 | Rv1565c | MAP1271c | 74 | hypothetical protein | Rv1565c.4599 | 6.15E-01 | 9.31E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.8 | 12.9 | 12.8 | 13.0 | 12.9 | 12.7 | 12.2 | 13.3 | 12.9 |
| 457 | Rv1819c | MAP1531c | 76 | Probable drug-transport transmembrane ATP-binding protein A | Rv1819c.1701 | 3.07E-01 | 7.75E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.3 | 12.3 | 12.4 | 12.3 | 12.7 | 12.0 | 13.4 | 13.0 |
| 458 | Rv1479 | MAP1205 | 93 | Probable transcriptional regulatory protein MoxR1 | Rv1479.4269 | 3.96E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.5 | 12.1 | 12.9 | 12.5 | 12.7 | 12.4 | 13.0 | 12.8 |
| 459 | Rv1456c | MAP1182c | 82 | Probable unidentified antibiotic-transport integral membrane A | Rv1456c.4246 | 2.08E-01 | 7.15E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.4 | 12.1 | 12.6 | 12.4 | 12.7 | 12.3 | 13.1 | 13.0 |
| 460 | Rv3369 | MAP2229 | 27 | hypothetical protein | Rv3369.2064 | 1.73E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.2 | 11.7 | 12.7 | 12.2 | 12.7 | 12.3 | 13.1 | 12.9 |
| 461 | Rv0270 | MAP3714 | 84 | Probable fatty-acid-CoA ligase FadD2 (fatty-acid-CoA synthetas | Rv0270.2655 | 7.47E-01 | 9.58E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.8 | 12.8 | 12.7 | 12.9 | 12.8 | 12.7 | 12.2 | 13.2 | 12.6 |
| 462 | Rv1320c | MAP2440 | 66 | Possible adenylate cyclase (ATP pyrophosphate-lyase) (adenyly | Rv1320c.2852 | 3.70E-01 | 8.32E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.5 | 12.2 | 12.8 | 12.6 | 12.7 | 12.4 | 13.0 | 12.7 |
| 463 | Rv1428c | MAP1160c | 83 | hypothetical protein | Rv1428c.3368 | 2.63E-01 | 7.62E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.2 | 11.6 | 12.8 | 12.2 | 12.7 | 12.2 | 13.3 | 12.7 |
| 464 | Rv2307B | MAP0522 | 29 | Hypothetical glycine rich protein | Rv2307B.2730 | 9.78E-01 | 9.90E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.7 | 12.7 | 12.8 | 12.7 | 12.7 | 12.4 | 13.1 | 12.8 |
| 465 | Rv1306 | MAP2455c | 79 | Probable ATP synthase B chain AtpF | Rv1306.1778 | 8.97E-01 | 9.77E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.6 | 11.6 | 13.7 | 12.9 | 12.7 | 12.3 | 13.2 | 12.9 |
| 466 | Rv0271c | MAP3716c | 84 | Probable acyl-CoA dehydrogenase FadE6 | Rv0271c.4413 | 8.02E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.8 | 12.5 | 13.1 | 12.7 | 12.7 | 12.3 | 13.2 | 12.8 |
| 467 | Rv0512 | MAP4005 | 91 | Probable delta-aminolevulinic acid dehydratase HemB (porpho | Rv0512.1079 | 3.51E-01 | 8.22E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.7 | 12.5 | 12.3 | 12.7 | 12.6 | 12.7 | 12.4 | 13.1 | 12.8 |
| 468 | Rv3695 | MAP0356c | 79 | Possible conserved membrane protein | Rv3695.2512 | 4.17E-03 | 6.07E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 12.4 | 11.8 | 11.6 | 12.1 | 12.0 | 12.7 | 12.4 | 13.0 | 12.7 |
| 469 | Rv0500 | MAP3991 | 81 | Probable pyrroline-5-carboxylate reductase ProC (P5CR) (P5C r | Rv0500.4421 | 4.59E-01 | 8.44E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.4 | 11.6 | 13.1 | 12.5 | 12.7 | 12.3 | 13.1 | 12.9 |
| 470 | Rv3916c | MAP4342c | 83 | hypothetical protein | Rv3916c.1323 | 3.90E-01 | 8.35E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.4 | 11.8 | 13.0 | 12.1 | 12.7 | 12.5 | 12.9 | 12.7 |
| 471 | Rv2307D | MAP0407c | 29 | Hypothetical protein | Rv2307D.672 | 7.07E-01 | 9.54E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.5 | 11.4 | 13.5 | 12.6 | 12.7 | 12.4 | 13.0 | 12.8 |
| 472 | Rv2892c | MAP1505 | 45 | PPE family protein PPE45 | Rv2892c.1508 | 6.90E-01 | 9.51E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.4 | 11.4 | 13.5 | 12.3 | 12.7 | 12.3 | 13.2 | 12.6 |
| 473 | Rv2617c | MAP1162 | 45 | Probable transmembrane protein | Rv2617c.3223 | 9.62E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.7 | 12.6 | 12.8 | 12.7 | 12.7 | 12.3 | 13.2 | 12.7 |
| 474 | Rv3728 | MAP3145c | 33 | Probable conserved two-domain membrane protein | Rv3728.2579 | 1.61E-01 | 6.83E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.3 | 12.2 | 12.4 | 12.3 | 12.7 | 12.2 | 13.2 | 12.7 |
| 475 | Rv1661 | MAP1370 | 70 | Probable polyketide synthase Pks7 | Rv1661-s1.287 | 7.04E-01 | 9.52E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.5 | 11.5 | 13.5 | 12.1 | 12.7 | 12.3 | 13.1 | 12.9 |
| 476 | Rv0468 | MAP3962 | 91 | 3-hydroxybutyryl-CoA dehydrogenase FadB2 (beta-hydroxybut | Rv0468.917 | 2.79E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.1 | 11.5 | 12.8 | 12.1 | 12.7 | 12.1 | 13.3 | 12.8 |
| 477 | Rv0355c | MAP3939c | 63 | PPE family protein PPE8 | Rv0355c-s1.31 | 1.05E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 12.5 | 12.1 | 11.9 | 12.3 | 12.1 | 12.7 | 12.4 | 13.0 | 12.7 |
| 478 | Rv0410c | MAP3893c | 86 | Serine/threonine-protein kinase PknG (protein kinase G) (STPK | Rv0410c.3154 | 8.82E-01 | 9.73E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.4 | 12.9 | 12.7 | 12.7 | 12.5 | 12.9 | 12.7 |
| 479 | Rv0438c | MAP3932c | 81 | Probable molybdopterin biosynthesis protein MoeA2 | Rv0438c.518 | 9.21E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.1 | 13.2 | 12.7 | 12.7 | 12.3 | 13.1 | 12.6 |
| 480 | Rv1917c | MAP3939c | 57 | PPE family protein PPE34 | Rv1917c.3461 | 5.43E-01 | 8.97E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.7 | 12.6 | 12.4 | 12.7 | 12.6 | 12.7 | 12.3 | 13.1 | 12.8 |
| 481 | Rv0451c | MAP1241c | 60 | Probable conserved membrane protein MmpS4 | Rv0451c.1517 | 9.24E-01 | 9.81E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.7 | 12.5 | 12.9 | 12.8 | 12.7 | 12.5 | 12.9 | 12.7 |
| 482 | Rv2259 | MAP2008 | 89 | S-nitrosomycothiol reductase MscR | Rv2259.792 | 2.22E-01 | 7.31E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.5 | 12.2 | 11.6 | 12.8 | 12.0 | 12.7 | 12.3 | 13.1 | 12.7 |
| 483 | Rv2524c | MAP0848 | 88 | Probable fatty acid synthase Fas (fatty acid synthetase) | Rv2524c-s5.28 | 7.88E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 11.9 | 13.3 | 12.5 | 12.7 | 12.3 | 13.0 | 12.8 |
| 484 | Rv0456c | MAP3949c | 83 | enoyl-CoA hydratase EchA2 (enoyl hydrase) (unsaturated acyl-C | Rv0456c.4392 | 2.33E-01 | 7.42E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.3 | 12.1 | 12.6 | 12.4 | 12.7 | 12.2 | 13.2 | 12.7 |
| 485 | Rv2681 | MAP2802 | 75 | Conserved hypothetical alanine rich protein | Rv2681.3985 | 8.51E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.8 | 12.3 | 13.2 | 12.8 | 12.7 | 12.1 | 13.3 | 12.9 |
| 486 | Rv2512c | MAP3759c | 47 | Transposase for insertion sequence element IS1081 | Rv2512c.3410 | 8.61E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 12.1 | 13.2 | 12.4 | 12.7 | 12.3 | 13.0 | 12.8 |
| 487 | Rv2717c | MAP2833c | 76 | hypothetical protein | Rv2717c.3021 | 5.36E-02 | 6.30E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 12.4 | 12.0 | 11.5 | 12.4 | 11.9 | 12.7 | 12.4 | 13.0 | 12.5 |
| 488 | Rv1193 | MAP2580c | 84 | Probable fatty-acid-CoA ligase FadD36 (fatty-acid-CoA syntheta | Rv1193.58 | 6.23E-01 | 9.31E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.8 | 12.9 | 12.3 | 13.5 | 12.7 | 12.7 | 12.4 | 13.0 | 12.6 |
| 489 | Rv2198c | MAP1938c | 59 | Probable conserved membrane protein MmpS3 | Rv2198c.3849 | 1.74E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.6 | 12.4 | 12.1 | 12.6 | 12.4 | 12.7 | 12.4 | 13.0 | 12.7 |
| 490 | Rv1127c | MAP2664 | 77 | Probable pyruvate, phosphate dikinase PpdK | Rv1127c.4417 | 8.22E-01 | 9.68E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.7 | 12.6 | 12.1 | 13.1 | 12.4 | 12.7 | 12.2 | 13.2 | 12.9 |
| 491 | Rv0773c | MAP0607c | 81 | Probable bifunctional acylase GgtA: cephalosporin acylase (GL- | Rv0773c.837 | 2.18E-01 | 7.30E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.5 | 12.2 | 11.7 | 12.7 | 12.2 | 12.7 | 12.3 | 13.1 | 12.8 |
| 492 | Rv0614 | MAP2472 | 45 | hypothetical protein | Rv0614.3970 | 1.57E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.4 | 12.3 | 12.5 | 12.4 | 12.7 | 12.4 | 13.0 | 12.8 |
| 493 | Rv1409 | MAP1136 | 78 | Probable bifunctional riboflavin biosynthesis protein RibG : dia | Rv1409.664 | 2.98E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.5 | 12.2 | 11.5 | 12.8 | 12.4 | 12.7 | 12.0 | 13.3 | 12.7 |
| 494 | Rv1842c | MAP1551c | 79 | hypothetical protein | Rv1842c.3701 | 9.45E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.7 | 12.7 | 12.2 | 13.2 | 12.5 | 12.7 | 12.3 | 13.0 | 12.7 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 495 | Rv0109 | MAP4144 | 61 | PE-PGRS family protein PE_PGRS1 | Rv0109.1405 | 6.51E-01 | 9.35E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.4 | 11.7 | 13.2 | 12.6 | 12.7 | 12.1 | 13.2 | 12.8 |
| 496 | Rv2881c | MAP2944c | 72 | Probable integral membrane phosphatidate cytidylyltransferas | Rv2881c.2511 | 4.55E-01 | 8.44E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.4 | 12.2 | 12.7 | 12.5 | 12.7 | 12.2 | 13.2 | 12.7 |
| 497 | Rv0099 | MAP2747 | 27 | Possible fatty-acid-CoA ligase FadD10 (fatty-acid-CoA syntheta | Rv0099.926 | 3.54E-01 | 8.22E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.4 | 12.0 | 12.8 | 12.5 | 12.7 | 12.3 | 13.0 | 12.7 |
| 498 | Rv2589 | MAP1041c | 85 | 4-aminobutyrate aminotransferase GabT (gamma-amino-N-bu | Rv2589.2839 | 2.83E-02 | 6.27E-01 | 1.00 | 2.38E-02 | 7.98E-01 | 12.5 | 12.0 | 11.7 | 12.3 | 12.1 | 12.7 | 12.5 | 12.8 | 12.7 |
| 499 | Rv2025c | MAP2784 | 40 | hypothetical protein | Rv2025c.3392 | 7.67E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.6 | 12.4 | 12.8 | 12.6 | 12.7 | 12.3 | 13.1 | 12.7 |
| 500 | Rv0146 | MAP3564 | 75 | Possible S-adenosylmethionine-dependent methyltransferase | Rv0146.3957 | 4.98E-01 | 8.80E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.3 | 11.6 | 13.1 | 12.1 | 12.7 | 12.2 | 13.1 | 12.7 |
| 501 | Rv1633 | MAP1335 | 95 | Probable excinuclease ABC (subunit B-helicase) UvrB | Rv1633.546 | 3.56E-01 | 8.22E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.4 | 12.0 | 12.8 | 12.2 | 12.7 | 12.2 | 13.1 | 12.7 |
| 502 | Rv2586c | MAP1044 | 74 | Probable protein-export membrane protein SecF | Rv2586c.1384 | 2.79E-01 | 7.74E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.8 | 13.1 | 12.7 | 13.4 | 13.0 | 12.7 | 12.1 | 13.2 | 12.9 |
| 503 | Rv3312A | MAP0342c | 74 | Secreted protein antigen | Rv3312A.3868 | 1.95E-01 | 6.98E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.2 | 11.8 | 12.6 | 12.1 | 12.7 | 12.2 | 13.1 | 12.6 |
| 504 | Rv1867 | MAP0898 | 78 | hypothetical protein | Rv1867.4584 | 8.16E-01 | 9.65E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.6 | 12.5 | 12.7 | 12.6 | 12.7 | 12.1 | 13.2 | 12.9 |
| 505 | Rv2159c | MAP1379 | 33 | hypothetical protein | Rv2159c.3960 | 7.23E-01 | 9.56E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.4 | 11.3 | 13.5 | 12.0 | 12.7 | 12.1 | 13.2 | 12.6 |
| 506 | Rv2195 | MAP1934 | 83 | Probable rieske iron-sulfur protein QcrA | Rv2195.3498 | 5.49E-01 | 8.97E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.8 | 13.2 | 11.8 | 14.6 | 12.8 | 12.7 | 12.3 | 13.0 | 12.7 |
| 507 | Rv1697 | MAP1404 | 90 | hypothetical protein | Rv1697.2688 | 9.95E-01 | 9.98E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.3 | 13.0 | 12.6 | 12.7 | 12.4 | 12.9 | 12.8 |
| 508 | Rv2999 | MAP1193c | 31 | Probable conserved lipoprotein LppY | Rv2999.3390 | 5.67E-01 | 9.03E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.6 | 12.6 | 12.5 | 12.7 | 12.6 | 12.7 | 12.5 | 12.9 | 12.6 |
| 509 | Rv0200 | MAP0767c | 30 | Possible conserved transmembrane protein | Rv0200.4127 | 5.53E-01 | 8.97E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.9 | 12.3 | 13.5 | 12.8 | 12.7 | 12.4 | 13.0 | 12.7 |
| 510 | Rv3818 | MAP0204c | 87 | hypothetical protein | Rv3818.3150 | 2.37E-01 | 7.47E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.6 | 12.3 | 12.0 | 12.7 | 12.2 | 12.7 | 12.4 | 12.9 | 12.8 |
| 511 | Rv0418 | MAP3906 | 80 | Probable lipoprotein aminopeptidase LpqL | Rv0418.249 | 2.98E-01 | 7.74E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.4 | 12.1 | 12.6 | 12.3 | 12.7 | 12.2 | 13.1 | 12.7 |
| 512 | Rv1006 | MAP0948 | 68 | hypothetical protein | Rv1006.903 | 3.54E-01 | 8.22E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.4 | 12.1 | 12.6 | 12.3 | 12.7 | 12.1 | 13.2 | 12.7 |
| 513 | Rv1245c | MAP2537 | 85 | Probable short-chain type dehydrogenase/reductase | Rv1245c.2212 | 1.73E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.5 | 12.1 | 11.6 | 12.6 | 12.3 | 12.7 | 12.3 | 13.0 | 12.8 |
| 514 | Rv2281 | MAP4041c | 31 | Putative phosphate-transport permease PitB | Rv2281.1695 | 6.20E-01 | 9.31E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.6 | 12.5 | 12.1 | 12.8 | 12.4 | 12.6 | 12.1 | 13.1 | 12.8 |
| 515 | Rv2666 | MAP3759c | 50 | Probable transposase for insertion sequence element IS1081 (f | Rv2666.476 | 8.02E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.6 | 12.5 | 11.6 | 13.4 | 12.5 | 12.6 | 12.3 | 13.0 | 12.5 |
| 516 | Rv2266 | MAP2015 | 83 | Probable cytochrome P450 124 Cyp124 | Rv2266.804 | 1.76E-01 | 6.83E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.4 | 11.9 | 11.2 | 12.6 | 11.7 | 12.6 | 12.0 | 13.3 | 12.5 |
| 517 | Rv1366 | MAP1047 | 27 | Hypothetical protein | Rv1366.477 | 2.97E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.2 | 11.5 | 12.8 | 12.4 | 12.6 | 12.2 | 13.1 | 12.8 |
| 518 | Rv3877 | MAP2598c | 26 | ESX conserved component EccD1 ESX-1 type VII secretion syste | Rv3877.2660 | 7.43E-01 | 9.57E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.6 | 12.5 | 12.0 | 13.1 | 12.7 | 12.6 | 12.2 | 13.1 | 12.6 |
| 519 | Rv2519 | MAP4144 | 41 | PE family protein PE26 | Rv2519.4388 | 7.76E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.4 | 13.1 | 12.8 | 12.6 | 12.2 | 13.0 | 12.8 |
| 520 | Rv0535 | MAP4030 | 78 | Probable 5'-methylthioadenosine phosphorylase Pnp (MTA ph | Rv0535.4227 | 2.49E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.5 | 12.3 | 12.2 | 12.4 | 12.3 | 12.6 | 12.4 | 12.9 | 12.7 |
| 521 | Rv0204c | MAP3639c | 84 | Probable conserved transmembrane protein | Rv0204c.230 | 4.31E-01 | 8.35E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.7 | 12.8 | 12.6 | 12.9 | 12.8 | 12.6 | 12.4 | 12.9 | 12.6 |
| 522 | Rv0752c | MAP4214c | 88 | Probable acyl-CoA dehydrogenase FadE9 | Rv0752c.1507 | 5.64E-01 | 9.02E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.9 | 13.3 | 11.5 | 15.1 | 12.7 | 12.6 | 12.0 | 13.3 | 12.6 |
| 523 | Rv2927c | MAP2997c | 93 | hypothetical protein | Rv2927c.739 | 9.61E-01 | 9.82E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.6 | 11.5 | 13.7 | 12.6 | 12.6 | 12.2 | 13.1 | 12.7 |
| 524 | Rv2957 | MAP1234 | 69 | Possible glycosyl transferase | Rv2957.1917 | 5.65E-02 | 6.39E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.4 | 12.0 | 11.6 | 12.3 | 12.1 | 12.6 | 12.2 | 13.1 | 12.5 |
| 525 | Rv2196 | MAP1935 | 89 | Probable ubiquinol-cytochrome C reductase QcrB (cytochrome | Rv2196.30 | 9.57E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.6 | 12.6 | 12.2 | 13.1 | 12.5 | 12.6 | 12.4 | 12.9 | 12.7 |
| 526 | Rv3388 | MAP4144 | 64 | PE-PGRS family protein PE_PGRS52 | Rv3388.3552 | 2.02E-01 | 7.15E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.2 | 11.8 | 12.5 | 12.1 | 12.6 | 12.1 | 13.2 | 12.7 |
| 527 | Rv3610c | MAP0448 | 85 | Membrane-bound protease FtsH (cell division protein) | Rv3610c.4419 | 7.93E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.7 | 12.5 | 12.9 | 12.8 | 12.6 | 12.2 | 13.1 | 12.7 |
| 528 | Rv2449c | MAP2272c | 80 | hypothetical protein | Rv2449c.1104 | 6.84E-01 | 9.46E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.5 | 12.2 | 12.9 | 12.5 | 12.6 | 12.2 | 13.0 | 12.6 |
| 529 | Rv3752c | MAP0279 | 92 | Possible cytidine/deoxycytidylate deaminase | Rv3752c.1868 | 9.53E-01 | 9.82E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.6 | 12.6 | 12.0 | 13.3 | 12.6 | 12.6 | 12.3 | 13.0 | 12.7 |
| 530 | Rv0174 | MAP3609 | 77 | Mce-family protein Mce1F | Rv0174.1209 | 1.82E-01 | 6.88E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.4 | 12.1 | 11.7 | 12.5 | 12.3 | 12.6 | 12.0 | 13.2 | 12.4 |
| 531 | Rv2834c | MAP2091 | 32 | Probable Sn-glycerol-3-phosphate transport integral membran | Rv2834c.1339 | 9.62E-01 | 9.82E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.6 | 12.1 | 13.1 | 12.4 | 12.6 | 12.1 | 13.2 | 12.9 |
| 532 | Rv1484 | MAP1210 | 89 | NADH-dependent enoyl-[acyl-carrier-protein] reductase InhA ( | Rv1484.4234 | 3.13E-01 | 7.78E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.5 | 12.3 | 11.9 | 12.7 | 12.3 | 12.6 | 12.2 | 13.0 | 12.8 |
| 533 | Rv2741 | MAP4144 | 64 | PE-PGRS family protein PE_PGRS47 | Rv2741.2082 | 8.21E-01 | 9.68E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.5 | 11.5 | 13.5 | 12.1 | 12.6 | 12.2 | 13.0 | 12.7 |
| 534 | Rv2678c | MAP2799c | 78 | Probable uroporphyrinogen decarboxylase HemE (uroporphyri | Rv2678c.3971 | 5.73E-01 | 9.06E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.4 | 11.8 | 13.0 | 12.4 | 12.6 | 12.2 | 13.0 | 12.8 |
| 535 | Rv2468c | MAP2288c | 81 | hypothetical protein | Rv2468c.3889 | 8.07E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.6 | 12.5 | 12.0 | 13.1 | 12.4 | 12.6 | 12.3 | 12.9 | 12.6 |
| 536 | Rv1059 | MAP0332 | 61 | hypothetical protein | Rv1059.487 | 4.22E-01 | 8.35E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.4 | 12.0 | 11.0 | 13.1 | 12.1 | 12.6 | 11.9 | 13.3 | 12.6 |
| 537 | Rv0980c | MAP144 | 55 | PE-PGRS family protein PE_PGRS18 | Rv0980c.3707 | 3.04E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.5 | 12.4 | 12.2 | 12.6 | 12.4 | 12.6 | 12.3 | 12.9 | 12.7 |
| 538 | Rv3533c | MAP3939c | 57 | PPE family protein PPE62 | Rv3533c.54 | 2.04E-01 | 7.15E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 12.8 | 13.1 | 12.6 | 13.7 | 13.2 | 12.6 | 12.3 | 12.9 | 12.7 |
| 539 | Rv0552 | MAP2524c | 79 | hypothetical protein | Rv0552.1700 | 5.24E-01 | 8.93E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 12.8 | 12.4 | 13.2 | 13.0 | 12.6 | 12.3 | 12.9 | 12.6 |
| 540 | Rv0645c | MAP4117c | 73 | Methoxy mycolic acid synthase 1 MmaA1 (methyl mycolic acid | Rv0645c.2202 | 6.75E-01 | 9.46E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.6 | 12.7 | 12.3 | 13.2 | 12.9 | 12.6 | 12.2 | 13.0 | 12.7 |
| 541 | Rv2077c | MAP1217c | 61 | Possible conserved transmembrane protein | Rv2077c.783 | 9.43E-01 | 9.82E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.6 | 12.0 | 13.1 | 12.4 | 12.6 | 12.2 | 13.0 | 12.7 |
| 542 | Rv1635c | MAP1338c | 68 | Probable mannosyltransferase Probable conserved transmemb | Rv1635c.1527 | 6.08E-01 | 9.25E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.3 | 11.6 | 13.1 | 12.3 | 12.6 | 12.2 | 13.1 | 12.6 |
| 543 | Rv0743c | MAP1322 | 35 | Hypothetical protein | Rv0743c.432 | 4.26E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.3 | 11.6 | 12.9 | 12.5 | 12.6 | 12.2 | 13.0 | 12.8 |
| 544 | Rv1631 | MAP1326 | 77 | Probable dephospho-CoA kinase CoaE (dephosphocoenzyme a | Rv1631.4276 | 3.00E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.5 | 12.2 | 11.8 | 12.7 | 12.1 | 12.6 | 12.2 | 13.0 | 12.6 |
| 545 | Rv0420c | MAP0118 | 43 | Possible transmembrane protein | Rv0420c.4462 | 7.43E-01 | 9.57E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.6 | 12.7 | 12.5 | 12.8 | 12.7 | 12.6 | 12.3 | 12.9 | 12.7 |
| 546 | Rv3205c | MAP3305c | 87 | hypothetical protein | Rv3205c.958 | 9.40E-02 | 6.48E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.5 | 12.2 | 12.0 | 12.4 | 12.2 | 12.6 | 12.3 | 12.9 | 12.7 |
| 547 | Rv1501 | MAP3160 | 36 | hypothetical protein | Rv1501.766 | 1.73E-01 | 6.83E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.4 | 11.9 | 11.3 | 12.5 | 12.2 | 12.6 | 12.0 | 13.2 | 12.4 |
| 548 | Rv1325c | MAP4144 | 62 | hypothetical protein | Rv1325c.1148 | 3.39E-01 | 8.15E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.2 | 11.6 | 12.7 | 12.1 | 12.6 | 12.1 | 13.1 | 12.7 |
| 549 | Rv2376c | MAP2167c | 75 | Low molecular weight antigen CFP2 (low molecular weight pro | Rv2376c.1489 | 4.53E-01 | 8.44E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.4 | 12.1 | 11.0 | 13.2 | 12.2 | 12.6 | 12.2 | 13.0 | 12.5 |
| 550 | Rv2773c | MAP2878c | 91 | Dihydrodipicolinate reductase DapB (DHPR) | Rv2773c.450 | 4.21E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.2 | 11.6 | 12.9 | 12.5 | 12.6 | 12.2 | 13.0 | 12.6 |
| 551 | Rv2919c | MAP2987c | 98 | Probable nitrogen regulatory protein P-II GlnB | Rv2919c.913 | 3.87E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.4 | 12.0 | 12.7 | 12.3 | 12.6 | 12.3 | 12.9 | 12.8 |
| 552 | Rv1281c | MAP2490 | 84 | Probable oligopeptide-transport ATP-binding protein ABC tran | Rv1281c.246 | 8.89E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.4 | 12.0 | 11.7 | 12.4 | 12.2 | 12.6 | 12.3 | 12.9 | 12.7 |
| 553 | Rv0355c | MAP3939c | 63 | PPE family protein PPE8 | Rv0355c-s3.2 | 5.55E-01 | 8.97E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.4 | 12.1 | 12.8 | 12.5 | 12.6 | 12.3 | 12.9 | 12.6 |
| 554 | Rv2219A | MAP1961c | 68 | Probable conserved membrane protein | Rv2219A.1567 | 7.30E-01 | 9.56E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.6 | 12.7 | 12.1 | 13.4 | 12.7 | 12.6 | 12.0 | 13.1 | 12.5 |
| 555 | Rv1771 | MAP0081 | 34 | L-gulono-1,4-lactone dehydrogenase | Rv1771.1827 | 8.57E-01 | 9.70E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.6 | 12.7 | 11.6 | 13.8 | 13.2 | 12.6 | 12.1 | 13.0 | 12.7 |
| 556 | Rv0189c | MAP3631c | 91 | Probable dihydroxy-acid dehydratase IlvD (dad) | Rv0189c.2268 | 5.40E-01 | 8.97E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 12.1 | 12.7 | 12.4 | 12.6 | 12.1 | 13.0 | 12.5 |
| 557 | Rv2462c | MAP2282c | 77 | Probable trigger factor (TF) protein Tig | Rv2462c.2923 | 4.03E-01 | 8.35E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 12.7 | 12.8 | 12.4 | 13.2 | 12.7 | 12.6 | 12.3 | 12.9 | 12.5 |
| 558 | Rv3480c | MAP0347c | 38 | Possible triacylglycerol synthase (diacylglycerol acyltransferase | Rv3480c.3816 | 4.90E-01 | 8.77E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.3 | 11.7 | 12.9 | 12.3 | 12.6 | 12.3 | 12.9 | 12.7 |
| 559 | Rv1901 | MAP1625 | 81 | Probable CinA-like protein CinA | Rv1901.2533 | 8.51E-01 | 9.70E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.6 | 12.6 | 12.3 | 13.0 | 12.8 | 12.6 | 12.3 | 12.8 | 12.6 |
| 560 | Rv1911c | MAP2411 | 56 | Probable lipoprotein LppC | Rv1911c.730 | 3.86E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.4 | 12.1 | 11.4 | 12.9 | 12.4 | 12.6 | 12.3 | 12.9 | 12.5 |
| 561 | Rv1920 | MAP0072c | 41 | Probable membrane protein | Rv1920.4509 | 2.26E-01 | 7.31E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 12.6 | 12.8 | 12.7 | 13.0 | 12.8 | 12.6 | 12.2 | 12.9 | 12.6 |
| 562 | Rv0336 | MAP4176 | 68 | Conserved 13E12 repeat family protein | Rv0336.4016 | 6.33E-01 | 9.31E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.5 | 12.3 | 12.7 | 12.4 | 12.6 | 12.3 | 12.8 | 12.6 |
| 563 | Rv0685 | MAP0364c | 97 | Probable iron-regulated elongation factor TU Tuf (EF-TU) | Rv0685.1769 | 4.21E-01 | 8.35E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.4 | 12.2 | 11.4 | 12.9 | 12.4 | 12.6 | 12.3 | 12.8 | 12.6 |
| 564 | Rv0172 | MAP3607 | 80 | Mce-family protein Mce1D | Rv0172.631 | 1.04E-01 | 6.48E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 12.8 | 13.1 | 12.9 | 13.4 | 13.1 | 12.6 | 12.0 | 13.1 | 12.6 |
| 565 | Rv3126c | MAP1465c | 63 | Hypothetical protein | Rv3126c.1777 | 7.91E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 11.7 | 13.2 | 12.6 | 12.6 | 12.2 | 12.9 | 12.7 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 566 | Rv2937 | MAP1237c | 31 | Daunorubicin-dim-transport integral membrane protein ABC tr | Rv2937.2203 | 6.92E-01 | 9.51E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 12.1 | 12.8 | 12.5 | 12.6 | 12.0 | 13.1 | 12.6 |
| 567 | Rv2174 | MAP1912 | 82 | Alpha(1->6)mannosyltransferase Possible conserved integral m | Rv2174.2572 | 5.10E-01 | 8.89E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.5 | 12.4 | 12.1 | 12.6 | 12.4 | 12.6 | 12.1 | 13.0 | 12.7 |
| 568 | Rv2347c | MAP1508 | 88 | Putative ESAT-6 like protein EsxP (ESAT-6 like protein 7) | Rv2347c.1771 | 5.11E-01 | 8.89E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.4 | 12.2 | 11.3 | 13.1 | 12.2 | 12.6 | 12.3 | 12.8 | 12.6 |
| 569 | Rv0246 | MAP1796c | 32 | Probable conserved integral membrane protein | Rv0246.227 | 9.24E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.6 | 11.9 | 13.3 | 12.3 | 12.6 | 12.2 | 12.9 | 12.5 |
| 570 | Rv0024 | MAP0036 | 68 | Putative secreted protein P60-related protein | Rv0024.172 | 6.45E-01 | 9.34E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.6 | 12.6 | 12.4 | 12.9 | 12.7 | 12.6 | 12.2 | 12.9 | 12.5 |
| 571 | Rv0751c | MAP0744c | 81 | Probable 3-hydroxyisobutyrate dehydrogenase MmsB (hibadh) | Rv0751c.1340 | 8.52E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.5 | 12.5 | 12.0 | 13.0 | 12.3 | 12.5 | 12.2 | 12.9 | 12.7 |
| 572 | Rv3067 | MAP3418 | 44 | hypothetical protein | Rv3067.3306 | 4.80E-01 | 8.69E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.5 | 12.3 | 11.9 | 12.8 | 12.4 | 12.5 | 12.3 | 12.8 | 12.5 |
| 573 | Rv3826 | MAP3752 | 62 | Probable fatty-acid-AMP ligase FadD23 (fatty-acid-AMP synthe | Rv3826.638 | 7.20E-01 | 9.56E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.3 | 11.2 | 13.4 | 12.0 | 12.5 | 12.1 | 13.0 | 12.6 |
| 574 | Rv0713 | MAP4173 | 65 | Probable conserved transmembrane protein | Rv0713.1479 | 5.45E-01 | 8.97E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.5 | 12.3 | 11.5 | 13.0 | 12.3 | 12.5 | 12.2 | 12.9 | 12.5 |
| 575 | Rv3203 | MAP2932c | 67 | Possible lipase LipV | Rv3203.3906 | 8.66E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 11.4 | 13.5 | 12.0 | 12.5 | 12.2 | 12.9 | 12.5 |
| 576 | Rv2185c | MAP1923c | 76 | Conserved protein TB16.3 | Rv2185c.1486 | 4.14E-01 | 8.35E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.4 | 12.2 | 11.4 | 12.9 | 12.1 | 12.5 | 12.3 | 12.8 | 12.5 |
| 577 | Rv3310 | MAP3432 | 75 | Acid phosphatase (acid phosphomonoesterase) (phosphomonc | Rv3310.1919 | 2.52E-01 | 7.60E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.5 | 12.3 | 12.1 | 12.5 | 12.4 | 12.5 | 12.2 | 12.9 | 12.7 |
| 578 | Rv3140 | MAP3189 | 88 | Probable acyl-CoA dehydrogenase FadE23 | Rv3140.2058 | 3.71E-01 | 8.32E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.7 | 12.9 | 12.3 | 13.6 | 12.9 | 12.5 | 12.1 | 13.0 | 12.6 |
| 579 | Rv1566c | MAP1272c | 77 | Possible Inv protein | Rv1566c.1773 | 6.30E-01 | 9.31E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.4 | 12.1 | 10.8 | 13.4 | 12.1 | 12.5 | 11.9 | 13.2 | 12.5 |
| 580 | Rv3527 | MAP0538c | 77 | Hypothetical protein | Rv3527.422 | 6.72E-01 | 9.46E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.3 | 11.4 | 13.2 | 12.4 | 12.5 | 12.2 | 12.9 | 12.7 |
| 581 | Rv1866 | MAP0708 | 78 | hypothetical protein | Rv1866.1131 | 6.42E-01 | 9.33E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.6 | 12.8 | 12.0 | 13.6 | 12.6 | 12.5 | 12.2 | 12.9 | 12.8 |
| 582 | Rv2902c | MAP2970c | 84 | Probable ribonuclease HII protein RnhB (RNase HII) | Rv2902c.4233 | 6.55E-01 | 9.36E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.6 | 12.8 | 11.8 | 13.9 | 12.5 | 12.5 | 12.2 | 12.9 | 12.7 |
| 583 | Rv2155c | MAP1899c | 79 | Probable UDP-N-acetylmuramoylalanine-D-glutamate ligase M | Rv2155c.4583 | 5.66E-01 | 9.02E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 12.1 | 12.7 | 12.3 | 12.5 | 12.2 | 12.9 | 12.6 |
| 584 | Rv0632c | MAP4102c | 81 | Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsatur | Rv0632c.3523 | 5.20E-01 | 8.93E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.7 | 13.0 | 11.9 | 14.1 | 12.7 | 12.5 | 12.2 | 12.8 | 12.6 |
| 585 | Rv0517 | MAP4008 | 77 | Possible membrane acyltransferase | Rv0517.516 | 8.95E-01 | 9.77E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.4 | 11.5 | 13.4 | 12.6 | 12.5 | 11.8 | 13.2 | 12.8 |
| 586 | Rv3497c | MAP0110 | 81 | Mce-family protein Mce4C | Rv3497c.2084 | 9.15E-01 | 9.81E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.6 | 12.6 | 11.6 | 13.6 | 12.2 | 12.5 | 12.3 | 12.8 | 12.5 |
| 587 | Rv3336c | MAP3453c | 86 | Probable tryptophanyl-tRNA synthetase TrpS (tryptophan--tRN | Rv3336c.4248 | 7.36E-01 | 9.57E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.5 | 12.4 | 11.6 | 13.1 | 12.0 | 12.5 | 11.9 | 13.1 | 12.5 |
| 588 | Rv3234c | MAP3347c | 83 | Putative triacylglycerol synthase (diacylglycerol acyltransferase | Rv3234c.2205 | 4.49E-02 | 6.27E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.4 | 12.0 | 11.9 | 12.1 | 12.0 | 12.5 | 12.1 | 12.9 | 12.8 |
| 589 | Rv0815c | MAP0645c | 90 | Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like p | Rv0815c.767 | 1.15E-01 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.3 | 11.7 | 11.1 | 12.4 | 11.8 | 12.5 | 12.1 | 13.0 | 12.7 |
| 590 | Rv0462 | MAP3956 | 90 | Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase ( | Rv0462.2634 | 6.61E-01 | 9.36E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.6 | 12.7 | 12.2 | 13.2 | 12.5 | 12.5 | 12.2 | 12.9 | 12.6 |
| 591 | Rv1869c | MAP1579c | 77 | Probable reductase | Rv1869c.2259 | 2.27E-01 | 7.31E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.3 | 12.0 | 11.4 | 12.5 | 11.8 | 12.5 | 12.0 | 13.1 | 12.7 |
| 592 | Rv0104 | MAP0938 | 37 | hypothetical protein | Rv0104.3143 | 8.01E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 11.2 | 13.5 | 12.2 | 12.5 | 12.2 | 12.9 | 12.5 |
| 593 | Rv3136 | MAP3184 | 53 | PPE family protein PPE51 | Rv3136.3214 | 6.85E-01 | 9.46E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.4 | 11.7 | 13.0 | 12.1 | 12.5 | 12.1 | 13.0 | 12.6 |
| 594 | Rv1135c | MAP3939c | 58 | PPE family protein PPE16 | Rv1135c.252 | 8.10E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.4 | 11.3 | 13.4 | 12.1 | 12.5 | 12.1 | 13.0 | 12.5 |
| 595 | Rv1385 | MAP1120 | 82 | Probable orotidine 5'-phosphate decarboxylase PyrF (OMP dec | Rv1385.3657 | 7.18E-01 | 9.56E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.5 | 12.6 | 12.2 | 13.0 | 12.6 | 12.5 | 12.2 | 12.8 | 12.5 |
| 596 | Rv2324 | MAP2096 | 91 | Probable transcriptional regulatory protein (probably AsnC-fan | Rv2324.2156 | 7.17E-01 | 9.56E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.5 | 12.4 | 12.2 | 12.6 | 12.5 | 12.5 | 12.2 | 12.8 | 12.4 |
| 597 | Rv0978c | MAP4144 | 55 | PE-PGRS family protein PE_PGRS17 | Rv0978c.3097 | 8.43E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 11.8 | 13.1 | 12.6 | 12.5 | 12.0 | 13.0 | 12.7 |
| 598 | Rv0222 | MAP3658 | 85 | Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsatur | Rv0222.3813 | 9.23E-01 | 9.81E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.5 | 12.5 | 12.0 | 13.0 | 12.7 | 12.5 | 12.1 | 12.9 | 12.5 |
| 599 | Rv1781c | MAP1500c | 81 | Probable 4-alpha-glucanotransferase MalQ (amylomaltase) (di | Rv1781c.4021 | 4.44E-01 | 8.42E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.4 | 12.3 | 12.0 | 12.6 | 12.2 | 12.5 | 12.2 | 12.8 | 12.6 |
| 600 | Rv2358 | MAP2138 | 74 | Probable transcriptional regulatory protein SmtB (probably Ars | Rv2358.4167 | 9.08E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.6 | 12.1 | 13.0 | 12.7 | 12.5 | 11.9 | 13.1 | 12.5 |
| 601 | Rv3058c | MAP3108c | 70 | Possible transcriptional regulatory protein (probably TetR-fami | Rv3058c.4494 | 4.32E-01 | 8.35E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.6 | 12.8 | 12.4 | 13.1 | 12.7 | 12.5 | 12.0 | 13.0 | 12.5 |
| 602 | Rv3883c | MAP3787 | 45 | Membrane-anchored mycosin MycP1 (serine protease) (subtili | Rv3883c.3793 | 8.41E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.6 | 11.4 | 13.8 | 12.0 | 12.5 | 12.2 | 12.8 | 12.6 |
| 603 | Rv3627c | MAP0436 | 80 | hypothetical protein | Rv3627c.3209 | 4.19E-01 | 8.35E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.5 | 12.6 | 12.5 | 12.8 | 12.7 | 12.5 | 12.2 | 12.8 | 12.4 |
| 604 | Rv1906c | MAP1630c | 54 | hypothetical protein | Rv1906c.2061 | 2.97E-01 | 7.74E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.3 | 11.8 | 10.9 | 12.7 | 12.3 | 12.5 | 11.8 | 13.2 | 12.2 |
| 605 | Rv3347c | MAP2121c | 61 | Membrane protein | Rv3347c-sC.46 | 7.44E-01 | 9.57E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.5 | 12.4 | 12.1 | 12.7 | 12.4 | 12.5 | 12.0 | 13.0 | 12.6 |
| 606 | Rv3531c | MAP0056c | 88 | Hypothetical protein | Rv3531c.210 | 7.32E-01 | 9.56E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.5 | 12.6 | 12.0 | 13.2 | 12.5 | 12.5 | 12.0 | 13.0 | 12.4 |
| 607 | Rv0788 | MAP0626 | 92 | Probable phosphoribosylformylglycinamidine synthase I PURG | Rv0788.726 | 6.28E-01 | 9.31E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.6 | 12.9 | 11.5 | 14.4 | 12.2 | 12.5 | 12.0 | 13.0 | 12.4 |
| 608 | Rv1481 | MAP1207 | 92 | Probable membrane protein | Rv1481.1080 | 5.87E-01 | 9.13E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.4 | 12.3 | 11.9 | 12.8 | 12.2 | 12.5 | 12.2 | 12.7 | 12.6 |
| 609 | Rv1371 | MAP0218 | 26 | Probable conserved membrane protein | Rv1371.1404 | 3.93E-01 | 8.35E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.6 | 12.7 | 12.6 | 12.8 | 12.7 | 12.5 | 12.0 | 13.0 | 12.6 |
| 610 | Rv1816 | MAP1528 | 80 | Possible transcriptional regulatory protein | Rv1816.734 | 4.87E-01 | 8.77E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.6 | 12.8 | 12.1 | 13.4 | 12.7 | 12.5 | 12.2 | 12.8 | 12.6 |
| 611 | Rv2400c | MAP2213c | 77 | Probable sulfate-binding lipoprotein SubI | Rv2400c.3676 | 5.37E-01 | 8.97E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.6 | 12.8 | 12.0 | 13.5 | 12.9 | 12.5 | 12.2 | 12.7 | 12.5 |
| 612 | Rv3141 | MAP0263c | 84 | Probable NADPH quinone oxidoreductase FadB4 (NADPH:quin | Rv3141.918 | 8.32E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.4 | 12.3 | 12.5 | 12.5 | 12.5 | 12.0 | 12.9 | 12.5 |
| 613 | Rv2781c | MAP2889c | 78 | Possible alanine rich oxidoreductase | Rv2781c.4538 | 9.00E-01 | 9.78E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.5 | 12.5 | 11.9 | 13.1 | 12.3 | 12.5 | 12.0 | 12.9 | 12.7 |
| 614 | Rv0361 | MAP3863c | 68 | Probable conserved membrane protein | Rv0361.1241 | 9.51E-01 | 9.82E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.5 | 12.5 | 11.7 | 13.3 | 12.6 | 12.5 | 12.1 | 12.9 | 12.6 |
| 615 | Rv3558 | MAP3939c | 51 | PPE family protein PPE64 | Rv3558.4106 | 9.14E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.5 | 12.4 | 11.7 | 13.2 | 12.3 | 12.5 | 12.2 | 12.7 | 12.6 |
| 616 | Rv2520c | MAP0103c | 71 | Possible conserved membrane protein | Rv2520c.2352 | 1.38E-01 | 6.83E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 12.6 | 12.9 | 12.9 | 12.9 | 12.9 | 12.5 | 12.0 | 13.0 | 12.4 |
| 617 | Rv3105c | MAP3175c | 93 | Probable peptide chain release factor 2 PrfB (RF-2) | Rv3105c.2824 | 6.83E-02 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.3 | 12.0 | 11.7 | 12.3 | 11.9 | 12.5 | 12.2 | 12.8 | 12.5 |
| 618 | Rv3623 | MAP0440c | 73 | Probable conserved lipoprotein LpqG | Rv3623.1526 | 7.52E-01 | 9.61E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.4 | 12.3 | 11.4 | 13.2 | 12.3 | 12.5 | 12.2 | 12.7 | 12.5 |
| 619 | Rv1194c | MAP1995 | 27 | hypothetical protein | Rv1194c.4555 | 8.77E-01 | 9.72E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.5 | 12.5 | 11.8 | 13.2 | 12.2 | 12.5 | 12.0 | 12.9 | 12.5 |
| 620 | Rv1016c | MAP0981c | 67 | Probable conserved lipoprotein LpqT | Rv1016c.48 | 6.95E-01 | 9.51E-01 | 0.42 | 7.95E-01 | 9.80E-01 | 12.5 | 12.5 | 12.3 | 12.8 | 12.5 | 12.5 | 12.1 | 12.8 | 12.5 |
| 621 | Rv3392c | MAP0135 | 70 | Cyclopropane-fatty-acyl-phospholipid synthase 1 CmaA1 (cyclo | Rv3392c.4226 | 1.68E-01 | 6.83E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.3 | 12.0 | 11.5 | 12.4 | 11.9 | 12.5 | 12.1 | 12.8 | 12.5 |
| 622 | Rv2928 | MAP3745 | 29 | Probable thioesterase TesA | Rv2928.3350 | 9.45E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.4 | 12.4 | 12.3 | 12.6 | 12.4 | 12.5 | 12.2 | 12.7 | 12.5 |
| 623 | Rv0671 | MAP4288 | 52 | Possible conserved lipoprotein LpqP | Rv0671.3068 | 2.84E-01 | 7.74E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.4 | 12.3 | 12.1 | 12.5 | 12.3 | 12.4 | 12.2 | 12.7 | 12.5 |
| 624 | Rv2311 | MAP2290c | 31 | hypothetical protein | Rv2311.4477 | 3.34E-01 | 8.11E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.6 | 12.8 | 12.3 | 13.3 | 12.6 | 12.4 | 12.1 | 12.8 | 12.5 |
| 625 | Rv3068c | MAP3146c | 86 | Probable phosphoglucomutase PgmA (glucose phosphomutase | Rv3068c.3134 | 7.66E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.4 | 12.3 | 11.4 | 13.2 | 12.2 | 12.4 | 12.0 | 12.9 | 12.5 |
| 626 | Rv0855 | MAP0785 | 84 | Probable fatty-acid-CoA racemase Far | Rv0855.3104 | 6.71E-01 | 9.46E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.5 | 12.8 | 11.6 | 13.9 | 12.2 | 12.4 | 12.1 | 12.8 | 12.6 |
| 627 | Rv1334 | MAP1917c | 52 | Possible hydrolase | Rv1334.1492 | 3.98E-01 | 8.35E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.3 | 12.0 | 11.1 | 12.8 | 12.2 | 12.4 | 12.2 | 12.7 | 12.5 |
| 628 | Rv1196 | MAP1505 | 41 | PPE family protein PPE18 | Rv1196.4560 | 8.04E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.5 | 12.5 | 12.0 | 13.0 | 12.5 | 12.4 | 12.0 | 12.9 | 12.3 |
| 629 | Rv3028c | MAP3060c | 91 | Probable electron transfer flavoprotein (alpha-subunit) FixB (al | Rv3028c.3962 | 7.88E-01 | 9.65E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.4 | 12.3 | 11.6 | 13.0 | 12.0 | 12.4 | 11.8 | 13.1 | 12.7 |
| 630 | Rv1478 | MAP1204 | 78 | Possible invasion protein | Rv1478.1779 | 9.58E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.4 | 12.4 | 11.6 | 13.2 | 12.6 | 12.4 | 12.1 | 12.8 | 12.4 |
| 631 | Rv3346c | MAP3462c | 69 | Conserved transmembrane protein | Rv3346c.98 | 3.63E-01 | 8.31E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.4 | 12.3 | 12.2 | 12.4 | 12.2 | 12.4 | 12.1 | 12.7 | 12.4 |
| 632 | Rv2893 | MAP0867c | 33 | Possible oxidoreductase | Rv2893.3385 | 2.24E-01 | 7.31E-01 | 0.78 | 2.62E-01 | 8.76E-01 | 12.3 | 12.0 | 11.6 | 12.4 | 12.2 | 12.4 | 12.1 | 12.8 | 12.6 |
| 633 | Rv1527c | MAP1636c | 68 | Probable polyketide synthase Pks5 | Rv1527c-s1.40 | 5.69E-01 | 9.04E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.5 | 12.8 | 11.8 | 13.8 | 13.1 | 12.4 | 11.8 | 13.0 | 12.4 |
| 634 | Rv3661 | MAP0414c | 87 | hypothetical protein | Rv3661.4515 | 7.83E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.5 | 12.2 | 12.8 | 12.4 | 12.4 | 11.9 | 12.9 | 12.5 |
| 635 | Rv0881 | MAP0820 | 84 | Possible rRNA methyltransferase (rRNA methylase) | Rv0881.2775 | 8.76E-01 | 9.72E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.4 | 12.0 | 12.9 | 12.4 | 12.4 | 12.1 | 12.7 | 12.5 |
| 636 | Rv1133c | MAP2661 | 86 | Probable 5-methyltetrahydropteroyltriglutamate--homocystein | Rv1133c.1709 | 7.68E-01 | 9.65E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.5 | 11.8 | 13.2 | 12.2 | 12.4 | 12.1 | 12.7 | 12.4 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 637 | Rv3162c | MAP1089 | 41 | Possible integral membrane protein | Rv3162c.707 | 5.82E-01 | 9.11E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.3 | 12.0 | 11.0 | 13.0 | 12.2 | 12.4 | 11.7 | 13.1 | 12.1 |
| 638 | Rv0538 | MAP4034 | 50 | Possible conserved membrane protein | Rv0538.2050 | 9.03E-01 | 9.80E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.5 | 11.4 | 13.6 | 12.1 | 12.4 | 11.8 | 13.0 | 12.4 |
| 639 | Rv1589 | MAP1283 | 89 | Probable biotin synthetase BioB | Rv1589.4244 | 3.93E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.3 | 12.1 | 11.8 | 12.4 | 12.2 | 12.4 | 11.8 | 12.9 | 12.5 |
| 640 | Rv1021 | MAP0988 | 74 | hypothetical protein | Rv1021.3969 | 4.13E-01 | 8.35E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.3 | 12.0 | 11.5 | 12.6 | 11.8 | 12.4 | 11.8 | 13.0 | 12.3 |
| 641 | Rv2027c | MAP2078c | 44 | Two component sensor histidine kinase DosT | Rv2027c.1690 | 2.77E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.3 | 12.0 | 11.7 | 12.3 | 12.2 | 12.4 | 11.8 | 12.9 | 12.5 |
| 642 | Rv1699 | MAP1406 | 91 | Probable CTP synthase PyrG | Rv1699.3714 | 9.92E-01 | 9.98E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.4 | 12.4 | 11.7 | 13.1 | 12.4 | 12.4 | 12.0 | 12.7 | 12.5 |
| 643 | Rv2630 | MAP1448c | 27 | Hypothetical protein | Rv2630.4183 | 6.99E-01 | 9.51E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.4 | 12.5 | 12.1 | 12.8 | 12.6 | 12.4 | 12.1 | 12.6 | 12.3 |
| 644 | Rv2033c | MAP1763c | 84 | hypothetical protein | Rv2033c.1328 | 9.93E-01 | 9.98E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.4 | 11.9 | 12.9 | 12.2 | 12.4 | 12.1 | 12.7 | 12.5 |
| 645 | Rv1977 | MAP4059 | 24 | hypothetical protein | Rv1977.492 | 2.89E-01 | 7.74E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.2 | 12.0 | 11.5 | 12.5 | 12.1 | 12.4 | 11.9 | 12.9 | 12.3 |
| 646 | Rv0126 | MAP3528 | 91 | Trehalose synthase TreS | Rv0126.1402 | 1.96E-01 | 6.98E-01 | 0.17 | 1.67E-01 | 8.62E-01 | 12.5 | 12.8 | 12.6 | 13.1 | 12.7 | 12.4 | 11.9 | 12.9 | 12.4 |
| 647 | Rv3493c | MAP0570 | 75 | Conserved hypothetical Mce associated alanine and valine rich | Rv3493c.2473 | 4.60E-02 | 6.27E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.2 | 11.9 | 11.8 | 12.1 | 12.0 | 12.4 | 12.1 | 12.7 | 12.5 |
| 648 | Rv1865c | MAP1574c | 78 | Probable short-chain type dehydrogenase | Rv1865c.1040 | 7.59E-01 | 9.64E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.4 | 12.6 | 11.5 | 13.7 | 12.1 | 12.4 | 12.0 | 12.8 | 12.3 |
| 649 | Rv3243c | MAP2534c | 27 | hypothetical protein | Rv3243c.1334 | 7.00E-01 | 9.51E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.3 | 12.2 | 11.7 | 12.6 | 12.3 | 12.4 | 11.4 | 13.3 | 12.2 |
| 650 | Rv2207 | MAP1948 | 83 | Probable nicotinate-nucleotide-dimethylbenzimidazol phosphc | Rv2207.2341 | 5.76E-01 | 9.06E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.5 | 12.4 | 12.6 | 12.5 | 12.4 | 12.0 | 12.7 | 12.4 |
| 651 | Rv1639c | MAP0749c | 72 | hypothetical protein | Rv1639c.1693 | 1.67E-01 | 6.83E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.2 | 12.0 | 11.7 | 12.3 | 12.0 | 12.4 | 12.0 | 12.8 | 12.5 |
| 652 | Rv3536c | MAP0531 | 82 | Probable hydratase | Rv3536c.2778 | 7.23E-01 | 9.56E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.4 | 12.6 | 11.6 | 13.6 | 12.3 | 12.4 | 12.0 | 12.7 | 12.5 |
| 653 | Rv1045 | MAP0369 | 35 | Hypothetical protein | Rv1045.3519 | 9.73E-03 | 6.27E-01 | 0.06 | 4.76E-02 | 7.98E-01 | 12.7 | 13.2 | 13.1 | 13.4 | 13.3 | 12.4 | 11.9 | 12.8 | 12.3 |
| 654 | Rv2276 | MAP2033 | 29 | Cytochrome P450 121 Cyp121 | Rv2276.646 | 6.99E-01 | 9.51E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.3 | 12.2 | 11.3 | 13.0 | 12.0 | 12.4 | 12.0 | 12.7 | 12.4 |
| 655 | Rv1895 | MAP1621 | 78 | Possible dehydrogenase | Rv1895.4264 | 7.40E-01 | 9.57E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.4 | 12.5 | 11.9 | 13.1 | 12.3 | 12.4 | 11.7 | 13.0 | 12.4 |
| 656 | Rv1491c | MAP1224c | 65 | hypothetical protein | Rv1491c.2770 | 4.11E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.3 | 12.1 | 11.8 | 12.5 | 12.2 | 12.4 | 12.0 | 12.7 | 12.3 |
| 657 | Rv0801 | MAP0633 | 76 | hypothetical protein | Rv0801.4442 | 8.27E-01 | 9.70E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.4 | 12.4 | 11.8 | 13.1 | 12.6 | 12.3 | 12.0 | 12.6 | 12.5 |
| 658 | Rv3709c | MAP0311c | 93 | Aspartokinase Ask (aspartate kinase) [contains: aspartokinase a | Rv3709c.1821 | 8.49E-01 | 9.70E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.4 | 12.4 | 11.6 | 13.3 | 12.8 | 12.3 | 12.0 | 12.7 | 12.6 |
| 659 | Rv0331 | MAP579c | 27 | Possible dehydrogenase/reductase | Rv0331.2247 | 1.01E-01 | 6.48E-01 | 0.89 | 9.52E-02 | 7.98E-01 | 12.1 | 11.6 | 11.1 | 12.2 | 11.8 | 12.3 | 11.9 | 12.8 | 12.5 |
| 660 | Rv3871 | MAP4241 | 38 | ESX conserved component EccCb1 ESX-1 type VII secretion syst | Rv3871.605 | 2.80E-01 | 7.74E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.4 | 12.7 | 12.5 | 12.8 | 12.7 | 12.3 | 11.8 | 12.8 | 12.3 |
| 661 | Rv2116 | MAP1840 | 55 | Conserved lipoprotein LppK | Rv2116.4126 | 7.31E-01 | 9.56E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.4 | 12.7 | 11.0 | 14.4 | 12.2 | 12.3 | 12.1 | 12.6 | 12.3 |
| 662 | Rv1445c | MAP1174c | 79 | Probable 6-phosphogluconolactonase DevB (6PGL) | Rv1445c.653 | 3.88E-01 | 8.35E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 12.5 | 12.9 | 11.9 | 13.8 | 13.3 | 12.3 | 11.8 | 12.9 | 12.3 |
| 663 | Rv0455c | MAP3948c | 79 | hypothetical protein | Rv0455c.1483 | 7.61E-01 | 9.64E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.3 | 12.1 | 11.1 | 13.2 | 12.0 | 12.3 | 12.0 | 12.6 | 12.3 |
| 664 | Rv3182 | MAP4269c | 48 | hypothetical protein | Rv3182.4153 | 2.22E-01 | 7.31E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 12.2 | 12.0 | 11.7 | 12.3 | 12.0 | 12.3 | 12.1 | 12.5 | 12.4 |
| 665 | Rv2476c | MAP0863 | 83 | Probable NAD-dependent glutamate dehydrogenase Gdh (NAD | Rv2476c-s2.14 | 8.87E-01 | 9.75E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.3 | 12.4 | 11.3 | 13.4 | 12.1 | 12.3 | 12.0 | 12.6 | 12.4 |
| 666 | Rv0103c | MAP4284 | 47 | Probable cation-transporter P-type ATPase B CtpB | Rv0103c.1414 | 2.08E-01 | 7.15E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.4 | 12.6 | 12.4 | 12.7 | 12.6 | 12.3 | 11.9 | 12.7 | 12.4 |
| 667 | Rv0464c | MAP3958c | 67 | hypothetical protein | Rv0464c.2354 | 5.57E-01 | 8.97E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.3 | 12.5 | 12.2 | 12.8 | 12.3 | 12.3 | 11.8 | 12.8 | 12.4 |
| 668 | Rv1362c | MAP0750c | 70 | Possible membrane protein | Rv1362c.3616 | 7.48E-01 | 9.58E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.3 | 12.4 | 12.1 | 12.7 | 12.3 | 12.3 | 11.8 | 12.8 | 12.1 |
| 669 | Rv1809 | MAP1153 | 62 | PPE family protein PPE33 | Rv1809.52 | 4.98E-01 | 8.80E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.4 | 12.7 | 11.8 | 13.6 | 12.5 | 12.3 | 11.8 | 12.7 | 12.3 |
| 670 | Rv1067c | MAP4144 | 59 | PE-PGRS family protein PE_PGRS19 | Rv1067c.4309 | 5.46E-01 | 8.97E-01 | 0.58 | 7.95E-01 | 9.80E-01 | 12.2 | 12.0 | 11.2 | 12.7 | 11.8 | 12.3 | 11.9 | 12.6 | 12.5 |
| 671 | Rv2107 | MAP2576c | 45 | PE family protein PE22 | Rv2107.2933 | 4.06E-01 | 8.35E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.2 | 12.1 | 11.8 | 12.4 | 12.0 | 12.3 | 12.0 | 12.5 | 12.4 |
| 672 | Rv3690 | MAP0361c | 68 | Probable conserved membrane protein | Rv3690.1604 | 9.24E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.2 | 12.2 | 11.3 | 13.1 | 12.0 | 12.3 | 11.9 | 12.6 | 12.4 |
| 673 | Rv0432 | MAP3921 | 73 | Periplasmic superoxide dismutase [Cu-Zn] SodC | Rv0432.2344 | 5.33E-01 | 8.97E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 12.4 | 12.8 | 11.3 | 14.3 | 12.5 | 12.2 | 11.7 | 12.8 | 12.3 |
| 674 | Rv2393 | MAP2037 | 69 | Ferrochelatase Che1 | Rv2393.1039 | 4.45E-01 | 8.42E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 12.1 | 11.7 | 10.8 | 12.6 | 11.6 | 12.2 | 11.5 | 13.0 | 12.1 |
| 675 | Rv1263 | MAP2509c | 82 | Probable amidase AmiB2 (aminohydrolase) | Rv1263.2262 | 9.12E-01 | 9.81E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.2 | 12.2 | 11.4 | 12.9 | 11.8 | 12.2 | 11.8 | 12.7 | 12.4 |
| 676 | Rv0360c | MAP3864 | 85 | hypothetical protein | Rv0360c.2934 | 9.66E-01 | 9.84E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.2 | 12.2 | 11.3 | 13.1 | 12.0 | 12.2 | 12.0 | 12.5 | 12.3 |
| 677 | Rv0764c | MAP0598c | 79 | Cytochrome P450 51 Cyp51 (CYPL1) (P450-L1A1) (sterol 14-alpl | Rv0764c.2948 | 2.99E-01 | 7.74E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.1 | 11.7 | 11.2 | 12.2 | 11.9 | 12.2 | 11.4 | 13.0 | 11.9 |
| 678 | Rv1123c | MAP0740c | 75 | Possible peroxidase BpoB (non-haem peroxidase) | Rv1123c.2504 | 8.56E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.3 | 12.3 | 11.4 | 13.3 | 11.9 | 12.2 | 11.9 | 12.6 | 12.4 |
| 679 | Rv1387 | MAP3490 | 47 | PPE family protein PPE20 | Rv1387.1810 | 7.61E-01 | 9.64E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.3 | 12.4 | 11.9 | 12.9 | 12.3 | 12.2 | 11.3 | 13.1 | 12.0 |
| 680 | Rv3800c | MAP0220 | 82 | Polyketide synthase Pks13 | Rv3800c-s1.27 | 9.94E-01 | 9.98E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.2 | 12.2 | 11.2 | 13.2 | 11.8 | 12.2 | 11.9 | 12.5 | 12.2 |
| 681 | Rv0453 | MAP3490 | 58 | PPE family protein PPE11 | Rv0453.1699 | 9.43E-01 | 9.82E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.2 | 12.2 | 11.7 | 12.8 | 12.2 | 12.2 | 11.9 | 12.5 | 12.3 |
| 682 | Rv0951 | MAP0896 | 89 | Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta) | Rv0951.1952 | 9.55E-01 | 9.82E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.2 | 12.2 | 11.1 | 13.4 | 11.8 | 12.2 | 11.5 | 12.9 | 11.8 |
| 683 | Rv2387 | MAP2206 | 78 | hypothetical protein | Rv2387.1682 | 3.74E-01 | 8.34E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 12.1 | 11.8 | 11.1 | 12.5 | 11.7 | 12.2 | 11.8 | 12.6 | 12.4 |
| 684 | Rv2933 | MAP3764c | 38 | Phenolpthiocerol synthesis type-I polyketide synthase PpsC | Rv2933-s4.27( | 7.24E-01 | 9.56E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.1 | 12.0 | 10.9 | 13.0 | 11.7 | 12.2 | 11.8 | 12.6 | 12.2 |
| 685 | Rv0905 | MAP0840 | 91 | Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsatura | Rv0905.1205 | 8.72E-01 | 9.70E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 12.2 | 12.3 | 11.6 | 12.9 | 12.0 | 12.2 | 11.7 | 12.7 | 12.3 |
| 686 | Rv1975 | MAP0281 | 70 | hypothetical protein | Rv1975.2646 | 9.36E-01 | 9.82E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.2 | 12.2 | 11.8 | 12.6 | 12.1 | 12.2 | 11.7 | 12.6 | 11.9 |
| 687 | Rv1394c | MAP0086 | 27 | Probable cytochrome P450 132 Cyp132 | Rv1394c.1786 | 9.20E-01 | 9.81E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.1 | 12.1 | 11.1 | 13.1 | 12.0 | 12.2 | 11.7 | 12.6 | 12.4 |
| 688 | Rv2490c | MAP4144 | 62 | PE-PGRS family protein PE_PGRS43 | Rv2490c-s2.84 | 8.59E-01 | 9.70E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.1 | 12.0 | 10.9 | 13.1 | 11.7 | 12.1 | 11.7 | 12.6 | 12.1 |
| 689 | Rv3567c | MAP0500 | 88 | Possible oxidoreductase Possible 3-hydroxy-9,10-seconandrost | Rv3567c.1294 | 6.49E-01 | 9.34E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.2 | 12.4 | 11.5 | 13.2 | 12.1 | 12.1 | 11.9 | 12.4 | 12.2 |
| 690 | Rv2091c | MAP1826c | 62 | Probable membrane protein | Rv2091c.75 | 4.37E-02 | 6.27E-01 | 0.00 | 2.38E-02 | 7.98E-01 | 12.4 | 12.9 | 12.5 | 13.3 | 12.8 | 12.1 | 11.9 | 12.4 | 12.2 |
| 691 | Rv2606c | MAP2710c | 92 | Possible pyridoxine biosynthesis protein SnzP | Rv2606c.3370 | 2.54E-02 | 6.27E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 11.9 | 11.4 | 11.1 | 11.8 | 11.5 | 12.1 | 11.8 | 12.4 | 12.1 |
| 692 | Rv2162c | MAP4144 | 66 | PE-PGRS family protein PE_PGRS38 | Rv2162c.59 | 1.73E-02 | 6.27E-01 | 0.00 | 2.38E-02 | 7.98E-01 | 12.5 | 13.3 | 12.9 | 13.8 | 13.3 | 12.1 | 11.8 | 12.3 | 12.2 |
| 693 | Rv3431c | MAP2274 | 64 | Possible transposase (fragment) | Rv3431c.756 | 2.89E-01 | 7.74E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 11.9 | 11.5 | 10.7 | 12.3 | 11.6 | 12.1 | 11.7 | 12.5 | 12.1 |
| 694 | Rv3791 | MAP0234c | 88 | Decaprenylphosphoryl-D-2-keto erythro pentose reductase | Rv3791.747 | 7.98E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.0 | 11.9 | 10.6 | 13.2 | 11.7 | 12.1 | 11.6 | 12.5 | 12.1 |
| 695 | Rv3345c | MAP4144 | 60 | PE-PGRS family protein PE_PGRS50 | Rv3345c-s3.43 | 6.95E-01 | 9.51E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.1 | 12.2 | 11.5 | 13.0 | 12.0 | 12.1 | 11.7 | 12.4 | 12.2 |
| 696 | Rv3643 | MAP0158 | 47 | Hypothetical protein | Rv3643.2979 | 8.97E-02 | 6.48E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 11.9 | 11.7 | 11.6 | 11.8 | 11.7 | 12.1 | 11.7 | 12.4 | 12.2 |
| 697 | Rv0038 | MAP0045 | 91 | hypothetical protein | Rv0038.4193 | 1.01E-01 | 6.48E-01 | 0.94 | 4.76E-02 | 7.98E-01 | 11.7 | 11.1 | 10.6 | 11.6 | 10.9 | 12.1 | 11.2 | 12.9 | 11.7 |
| 698 | Rv1615 | MAP4311c | 31 | Probable membrane protein | Rv1615.4468 | 6.36E-01 | 9.31E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.1 | 12.3 | 11.6 | 13.0 | 12.0 | 12.0 | 11.4 | 12.7 | 12.4 |
| 699 | Rv3288c | MAP0383 | 79 | Putative protein UsfY | Rv3288c.2150 | 3.01E-01 | 7.74E-01 | 0.22 | 2.62E-01 | 8.76E-01 | 12.2 | 12.6 | 11.9 | 13.3 | 12.3 | 12.0 | 11.4 | 12.6 | 12.0 |
| 700 | Rv1463 | MAP1189 | 90 | Probable conserved ATP-binding protein ABC transporter | Rv1463.2204 | 4.53E-01 | 8.44E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.1 | 12.2 | 11.9 | 12.6 | 12.1 | 12.0 | 11.6 | 12.5 | 12.1 |
| 701 | Rv2486 | MAP2306 | 82 | Probable enoyl-CoA hydratase EchA14 (enoyl hydrase) (unsatu | Rv2486.3807 | 8.62E-01 | 9.70E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.0 | 11.9 | 11.4 | 12.5 | 11.7 | 12.0 | 11.7 | 12.3 | 12.1 |
| 702 | Rv3633 | MAP3160 | 37 | hypothetical protein | Rv3633.3658 | 1.57E-01 | 6.83E-01 | 0.83 | 1.67E-01 | 8.62E-01 | 11.8 | 11.3 | 11.0 | 11.6 | 11.4 | 12.0 | 11.2 | 12.8 | 11.7 |
| 703 | Rv1450c | MAP4144 | 56 | PE-PGRS family protein PE_PGRS27 | Rv1450c-s2.28 | 6.49E-01 | 9.34E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.1 | 12.4 | 11.0 | 13.7 | 12.3 | 12.0 | 11.4 | 12.6 | 11.6 |
| 704 | Rv0826 | MAP0660 | 83 | hypothetical protein | Rv0826.2957 | 7.99E-01 | 9.65E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 12.0 | 12.1 | 11.4 | 12.8 | 12.0 | 12.0 | 11.6 | 12.4 | 12.0 |
| 705 | Rv0673 | MAP2395c | 92 | Possible enoyl-CoA hydratase EchA4 (enoyl hydrase) (unsatura | Rv0673.3236 | 3.59E-01 | 8.25E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 11.8 | 11.6 | 11.1 | 12.1 | 11.6 | 12.0 | 11.6 | 12.3 | 11.9 |
| 706 | Rv1840c | MAP4144 | 63 | PE-PGRS family protein PE_PGRS34 | Rv1840c.1498 | 8.83E-01 | 9.73E-01 | 0.61 | 7.14E-01 | 9.59E-01 | 11.9 | 11.8 | 10.2 | 13.4 | 11.5 | 11.9 | 11.5 | 12.4 | 11.9 |
| 707 | Rv3588c | MAP0470 | 78 | Beta-carbonic anhydrase CanB | Rv3588c.2469 | 7.86E-01 | 9.65E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 12.0 | 12.0 | 11.5 | 12.5 | 11.8 | 11.9 | 11.6 | 12.3 | 11.9 |

# Table S3 continued

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 708 | Rv1244 | MAP2539c | 71 | Probable lipoprotein LpqZ | Rv1244.2635 | 3.67E-01 | 8.32E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 11.8 | 11.5 | 10.9 | 12.2 | 11.6 | 11.9 | 11.5 | 12.3 | 12.0 |
| 709 | Rv2964 | MAP0902 | 41 | Probable formyltetrahydrofolate deformylase PurU (formyl-FH | Rv2964.3373 | 5.85E-01 | 9.12E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 12.0 | 12.1 | 11.7 | 12.6 | 12.1 | 11.9 | 11.3 | 12.5 | 11.8 |
| 710 | Rv3704c | MAP0306c | 74 | Glutamate--cysteine ligase GshA (gamma-glutamylcysteine syn | Rv3704c.1955 | 3.87E-01 | 8.35E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 12.1 | 12.4 | 11.5 | 13.3 | 12.5 | 11.9 | 11.4 | 12.4 | 11.9 |
| 711 | Rv3282 | MAP3401 | 65 | hypothetical protein | Rv3282.1304 | 7.31E-01 | 9.56E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 12.0 | 12.1 | 10.9 | 13.3 | 12.0 | 11.9 | 11.5 | 12.3 | 11.9 |
| 712 | Rv2074 | MAP1820 | 93 | Possible pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidas | Rv2074.1283 | 6.60E-01 | 9.36E-01 | 0.56 | 9.05E-01 | 9.80E-01 | 11.8 | 11.6 | 10.9 | 12.3 | 11.6 | 11.9 | 11.0 | 12.7 | 11.6 |
| 713 | Rv1061 | MAP1010 | 75 | hypothetical protein | Rv1061.3931 | 2.32E-01 | 7.42E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 11.7 | 11.4 | 10.9 | 11.8 | 11.2 | 11.8 | 11.3 | 12.3 | 12.0 |
| 714 | Rv3608c | MAP0450 | 81 | Dihydropteroate synthase 1 FolP (DHPS 1) (dihydropteroate py | Rv3608c.1912 | 5.85E-01 | 9.12E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 11.8 | 12.1 | 10.9 | 13.2 | 11.8 | 11.7 | 11.4 | 12.0 | 11.7 |
| 715 | Rv1024 | MAP0991 | 73 | Possible conserved membrane protein | Rv1024.3517 | 7.53E-01 | 9.61E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 11.7 | 11.9 | 11.1 | 12.7 | 11.5 | 11.7 | 11.2 | 12.1 | 11.8 |
| 716 | Rv0208c | MAP3643c | 66 | Hypothetical methlytransferase (methylase) | Rv0208c.460 | 1.10E-01 | 6.48E-01 | 0.11 | 9.52E-02 | 7.98E-01 | 12.0 | 12.6 | 11.8 | 13.3 | 12.5 | 11.6 | 11.2 | 12.1 | 11.6 |
| 717 | Rv2231c | MAP1983c | 29 | Possible aminotransferase CobC | Rv2231c.4261 | 4.90E-01 | 8.77E-01 | 0.67 | 5.48E-01 | 9.11E-01 | 11.5 | 11.3 | 11.0 | 11.7 | 11.2 | 11.6 | 11.1 | 12.0 | 11.9 |
| 718 | Rv1665 | MAP1372 | 76 | Chalcone synthase Pks11 | Rv1665.1643 | 5.36E-01 | 8.97E-01 | 0.72 | 3.81E-01 | 8.90E-01 | 11.4 | 11.3 | 10.9 | 11.6 | 11.4 | 11.5 | 11.0 | 11.9 | 11.6 |
| 719 | Rv3390 | MAP3481 | 67 | Probable conserved lipoprotein LpqD | Rv3390.3205 | 7.57E-01 | 9.64E-01 | 0.39 | 7.14E-01 | 9.59E-01 | 11.5 | 11.6 | 10.7 | 12.4 | 11.9 | 11.4 | 11.0 | 11.9 | 11.5 |
| 720 | Rv2200c | MAP1940c | 79 | Probable transmembrane cytochrome C oxidase (subunit II) Ct | Rv2200c.2919 | 4.18E-01 | 8.35E-01 | 0.33 | 5.48E-01 | 9.11E-01 | 11.6 | 11.9 | 10.9 | 12.9 | 11.6 | 11.4 | 11.1 | 11.8 | 11.4 |
| 721 | Rv3834c | MAP0197 | 88 | SERYL-tRNA synthetase SerS (serine--tRNA ligase) (SERRS) (seri | Rv3834c.3688 | 9.79E-01 | 9.90E-01 | 0.50 | 1.00E+00 | 1.00E+00 | 11.4 | 11.4 | 9.3 | 13.6 | 10.5 | 11.4 | 10.2 | 12.6 | 10.9 |
| 722 | Rv3372 | MAP1747c | 73 | Trehalose 6-phosphate phosphatase OtsB2 (trehalose-phospha | Rv3372.2531 | 6.02E-01 | 9.20E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 11.3 | 11.6 | 10.3 | 12.8 | 11.2 | 11.2 | 11.0 | 11.4 | 11.2 |
| 723 | Rv0993 | MAP0924 | 88 | UTP--glucose-1-phosphate uridylyltransferase GalU (UDP-gluc | Rv0993.2505 | 3.16E-01 | 7.83E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 11.5 | 12.2 | 10.7 | 13.6 | 11.8 | 11.2 | 10.6 | 11.8 | 11.4 |
| 724 | Rv2268c | MAP2584 | 34 | Probable cytochrome P450 128 Cyp128 | Rv2268c.4099 | 2.06E-01 | 7.15E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 11.5 | 12.2 | 11.1 | 13.3 | 12.4 | 11.2 | 11.0 | 11.3 | 11.2 |
| 725 | Rv0148 | MAP3567 | 88 | Probable short-chain type dehydrogenase/reductase | Rv0148.1907 | 9.73E-01 | 9.89E-01 | 0.44 | 9.05E-01 | 9.80E-01 | 11.0 | 11.0 | 10.3 | 11.7 | 11.1 | 11.0 | 10.6 | 11.4 | 11.1 |
| 726 | Rv2184c | MAP1922c | 81 | hypothetical protein | Rv2184c.1373 | 6.53E-04 | 2.38E-01 | 0.00 | 2.38E-02 | 7.98E-01 | 11.5 | 12.8 | 12.4 | 13.1 | 12.8 | 10.9 | 10.4 | 11.4 | 11.2 |
| 727 | Rv2252 | MAP2005 | 79 | Diacylglycerol kinase | Rv2252.4240 | 3.47E-01 | 8.22E-01 | 0.28 | 3.81E-01 | 8.90E-01 | 10.9 | 11.6 | 9.9 | 13.4 | 11.5 | 10.6 | 10.3 | 10.8 | 10.7 |
| 728 | Rv2315c | MAP2089c | 85 | hypothetical protein | Rv2315c.2860 | 7.76E-06 | 5.66E-03 | 0.00 | 2.38E-02 | 7.98E-01 | 11.3 | 13.0 | 12.7 | 13.2 | 12.9 | 10.5 | 10.3 | 10.7 | 10.5 |
| 729 | Rv2349c | MAP2149c | 33 | Probable phospholipase C 3 PlcC | Rv2349c.3255 | 1.48E-01 | 6.83E-01 | 0.06 | 4.89E-02 | 7.98E-01 | 10.8 | 12.1 | 10.5 | 13.7 | 12.8 | 10.2 | 9.9 | 10.6 | 10.0 |

[a] Rank=Strongest to weakest mean signal intensity among clinical cows.

[b] Mean all samples=signal intensity average of all subclinical and clinical serum samples.

# Table S4

Table S4. Top 30 differentially reactive *Mtb* proteins ranked by P-value

| **TB protein** | **MAP K-10 locus tag** | **Description** | **P-value[a]** | **BH P-value[b]** | **Mean Subclinical Cows (95% CI)** | **Mean Clinical Cows (95% CI)** |
|---|---|---|---|---|---|---|
| Rv2315c | MAP2089c | Hypothetical protein | 7.80E-06 | 5.70E-03 | 13.0 (12.7-13.2) | 10.5 (10.3-10.7) |
| Rv2184c | MAP1922c | Hypothetical protein | 6.50E-04 | 2.40E-01 | 12.8 (12.4-13.1) | 10.9 (10.4-11.4) |
| Rv1968 | MAP2114c | Mce-family protein Mce3C | 2.20E-03 | 4.10E-01 | 13.0 (13.0-13.1) | 13.6 (13.4-13.7) |
| Rv2878c | MAP2942c | Soluble secreted antigen Mpt53 precursor | 2.30E-03 | 4.10E-01 | 11.7 (11.0-12.4) | 14.8 (14.3-15.2) |
| Rv3695 | MAP0356c | Possible conserved membrane protein | 4.20E-03 | 6.10E-01 | 11.8 (11.6-12.1) | 12.7 (12.4-13.0) |
| Rv1290c | MAP1726c | Hypothetical protein | 6.30E-03 | 6.30E-01 | 11.7 (11.5-11.9) | 12.9 (12.4-13.5) |
| Rv0442c | MAP3939c | PPE family protein PPE10 | 8.90E-03 | 6.30E-01 | 12.8 (12.6-12.9) | 13.7 (13.2-14.1) |
| Rv0312 | MAP3800 | Conserved hypothetical proline and threonine rich protein | 9.10E-03 | 6.30E-01 | 12.5 (12.3-12.6) | 12.9 (12.7-13.1) |
| Rv1045 | MAP0369 | Hypothetical protein | 9.70E-03 | 6.30E-01 | 13.2 (13.1-13.4) | 12.4 (11.9-12.8) |
| Rv0355c | MAP3939c | PPE family protein PPE8 | 1.10E-02 | 6.30E-01 | 12.1 (11.9-12.3) | 12.7 (12.4-13.0) |
| Rv2962c | MAP2851c | Possible glycosyl transferase | 1.10E-02 | 6.30E-01 | 12.3 (12.0-12.7) | 13.2 (12.9-13.4) |
| Rv1779c | MAP1493c | Possible integral membrane protein | 1.20E-02 | 6.30E-01 | 12.4 (12.2-12.6) | 13.1 (12.8-13.5) |
| Rv3267 | MAP3381 | Conserved protein (CPSA-related protein) | 1.40E-02 | 6.30E-01 | 13.3 (13.1-13.4) | 13.7 (13.5-13.9) |
| Rv2162c | MAP4144 | PE-PGRS family protein PE_PGRS38 | 1.70E-02 | 6.30E-01 | 13.3 (12.9-13.8) | 12.1 (11.8-12.3) |
| Rv0901 | MAP2837c | Possible conserved exported or membrane protein | 1.80E-02 | 6.30E-01 | 12.3 (12.1-12.5) | 12.9 (12.6-13.3) |
| Rv0155 | MAP3572 | Probable NAD(P) transhydrogenase (subunit alpha) PntAa | 1.90E-02 | 6.30E-01 | 12.5 (12.2-12.8) | 13.1 (12.9-13.3) |
| Rv3884c | MAP0167 | ESX conserved component EccA2 ESX-2 type VII secretion system protein Probable CbxX/CfqX family protein | 2.00E-02 | 6.30E-01 | 12.3 (12.2-12.5) | 12.9 (12.6-13.3) |
| Rv2458 | MAP2279 | Probable homocysteine S-methyltransferase MmuM | 2.10E-02 | 6.30E-01 | 12.5 (12.3-12.7) | 13.0 (12.8-13.3) |
| Rv0729 | MAP4195 | Possible D-xylulose kinase XylB | 2.30E-02 | 6.30E-01 | 12.5 (12.3-12.6) | 13.0 (12.7-13.3) |
| Rv3629c | MAP0434 | Probable conserved integral membrane protein | 2.40E-02 | 6.30E-01 | 12.7 (12.5-12.9) | 13.2 (12.9-13.4) |
| Rv1145 | MAP2635c | Probable conserved transmembrane transport protein MmpL13a | 2.50E-02 | 6.30E-01 | 12.6 (12.3-12.9) | 13.4 (13.0-13.7) |
| Rv0535 | MAP4030 | Probable 5'-methylthioadenosine phosphorylase Pnp | 2.50E-02 | 6.30E-01 | 12.3 (12.2-12.4) | 12.6 (12.4-12.9) |
| Rv2606c | MAP2710c | Possible pyridoxine biosynthesis protein SnzP | 2.50E-02 | 6.30E-01 | 11.4 (11.1-11.8) | 12.1 (11.8-12.4) |
| Rv3869 | MAP3779 | ESX conserved component EccB1 ESX-1 type VII secretion system protein Possible membrane protein | 2.50E-02 | 6.30E-01 | 12.7 (12.4-13.0) | 13.4 (13.1-13.7) |
| Rv0959 | MAP0906 | hypothetical protein | 2.60E-02 | 6.30E-01 | 12.4 (12.3-12.5) | 12.8 (12.6-13.1) |
| Rv3163c | MAP3217c | Possible conserved secreted protein | 2.70E-02 | 6.30E-01 | 12.5 (12.3-12.7) | 13.1 (12.7-13.4) |
| Rv3766 | MAP1313c | Hypothetical protein | 2.80E-02 | 6.30E-01 | 13.4 (13.3-13.5) | 13.9 (13.6-14.3) |
| Rv3470c | MAP3038c | Probable acetolactate synthase (large subunit) IlvB2 | 2.80E-02 | 6.30E-01 | 12.1 (11.9-12.4) | 12.9 (12.4-13.3) |
| Rv2051c | MAP1800c | Polyprenol-monophosphomannose synthase Ppm1 | 2.80E-02 | 6.30E-01 | 12.7 (12.5-13.0) | 13.4 (13.0-13.7) |
| Rv2589 | MAP1041c | 4-aminobutyrate aminotransferase GabT | 2.80E-02 | 6.30E-01 | 12.0 (11.7-12.3) | 12.7 (12.5-12.8) |

[a] Student’s T-test P value; 5.0E-2 = 0.05.

[b] P-value adjusted for the false discovery rate using the Benjamini-Hochberg (BH) method.

# Table S5

**Table S5. Mtb proteins with the highest infection to control ratios**

| Mtb ID | MAP ID | SubClinical/Neg | Clinical/Neg | Description |
|---|---|---|---|---|
| Rv2315c | MAP2089c | 3.17 | 1.90 | hypothetical protein |
| Rv0993 | No ortholog | 2.30 | 2.03 | UTP--glucose-1-phosphate uridylyltransferase GalU (UDP-glucose pyrophosphorylase) (UDPGP) (alpha-D-glucosyl-1-phosphate uridylyltransferase) (uridine diphosphoglucose pyrophosphorylase) |
| Rv0752c | MAP4214c | 2.28 | 2.06 | Probable acyl-CoA dehydrogenase FadE9 |
| Rv2252 | MAP2005 | 2.26 | 2.00 | Diacylglycerol kinase |
| Rv2162c | No ortholog | 2.22 | 1.99 | PE-PGRS family protein PE_PGRS38 |
| Rv0172 | MAP3607 | 2.03 | 2.05 | Mce-family protein Mce1D |
| Rv2349c | MAP2149c | 2.01 | 1.87 | Probable phospholipase C 3 PlcC |
| Rv3704c | MAP0306c | 1.98 | 2.06 | Glutamate--cysteine ligase GshA (gamma-glutamylcysteine synthetase) (gamma-ECS) (GCS) (gamma-glutamyl-L-cysteine synthetase) |
| Rv3175 | No ortholog | 1.93 | 2.01 | Possible amidase (aminohydrolase) |
| Rv0938 | MAP0880 | 1.88 | 2.01 | ATP dependent DNA ligase LigD (ATP dependent polydeoxyribonucleotide synthase) (thermostable DNA ligase) (ATP dependent polynucleotide ligase) (sealase) (DNA repair enzyme) (DNA joinase) |
| Rv2921c | MAP2989c | 1.88 | 2.01 | Probable cell division protein FtsY (SRP receptor) (signal recognition particle receptor) |
| Rv2195 | MAP1934 | 1.83 | 2.04 | Probable rieske iron-sulfur protein QcrA |
| Rv0432 | MAP2131c | 1.81 | 2.03 | Periplasmic superoxide dismutase [Cu-Zn] SodC |
| Rv1445c | MAP1174c | 1.77 | 2.03 | Probable 6-phosphogluconolactonase DevB (6PGL) |
| Rv1045 | No ortholog | 1.73 | 1.99 | Hypothetical protein |
| Rv3651 | MAP0421c | 1.71 | 1.97 | hypothetical protein |
| Rv1527c-s1 | No ortholog | 1.71 | 2.05 | Probable polyketide synthase Pks5 |
| Rv0458 | MAP3952 | 1.70 | 2.02 | Probable aldehyde dehydrogenase |
| Rv1020-s1 | No ortholog | 1.70 | 2.09 | Probable transcription-repair coupling factor Mfd (TRCF) |