

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plates 1-42**

Catalog No. NR-19274

**Table 1: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 1 (ZMTDA), NR-19637**

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 71201 | A01           | 124        | Rv1572c  | hypothetical protein Rv1572c                                     | NP_216088.2      | 2                         |
| 71005 | A02           | 151        | Rv3461c  | 50S ribosomal protein L36 (rpmJ)                                 | NP_217978.1      | 2                         |
| 71053 | A03           | 181        | Rv3924c  | 50S ribosomal protein L34 (rpmH)                                 |                  | 2                         |
| 71013 | A04           | 184        | Rv2452c  | hypothetical protein Rv2452c                                     | NP_216968.1      | 2                         |
| 71167 | A05           | 193        | Rv0657c  | hypothetical protein Rv0657c                                     | NP_215171.1      | 2.69948187                |
| 71177 | A06           | 211        | Rv0666   | hypothetical protein Rv0666                                      | NP_215180.1      | 2                         |
| 71225 | A07           | 214        | Rv1693   | hypothetical protein Rv1693                                      | NP_216209.1      | 2                         |
| 71073 | A08           | 217        | Rv2099c  | PE family protein (PE21)   |                  | 2                         |
| 70874 | A09           | 220        | Rv0810c  | hypothetical protein Rv0810c                                     | NP_215325.1      | 2                         |
| 70913 | A10           | 223        | Rv2371   | PE-PGRS family protein (PE_PGRS40)                               | YP_177875.1      | 2                         |
| 71141 | A11           | 229        | Rv2806   | hypothetical protein Rv2806                                      | NP_217322.1      | 2                         |
| 71121 | A12           | 235        | Rv1113   | hypothetical protein Rv1113                                      | NP_215629.1      | 1.99574468                |
| 71181 | B01           | 241        | Rv3648c  | cold shock protein A (cspA)                                      | NP_218165.1      | 2                         |
| 70937 | B02           | 244        | Rv0763c  | ferredoxin   | NP_215277.1      | 2                         |
| 70966 | B03           | 247        | Rv1054   | integrase  | NP_215570.2      | 1.27530364                |
| 71145 | B04           | 253        | Rv2377c  | putative protein MbtH (mbtH)                                     | NP_216893.1      | 2                         |
| 70861 | B05           | 253        | Rv2830c  | hypothetical protein Rv2830c                                     | NP_217346.1      | 2                         |
| 70853 | B06           | 253        | Rv3221c  | anti-sigma factor  | YP_177945.1      | 2                         |
| 71210 | B07           | 256        | Rv1893   | hypothetical protein Rv1893                                      | NP_216409.1      | 2                         |
| 71062 | B08           | 259        | Rv0378   | glycine rich protein   | NP_214892.1      | 1.99227799                |
| 71214 | B09           | 259        | Rv0699   | hypothetical protein Rv0699                                      | NP_215213.1      | 2                         |
| 71097 | B10           | 259        | Rv1584c  | phiRv1 phage protein   | NP_216100.1      | 2                         |
| 70933 | B11           | 259        | Rv2493   | hypothetical protein Rv2493                                      | NP_217009.1      | 2                         |
| 71033 | B12           | 262        | Rv2049c  | hypothetical protein Rv2049c                                     | NP_216565.1      | 2                         |
| 71217 | C01           | 265        | Rv0298   | hypothetical protein Rv0298                                      | NP_214812.1      | 2                         |
| 71030 | C02           | 268        | Rv0947c  | putative mycolyl transferase                                     |                  | 1.94776119                |
| 70953 | C03           | 271        | Rv2663   | hypothetical protein Rv2663                                      | NP_217179.1      | 2                         |
| 71022 | C04           | 277        | Rv3053c  | glutaredoxin electron transport protein NrdH (nrdH)              | NP_217569.1      | 2                         |
| 70869 | C05           | 280        | Rv3321c  | hypothetical protein Rv3321c                                     | NP_217838.1      | 2                         |
| 71001 | C06           | 283        | Rv0608   | hypothetical protein Rv0608                                      | NP_215122.1      | 2                         |
| 71169 | C07           | 283        | Rv0750   | hypothetical protein Rv0750                                      | NP_215264.1      | 2                         |
| 71154 | C08           | 283        | Rv2595   | hypothetical protein Rv2595                                      | NP_217111.1      | 2                         |
| 70987 | C09           | 283        | Rv2654c  | phiRv2 prophage protein  | NP_217170.1      | 1.61837456                |
| 70929 | C10           | 286        | Rv3022c  | PE family protein (PE29)   | YP_177685.1      | 2                         |
| 70981 | C11           | 292        | Rv0689c  | hypothetical protein Rv0689c                                     | NP_215203.1      | 1.99657534                |
| 70886 | C12           | 292        | Rv2975c  | hypothetical protein Rv2975c                                     | NP_217491.1      | 1.85958904                |
| 71230 | D01           | 292        | Rv3654c  | hypothetical protein Rv3654c                                     | NP_218171.1      | -                         |
| 70957 | D02           | 295        | Rv1398c  | hypothetical protein Rv1398c                                     | NP_215914.1      | 2                         |
| 71133 | D03           | 295        | Rv2342   | hypothetical protein Rv2342                                      | NP_216858.1      | 2                         |
| 70973 | D04           | 322        | Rv0882   | hypothetical protein Rv0882                                      | NP_215397.1      | 2                         |
| 70926 | D05           | 322        | Rv1037c  | putative ESAT-6 like protein ESXI (ESAT-6 like protein 1) (esxI) | NP_215553.1      | 2                         |
| 70857 | D06           | 322        | Rv2346c  | putative ESAT-6 like protein ESXO (ESAT-6 like protein 6) (esxO) | NP_216862.1      | 2                         |
| 71105 | D07           | 325        | Rv0150c  | hypothetical protein Rv0150c                                     | NP_214664.1      | 2                         |
| 71113 | D08           | 325        | Rv3875   | 6 kDa early secretory antigenic target ESXA (ESAT-6) (esxA)      | YP_178023.1      | 2                         |

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|-------|---------------|------------|----------|--|------------------|---------------------------|
| 71173 | D09           | 325        | Rv3890c  | ESAT-6 like protein ESXC (ESAT-6 like protein 11) (esxC)                                     | NP_218407.1      | 2                         |
| 71045 | D10           | 328        | Rv0053   | 30S ribosomal protein S6 (rpsF)  | NP_214567.1      | 2                         |
| 70962 | D11           | 328        | Rv0190   | hypothetical protein Rv0190  | NP_214704.1      | 2                         |
| 70893 | D12           | 328        | Rv0288   | low molecular weight protein antigen 7 ESXH (10 kDa antigen) (CFP-7) (protein TB10.4) (esxH) | NP_214802.1      | 2                         |
| 70949 | E01           | 328        | Rv0829   | hypothetical protein Rv0829  | NP_215344.1      | 2                         |
| 71025 | E02           | 328        | Rv2146c  | transmembrane protein  | NP_216662.1      | 2                         |
| 70997 | E03           | 328        | Rv2433c  | hypothetical protein Rv2433c   | NP_216949.1      | 2                         |
| 71185 | E04           | 328        | Rv3019c  | secreted ESAT-6 like protein ESXR (TB10.3) (ESAT-6 like protein 9) (esxR)                    | NP_217535.1      | 2                         |
| 70882 | E05           | 331        | Rv0250c  | hypothetical protein Rv0250c   | NP_214764.1      | 2                         |
| 71089 | E06           | 331        | Rv0287   | hypothetical protein Rv0287 (esxG)   | NP_214801.1      | 1.83685801                |
| 70905 | E07           | 331        | Rv0508   | hypothetical protein Rv0508  | NP_215022.1      | 2                         |
| 71137 | E08           | 331        | Rv1012   | hypothetical protein Rv1012  | NP_215528.1      | 2                         |
| 71093 | E09           | 331        | Rv2117   | hypothetical protein Rv2117  | NP_216633.1      | 2                         |
| 71206 | E10           | 331        | Rv2561   | hypothetical protein Rv2561  | NP_217077.1      | 2                         |
| 70990 | E11           | 331        | Rv3020c  | Esat-6 like protein EsxS (esxS)  | YP_177919.1      | 2                         |
| 71157 | E12           | 334        | Rv0968   | hypothetical protein Rv0968  | NP_215483.1      | 2                         |
| 71110 | F01           | 334        | Rv1197   | Esat-6 like protein EsxK (Esat-6 like protein 3) (esxK)                                      | NP_215713.1      | 2                         |
| 71010 | F02           | 334        | Rv1951c  | hypothetical protein Rv1951c   | NP_216467.1      | 2                         |
| 70979 | F03           | 334        | Rv1959c  | hypothetical protein Rv1959c   | NP_216475.1      | 2.31137725                |
| 70969 | F04           | 334        | Rv2107   | PE family protein (PE22)   | YP_177858.1      | 2                         |
| 70865 | F05           | 334        | Rv2347c  | putative ESAT-6 like protein ESXP (ESAT-6 like protein 7) (esxP)                             | NP_216863.1      | 2                         |
| 71066 | F06           | 334        | Rv3477   | PE family protein (PE31)   | YP_177975.1      | 1.90419162                |
| 71191 | F07           | 337        | Rv0514   | transmembrane protein  | NP_215028.1      | 1.23442136                |
| 71149 | F08           | 337        | Rv0916c  | PE family protein (PE7)  | YP_177766.1      | -                         |
| 71198 | F09           | 337        | Rv1791   | PE family protein (PE19)   | YP_177837.1      | 1.77744807                |
| 71305 | F10           | 337        | Rv1806   | PE family protein (PE20)   | YP_177843.1      | 2                         |
| 71314 | F11           | 337        | Rv2271   | hypothetical protein Rv2271  | NP_216787.1      | 2                         |
| 71393 | F12           | 337        | Rv2431c  | PE family protein (PE25)   | YP_177882.1      | 2                         |
| 71449 | G01           | 337        | Rv2489c  | hypothetical protein Rv2489c   | NP_217005.1      | 2                         |
| 71425 | G02           | 337        | Rv3012c  | aspartyl/glutamyl-tRNA amidotransferase subunit C (gatC)                                     | NP_217528.1      | 2                         |
| 71281 | G03           | 337        | Rv3155   | NADH dehydrogenase subunit K (nuoK)  | NP_217671.1      | 2                         |
| 71278 | G04           | 337        | Rv3407   | hypothetical protein Rv3407  | NP_217924.1      | 2                         |
| 71513 | G05           | 337        | Rv3872   | PE family-related protein (PE35)   | YP_178021.1      | 2                         |
| 71557 | G06           | 340        | Rv0299   | hypothetical protein Rv0299  | NP_214813.1      | 2                         |
| 71270 | G07           | 340        | Rv0543c  | hypothetical protein Rv0543c   | NP_215057.1      | 2                         |
| 71367 | G08           | 340        | Rv2369c  | hypothetical protein Rv2369c   | NP_216885.1      | 2.2                       |
| 71369 | G09           | 340        | Rv2699c  | hypothetical protein Rv2699c   | NP_217215.1      | 1.99411765                |
| 71347 | G10           | 340        | Rv3418c  | co-chaperonin GroES (groES)  | NP_217935.1      | 2.25588235                |
| 71473 | G11           | 340        | Rv3444c  | putative ESAT-6 like protein ESXT (esxT)   | NP_217961.1      | 2                         |
| 71386 | G12           | 340        | Rv3760   | hypothetical protein Rv3760  | NP_218277.1      | 2                         |
| 71453 | H01           | 340        | Rv3874   | 10 kDa culture filtrate antigen EsxB (esxB)  | NP_218391.1      | 2                         |
| 71569 | H02           | 343        | Rv0700   | 30S ribosomal protein S10 (rpsJ)   | NP_215214.1      | 2                         |
| 71553 | H03           | 343        | Rv0793   | hypothetical protein Rv0793  | NP_215308.1      | 2                         |
| 71265 | H04           | 343        | Rv2021c  | transcriptional regulatory protein   | NP_216537.1      | 2                         |
| 71525 | H05           | 343        | Rv2056c  | 30S ribosomal protein S14 (rpsN)   | NP_216572.1      | 2                         |
| 71534 | H06           | 343        | Rv2901c  | hypothetical protein Rv2901c   | NP_217417.1      | 1.89212828                |
| 71598 | H07           | 346        | Rv0285   | PE family protein (PE5)  | YP_177710.1      | 1.93930636                |
| 71578 | H08           | 346        | Rv0430   | hypothetical protein Rv0430  | NP_214944.1      | 2                         |

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|-------|---------------|------------|----------|------------------------------|------------------|---------------------------|
| 71493 | H09           | 346        | Rv0659c  | hypothetical protein Rv0659c | NP_215173.1      | 2                         |
| 71537 | H10           | 346        | Rv1898   | hypothetical protein Rv1898  | NP_216414.1      | 2                         |
| 71401 | H11           | 346        | Rv3385c  | hypothetical protein Rv3385c | NP_217902.1      | 2                         |
| 71405 | H12           | 349        | Rv0603   | hypothetical protein Rv0603  | NP_215117.1      | 1.88825215                |

Table 2: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 2 (ZMTDB), NR-19638

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 71363 | A01           | 349        | Rv1102c  | hypothetical protein Rv1102c  | NP_215618.1      | 2                         |
| 71397 | A02           | 349        | Rv1772   | hypothetical protein Rv1772   | NP_216288.1      | 2                         |
| 71322 | A03           | 349        | Rv1953   | hypothetical protein Rv1953   | NP_216469.1      | 1.905444126               |
| 71489 | A04           | 349        | Rv2809   | hypothetical protein Rv2809   | NP_217325.1      | 2                         |
| 71466 | A05           | 349        | Rv3440c  | hypothetical protein Rv3440c  | NP_217957.1      | 2                         |
| 71351 | A06           | 349        | Rv3615c  | hypothetical protein Rv3615c  | NP_218132.1      | 2                         |
| 71431 | A07           | 349        | Rv3865   | hypothetical protein Rv3865   | NP_218382.1      | 2.191977077               |
| 71590 | A08           | 349        | Rv3905c  | hypothetical protein Rv3905c  | NP_218422.1      | 2                         |
| 71378 | A09           | 367        | Rv0030   | hypothetical protein Rv0030   | NP_214544.1      | 2                         |
| 71485 | A10           | 370        | Rv3129   | hypothetical protein Rv3129   | YP_177933.1      | 2                         |
| 71285 | A11           | 370        | Rv3216   | acetyltransferase   | NP_217732.1      | 2                         |
| 71297 | A12           | 385        | Rv0801   | hypothetical protein Rv0801   | NP_215316.1      | 2                         |
| 71414 | B01           | 385        | Rv1466   | hypothetical protein Rv1466   | NP_215982.1      | 1.994805195               |
| 71294 | B02           | 394        | Rv0253   | nitrite reductase   | NP_214767.1      | -                         |
| 71263 | B03           | 397        | Rv1767   | hypothetical protein Rv1767   | NP_216283.1      | 2.549118388               |
| 71518 | B04           | 400        | Rv1089   | PE family protein   | YP_177785.1      | -                         |
| 71602 | B05           | 400        | Rv2658c  | prophage protein  | NP_217174.1      | 2                         |
| 71618 | B06           | 400        | Rv3922c  | hypothetical protein Rv3922c  | NP_218439.1      | -                         |
| 71502 | B07           | 403        | Rv1311   | F0F1 ATP synthase subunit epsilon   | NP_215827.1      | 1.990074442               |
| 71575 | B08           | 406        | Rv0662c  | hypothetical protein Rv0662c  | NP_215176.1      | 1.884236453               |
| 71506 | B09           | 406        | Rv0714   | 50S ribosomal protein L14   | NP_215228.1      | 2                         |
| 71353 | B10           | 406        | Rv2087   | hypothetical protein Rv2087   | NP_216603.2      | 2                         |
| 71471 | B11           | 412        | Rv2206   | transmembrane protein   | NP_216722.2      | 1.601941748               |
| 71585 | B12           | 417        | Rv0857   | hypothetical protein Rv0857   | NP_215372.2      | 1.932853717               |
| 71254 | C01           | 421        | Rv1761c  | hypothetical protein Rv1761c  | NP_216277.1      | 2.589073634               |
| 71317 | C02           | 422        | Rv2863   | hypothetical protein Rv2863   | NP_217379.1      | 2                         |
| 71342 | C03           | 424        | Rv2898c  | hypothetical protein Rv2898c  | NP_217414.1      | 2                         |
| 71543 | C04           | 427        | Rv0367c  | hypothetical protein Rv0367c  | NP_214881.1      | 1.606557377               |
| 71433 | C05           | 427        | Rv1052   | hypothetical protein Rv1052   | NP_215568.1      | 1.927400468               |
| 71439 | C06           | 427        | Rv2570   | hypothetical protein Rv2570   | NP_217086.1      | 1.995316159               |
| 71637 | C07           | 493        | Rv0985c  | large-conductance mechanosensitive channel  | NP_215500.1      | 2                         |
| 71682 | C08           | 502        | Rv2576c  | hypothetical protein Rv2576c  | NP_217092.1      | 2                         |
| 72342 | C09           | 514        | Rv1276c  | hypothetical protein Rv1276c  | NP_215792.1      | 2.342412451               |
| 72197 | C10           | 514        | Rv2239c  | hypothetical protein Rv2239c  | NP_216755.1      | 2                         |
| 72186 | C11           | 514        | Rv2730   | hypothetical protein Rv2730   | NP_217246.1      | 2                         |
| 72351 | C12           | 514        | Rv3437   | transmembrane protein   | NP_217954.1      | 2                         |
| 72178 | D01           | 517        | Rv0374c  | carbon monoxide dehydrogenase small subunit   | NP_214888.1      | 1.998065764               |
| 72278 | D02           | 517        | Rv1926c  | immunogenic protein MPT63 (antigen MPT63/MPB63) (16 kDa immunoprotective extracellular protein) | NP_216442.1      | 1.620889749               |
| 72017 | D03           | 517        | Rv3581c  | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase   | NP_218098.1      | 2                         |
| 72026 | D04           | 520        | Rv0307c  | hypothetical protein Rv0307c  | NP_214821.1      | 1.907692308               |
| 72101 | D05           | 520        | Rv3165c  | hypothetical protein Rv3165c  | NP_217681.1      | 2                         |
| 72042 | D06           | 520        | Rv3172c  | hypothetical protein Rv3172c  | NP_217688.1      | 2                         |
| 72117 | D07           | 520        | Rv3237c  | hypothetical protein Rv3237c  | NP_217754.1      | 2                         |

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|-------|---------------|------------|----------|--|------------------|---------------------------|
| 72135 | D08           | 520        | Rv3492c  | Mce associated protein                                 | NP_218009.1      | 2.380769231               |
| 72242 | D09           | 520        | Rv3831   | hypothetical protein Rv3831                            | NP_218348.1      | 2.130769231               |
| 72023 | D10           | 523        | Rv1287   | hypothetical protein Rv1287                            | NP_215803.1      | 2.361376673               |
| 72238 | D11           | 523        | Rv2633c  | hypothetical protein Rv2633c                           | NP_217149.1      | 2                         |
| 72327 | D12           | 523        | Rv2965c  | phosphopantetheine adenyllyltransferase                | NP_217481.1      | 2.223709369               |
| 72158 | E01           | 526        | Rv0245   | oxidoreductase   | NP_214759.1      | 1.998098859               |
| 72115 | E02           | 526        | Rv2035   | hypothetical protein Rv2035                            | NP_216551.1      | 2.933460076               |
| 72306 | E03           | 529        | Rv2327   | hypothetical protein Rv2327                            | NP_216843.1      | 2.737240076               |
| 72378 | E04           | 532        | Rv0431   | putative tuberculin related peptide                    | NP_214945.1      | 1.859022556               |
| 72191 | E05           | 535        | Rv2719c  | hypothetical protein Rv2719c                           | NP_217235.1      | 1.439252336               |
| 72357 | E06           | 538        | Rv1506c  | hypothetical protein Rv1506c                           | NP_216022.1      | 2                         |
| 72053 | E07           | 538        | Rv2616   | hypothetical protein Rv2616                            | NP_217132.1      | 2                         |
| 72374 | E08           | 541        | Rv0201c  | hypothetical protein Rv0201c                           | NP_214715.1      | 1.754158965               |
| 72273 | E09           | 568        | Rv3425   | PPE family protein                                     | YP_177971.1      | 2                         |
| 72009 | E10           | 576        | Rv2987c  | isopropylmalate isomerase small subunit                | NP_217503.1      | 2                         |
| 72171 | E11           | 583        | Rv0733   | adenylate kinase                                       | NP_215247.1      | 2.123499142               |
| 72361 | E12           | 583        | Rv1105   | hypothetical protein Rv1105                            |                  | 2                         |
| 72173 | F01           | 589        | Rv1503c  | hypothetical protein Rv1503c                           | NP_216019.1      | 2                         |
| 72249 | F02           | 592        | Rv1150   | possible transposase fragment                          |                  | -                         |
| 72097 | F03           | 595        | Rv2499c  | oxidase regulatory-like protein                        | NP_217015.1      | 1.996638655               |
| 72073 | F04           | 598        | Rv1476   | hypothetical protein Rv1476                            | NP_215992.1      | 1.996655518               |
| 72067 | F05           | 607        | Rv1727   | hypothetical protein Rv1727                            | NP_216243.1      | -                         |
| 72093 | F06           | 610        | Rv1388   | putative integration host factor MIHF                  | NP_215904.1      | 2                         |
| 72165 | F07           | 610        | Rv2879c  | hypothetical protein Rv2879c                           | NP_217395.1      | -                         |
| 72126 | F08           | 613        | Rv3770c  | hypothetical protein Rv3770A                           | YP_178012.1      | 1.345840131               |
| 72299 | F09           | 616        | Rv3647c  | hypothetical protein Rv3647c                           | NP_218164.1      | 2.211038961               |
| 72369 | F10           | 643        | Rv0612   | hypothetical protein Rv0612                            | NP_215126.1      | 1.99222395                |
| 72417 | F11           | 643        | Rv2022c  | hypothetical protein Rv2022c                           | NP_216538.1      | 2                         |
| 72663 | F12           | 646        | Rv0038   | hypothetical protein Rv0038                            | NP_214552.1      | 2.578947368               |
| 72581 | G01           | 649        | Rv0995   | ribosomal-protein-alanine acetyltransferase            | NP_215510.1      | 2                         |
| 72652 | G02           | 652        | Rv1210   | DNA-3-methyladenine glycosylase I                      | NP_215726.1      | 2                         |
| 72477 | G03           | 652        | Rv3055   | TetR family transcriptional regulator                  | NP_217571.1      | 2                         |
| 72464 | G04           | 658        | Rv0779c  | transmembrane protein                                  | NP_215293.1      | 1.772036474               |
| 72549 | G05           | 658        | Rv3189   | hypothetical protein Rv3189                            | NP_217705.1      | 1.993920973               |
| 72676 | G06           | 670        | Rv2680   | hypothetical protein Rv2680                            | NP_217196.1      | 1.937313433               |
| 72700 | G07           | 673        | Rv3153   | NADH dehydrogenase subunit I                           | NP_217669.1      | 2                         |
| 72631 | G08           | 679        | Rv0175   | mce associated membrane protein                        | NP_214689.1      | 2.402061856               |
| 72415 | G09           | 682        | Rv2983   | hypothetical protein Rv2983                            | NP_217499.1      | 2                         |
| 72603 | G10           | 682        | Rv2986c  | DNA-binding protein HU                                 | NP_217502.1      | 2.315249267               |
| 72593 | G11           | 685        | Rv0358   | hypothetical protein Rv0358                            | NP_214872.1      | 1.448175182               |
| 72637 | G12           | 685        | Rv0956   | phosphoribosylglycinamide formyltransferase            | NP_215471.1      | 3.075912409               |
| 72501 | H01           | 685        | Rv1907c  | hypothetical protein Rv1907c                           |                  | 2                         |
| 72405 | H02           | 685        | Rv2506   | TetR family transcriptional regulator                  | NP_217022.1      | 2                         |
| 72496 | H03           | 691        | Rv0348   | transcriptional regulatory protein                     | NP_214862.1      | 2                         |
| 72521 | H04           | 691        | Rv2612c  | CDP-diacylglycerol--inositol 3-phosphatidyltransferase | YP_177894.1      | 2                         |
| 72437 | H05           | 694        | Rv0309   | hypothetical protein Rv0309                            | NP_214823.1      | 2                         |
| 72702 | H06           | 694        | Rv1332   | transcriptional regulatory protein                     | NP_215848.1      | 2                         |
| 72507 | H07           | 694        | Rv1587c  | REP13E12 repeat-containing protein                     | NP_216103.2      | 3.095100865               |
| 72556 | H08           | 694        | Rv2086   | hypothetical protein Rv2086                            | NP_216602.2      | 2                         |
| 72517 | H09           | 694        | Rv2637   | transmembrane protein DedA                             | NP_217153.1      | 1.998559078               |
| 72537 | H10           | 697        | Rv2301   | cutinase CUT2  | NP_216817.2      | 2                         |
| 72609 | H11           | 697        | Rv2543   | lipoprotein LppA                                       | NP_217059.1      | 2                         |
| 72498 | H12           | 697        | Rv3000   | transmembrane protein                                  | NP_217516.1      | 2.56097561                |

Table 3: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 3 (ZMTDC), NR-19639

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 72677 | A01           | 700        | Rv0085   | hydrogenase HycP (hycP)  | NP_214599.1      | 2                         |
| 72733 | A02           | 700        | Rv0540   | hypothetical protein Rv0540  | NP_215054.1      | 1.93                      |
| 72473 | A03           | 700        | Rv1362c  | hypothetical protein Rv1362c   | NP_215878.1      | 2                         |
| 72714 | A04           | 703        | Rv3323c  | MOAD-MOAE fusion protein MOAX (moaX)   | YP_177959.1      | 1.87339972                |
| 72741 | A05           | 712        | Rv0649   | malonyl CoA-acyl carrier protein transacylase (fabD2)                        | YP_177744.1      | 1.09410112                |
| 72754 | A06           | 712        | Rv0962c  | lipoprotein LprP (lprP)  | NP_215477.1      | -                         |
| 72616 | A07           | 712        | Rv2014   | transposase  | NP_216530.2      | 1.99157303                |
| 72580 | A08           | 712        | Rv2607   | pyridoxamine 5'-phosphate Oxidase (pdxH)                                     | NP_217123.1      | 1.99157303                |
| 72458 | A09           | 718        | Rv0229c  | hypothetical protein Rv0229c   | NP_214743.1      | 1.99860724                |
| 72689 | A10           | 718        | Rv1016c  | lipoprotein LpqT (lpqT)  | NP_215532.1      | 2.96657382                |
| 72409 | A11           | 718        | Rv1570   | dithiobiotin synthetase (bioD)   | NP_216086.1      | 1.60724234                |
| 72717 | A12           | 727        | Rv3268   | hypothetical protein Rv3268  | NP_217785.1      | 1.75240715                |
| 72481 | B01           | 730        | Rv0059   | hypothetical protein Rv0059  | NP_214573.1      | 1.99726027                |
| 72761 | B02           | 730        | Rv1566c  | inv protein  | NP_216082.1      | 1.75068493                |
| 72533 | B03           | 733        | Rv1710   | hypothetical protein Rv1710  | NP_216226.1      | 2                         |
| 72746 | B04           | 736        | Rv0013   | para-aminobenzoate synthase component II (trpG)                              | YP_177615.1      | 2.74592391                |
| 72585 | B05           | 739        | Rv2227   | hypothetical protein Rv2227  | NP_216743.1      | 2                         |
| 72515 | B06           | 742        | Rv2013   | transposase  | NP_216529.2      | 2                         |
| 72659 | B07           | 742        | Rv3765c  | two component transcriptional regulatory protein                             | NP_218282.1      | 1.96361186                |
| 72618 | B08           | 748        | Rv2135c  | hypothetical protein Rv2135c   | NP_216651.1      | 1.97593583                |
| 72472 | B09           | 748        | Rv3519   | hypothetical protein Rv3519  | NP_218036.1      | 2                         |
| 72653 | B10           | 754        | Rv0308   | integral membrane protein  | NP_214822.1      | 2                         |
| 72485 | B11           | 754        | Rv0639   | transcription antitermination protein NusG (nusG)                            | NP_215153.1      | 2                         |
| 72421 | B12           | 760        | Rv1078   | proline-rich antigen (pra)   | NP_215594.1      | 1.98815789                |
| 72433 | C01           | 760        | Rv2525c  | hypothetical protein Rv2525c   | NP_217041.1      | 3.08552632                |
| 72729 | C02           | 763        | Rv0275c  | TetR family transcriptional regulator  | YP_177706.1      | 1.70249017                |
| 72695 | C03           | 766        | Rv3287c  | anti-sigma factor rsbW (sigma negative effector) (rsbW)                      | NP_217804.2      | 3.02610966                |
| 72725 | C04           | 769        | Rv1748   | hypothetical protein Rv1748  | NP_216264.1      | 3.11053316                |
| 72547 | C05           | 772        | Rv0387c  | PPE family protein   | NP_214901.1      | 2.02720207                |
| 72441 | C06           | 775        | Rv1603   | phosphoribosyl isomerase A (hisA)  | NP_216119.1      | 1.8916129                 |
| 72529 | C07           | 778        | Rv0625c  | transmembrane protein  | NP_215139.1      | 1.83547558                |
| 72402 | C08           | 778        | Rv1164   | respiratory nitrate reductase subunit gamma NarI (narI)                      | NP_215680.1      | 1.8496144                 |
| 72621 | C09           | 778        | Rv2573   | 2-dehydropantoate 2-reductase  | NP_217089.2      | 1.30719794                |
| 72541 | C10           | 778        | Rv3653   | PE-PGRS family-related protein (PE_PGRS61)                                   | YP_178002.1      | 1.46272494                |
| 72766 | C11           | 781        | Rv0606   | hypothetical protein Rv0606  | NP_215120.1      | 1.9346991                 |
| 72510 | C12           | 781        | Rv0757   | two component system response transcriptional positive regulator PHOP (phoP) | NP_215271.1      | 2                         |
| 72527 | D01           | 781        | Rv1350   | 3-ketoacyl-(acyl-carrier-protein) reductase (fabG)                           | NP_215866.1      | 2.30985915                |
| 72667 | D02           | 781        | Rv1553   | fumarate reductase iron-sulfur subunit FrdB (frdB)                           | NP_216069.1      | 2.48015365                |
| 72641 | D03           | 781        | Rv3451   | cutinase precursor CUT3 (cut3)   | NP_217968.2      | 2.29961588                |
| 72625 | D04           | 781        | Rv3550   | enoyl-CoA hydratase (echA20)   | NP_218067.1      | 2.03072983                |
| 72705 | D05           | 784        | Rv0247c  | fumarate reductase iron-sulfur subunit                                       | NP_214761.1      | 1.83290816                |
| 72771 | D06           | 784        | Rv0769   | short chain dehydrogenase  | NP_215283.1      | 2.10714286                |
| 72597 | D07           | 787        | Rv0184   | hypothetical protein Rv0184  | NP_214698.1      | 1.85387548                |
| 72757 | D08           | 787        | Rv0494   | GntR family transcriptional regulator  | NP_215008.2      | 1.88437103                |
| 72390 | D09           | 787        | Rv2208   | cobalamin synthase (cobS)  | NP_216724.1      | 2.57814485                |
| 72681 | D10           | 790        | Rv1144   | short-chain type dehydrogenase/reductase                                     | NP_215660.1      | 1.91265823                |
| 72633 | D11           | 790        | Rv2516c  | hypothetical protein Rv2516c   | NP_217032.2      | 1.94050633                |
| 72591 | D12           | 793        | Rv0116c  | hypothetical protein Rv0116c   | NP_214630.1      | 2.50189155                |
| 72685 | E01           | 793        | Rv2403c  | lipoprotein LppR (lppR)  | NP_216919.1      | 1.89281211                |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 72569 | E02           | 796        | Rv1491c  | hypothetical protein Rv1491c   | NP_216007.1      | 1.97613065                |
| 72648 | E03           | 796        | Rv2667   | ATP-dependent protease ATP-binding subunit ClpC2 (clpC2)   | YP_177897.1      | 2                         |
| 72557 | E04           | 796        | Rv2686c  | antibiotic ABC transporter transmembrane protein   | NP_217202.1      | 1.55778894                |
| 72956 | E05           | 799        | Rv1424c  | hypothetical protein Rv1424c   | NP_215940.1      | 2                         |
| 72780 | E06           | 802        | Rv1056   | hypothetical protein Rv1056  | NP_215572.1      | 1.99625935                |
| 73123 | E07           | 805        | Rv0091   | bifunctional 5'-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase (mtn)   | NP_214605.1      | 2.7068323                 |
| 73002 | E08           | 805        | Rv2237   | hypothetical protein Rv2237  | NP_216753.1      | 2.94782609                |
| 72959 | E09           | 805        | Rv3297   | endonuclease VIII (nei)  | NP_217814.1      | 3.08447205                |
| 73116 | E10           | 808        | Rv0446c  | transmembrane protein  | NP_214960.1      | 2                         |
| 73029 | E11           | 808        | Rv2486   | enoyl-CoA hydratase (echA14)   | NP_217002.1      | 1.94554455                |
| 73135 | E12           | 808        | Rv3455c  | tRNA pseudouridine synthase A (truA)   | NP_217972.2      | 2.9009901                 |
| 73005 | F01           | 808        | Rv3662c  | hypothetical protein Rv3662c   | NP_218179.1      | 1.50371287                |
| 73055 | F02           | 811        | Rv2189c  | hypothetical protein Rv2189c   | NP_216705.1      | 2.37731196                |
| 73139 | F03           | 814        | Rv3839   | hypothetical protein Rv3839  | NP_218356.1      | 1.47788698                |
| 72818 | F04           | 823        | Rv2928   | thioesterase TESA (tesA)   | NP_217444.1      | 1.87970838                |
| 72884 | F05           | 823        | Rv3286c  | RNA polymerase sigma factor SigF (sigF)  | NP_217803.1      | 2                         |
| 73146 | F06           | 826        | Rv1086   | short (C15) chain Z-isoprenyl diphosphate synthase (Z-FPP synthase) (Z-farnesyl diphosphate synthase) (Z-FPP synthetase) (Z-farnesyl diphosphate synthetase) (geranyltranstransferase) (farnesyl pyrophosphate synthetase) | NP_215602.1      | 2.60290557                |
| 72835 | F07           | 826        | Rv3559c  | short chain dehydrogenase  | NP_218076.1      | 2.0472155                 |
| 72918 | F08           | 829        | Rv3516   | enoyl-CoA hydratase (echA19)   | NP_218033.1      | 2.51507841                |
| 72872 | F09           | 829        | Rv3833   | AraC family transcriptional regulator  | NP_218350.1      | 1.95778046                |
| 72813 | F10           | 832        | Rv0466   | hypothetical protein Rv0466  | NP_214980.1      | 1.90024039                |
| 72890 | F11           | 832        | Rv1008   | deoxyribonuclease TatD (YjjV protein) (tatD)   | NP_215524.1      | 1.88221154                |
| 72979 | F12           | 832        | Rv3351c  | hypothetical protein Rv3351c   | NP_217868.1      | 2.37980769                |
| 72929 | G01           | 835        | Rv1964   | integral membrane protein YrbE3A (yrbE3A)  | NP_216480.1      | 1.97844311                |
| 73009 | G02           | 835        | Rv2362c  | DNA repair protein RecO (recO)   | NP_216878.1      | 1.62994012                |
| 72916 | G03           | 835        | Rv2702   | polyphosphate glucokinase PPGK (polyphosphate-glucose phosphotransferase) (ppgK)   | NP_217218.1      | 1.99281437                |
| 73079 | G04           | 838        | Rv3213c  | SOJ/PARA-like protein  | NP_217729.1      | 2.87350835                |
| 72966 | G05           | 839        | Rv2631   | hypothetical protein Rv2631  | NP_217147.2      | 2.81883194                |
| 72832 | G06           | 841        | Rv2131c  | monophosphatase CysQ (cysQ)  | NP_216647.1      | 1.90249703                |
| 72799 | G07           | 844        | Rv1141c  | enoyl-CoA hydratase (echA11)   | NP_215657.1      | 3.08530806                |
| 72839 | G08           | 844        | Rv2464c  | DNA glycosylase  | NP_216980.1      | 3.08649289                |
| 72942 | G09           | 844        | Rv3307   | purine nucleoside phosphorylase (deoD)   | NP_217824.1      | 2.32701422                |
| 72885 | G10           | 847        | Rv0971c  | enoyl-CoA hydratase (echA7)  | NP_215486.1      | 1.97048406                |
| 72976 | G11           | 850        | Rv0839   | hypothetical protein Rv0839  | NP_215354.1      | 2                         |
| 73094 | G12           | 850        | Rv1613   | tryptophan synthase subunit alpha (trpA)   | NP_216129.1      | 1.81882353                |
| 73149 | H01           | 850        | Rv2813   | hypothetical protein Rv2813  | NP_217329.1      | 2.73882353                |
| 73067 | H02           | 856        | Rv1718   | hypothetical protein Rv1718  | NP_216234.1      | 3.27336449                |
| 73105 | H03           | 856        | Rv3600c  | pantothenate kinase  | NP_218117.1      | 2.99649533                |
| 72898 | H04           | 859        | Rv0079   | hypothetical protein Rv0079  | NP_214593.1      | 3.13853318                |
| 72782 | H05           | 859        | Rv0249c  | succinate dehydrogenase membrane anchor subunit  | NP_214763.1      | 1.65308498                |
| 72981 | H06           | 859        | Rv1339   | hypothetical protein Rv1339  | NP_215855.1      | 2.18044237                |
| 73042 | H07           | 859        | Rv2622   | methyltransferase (methylase)  | NP_217138.1      | 1.774156                  |
| 72807 | H08           | 862        | Rv1403c  | putative methyltransferase   | NP_215919.1      | 3.54060325                |
| 73125 | H09           | 862        | Rv3030   | hypothetical protein Rv3030  | NP_217546.1      | 2.16589327                |
| 72852 | H10           | 865        | Rv0687   | 3-ketoacyl-(acyl-carrier-protein) reductase (fabG)   | NP_215201.1      | 2                         |
| 73110 | H11           | 865        | Rv1040c  | PE family protein (PE8)  | YP_177779.1      | 2.67630058                |
| 72861 | H12           | 865        | Rv2769c  | PE family protein (PE27)   | YP_177907.1      | 1.63468208                |

Table 4: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 4 (ZMTDD), NR-19640

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 73090 | A01           | 865        | Rv2957   | glycosyl transferase   | NP_217473.1      | 4.04277457                |
| 73154 | A02           | 868        | Rv0153c  | phosphotyrosine protein phosphatase PTPB (protein-tyrosine-phosphatase) (PTPase) (ptbB)      | NP_214667.1      | 1.73041475                |
| 72826 | A03           | 868        | Rv2136c  | undecaprenyl pyrophosphate phosphatase (uppP)  | NP_216652.1      | 3.29608295                |
| 72860 | A04           | 868        | Rv2938   | daunorubicin-DIM-transport integral membrane protein ABC transporter DrrC (drrC)             | NP_217454.1      | 2                         |
| 72841 | A05           | 871        | Rv3487c  | esterase/lipase LipF (lipF)  | NP_218004.1      | 3.05740528                |
| 72874 | A06           | 874        | Rv1460   | transcriptional regulatory protein   | NP_215976.2      | 1.49084668                |
| 73097 | A07           | 874        | Rv2119   | hypothetical protein Rv2119  | NP_216635.1      | 3.03546911                |
| 72854 | A08           | 877        | Rv2409c  | hypothetical protein Rv2409c   | NP_216925.1      | 3.26567845                |
| 72971 | A09           | 880        | Rv3243c  | hypothetical protein Rv3243c   | NP_217760.1      | 3.43977273                |
| 72936 | A10           | 880        | Rv3438   | hypothetical protein Rv3438  | NP_217955.1      | 1.9625                    |
| 73046 | A11           | 880        | Rv3783   | O-antigen/lipopolysaccharide transport integral membrane protein ABC transporter RfbD (rfbD) | NP_218300.1      | 3.92840909                |
| 72911 | A12           | 880        | Rv3878   | hypothetical protein Rv3878  | NP_218395.1      | 3.08977273                |
| 73014 | B01           | 883        | Rv2605c  | acyl-CoA thioesterase II (tesB2)   | NP_217121.1      | 2.93318233                |
| 72926 | B02           | 883        | Rv3333c  | hypothetical protein Rv3333c   | NP_217850.1      | 1.66591166                |
| 73131 | B03           | 886        | Rv1978   | hypothetical protein Rv1978  | NP_216494.1      | 3.87358916                |
| 72922 | B04           | 892        | Rv2313c  | hypothetical protein Rv2313c   | NP_216829.1      | 1.72309417                |
| 72879 | B05           | 892        | Rv3435c  | transmembrane protein  | NP_217952.1      | 3.55605381                |
| 72810 | B06           | 892        | Rv3810   | exported repetitive protein precursor PirG (cell surface protein) (EXP53) (pirG)             | NP_218327.1      | 1.70852018                |
| 72961 | B07           | 895        | Rv1062   | hypothetical protein Rv1062  | NP_215578.1      | 2.87932961                |
| 73037 | B08           | 895        | Rv1472   | enoyl-CoA hydratase (echA12)   | NP_215988.1      | 2.95642458                |
| 72801 | B09           | 898        | Rv0375c  | carbon monoxide dehydrogenase medium subunit   | NP_214889.1      | 3.04565702                |
| 72994 | B10           | 898        | Rv0436c  | CDP-diacylglycerol--serine O-phosphatidyltransferase (pssA)                                  | NP_214950.1      | 3.80400891                |
| 73141 | B11           | 898        | Rv1118c  | hypothetical protein Rv1118c   | NP_215634.1      | 2.97772829                |
| 72990 | B12           | 898        | Rv1244   | lipoprotein LpqZ (lpqZ)  | NP_215760.1      | 1.29064588                |
| 73034 | C01           | 901        | Rv0470c  | hypothetical protein Rv0470A   | YP_177622.1      | 2.88346282                |
| 72938 | C02           | 901        | Rv1455   | hypothetical protein Rv1455  | NP_215971.1      | 1.32297447                |
| 73073 | C03           | 901        | Rv1920   | hypothetical protein Rv1920  | NP_216436.1      | 2.98224195                |
| 73027 | C04           | 901        | Rv2877c  | integral membrane protein  | YP_177912.1      | 3.24750277                |
| 73049 | C05           | 901        | Rv3057c  | short chain dehydrogenase  | NP_217573.1      | 3.02219756                |
| 73082 | C06           | 904        | Rv0881   | rRNA methyltransferase   | NP_215396.1      | 1.67035398                |
| 73087 | C07           | 904        | Rv2161c  | hypothetical protein Rv2161c   | NP_216677.1      | 3.20685841                |
| 73101 | C08           | 907        | Rv2275   | hypothetical protein Rv2275  | NP_216791.1      | 2.98235943                |
| 73022 | C09           | 907        | Rv2924c  | formamidopyrimidine-DNA glycosylase (fpg)  | NP_217440.1      | 2.73980154                |
| 72951 | C10           | 907        | Rv2937   | daunorubicin-DIM-transport integral membrane protein ABC transporter DrrB (drrB)             | NP_217453.1      | 1.22601985                |
| 72986 | C11           | 907        | Rv3335c  | integral membrane protein  | NP_217852.1      | 1.52701213                |
| 72865 | C12           | 907        | Rv3555c  | hypothetical protein Rv3555c   | NP_218072.1      | 2.94928335                |
| 73161 | D01           | 910        | Rv1189   | RNA polymerase sigma factor SigI (sigI)  | NP_215705.1      | 1.58571429                |
| 73234 | D02           | 911        | Rv1282c  | oligopeptide-transport integral membrane protein ABC transporter OppC (oppC)                 | NP_215798.1      | 3.54226125                |
| 73369 | D03           | 913        | Rv2911   | D-alanyl-D-alanine carboxypeptidase (dacB2)  | YP_177914.1      | 1.59255203                |
| 73518 | D04           | 916        | Rv0534c  | 1,4-dihydroxy-2-naphthoate octaprenyltransferase   | NP_215048.1      | 1.38209607                |
| 73285 | D05           | 922        | Rv1369c  | transposase  | NP_215885.1      | 1.54121475                |
| 73215 | D06           | 922        | Rv2026c  | hypothetical protein Rv2026c   | NP_216542.1      | 1.78308026                |
| 73390 | D07           | 922        | Rv3395c  | hypothetical protein Rv3395A   | YP_177969.1      | 3.57375271                |
| 73210 | D08           | 925        | Rv0289   | hypothetical protein Rv0289  | NP_214803.1      | 1.3372973                 |
| 73457 | D09           | 925        | Rv2886c  | resolvase  | NP_217402.1      | 1.47459459                |
| 73424 | D10           | 925        | Rv3232c  | transcriptional regulatory protein PvdS (pvdS)   | NP_217749.1      | 1.70054054                |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 73381 | D11           | 928        | Rv0495c  | hypothetical protein Rv0495c  | NP_215009.1      | 1.5700431                 |
| 73329 | D12           | 928        | Rv2751   | hypothetical protein Rv2751   | NP_217267.1      | 3.72198276                |
| 73522 | E01           | 931        | Rv1076   | lipase LipU (lipU)  | NP_215592.1      | 1.4650913                 |
| 73313 | E02           | 931        | Rv2415c  | hypothetical protein Rv2415c  | NP_216931.1      | 1.58539205                |
| 73326 | E03           | 934        | Rv2793c  | tRNA pseudouridine synthase B (truB)  | NP_217309.1      | 3.25481799                |
| 73380 | E04           | 943        | Rv0936   | phosphate ABC transporter transmembrane protein (pstA2)                                 | NP_215451.1      | 1.8388123                 |
| 73373 | E05           | 946        | Rv0281   | hypothetical protein Rv0281   | NP_214795.1      | 1.42494715                |
| 73396 | E06           | 946        | Rv0428c  | hypothetical protein Rv0428c  | NP_214942.1      | 1.86786469                |
| 73441 | E07           | 946        | Rv0650   | sugar kinase  | NP_215164.1      | 2.83192389                |
| 73481 | E08           | 946        | Rv1486c  | hypothetical protein Rv1486c  | NP_216002.2      | 3.54862579                |
| 73525 | E09           | 946        | Rv2458   | homocysteine methyltransferase (mmuM)   | NP_216974.1      | 3.77484144                |
| 73505 | E10           | 949        | Rv2835c  | sn-glycerol-3-phosphate transport integral membrane protein ABC transporter UGPA (ugpA) | NP_217351.1      | 1.46786091                |
| 73297 | E11           | 952        | Rv1111c  | hypothetical protein Rv1111c  | NP_215627.2      | 1.52521008                |
| 73409 | E12           | 952        | Rv1324   | thioredoxin   | NP_215840.1      | 1.51365546                |
| 73229 | F01           | 952        | Rv3298c  | esterase lipoprotein LpqC (lpqC)  | NP_217815.1      | 3.3802521                 |
| 73406 | F02           | 955        | Rv0930   | phosphate ABC transporter transmembrane protein   | NP_215445.2      | 1.41884817                |
| 73266 | F03           | 964        | Rv0142   | hypothetical protein Rv0142   | NP_214656.1      | 1.48858921                |
| 73264 | F04           | 964        | Rv3665c  | peptide ABC transporter transmembrane protein (dppB)                                    | NP_218182.1      | 1.5                       |
| 73366 | F05           | 967        | Rv2252   | diacylglycerol kinase   | NP_216768.1      | 2.44984488                |
| 73358 | F06           | 967        | Rv2776c  | oxidoreductase  | NP_217292.1      | 1.48293692                |
| 73480 | F07           | 970        | Rv2334   | cysteine synthase A CysK1 (cysK1)   | YP_177868.1      | 1.79484536                |
| 73172 | F08           | 970        | Rv3695   | hypothetical protein Rv3695   | NP_218212.1      | 1.81237113                |
| 73454 | F09           | 976        | Rv1092c  | pantothenate kinase (coaA)  | NP_215608.1      | 1.85553279                |
| 73207 | F10           | 976        | Rv2282c  | LysR family transcriptional regulator   | NP_216798.1      | 2.57172131                |
| 73302 | F11           | 979        | Rv0796   | transposase IS6110  | NP_215311.1      | 1.46067416                |
| 73431 | F12           | 982        | Rv0233   | ribonucleotide-diphosphate reductase subunit beta                                       | NP_214747.1      | 2.59775967                |
| 73339 | G01           | 982        | Rv2727c  | tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)                               | NP_217243.1      | 1.88289206                |
| 73356 | G02           | 982        | Rv2824c  | hypothetical protein Rv2824c  | NP_217340.1      | 1.74541752                |
| 73228 | G03           | 982        | Rv2905   | alanine rich lipoprotein LppW (lppW)  | NP_217421.1      | 1.43584521                |
| 73220 | G04           | 982        | Rv3485c  | short chain dehydrogenase   | NP_218002.1      | 1.79327902                |
| 73433 | G05           | 982        | Rv3767c  | hypothetical protein Rv3767c  | NP_218284.1      | 2.59063136                |
| 73474 | G06           | 988        | Rv0604   | lipoprotein lpqo (lpqO)   | NP_215118.1      | 2.52732794                |
| 73534 | G07           | 988        | Rv1296   | homoserine kinase (thrB)  | NP_215812.1      | 2.53846154                |
| 73203 | G08           | 988        | Rv1845c  | hypothetical protein Rv1845c  | NP_216361.1      | 1.6417004                 |
| 73180 | G09           | 988        | Rv2413c  | hypothetical protein Rv2413c  | NP_216929.1      | 1.79149798                |
| 73183 | G10           | 991        | Rv1201c  | transferase   | NP_215717.1      | 1.23713421                |
| 73426 | G11           | 991        | Rv2985   | hydrolase MutT1 (mutT1)   | NP_217501.1      | 2.65489405                |
| 73485 | G12           | 994        | Rv3176c  | epoxide hydrolase MesT (mesT)   | YP_177938.1      | 2.46177062                |
| 73258 | H01           | 997        | Rv0787   | hypothetical protein Rv0787   | NP_215301.1      | 1.37311936                |
| 73495 | H02           | 997        | Rv1399c  | lipase LipH (lipH)  | NP_215915.1      | 2.45135406                |
| 73467 | H03           | 997        | Rv3683   | hypothetical protein Rv3683   | NP_218200.1      | 2.23570712                |
| 73397 | H04           | 1000       | Rv1400c  | lipase LipI (lipI)  | NP_215916.1      | 2.391                     |
| 73513 | H05           | 1000       | Rv1949c  | hypothetical protein Rv1949c  | NP_216465.1      | 1.483                     |
| 73173 | H06           | 1009       | Rv1336   | cysteine synthase B CysM (cysM)   | NP_215852.1      | 1.40336967                |
| 73197 | H07           | 1009       | Rv3625c  | cell cycle protein MESJ (mesJ)  | NP_218142.1      | 1.52923687                |
| 73501 | H08           | 1015       | Rv2893   | oxidoreductase  | NP_217409.1      | 1.34679803                |
| 73449 | H09           | 1018       | Rv1538c  | L-aparaginase ansA (ansA)   | NP_216054.1      | 1.35265226                |
| 73401 | H10           | 1027       | Rv1188   | proline dehydrogenase   | NP_215704.1      | 1.39240506                |
| 73537 | H11           | 1027       | Rv2649   | transposase IS6110  | NP_217165.1      | 2.3962999                 |
| 73241 | H12           | 1027       | Rv3382c  | LYTB-like protein LYTB1 (lytB1)   | YP_177967.1      | 1.42161636                |



Table 5: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 5 (ZMTDE), NR-19641

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 73387 | A01           | 1030       | Rv1681   | molybdopterin biosynthesis protein MoeX   | NP_216197.1      | 2.621359223               |
| 73419 | A02           | 1030       | Rv3694c  | transmembrane protein   | NP_218211.1      | 3.186407767               |
| 73351 | A03           | 1033       | Rv3261   | LPPG:FO 2-phospho-L-lactate transferase   | NP_217778.1      | 1.181994192               |
| 73165 | A04           | 1033       | Rv3464   | dTDP-glucose 4,6-dehydratase RMLB   | NP_217981.1      | 1.460793804               |
| 73251 | A05           | 1036       | Rv1285   | sulfate adenylyltransferase subunit 2   | NP_215801.1      | 3.283783784               |
| 73790 | A06           | 1039       | Rv2424c  | transposase   | NP_216940.1      | 3.204042348               |
| 73767 | A07           | 1039       | Rv3001c  | ketol-acid reductoisomerase   | NP_217517.1      | 3.769008662               |
| 73743 | A08           | 1042       | Rv1912c  | oxidoreductase FADB5  | NP_216428.1      | 1.657389635               |
| 73802 | A09           | 1060       | Rv0129c  | secreted antigen 85-C FBPC (85C) (antigen 85 complex C) (AG58C) (MycolyI transferase 85C) (fibronectin-binding protein C) | YP_177694.1      | 2.737735849               |
| 73748 | A10           | 1060       | Rv0885   | hypothetical protein  | NP_215400.1      | 1.63490566                |
| 73834 | A11           | 1060       | Rv3194c  | hypothetical protein  | NP_217710.1      | 3.544339623               |
| 73898 | A12           | 1062       | Rv2568c  | hypothetical protein  | NP_217084.1      | 2.425612053               |
| 73787 | B01           | 1063       | Rv1043c  | hypothetical protein  | NP_215559.1      | 3.645343368               |
| 73705 | B02           | 1072       | Rv2592c  | Holliday junction DNA helicase RuvB   | NP_217108.1      | 2.014925373               |
| 73711 | B03           | 1078       | Rv0536   | UDP-glucose 4-epimerase   | YP_177737.1      | 3.130797774               |
| 73878 | B04           | 1078       | Rv1168c  | PPE family protein  | YP_177791.1      | 1.386827458               |
| 73761 | B05           | 1078       | Rv1520   | sugar transferase   | NP_216036.1      | 2.045454545               |
| 73679 | B06           | 1078       | Rv3056   | DNA polymerase IV   | NP_217572.1      | 3.046382189               |
| 73633 | B07           | 1081       | Rv0791c  | hypothetical protein  | NP_215306.1      | 2.061054579               |
| 73736 | B08           | 1081       | Rv1523   | methyltransferase   | NP_216039.1      | 1.55226642                |
| 73755 | B09           | 1081       | Rv2167c  | transposase   | NP_216683.1      | 3.183163737               |
| 73830 | B10           | 1087       | Rv0072   | glutamine-transport transmembrane protein ABC transporter   | NP_214586.1      | 3.530818767               |
| 73567 | B11           | 1096       | Rv3659c  | hypothetical protein  | YP_178003.1      | 2.832116788               |
| 73883 | B12           | 1099       | Rv1940   | riboflavin biosynthesis protein ribA1 (GTP cyclohydrolase II)   | YP_177851.1      | 3.295723385               |
| 73541 | C01           | 1105       | Rv0125   | serine protease PepA  | NP_214639.1      | 1.31040724                |
| 73674 | C02           | 1105       | Rv2571c  | transmembrane alanine and valine and leucine rich protein   | NP_217087.1      | 2.857918552               |
| 73694 | C03           | 1108       | Rv2777c  | hypothetical protein  |                  | 1.324909747               |
| 73557 | C04           | 1111       | Rv2678c  | uroporphyrinogen decarboxylase  | NP_217194.1      | 1.96039604                |
| 73682 | C05           | 1114       | Rv3586   | DNA integrity scanning protein DisA   | NP_218103.1      | 3.527827648               |
| 73686 | C06           | 1117       | Rv1184c  | hypothetical protein  | NP_215700.1      | 1.368845121               |
| 73779 | C07           | 1117       | Rv2156c  | phospho-N-acetylmuramoyl-pentapeptide-transferase   | NP_216672.1      | 3.290062668               |
| 73915 | C08           | 1117       | Rv3044   | FEIII-dicitrate-binding periplasmic lipoprotein   | NP_217560.1      | 3.347358997               |
| 73855 | C09           | 1120       | Rv3035   | hypothetical protein  | NP_217551.1      | 2.814285714               |
| 73895 | C10           | 1126       | Rv0542c  | O-succinylbenzoic acid--CoA ligase  | NP_215056.1      | 2.376554174               |
| 73798 | C11           | 1132       | Rv2231c  | hypothetical protein  | NP_216747.1      | 1.348939929               |
| 73630 | C12           | 1132       | Rv3468c  | dTDP-glucose 4,6-dehydratase  | YP_177974.1      | 3.617491166               |
| 73647 | D01           | 1135       | Rv1787   | PPE family protein  | YP_177833.1      | 2.903964758               |
| 73922 | D02           | 1138       | Rv3921c  | putative inner membrane protein translocase component YidC  | NP_218438.1      | 2.775922671               |
| 73614 | D03           | 1141       | Rv0205   | transmembrane protein   | NP_214719.1      | 2.862401402               |
| 73824 | D04           | 1147       | Rv1936   | monooxygenase   | NP_216452.1      | 1.401918047               |
| 73723 | D05           | 1156       | Rv2535c  | cytoplasmic peptidase PepQ  | NP_217051.1      | 3.553633218               |
| 73619 | D06           | 1156       | Rv2856   | nickel-transport integral membrane protein  | NP_217372.1      | 3.128027682               |
| 73639 | D07           | 1159       | Rv1516c  | sugar transferase   | NP_216032.2      | 3.391716997               |
| 73874 | D08           | 1165       | Rv2089c  | dipeptidase PepE  | NP_216605.1      | 1.32360515                |
| 73643 | D09           | 1168       | Rv0433   | carboxylate-amine ligase  | NP_214947.1      | 2.906678082               |
| 73597 | D10           | 1168       | Rv2439c  | gamma-glutamyl kinase   | NP_216955.1      | 1.927226027               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 73657 | D11           | 1171       | Rv1479   | transcriptional regulatory protein MOXR1                                    | YP_177816.1      | 1.935952178               |
| 73815 | D12           | 1171       | Rv3562   | acyl-CoA dehydrogenase FADE31   | NP_218079.1      | 3.108454313               |
| 73826 | E01           | 1174       | Rv0557   | mannosyltransferase PIMB  | NP_215071.1      | 3.27427598                |
| 73739 | E02           | 1177       | Rv2150c  | cell division protein FtsZ  | NP_216666.1      | 3.204757859               |
| 73794 | E03           | 1177       | Rv2184c  | hypothetical protein  | NP_216700.1      | 1.23364486                |
| 73689 | E04           | 1180       | Rv0062   | endo-1,4-beta-glucanase   | YP_177689.1      | 1.902542373               |
| 73918 | E05           | 1183       | Rv2951c  | oxidoreductase  | NP_217467.1      | 1.284023669               |
| 73850 | E06           | 1186       | Rv3161c  | dioxygenase   | NP_217677.1      | 1.336424958               |
| 73752 | E07           | 1189       | Rv0628c  | enoyl-CoA hydratase   | NP_215146.1      | 1.347350715               |
| 73671 | E08           | 1189       | Rv3332   | N-acetylglucosamine-6-phosphate deacetylase                                 | NP_217849.1      | 3.110176619               |
| 73583 | E09           | 1192       | Rv2164c  | hypothetical protein  | NP_216680.1      | 3.367449664               |
| 73627 | E10           | 1192       | Rv3495c  | MCE-family lipoprotein LprN   | NP_218012.1      | 2.944630872               |
| 73758 | E11           | 1195       | Rv2190c  | hypothetical protein Rv2190c  | NP_216706.1      | 2.389958159               |
| 73809 | E12           | 1198       | Rv0115   | D-alpha-D-heptose-7-phosphate kinase  | NP_214629.1      | 1.446577629               |
| 73902 | F01           | 1198       | Rv1569   | 8-amino-7-oxononanoate synthase   | YP_177822.1      | 3.136894825               |
| 73807 | F02           | 1198       | Rv3540c  | lipid-transfer protein  | NP_218057.1      | 2.939899833               |
| 73714 | F03           | 1198       | Rv3556c  | acetyl-CoA acetyltransferase  | NP_218073.1      | 3.373956594               |
| 73866 | F04           | 1201       | Rv2868c  | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase                        | NP_217384.1      | 3.331390508               |
| 73546 | F05           | 1207       | Rv0823c  | transcriptional regulatory protein  | NP_215338.1      | 2.788732394               |
| 73729 | F06           | 1207       | Rv3305c  | N-acyl-L-amino acid amidohydrolase  | YP_177955.1      | 1.694283347               |
| 74077 | F07           | 1210       | Rv2072c  | precorrin-6y methyltransferase CobL   | NP_216588.1      | 2.924793388               |
| 73980 | F08           | 1210       | Rv3860   | hypothetical protein  | NP_218377.1      | 1.442975207               |
| 73989 | F09           | 1213       | Rv1196   | PPE family protein  | YP_177795.1      | 1.981038747               |
| 74152 | F10           | 1213       | Rv3546   | acetyl-CoA acetyltransferase  | NP_218063.1      | 1.480626546               |
| 74101 | F11           | 1219       | Rv1131   | citrate synthase  | NP_215647.1      | 2.671862182               |
| 74125 | F12           | 1219       | Rv1372   | hypothetical protein  | YP_177803.1      | 2.40607055                |
| 74083 | G01           | 1219       | Rv1785c  | cytochrome P450 143   | NP_216301.1      | 3.007383101               |
| 74173 | G02           | 1219       | Rv2495c  | branched-chain alpha-keto acid dehydrogenase subunit E2                     | NP_217011.1      | 2.673502871               |
| 74203 | G03           | 1222       | Rv2500c  | acyl-CoA dehydrogenase  | NP_217016.1      | 3.103109656               |
| 73985 | G04           | 1225       | Rv0400c  | acyl-CoA dehydrogenase FADE7  | NP_214914.1      | 1.192653061               |
| 74250 | G05           | 1225       | Rv3618   | monooxygenase   | NP_218135.1      | 2.10122449                |
| 74085 | G06           | 1228       | Rv0694   | L-lactate dehydrogenase (cytochrome) LldD1                                  | NP_215208.1      | 1.199511401               |
| 73932 | G07           | 1228       | Rv2276   | cytochrome P450 121 CYP121  | NP_216792.1      | 1.457654723               |
| 74217 | G08           | 1231       | Rv2723   | integral membrane protein   | NP_217239.1      | 1.086108855               |
| 74137 | G09           | 1234       | Rv3778c  | aminotransferase  | NP_218295.1      | 1.06726094                |
| 74145 | G10           | 1237       | Rv2188c  | hypothetical protein  | NP_216704.2      | 2.73807599                |
| 73997 | G11           | 1240       | Rv1812c  | dehydrogenase   | NP_216328.1      | 3.044354839               |
| 74047 | G12           | 1243       | Rv3644c  | DNA polymerase III subunit delta'   | NP_218161.1      | 3.585679807               |
| 73946 | H01           | 1246       | Rv0593   | MCE-family lipoprotein LprL   | NP_215107.1      | 1.33788122                |
| 74302 | H02           | 1246       | Rv1627c  | lipid-transfer protein  | NP_216143.1      | 1.337078652               |
| 74117 | H03           | 1249       | Rv2542   | hypothetical protein  | NP_217058.1      | 2.15692554                |
| 74299 | H04           | 1252       | Rv1302   | undecapaprenyl-phosphate alpha-N-acetyl-glucosaminyltransferase             | NP_215818.1      | 3.090255591               |
| 73949 | H05           | 1252       | Rv1653   | bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein | NP_216169.1      | 2.748402556               |
| 74035 | H06           | 1255       | Rv1074c  | acetyl-CoA acetyltransferase  | NP_215590.1      | 3.000796813               |
| 74281 | H07           | 1255       | Rv1256c  | cytochrome P450 130 CYP130  | NP_215772.1      | 1.152191235               |
| 74003 | H08           | 1255       | Rv3330   | penicillin-binding protein DacB1  | NP_217847.1      | 3.419123506               |
| 74258 | H09           | 1261       | Rv2067c  | hypothetical protein  | NP_216583.1      | 2.087232355               |
| 74210 | H10           | 1261       | Rv3786c  | hypothetical protein  | NP_218303.1      | 2.069785884               |
| 74058 | H11           | 1264       | Rv2518c  | lipoprotein LppS  | NP_217034.1      | 2.053797468               |
| 74141 | H12           | 1267       | Rv3640c  | transposase   | NP_218157.1      | 1.055248619               |

Table 6: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 6 (ZMTDF), NR-19642

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 73969 | A01           | 1270       | Rv1968   | MCE-family protein MCE3C (mce3C)  | NP_216484.1      | 2.71259843                |
| 74230 | A02           | 1270       | Rv2153c  | undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase (murG) | NP_216669.1      | 1.29133858                |
| 74007 | A03           | 1270       | Rv3899c  | hypothetical protein Rv3899c  | NP_218416.1      | 3.44251969                |
| 73981 | A04           | 1273       | Rv0597c  | hypothetical protein Rv0597c  | NP_215111.1      | 1.17910448                |
| 74245 | A05           | 1276       | Rv0914c  | acetyl-CoA acetyltransferase  | NP_215429.1      | 2.92319749                |
| 74278 | A06           | 1279       | Rv2627c  | hypothetical protein Rv2627c  | NP_217143.1      | 2.08131353                |
| 74153 | A07           | 1279       | Rv2943   | IS1533 transposase  | NP_217459.1      | 2.69898358                |
| 74011 | A08           | 1279       | Rv3578   | arsenical PUMP integral membrane protein ArsB2 (arsB2)                                  | NP_218095.1      | 1.30492572                |
| 74093 | A09           | 1279       | Rv3621c  | PPE family protein (PPE65)  | YP_177998.1      | 2.57154027                |
| 74105 | A10           | 1279       | Rv3712   | ligase  | NP_218229.1      | 2.84519156                |
| 73940 | A11           | 1282       | Rv1872c  | L-lactate dehydrogenase (cytochrome) LldD2 (lldD2)                                      | NP_216388.1      | 1.14898596                |
| 74242 | A12           | 1285       | Rv3775   | lipase LipE (lipE)  | NP_218292.1      | 2.06692607                |
| 74161 | B01           | 1291       | Rv0545c  | inorganic phosphate transporter (pitA)  | NP_215059.1      | 1.15491867                |
| 74053 | B02           | 1300       | Rv1426c  | esterase LipO (lipO)  | NP_215942.1      | 1.76                      |
| 74067 | B03           | 1303       | Rv3190c  | hypothetical protein Rv3190c  | NP_217706.1      | 3.09593246                |
| 74071 | B04           | 1309       | Rv0915c  | PPE family protein (PPE14)  | YP_177765.1      | 3.12605042                |
| 73995 | B05           | 1313       | Rv1969   | MCE-family protein MCE3D (mce3D)  | NP_216485.1      | 3.09444021                |
| 74051 | B06           | 1318       | Rv2677c  | protoporphyrinogen Oxidase (hemY)   | YP_177675.1      | 1.82397572                |
| 74305 | B07           | 1324       | Rv1771   | oxidoreductase  | NP_216287.1      | 1.10574018                |
| 74221 | B08           | 1324       | Rv2266   | cytochrome P450 124 CYP124 (cyp124)   | NP_216782.1      | 2.78776435                |
| 73936 | B09           | 1333       | Rv0896   | type II citrate synthase (glfA)   | NP_215411.1      | 1.38934734                |
| 74273 | B10           | 1339       | Rv1095   | PhoH-like protein PhoH2 (phosphate starvation-inducible protein PsiH) (phoH)            | NP_215611.1      | 2.6982823                 |
| 74013 | B11           | 1339       | Rv2673   | integral membrane protein   | NP_217189.1      | 2.78416729                |
| 73941 | B12           | 1339       | Rv3545c  | cytochrome P450 125 (cyp125)  | NP_218062.1      | 2.74159821                |
| 74295 | C01           | 1342       | Rv0576   | ArsR family transcriptional regulator   | NP_215090.1      | 2.78539493                |
| 74089 | C02           | 1345       | Rv1232c  | hypothetical protein Rv1232c  | NP_215748.1      | 2.20817844                |
| 73958 | C03           | 1345       | Rv1783   | hypothetical protein Rv1783   | NP_216299.1      | 2.07806691                |
| 74019 | C04           | 1351       | Rv1568   | adenosylmethionine--8-amino-7-oxononanoate transaminase (bioA)                          | NP_216084.1      | 2.45965951                |
| 74027 | C05           | 1354       | Rv2246   | 3-oxoacyl-(acyl carrier protein) synthase II (kasB)                                     | NP_216762.1      | 2.95199409                |
| 74185 | C06           | 1354       | Rv2681   | hypothetical protein Rv2681   | NP_217197.1      | 2.6661743                 |
| 74234 | C07           | 1357       | Rv0449c  | hypothetical protein Rv0449c  | NP_214963.1      | 2.0412675                 |
| 74285 | C08           | 1357       | Rv2041c  | sugar-binding lipoprotein   | NP_216557.1      | 2.76934414                |
| 73926 | C09           | 1360       | Rv2318   | periplasmic sugar-binding lipoprotein UspC (uspC)                                       | NP_216834.1      | 1.94926471                |
| 73962 | C10           | 1360       | Rv3693   | hypothetical protein Rv3693   | NP_218210.1      | 1.82647059                |
| 74445 | C11           | 1363       | Rv0393   | 13E12 repeat family protein   | NP_214907.1      | 2.26118855                |
| 74403 | C12           | 1375       | Rv2508c  | hypothetical protein Rv2508c  | NP_217024.1      | 2.76363636                |
| 74646 | D01           | 1378       | Rv0902c  | two component sensor histidine kinase PRRB (prbB)                                       | NP_215417.1      | 2.00435414                |
| 74542 | D02           | 1378       | Rv3371   | hypothetical protein Rv3371   | NP_217888.1      | 1.73222061                |
| 74381 | D03           | 1387       | Rv3835   | hypothetical protein Rv3835   | NP_218352.1      | 2.58399423                |
| 74326 | D04           | 1405       | Rv0955   | integral membrane protein   | NP_215470.1      | 2.46690391                |
| 74449 | D05           | 1405       | Rv1257c  | oxidoreductase  | NP_215773.1      | 3.59572954                |
| 74613 | D06           | 1417       | Rv2791c  | transposase   | NP_217307.1      | 3.27875794                |
| 74642 | D07           | 1420       | Rv3881c  | hypothetical protein Rv3881c  | NP_218398.1      | 2.66056338                |
| 74511 | D08           | 1423       | Rv1726   | oxidoreductase  | NP_216242.1      | 4.11665495                |
| 74661 | D09           | 1423       | Rv2615c  | PE-PGRS family protein (PE_PGRS45)  | YP_177895.1      | 2.91848208                |
| 74333 | D10           | 1429       | Rv0096   | PPE family protein (PPE1)   | YP_177690.1      | 3.31980406                |
| 74621 | D11           | 1429       | Rv0573c  | nicotinate phosphoribosyltransferase  | NP_215087.1      | 3.51574528                |
| 74371 | D12           | 1429       | Rv1537   | DNA polymerase IV (dinX)  | NP_216053.2      | 3.5703289                 |
| 74386 | E01           | 1432       | Rv0983   | serine protease PepD (pepD)   | NP_215498.1      | 2.47835196                |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 74349 | E02           | 1432       | Rv1077   | cystathionine beta-synthase CBS (Serine sulfhydryase) (Beta-thionase) (hemoprotein H-450) (cbs)              | YP_177782.1      | 3.2122905                 |
| 74658 | E03           | 1435       | Rv0296c  | sulfatase  | YP_177712.1      | 2.58885017                |
| 74549 | E04           | 1438       | Rv2462c  | trigger factor (tig)   | NP_216978.1      | 3.59318498                |
| 74628 | E05           | 1441       | Rv3448   | integral membrane protein  | NP_217965.1      | 1.10825815                |
| 74319 | E06           | 1444       | Rv1614   | prolipoprotein diacylglycerol transferase (lgt)  | NP_216130.1      | 3.64265928                |
| 74577 | E07           | 1444       | Rv3820c  | polyketide synthase associated protein PapA2 (papA2)   | YP_178020.1      | 3.55955679                |
| 74514 | E08           | 1447       | Rv0221   | hypothetical protein Rv0221  | NP_214735.1      | 2.5252246                 |
| 74358 | E09           | 1447       | Rv0261c  | integral membrane nitrite extrusion protein NarK3 (narK3)  | NP_214775.1      | 2.57636489                |
| 74619 | E10           | 1447       | Rv2812   | transposase  | NP_217328.1      | 3.96199032                |
| 74601 | E11           | 1447       | Rv3580c  | cysteinyI-tRNA synthetase (cysS)   | YP_177992.1      | 1.02280581                |
| 74397 | E12           | 1450       | Rv0392c  | membrane NADH dehydrogenase (ndhA)   | NP_214906.1      | 1.01172414                |
| 74650 | F01           | 1450       | Rv2522c  | hypothetical protein Rv2522c   | NP_217038.1      | 1.93103448                |
| 74683 | F02           | 1450       | Rv2974c  | hypothetical protein Rv2974c   | NP_217490.1      | 2.62758621                |
| 74606 | F03           | 1450       | Rv3450c  | hypothetical protein Rv3450c   | NP_217967.1      | 2.5937931                 |
| 74671 | F04           | 1459       | Rv1576c  | phiRV1 phage protein   | NP_216092.1      | 3.91432488                |
| 74421 | F05           | 1459       | Rv2888c  | Amidase (amiC)   | NP_217404.1      | 3.60246744                |
| 74537 | F06           | 1462       | Rv1098c  | fumarate hydratase (fumC)  | NP_215614.1      | 3.02941176                |
| 74379 | F07           | 1465       | Rv2655c  | phiRv2 prophage protein  | NP_217171.1      | 3.90443686                |
| 74673 | F08           | 1465       | Rv3375   | amidase AmiD (amiD)  | NP_217892.1      | 3.46416382                |
| 74405 | F09           | 1465       | Rv3764c  | two component sensor kinase  | NP_218281.1      | 3.48191126                |
| 74534 | F10           | 1480       | Rv2425c  | hypothetical protein Rv2425c   | NP_216941.1      | 2.23243243                |
| 74589 | F11           | 1480       | Rv3869   | hypothetical protein Rv3869  | NP_218386.1      | 2.76216216                |
| 74630 | F12           | 1480       | Rv3907c  | poly(A) polymerase (pcnA)  | YP_178026.1      | 2.49324324                |
| 74559 | G01           | 1483       | Rv0591   | MCE-family protein MCE2C (mce2C)   | NP_215105.1      | 3.55428186                |
| 74354 | G02           | 1483       | Rv2434c  | transmembrane protein  | NP_216950.1      | 2.57518543                |
| 74495 | G03           | 1495       | Rv1844c  | 6-phosphogluconate dehydrogenase (gnd1)  | YP_177848.1      | 3.63745819                |
| 74419 | G04           | 1498       | Rv1129c  | transcriptional regulator protein  | NP_215645.1      | 3.81041389                |
| 74361 | G05           | 1501       | Rv0442c  | PPE family protein (PPE10)   | YP_177726.1      | 3.39573618                |
| 74529 | G06           | 1501       | Rv1226c  | hypothetical protein Rv1226c   | NP_215742.1      | 3.42771486                |
| 74637 | G07           | 1507       | Rv2127   | L-asparagine permease ansP1 (ansP1)  | YP_177863.1      | 3.3384207                 |
| 74329 | G08           | 1507       | Rv3854c  | monooxygenase ETHA (ethA)  | NP_218371.1      | 3.52753816                |
| 74677 | G09           | 1516       | Rv0143c  | transmembrane protein  | NP_214657.1      | 3.26253298                |
| 74505 | G10           | 1516       | Rv2519   | PE family protein (PE26)   | YP_177888.1      | 3.18205805                |
| 74437 | G11           | 1516       | Rv3059   | cytochrome P450 136 (cyp136)   | NP_217575.1      | 2.94129288                |
| 74434 | G12           | 1519       | Rv0343   | isoniazid inductible gene protein INIC (iniC)  | NP_214857.1      | 2.57077024                |
| 74690 | H01           | 1519       | Rv3303c  | flavoprotein disulfide reductase (lpdA)  | NP_217820.1      | 2.3805135                 |
| 74502 | H02           | 1522       | Rv0255c  | cobyric acid synthase (cobQ1)  | YP_177703.1      | 2.4434954                 |
| 74429 | H03           | 1522       | Rv1867   | acetyl-CoA acetyltransferase   | NP_216383.1      | 3.08081472                |
| 74413 | H04           | 1522       | Rv2152c  | UDP-N-acetylmuramate--L-alanine ligase (murC)  | NP_216668.1      | 3.53088042                |
| 74321 | H05           | 1522       | Rv3011c  | aspartyl/glutamyl-tRNA amidotransferase subunit A (gatA)   | NP_217527.1      | 2.51445466                |
| 74465 | H06           | 1522       | Rv3293   | piperideine-6-carboxylic acid dehydrogenase  | YP_177953.1      | 2.84362681                |
| 74485 | H07           | 1525       | Rv0904c  | putative acetyl-coenzyme A carboxylase carboxyl transferase (subunit BETA) ACCD3 (ACCASE BETA chain) (accD3) | NP_215419.1      | 3.33377049                |
| 74598 | H08           | 1525       | Rv2725c  | GTP-binding protein HflX (hflX)  | NP_217241.1      | 2.54557377                |
| 74341 | H09           | 1525       | Rv3083   | monooxygenase  | NP_217599.1      | 3.32131148                |
| 74930 | H10           | 1525       | Rv3175   | amidase  | NP_217691.1      | 2.44918033                |
| 74890 | H11           | 1528       | Rv0109   | PE-PGRS family protein (PE_PGRS1)  | YP_177692.1      | 1.56479058                |
| 74945 | H12           | 1531       | Rv1376   | hypothetical protein Rv1376  | NP_215892.1      | 3.29196604                |

Table 7: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 7 (ZMTDG), NR-19643

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 74787 | A01           | 1534       | Rv2004c  | hypothetical protein   | NP_216520.1      | 3.322685789               |
| 74777 | A02           | 1540       | Rv3490   | alpha,alpha-trehalose-phosphate synthase                     | NP_218007.1      | 3.507142857               |
| 74918 | A03           | 1549       | Rv0336   | 13E12 repeat family protein                                  | NP_214850.1      | 2.276307295               |
| 74957 | A04           | 1555       | Rv0895   | hypothetical protein   | NP_215410.1      | 3.427652733               |
| 74903 | A05           | 1558       | Rv0147   | aldehyde dehydrogenase                                       | NP_214661.1      | 3.486521181               |
| 74866 | A06           | 1561       | Rv3062   | ATP-dependent DNA ligase                                     | NP_217578.1      | 3.624599616               |
| 74906 | A07           | 1561       | Rv3561   | acyl-CoA synthetase  | NP_218078.1      | 2.864189622               |
| 75055 | A08           | 1564       | Rv0592   | MCE-family protein MCE2D                                     | NP_215106.1      | 4.098465473               |
| 74893 | A09           | 1567       | Rv3698   | hypothetical protein   | NP_218215.1      | 5.124441608               |
| 74971 | A10           | 1567       | Rv3887c  | transmembrane protein  | NP_218404.1      | 4.257817486               |
| 74921 | A11           | 1573       | Rv0234c  | succinic semialdehyde dehydrogenase                          | NP_216247.2      | 4.27972028                |
| 74810 | A12           | 1576       | Rv2209   | integral membrane protein                                    | NP_216725.1      | 3.556472081               |
| 74897 | B01           | 1576       | Rv2733c  | hypothetical protein   | NP_217249.1      | 3.277284264               |
| 74697 | B02           | 1582       | Rv2414c  | hypothetical protein   | NP_216930.1      | 5.06573957                |
| 75046 | B03           | 1585       | Rv0171   | MCE-family protein MCE1C                                     | NP_214685.1      | 2.998107256               |
| 75041 | B04           | 1585       | Rv2213   | leucyl aminopeptidase  | NP_216729.1      | 5.203154574               |
| 74833 | B05           | 1585       | Rv2329c  | nitrite extrusion protein 1 NarK1                            | NP_216845.1      | 3.013249211               |
| 74994 | B06           | 1585       | Rv3509c  | hypothetical protein   | NP_218026.1      | 3.176656151               |
| 75037 | B07           | 1588       | Rv2174   | integral membrane protein                                    | NP_216690.1      | 4.08186398                |
| 74737 | B08           | 1594       | Rv0453   | PPE family protein   | YP_177727.1      | 2.640526976               |
| 74938 | B09           | 1597       | Rv3776   | hypothetical protein   | NP_218293.1      | 3.046963056               |
| 74758 | B10           | 1600       | Rv2223c  | exported protease  | NP_216739.1      | 3.515                     |
| 75058 | B11           | 1603       | Rv1345   | long-chain-fatty-acid--                                      | NP_215861.1      | 3.670617592               |
| 74769 | B12           | 1612       | Rv2154c  | FtsW-like protein FtsW                                       | NP_216670.1      | 4.265508685               |
| 74849 | C01           | 1612       | Rv3049c  | monooxygenase  | NP_217565.1      | 2.905086849               |
| 74713 | C02           | 1621       | Rv3211   | ATP-dependent RNA helicase RhlE                              | NP_217727.1      | 3.312152992               |
| 74927 | C03           | 1624       | Rv2672   | secreted protease  | NP_217188.1      | 3.253694581               |
| 74935 | C04           | 1627       | Rv2502c  | acetyl-/propionyl-CoA carboxylase subunit beta               | NP_217018.1      | 3.525507068               |
| 74981 | C05           | 1627       | Rv3737   | transmembrane protein  | NP_218254.1      | 4.163491088               |
| 74855 | C06           | 1636       | Rv0806c  | UDP-glucose-4-epimerase CpsY                                 | NP_215321.1      | 3.647310513               |
| 74989 | C07           | 1642       | Rv3308   | phosphomannomutase   | NP_217825.1      | 3.950669915               |
| 75069 | C08           | 1645       | Rv0897c  | oxidoreductase   | NP_215412.1      | 4.145896657               |
| 74838 | C09           | 1648       | Rv3379c  | 1-deoxy-D-xylulose-5-phosphate synthase                      | NP_217896.1      | 3.52973301                |
| 74843 | C10           | 1651       | Rv3885c  | hypothetical protein   | NP_218402.1      | 4.235614779               |
| 75035 | C11           | 1654       | Rv1186c  | hypothetical protein   | NP_215702.1      | 3.477629988               |
| 74953 | C12           | 1657       | Rv3811   | hypothetical protein   | YP_178018.1      | 3.02051901                |
| 74883 | D01           | 1666       | Rv0672   | acyl-CoA dehydrogenase FADE8                                 | NP_215186.1      | 3.662665066               |
| 74998 | D02           | 1672       | Rv1013   | acyl-CoA synthetase  | NP_215529.1      | 3.003588517               |
| 75005 | D03           | 1684       | Rv1217c  | tetrasin-transport integral membrane protein ABC transporter | NP_215733.1      | 3.866983373               |
| 75074 | D04           | 1687       | Rv2800   | hydrolase  | NP_217316.1      | 3.462359218               |
| 75065 | D05           | 1690       | Rv2100   | hypothetical protein   | NP_216616.1      | 3.956213018               |
| 74789 | D06           | 1696       | Rv0782   | oligopeptidase B   | NP_215295.2      | 4.264150943               |
| 74914 | D07           | 1699       | Rv0946c  | glucose-6-phosphate isomerase                                | NP_215461.1      | 3.380812243               |
| 74782 | D08           | 1702       | Rv0166   | acyl-CoA synthetase  | NP_214680.1      | 3.456521739               |
| 75449 | D09           | 1708       | Rv0256c  | PPE family protein   | YP_177704.1      | 4.266978923               |
| 75125 | D10           | 1729       | Rv1754c  | hypothetical protein   | NP_216270.1      | 4.053209948               |
| 75323 | D11           | 1741       | Rv3245c  | two component sensory transduction histidine kinase MTRB     | NP_217762.1      | 3.998276852               |
| 75289 | D12           | 1753       | Rv1550   | fatty-acid-CoA ligase  | NP_216066.1      | 4.19965773                |
| 75182 | E01           | 1768       | Rv0226c  | transmembrane protein  | NP_214740.1      | 3.182126697               |
| 75393 | E02           | 1774       | Rv1185c  | acyl-CoA synthetase  | NP_215701.1      | 4.117249154               |
| 75317 | E03           | 1786       | Rv3533c  | PPE family protein   | YP_177985.1      | 3.555431131               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 75110 | E04           | 1789       | Rv2565   | hypothetical protein   | NP_217081.1      | 3.474007826               |
| 75142 | E05           | 1792       | Rv3590c  | PE-PGRS family protein   | YP_177993.1      | 1.938616071               |
| 75129 | E06           | 1807       | Rv2088   | transmembrane serine/threonine-protein kinase J                                  | NP_216604.1      | 4.122302158               |
| 75453 | E07           | 1813       | Rv1280c  | periplasmic oligopeptide-binding lipoprotein OppA                                | NP_215796.1      | 4.079426365               |
| 75275 | E08           | 1813       | Rv3635   | transmembrane protein  | NP_218152.1      | 3.237727523               |
| 75262 | E09           | 1828       | Rv2572c  | aspartyl-tRNA synthetase   | NP_217088.1      | 2.791575492               |
| 75410 | E10           | 1843       | Rv0126   | trehalose synthase TRES  | NP_214640.1      | 2.295713511               |
| 75265 | E11           | 1846       | Rv1297   | transcription termination factor Rho   | NP_215813.1      | 2.908992416               |
| 75145 | E12           | 1867       | Rv2115c  | ATPase   | NP_216631.1      | 4.086234601               |
| 75330 | F01           | 1873       | Rv0244c  | acyl-CoA dehydrogenase FADE5   | NP_214758.1      | 2.849973305               |
| 75097 | F02           | 1876       | Rv1281c  | oligopeptide-transport ATP-binding protein ABC transporter OppD                  | NP_215797.1      | 4.065565032               |
| 75351 | F03           | 1885       | Rv1492   | methylmalonyl-CoA mutase small subunit   | NP_216008.1      | 4.187798408               |
| 75083 | F04           | 1885       | Rv2356c  | PPE family protein   | YP_177872.1      | 3.975066313               |
| 75339 | F05           | 1894       | Rv1768   | PE-PGRS family protein   | YP_177832.1      | 2.343189018               |
| 75191 | F06           | 1897       | Rv3884c  | CBXX/CFQX family protein   | NP_218401.1      | 4.112282551               |
| 75375 | F07           | 1900       | Rv1925   | acyl-CoA synthetase  | NP_216441.1      | 3.796315789               |
| 75345 | F08           | 1903       | Rv1551   | glycerol-3-phosphate acyltransferase   | NP_216067.1      | 3.280084078               |
| 75137 | F09           | 1933       | Rv0282   | hypothetical protein   | NP_214796.1      | 3.829280911               |
| 75238 | F10           | 1933       | Rv1272c  | drugs-transport transmembrane ATP-binding protein ABC transporter                | NP_215788.1      | 3.167615106               |
| 75206 | F11           | 1951       | Rv3801c  | acyl-CoA synthetase  | NP_218318.1      | 3.150691953               |
| 75253 | F12           | 1951       | Rv3808c  | bifunctional UDP-galactofuranosyl transferase GLFT                               | NP_218325.1      | 3.897488467               |
| 75333 | G01           | 1954       | Rv2682c  | 1-deoxy-D-xylulose-5-phosphate synthase  | YP_177898.1      | 3.217502559               |
| 75305 | G02           | 1972       | Rv3710   | 2-isopropylmalate synthase   | NP_218227.2      | 3.303245436               |
| 75113 | G03           | 1978       | Rv0248c  | succinate dehydrogenase flavoprotein subunit                                     | NP_214762.1      | 3.364509606               |
| 75219 | G04           | 1978       | Rv1420   | excinuclease ABC subunit C   | NP_215936.1      | 4.003538928               |
| 75367 | G05           | 1981       | Rv2299c  | heat shock protein 90  | NP_216815.1      | 3.467945482               |
| 75193 | G06           | 1993       | Rv3667   | acetyl-CoA synthetase  | NP_218184.1      | 3.538384345               |
| 75327 | G07           | 2008       | Rv2079   | hypothetical protein   | NP_216595.1      | 3.840139442               |
| 75170 | G08           | 2020       | Rv3743c  | cation transporter P-type ATPase CtpJ  | NP_218260.1      | 2.593069307               |
| 75159 | G09           | 2023       | Rv0102   | integral membrane protein  | NP_214616.1      | 3.739495798               |
| 75163 | G10           | 2032       | Rv0931c  | transmembrane serine/threonine-protein kinase D PKND (protein kinase D) (STPK D) | NP_215446.1      | 3.758366142               |
| 75117 | G11           | 2038       | Rv3779   | transmembrane protein alanine and leucine rich                                   | NP_218296.1      | 4.407752699               |
| 75443 | G12           | 2041       | Rv2395   | integral membrane protein  | NP_216911.1      | 4.24399804                |
| 75242 | H01           | 2059       | Rv0457c  | peptidase  | NP_214971.1      | 3.639630889               |
| 75437 | H02           | 2059       | Rv1084   | hypothetical protein   | NP_215600.1      | 4.066537154               |
| 75249 | H03           | 2071       | Rv1836c  | hypothetical protein   | NP_216352.1      | 4.142926123               |
| 75593 | H04           | 2101       | Rv1877   | integral membrane protein  | NP_216393.1      | 4.360780581               |
| 75691 | H05           | 2131       | Rv2326c  | transmembrane ATP-binding protein ABC transporter                                | NP_216842.1      | 3.916001877               |
| 75765 | H06           | 2182       | Rv0120c  | elongation factor G  | NP_214634.1      | 4.250229148               |
| 75579 | H07           | 2203       | Rv1564c  | maltooligosyltrehalose synthase TreX   | YP_177821.1      | 3.860190649               |
| 75622 | H08           | 2212       | Rv1781c  | 4-alpha-glucanotransferase MalQ  | NP_216297.1      | 3.775768535               |
| 75697 | H09           | 2266       | Rv2984   | polyphosphate kinase   | NP_217500.1      | 7.053398058               |
| 75799 | H10           | 2317       | Rv0938   | ATP-dependent DNA ligase   | NP_215453.1      | 3.981009927               |
| 75702 | H11           | 2350       | Rv0969   | metal cation transporter P-type ATPase CtpV                                      | NP_215484.1      | 3.098297872               |
| 75843 | H12           | 2353       | Rv0949   | ATP-dependent DNA helicase II UVRD1  | YP_177772.1      | 3.552911177               |

Table 8: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 8 (ZMTDH), NR-19644

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 75546 | A01           | 2401       | Rv0711   | arylsulfatase AtsA (atsA)  | NP_215225.1      | 4.06247397                |
| 75658 | A02           | 2410       | Rv2583c  | GTP pyrophosphokinase (relA)                                       | NP_217099.1      | 3.27344398                |
| 75758 | A03           | 2425       | Rv0585c  | integral membrane protein  | NP_215099.1      | 3.25113402                |
| 75734 | A04           | 2431       | Rv0908   | metal cation transporter ATPase P-type CtpE (ctpE)                 | NP_215423.1      | 3.65734266                |
| 75822 | A05           | 2464       | Rv1821   | preprotein translocase subunit SecA (secA2)                        | NP_216337.1      | 3.82102273                |
| 75669 | A06           | 2602       | Rv2047c  | hypothetical protein Rv2047c                                       | NP_216563.1      | 7.42928517                |
| 75835 | A07           | 2605       | Rv0987   | adhesion component transport transmembrane protein ABC transporter | NP_215502.1      | 3.72360845                |
| 76013 | A08           | 2914       | Rv0402c  | transmembrane transport protein Mmpl1 (mmpL1)                      | NP_214916.1      | 3.00789293                |
| 75997 | A09           | 2926       | Rv2339   | transmembrane transport protein Mmpl9 (mmpL9)                      | NP_216855.1      | 3.27785373                |
| 75985 | A10           | 2941       | Rv0450c  | transmembrane transport protein Mmpl4 (mmpL4)                      | NP_214964.1      | 3.36688201                |
| 75913 | A11           | 2944       | Rv0507   | transmembrane transport protein Mmpl2 (mmpL2)                      | NP_215021.1      | 3.43546196                |
| 75977 | A12           | 3265       | Rv3479   | hypothetical protein Rv3479  | NP_217996.2      | 3.27105666                |
| 76062 | B01           | 3307       | Rv3823c  | integral membrane transport protein (mmpL8)                        | NP_218340.1      | 3.60931358                |
| 76501 | B02           | 130        | MT1978   | hypothetical protein MT1978  | NP_336436.1      | 2                         |
| 76345 | B03           | 130        | MT3102   | hypothetical protein MT3102  | NP_337617.1      | 2                         |
| 76337 | B04           | 133        | MT1330   | hypothetical protein MT1330  | NP_335777.1      | 2                         |
| 76509 | B05           | 133        | MT1790   | hypothetical protein MT1790  | NP_336249.1      | 2                         |
| 76552 | B06           | 133        | MT2988.1 | hypothetical protein MT2988.1                                      | NP_337501.1      | 2                         |
| 76445 | B07           | 133        | MT3449.2 | hypothetical protein MT3449.2                                      | NP_337979.1      | 2                         |
| 76465 | B08           | 133        | MT3510.1 | hypothetical protein MT3510.1                                      | NP_338034.1      | 2                         |
| 76513 | B09           | 136        | MT0325   | hypothetical protein MT0325  | NP_334733.1      | 2                         |
| 76485 | B10           | 136        | MT0725   | hypothetical protein MT0725  | NP_335141.1      | 2                         |
| 76561 | B11           | 136        | MT0835   | hypothetical protein MT0835  | NP_335263.1      | 2                         |
| 76497 | B12           | 136        | MT1057.1 | hypothetical protein MT1057.1                                      | YP_061208.1      | 2                         |
| 76184 | C01           | 136        | MT1342   | hypothetical protein MT1342  | NP_335790.1      | 2                         |
| 76233 | C02           | 136        | MT2165.1 | hypothetical protein MT2165.1                                      | NP_336634.1      | 2                         |
| 76297 | C03           | 136        | MT2803.1 | tRNA delta(2)-isopentenylpyrophosphate transferase                 | NP_337302.1      | 2                         |
| 76197 | C04           | 139        | MT1627   | hypothetical protein MT1627  | NP_336081.1      | 2                         |
| 76353 | C05           | 139        | MT1717   | hypothetical protein MT1717  | NP_336171.1      | 2                         |
| 76325 | C06           | 139        | MT2460   | hypothetical protein MT2460  | NP_336941.1      | 2                         |
| 76457 | C07           | 139        | MT3580.1 | hypothetical protein MT3580.1                                      | NP_338124.1      | 2                         |
| 76449 | C08           | 142        | MT3653.1 | hypothetical protein MT3653.1                                      | NP_338199.1      | 2                         |
| 76533 | C09           | 142        | MT3952   | hypothetical protein MT3952  | NP_338505.1      | 2                         |
| 76241 | C10           | 142        | MT3962   | hypothetical protein MT3962  | NP_338515.1      | -                         |
| 76213 | C11           | 145        | MT0827   | hypothetical protein MT0827  | NP_335255.1      | 2                         |
| 76189 | C12           | 145        | MT1759   | hypothetical protein MT1759  | NP_336217.1      | 2                         |
| 76489 | D01           | 145        | MT2011   | hypothetical protein MT2011  | NP_336469.1      | 2                         |
| 76521 | D02           | 148        | MT0450   | hypothetical protein MT0450  | NP_334859.1      | 2                         |
| 76357 | D03           | 148        | MT1107   | hypothetical protein MT1107  | NP_335549.1      | 2                         |
| 76280 | D04           | 148        | MT2364.1 | hypothetical protein MT2364.1                                      | NP_336837.1      | 2                         |
| 76421 | D05           | 148        | MT3520   | hypothetical protein MT3520  | NP_338044.1      | 2                         |
| 76477 | D06           | 151        | MT2438   | hypothetical protein MT2438  | NP_336918.1      | 2                         |
| 76229 | D07           | 154        | MT1367.1 | hypothetical protein MT1367.1                                      | NP_335817.1      | 2                         |
| 76462 | D08           | 154        | MT1909   | hypothetical protein MT1909  | NP_336366.1      | 2                         |
| 76365 | D09           | 154        | MT3427.1 | hypothetical protein MT3427.1                                      | NP_337956.1      | 2                         |
| 76246 | D10           | 157        | MT1116   | hypothetical protein MT1116  | NP_335558.1      | 2                         |
| 76270 | D11           | 157        | MT1166   | hypothetical protein MT1166  | NP_335609.1      | 2                         |
| 76437 | D12           | 157        | MT1285   | hypothetical protein MT1285  | NP_335729.1      | 2                         |
| 76201 | E01           | 157        | MT1488   | hypothetical protein MT1488  | NP_335937.1      | 2                         |
| 76261 | E02           | 157        | MT3449.1 | hypothetical protein MT3449.1                                      | NP_337978.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------------|------------------|---------------------------|
| 76520 | E03           | 160        | MT0598   | hypothetical protein MT0598   | NP_335007.1      | 1.98125                   |
| 76193 | E04           | 160        | MT1096.2 | hypothetical protein MT1096.2 | NP_335538.1      | -                         |
| 76369 | E05           | 160        | MT1760   | hypothetical protein MT1760   | NP_336218.1      | 2                         |
| 76429 | E06           | 160        | MT2027   | hypothetical protein MT2027   | NP_336488.1      | 2                         |
| 76537 | E07           | 163        | MT0159   | hypothetical protein MT0159   | NP_334569.1      | 2                         |
| 76331 | E08           | 166        | MT2514   | hypothetical protein MT2514   | NP_336997.1      | 2                         |
| 76341 | E09           | 166        | MT3145.1 | hypothetical protein MT3145.1 | NP_337664.1      | 2                         |
| 76209 | E10           | 169        | MT0291.2 | hypothetical protein MT0291.2 | NP_334699.1      | 2                         |
| 76362 | E11           | 169        | MT2722   | hypothetical protein MT2722   | NP_337222.1      | 2                         |
| 76333 | E12           | 169        | MT3762   | hypothetical protein MT3762   | NP_338312.1      | 2.83431953                |
| 76413 | F01           | 172        | MT3273   | hypothetical protein MT3273   | NP_337799.1      | 2                         |
| 76321 | F02           | 172        | MT3378   | hypothetical protein MT3378   | NP_337906.1      | -                         |
| 76405 | F03           | 172        | MT3744   | hypothetical protein MT3744   | NP_338290.1      | 2                         |
| 76301 | F04           | 175        | MT0009   | hypothetical protein MT0009   | NP_334417.1      | 2                         |
| 76305 | F05           | 175        | MT0521.1 | hypothetical protein MT0521.1 |                  | 1.92                      |
| 76397 | F06           | 175        | MT1822   | hypothetical protein MT1822   | NP_336278.1      | -                         |
| 76556 | F07           | 175        | MT2015   | hypothetical protein MT2015   | NP_336473.1      | 2                         |
| 76317 | F08           | 178        | MT0768.1 | hypothetical protein MT0768.1 | NP_335190.1      | 2                         |
| 76417 | F09           | 178        | MT1025.1 | hypothetical protein MT1025.1 | NP_335459.1      | -                         |
| 76442 | F10           | 178        | MT1401   | hypothetical protein MT1401   | NP_335850.1      | 2                         |
| 76544 | F11           | 178        | MT3032   | hypothetical protein MT3032   | NP_337544.1      | 2                         |
| 76377 | F12           | 178        | MT3135   | hypothetical protein MT3135   | NP_337652.1      | 2                         |
| 76381 | G01           | 178        | MT3207   | hypothetical protein MT3207   | NP_337733.1      | 2                         |
| 76274 | G02           | 184        | MT0771   | hypothetical protein MT0771   | NP_335193.1      | 2                         |
| 76259 | G03           | 184        | MT1192   | hypothetical protein MT1192   | NP_335635.1      | 2                         |
| 76285 | G04           | 184        | MT2653   | hypothetical protein MT2653   | NP_337152.1      | 2                         |
| 76253 | G05           | 184        | MT2993   | hypothetical protein MT2993   | NP_337506.1      | 1.60869565                |
| 76266 | G06           | 187        | MT0204.1 | hypothetical protein MT0204.1 | NP_334611.1      | 2                         |
| 76185 | G07           | 187        | MT1798   | hypothetical protein MT1798   | NP_336257.1      | 2                         |
| 76393 | G08           | 187        | MT2547.2 | hypothetical protein MT2547.2 | NP_337035.1      | 2                         |
| 76228 | G09           | 190        | MT0012   | hypothetical protein MT0012   | NP_334420.1      | 2                         |
| 76402 | G10           | 190        | MT0494   | hypothetical protein MT0494   | NP_334903.1      | -                         |
| 76281 | G11           | 190        | MT2007   | hypothetical protein MT2007   | NP_336465.1      | 1.91052632                |
| 76505 | G12           | 190        | MT2371   | hypothetical protein MT2371   | NP_336850.1      | 2                         |
| 76545 | H01           | 190        | MT3921   | hypothetical protein MT3921   | NP_338473.1      | 2                         |
| 76453 | H02           | 193        | MT0291.1 | hypothetical protein MT0291.1 | NP_334698.1      | 2                         |
| 76409 | H03           | 193        | MT1650   | hypothetical protein MT1650   | NP_336105.1      | 2                         |
| 76482 | H04           | 193        | MT2370.1 | hypothetical protein MT2370.1 | NP_336847.1      | -                         |
| 76385 | H05           | 193        | MT3535   | hypothetical protein MT3535   | NP_338061.1      | 2                         |
| 76557 | H06           | 196        | MT2736.1 | hypothetical protein MT2736.1 | NP_337238.1      | 2                         |
| 76530 | H07           | 196        | MT3131.1 | hypothetical protein MT3131.1 | NP_337648.1      | 2                         |
| 76221 | H08           | 199        | MT0932   | hypothetical protein MT0932   | NP_335365.1      | 2                         |
| 76351 | H09           | 199        | MT3718.2 | hypothetical protein MT3718.2 | NP_338265.1      | 2                         |
| 76250 | H10           | 202        | MT3210   | hypothetical protein MT3210   | NP_337736.1      | 2                         |
| 76433 | H11           | 205        | MT1821.1 | hypothetical protein MT1821.1 | NP_336277.1      | 2                         |
| 76218 | H12           | 205        | MT1839.1 | hypothetical protein MT1839.1 | NP_336297.1      | 2                         |

Table 9: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 9 (ZMTDI), NR-19645

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------------|------------------|---------------------------|
| 76473 | A01           | 205        | MT3284   | hypothetical protein MT3284   | NP_337811.1      | 1.11707317                |
| 76205 | A02           | 208        | MT2334.1 | hypothetical protein MT2334.1 | NP_336804.1      | 2                         |
| 76309 | A03           | 208        | MT2405   | hypothetical protein MT2405   | NP_336884.1      | 2                         |
| 76373 | A04           | 208        | MT2558   | hypothetical protein MT2558   | NP_337048.1      | 2                         |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)         | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---------------------------------|------------------|---------------------------|
| 76493 | A05           | 217        | MT2361.1 | hypothetical protein MT2361.1   | NP_336833.1      | 2                         |
| 76692 | A06           | 220        | MT0555   | hypothetical protein MT0555     | NP_334964.1      | 2                         |
| 76733 | A07           | 220        | MT2330.1 | hypothetical protein MT2330.1   | NP_336799.1      | 2                         |
| 76657 | A08           | 220        | MT3878   | hypothetical protein MT3878     | NP_338429.1      | 2                         |
| 76884 | A09           | 223        | MT0328   | hypothetical protein MT0328     | NP_334736.1      | 2                         |
| 76591 | A10           | 223        | MT4019   | hypothetical protein MT4019     | NP_338570.1      | 1.85201794                |
| 76706 | A11           | 226        | MT2779   | hypothetical protein MT2779     | NP_337281.1      | 2                         |
| 76565 | A12           | 229        | MT2283   | hypothetical protein MT2283     | NP_336754.1      | 1.82969432                |
| 76886 | B01           | 232        | MT2142   | hypothetical protein MT2142     | NP_336610.1      | 2                         |
| 76686 | B02           | 232        | MT2502   | hypothetical protein MT2502     | NP_336985.1      | 2                         |
| 76571 | B03           | 235        | MT3631   | hypothetical protein MT3631     | NP_338178.1      | 3.28510638                |
| 76890 | B04           | 241        | MT1747   | hypothetical protein MT1747     | NP_336203.1      | 2                         |
| 76874 | B05           | 247        | MT1025.3 | hypothetical protein MT1025.3   | NP_335461.1      | 2                         |
| 76915 | B06           | 247        | MT3279   | hypothetical protein MT3279     | NP_337806.1      | 2                         |
| 76671 | B07           | 250        | MT0066.2 | hypothetical protein MT0066.2   | NP_334476.1      | 3.312                     |
| 76683 | B08           | 250        | MT0085.1 | hypothetical protein MT0085.1   | NP_334496.1      | 2.444                     |
| 76664 | B09           | 250        | MT4026.1 | hypothetical protein MT4026.1   | NP_338577.1      | 2                         |
| 76837 | B10           | 253        | MT1479.1 | hypothetical protein MT1479.1   | NP_335930.1      | 2                         |
| 76633 | B11           | 253        | MT3013   | hypothetical protein MT3013     | NP_337526.1      | 2                         |
| 76946 | B12           | 256        | MT1172.1 | hypothetical protein MT1172.1   | NP_335617.1      | 2                         |
| 76893 | C01           | 256        | MT2316   | hypothetical protein MT2316     | NP_336784.1      | 2                         |
| 76761 | C02           | 262        | MT1409   | hypothetical protein MT1409     | NP_335858.1      | 2                         |
| 76757 | C03           | 265        | MT2285.2 | hypothetical protein MT2285.2   | NP_336757.1      | 2                         |
| 76605 | C04           | 265        | MT2617   | hypothetical protein MT2617     | NP_337114.1      | 2                         |
| 76769 | C05           | 268        | MT1535   | hypothetical protein MT1535     | NP_335988.1      | 2                         |
| 76938 | C06           | 268        | MT3532.1 | hypothetical protein MT3532.1   | NP_338057.1      | 2                         |
| 76802 | C07           | 271        | MT2122   | CopG family DNA-binding protein | NP_336588.1      | 2                         |
| 76861 | C08           | 277        | MT2593.2 | hypothetical protein MT2593.2   | NP_337086.1      | 2                         |
| 76810 | C09           | 280        | MT0772.2 | hypothetical protein MT0772.2   | NP_335196.1      | 1.99642857                |
| 76929 | C10           | 280        | MT2544   | hypothetical protein MT2544     | NP_337030.1      | 2                         |
| 76853 | C11           | 283        | MT0968.1 | hypothetical protein MT0968.1   | NP_335402.1      | 2                         |
| 76638 | C12           | 283        | MT2501   | hypothetical protein MT2501     | NP_336984.1      | 2                         |
| 76642 | D01           | 283        | MT3755   | hypothetical protein MT3755     | NP_338302.1      | 2                         |
| 76628 | D02           | 313        | MT0717.1 | hypothetical protein MT0717.1   | NP_335130.1      | 2                         |
| 76777 | D03           | 313        | MT1148   | hypothetical protein MT1148     | NP_335591.1      | 2                         |
| 76813 | D04           | 319        | MT2726   | hypothetical protein MT2726     | NP_337226.1      | 2                         |
| 76714 | D05           | 319        | MT2991   | acylphosphatase                 | NP_337504.1      | 2                         |
| 76821 | D06           | 322        | MT2401.1 | hypothetical protein MT2401.1   | NP_336880.1      | 2                         |
| 76654 | D07           | 325        | MT4035.1 | hypothetical protein MT4035.1   | NP_338587.1      | 2                         |
| 76918 | D08           | 328        | MT2837   | hypothetical protein MT2837     | NP_337342.1      | 2.18292683                |
| 76928 | D09           | 331        | MT3269   | hypothetical protein MT3269     | NP_337794.1      | 2                         |
| 76865 | D10           | 337        | MT1040.1 | hypothetical protein MT1040.1   | NP_335477.1      | 1.95845697                |
| 76789 | D11           | 340        | MT1182   | hypothetical protein MT1182     | NP_335626.1      | 2                         |
| 76788 | D12           | 340        | MT1305.1 | drug transporter                | NP_335733.1      | 2                         |
| 76749 | E01           | 340        | MT3858   | hypothetical protein MT3858     | NP_338408.1      | 1.95882353                |
| 76826 | E02           | 343        | MT0543   | hypothetical protein MT0543     | NP_334952.1      | 2                         |
| 76898 | E03           | 346        | MT0025   | hypothetical protein MT0025     | NP_334433.1      | -                         |
| 76614 | E04           | 358        | MT2554.2 | hypothetical protein MT2554.2   | NP_337044.1      | 2                         |
| 76718 | E05           | 361        | MT2637.1 | hypothetical protein MT2637.1   | NP_337136.1      | 2                         |
| 76730 | E06           | 364        | MT0692.1 | hypothetical protein MT0692.1   | NP_335104.1      | 2                         |
| 76617 | E07           | 364        | MT2123   | hypothetical protein MT2123     | NP_336589.1      | 1.99450549                |
| 76782 | E08           | 391        | MT2807   | hypothetical protein MT2807     | NP_337314.1      | 2                         |
| 76721 | E09           | 394        | MT1534   | hypothetical protein MT1534     | NP_335987.1      | 2                         |
| 76912 | E10           | 394        | MT1775   | hypothetical protein MT1775     | NP_336234.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID  | Description (Gene name)        | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|-----------|--------------------------------|------------------|---------------------------|
| 76944 | E11           | 406        | MT1329    | hypothetical protein MT1329    | NP_335776.1      | 2                         |
| 76836 | E12           | 412        | MT0270.1  | hypothetical protein MT0270.1  | NP_334675.1      | 2                         |
| 76674 | F01           | 418        | MT0066.1  | hypothetical protein MT0066.1  | NP_334475.1      | 2                         |
| 76582 | F02           | 421        | MT3974.1  | hypothetical protein MT3974.1  | NP_338529.1      | 2                         |
| 76610 | F03           | 424        | MT1083.1  | hypothetical protein MT1083.1  | NP_335522.1      | -                         |
| 76650 | F04           | 424        | MT1849.1  | hypothetical protein MT1849.1  | NP_336307.1      | 2                         |
| 76901 | F05           | 430        | MT2944    | hypothetical protein MT2944    | NP_337455.1      | 2                         |
| 76585 | F06           | 442        | MT1170    | hypothetical protein MT1170    | NP_335614.1      | 1.95022624                |
| 76698 | F07           | 442        | MT3139.1  | hypothetical protein MT3139.1  | NP_337657.1      | -                         |
| 76737 | F08           | 448        | MT2694    | hypothetical protein MT2694    | NP_337196.1      | 1.99553571                |
| 76799 | F09           | 451        | MT3037    | hypothetical protein MT3037    | NP_337549.1      | 3.12416851                |
| 76696 | F10           | 451        | MT3270.1  | hypothetical protein MT3270.1  | NP_337796.1      | 2                         |
| 76850 | F11           | 457        | MT2291    | hypothetical protein MT2286    | NP_336758.1      | 2                         |
| 76742 | F12           | 460        | MT2721    | hypothetical protein MT2721    | NP_337221.1      | 2                         |
| 76678 | G01           | 463        | MT3573.12 | hypothetical protein MT3573.12 | NP_338112.1      | 2                         |
| 76793 | G02           | 466        | MT0383    | hypothetical protein MT0383    | NP_334790.1      | 1.56866953                |
| 76593 | G03           | 478        | MT0487    | hypothetical protein MT0487    | NP_334896.1      | 1.37656904                |
| 76646 | G04           | 481        | MT2138.2  | hypothetical protein MT2138.2  | NP_336606.1      | 2                         |
| 76934 | G05           | 493        | MT2520.1  | hypothetical protein MT2520.1  | NP_337005.1      | 2                         |
| 76848 | G06           | 505        | MT2871    | hypothetical protein MT2871    | NP_337378.1      | 2                         |
| 76908 | G07           | 508        | MT0407    | hypothetical protein MT0407    | NP_334816.1      | 2                         |
| 76878 | G08           | 517        | MT0608    | hypothetical protein MT0608    | NP_335017.1      | 2                         |
| 76966 | G09           | 523        | MT0173    | hypothetical protein MT0173    | NP_334580.1      | 1.8585086                 |
| 77119 | G10           | 532        | MT0655    | hypothetical protein MT0655    | NP_335065.1      | 2.0018797                 |
| 77105 | G11           | 541        | MT1555.1  | hypothetical protein MT1555.1  | NP_336007.1      | 2                         |
| 77061 | G12           | 556        | MT3876    | hypothetical protein MT3876    | NP_338426.1      | 2                         |
| 77143 | H01           | 586        | MT0250    | hypothetical protein MT0250    | NP_334654.1      | 3.24232082                |
| 77013 | H02           | 592        | MT0470    | hypothetical protein MT0470    | NP_334879.1      | 2                         |
| 76971 | H03           | 595        | MT2626    | hypothetical protein MT2626    | NP_337123.1      | 2                         |
| 77145 | H04           | 616        | MT0392    | hypothetical protein MT0392    | NP_334800.1      | 1.62824675                |
| 76953 | H05           | 616        | MT2113    | hypothetical protein MT2113    | NP_336578.1      | 2                         |
| 77137 | H06           | 631        | MT1264.1  | hypothetical protein MT1264.1  | NP_335708.1      | 1.97305864                |
| 77129 | H07           | 634        | MT0525    | hypothetical protein MT0525    | NP_334934.1      | 2                         |
| 77122 | H08           | 646        | MT0614    | hypothetical protein MT0614    | NP_335024.1      | 3.53869969                |
| 77007 | H09           | 646        | MT2488.1  | hypothetical protein MT2488.1  | NP_336971.1      | 1.46594427                |
| 77025 | H10           | 655        | MT1029    | hypothetical protein MT1029    | NP_335465.1      | 1.99541985                |
| 76957 | H11           | 658        | MT2958.1  | hypothetical protein MT2958.1  | NP_337470.1      | 1.54711246                |
| 77098 | H12           | 664        | MT0610    | hypothetical protein MT0610    | NP_335020.1      | 1.37650602                |

Table 10: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 10 (ZMTDJ), NR-19646

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name) | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------|------------------|---------------------------|
| 76977 | A01           | 664        | MT1082   | hypothetical protein    | NP_335520.1      | 1.605421687               |
| 77029 | A02           | 673        | MT0903   | hypothetical protein    | NP_335331.1      | 1.930163447               |
| 77104 | A03           | 673        | MT3084   | hypothetical protein    | NP_337599.1      | -                         |
| 77020 | A04           | 679        | MT3503   | hypothetical protein    | NP_338026.1      | 2                         |
| 76973 | A05           | 685        | MT0726   | hypothetical protein    | NP_335142.1      | 2                         |
| 77056 | A06           | 715        | MT0177   | hypothetical protein    | NP_334583.1      | 2                         |
| 77034 | A07           | 748        | MT2934   | hypothetical protein    | NP_337445.1      | 3.965240642               |
| 77150 | A08           | 748        | MT3770   | hypothetical protein    | NP_338323.1      | 3.881016043               |
| 77001 | A09           | 847        | MT3393   | hypothetical protein    | NP_337922.1      | 1.551357733               |

Table 11: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 11 (ZMTLA), NR-19647

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------------|------------------|---------------------------|
| 10078 | A01           | 130        | Rv1028A  | membrane protein kdpF              | YP_177636.1      | 2.569230769               |
| 9941  | A02           |            | Rv1089A  | endo-1,4-beta-glucanase            |                  |                           |
| 9995  | A03           | 166        | Rv0157A  | CLONE IS INVALID                   |                  | 2                         |
| 39956 | A04           | 175        | Rv1434   | hypothetical protein               | NP_215950.1      | 1.84                      |
| 10102 | A05           | 175        | Rv0749A  | hypothetical protein               | YP_177632.1      | 1.988571429               |
| 39962 | A06           | 187        | Rv1119c  | hypothetical protein               | NP_215635.1      | 1.839572193               |
| 39963 | A07           | 190        | Rv0900   | hypothetical protein               | NP_215415.1      | 2                         |
| 39967 | A08           | 199        | Rv3613c  | hypothetical protein               | NP_218130.1      | 2.688442211               |
| 10003 | A09           | 199        | Rv3678A  | hypothetical protein               | YP_178004.1      | 2                         |
| 39972 | A10           | 202        | Rv3489   | hypothetical protein               | NP_218006.1      | 2.371287129               |
| 39970 | A11           | 202        | Rv2057c  | 50S ribosomal protein L33          | YP_177856.1      | -                         |
| 39973 | A12           | 205        | Rv3251c  | rubredoxin RUBA                    | NP_217768.1      | 2                         |
| 9978  | B01           | 205        | Rv0634B  | 50S ribosomal protein L33          | YP_177630.1      | 2                         |
| 10107 | B02           | 205        | Rv1706A  | PPE family protein                 | YP_177828.1      | -                         |
| 9942  | B03           | 208        | Rv2970A  | lipase/esterase LipN               | NP_217486.1      | 1.831730769               |
| 10020 | B04           |            | Rv0236A  | hypothetical protein               |                  |                           |
| 10073 | B05           | 211        | Rv0979A  | 50S ribosomal protein L32          | YP_177635.1      | -                         |
| 39980 | B06           | 217        | Rv0909   | hypothetical protein               | NP_215424.1      | 2                         |
| 39983 | B07           | 220        | Rv3250c  | rubredoxin RubB                    | NP_217767.1      | 2                         |
| 10009 | B08           | 220        | Rv2307D  | hypothetical protein               | YP_177667.1      | -                         |
| 39984 | B09           | 223        | Rv0717   | 30S ribosomal protein S14          | YP_177747.1      | 2                         |
| 39985 | B10           | 223        | Rv1116   | hypothetical protein               | NP_215632.1      | -                         |
| 10055 | B11           | 223        | Rv0755A  | transposase                        | YP_177633.1      | -                         |
| 39988 | B12           |            | Rv1766   | hypothetical protein               |                  |                           |
| 39990 | C01           | 229        | Rv1799   | lipoprotein LppT                   | NP_216315.1      | 1.969432314               |
| 39991 | C02           | 229        | Rv1950c  | hypothetical protein               | NP_216466.1      | 2                         |
| 39996 | C03           | 229        | Rv3643   | hypothetical protein               | NP_218160.1      | 1.602620087               |
| 10127 | C04           | 229        | Rv2307A  | glycine rich protein               | YP_177665.1      | -                         |
| 10061 | C05           | 229        | Rv1473A  | transcriptional regulatory protein | YP_177644.1      | -                         |
| 10014 | C06           | 229        | Rv3770B  | hypothetical protein               | NP_218287.1      | 2.807860262               |
| 39998 | C07           | 232        | Rv1642   | 50S ribosomal protein L35          | NP_216158.1      | 1.788793103               |
| 40000 | C08           | 232        | Rv2255c  | hypothetical protein               | NP_216771.1      | 2                         |
| 39999 | C09           | 232        | Rv2111c  | hypothetical protein               | NP_216627.1      | 2                         |
| 40002 | C10           | 232        | Rv3642c  | hypothetical protein               | NP_218159.1      | 2                         |
| 40001 | C11           | 232        | Rv2283   | hypothetical protein               | NP_216799.1      | 2                         |
| 40006 | C12           | 235        | Rv3857c  | hypothetical protein               | NP_218374.1      | 2                         |
| 40003 | D01           | 235        | Rv0722   | 50S ribosomal protein L30          | NP_215236.1      | 2                         |
| 40007 | D02           | 241        | Rv1786   | ferredoxin                         | NP_216302.1      | 2                         |
| 40008 | D03           | 241        | Rv2128   | transmembrane protein              | NP_216644.1      | 2                         |
| 10036 | D04           | 241        | Rv2401A  | hypothetical protein               | YP_177670.1      | 1.65560166                |
| 40011 | D05           | 244        | Rv0416   | sulfur carrier protein ThiS        | NP_214930.1      | 2.454918033               |
| 40019 | D06           | 244        | Rv3656c  | hypothetical protein               | NP_218173.1      | 2.348360656               |
| 40022 | D07           | 247        | Rv2304c  | hypothetical protein               | NP_216820.1      | 2                         |
| 40023 | D08           | 250        | Rv0031   | remnant of A transposase           | NP_214545.1      | 2                         |
| 40026 | D09           | 250        | Rv3745c  | hypothetical protein               | NP_218262.1      | 2                         |
| 40024 | D10           |            | Rv1740   | hypothetical protein               |                  |                           |
| 9960  | D11           | 250        | Rv1498A  | methyltransferase                  | NP_216014.1      | 2.632                     |
| 40027 | D12           | 253        | Rv0379   | protein transport protein          | YP_177722.1      | 2                         |
| 40031 | E01           | 253        | Rv1952   | hypothetical protein               | NP_216468.1      | 2.498023715               |
| 40038 | E02           | 253        | Rv3751   | integrase                          | NP_218268.1      | 2                         |
| 9976  | E03           | 253        | Rv1765A  | hypothetical protein               | NP_216281.1      | 3.47826087                |
| 40043 | E04           | 256        | Rv2401   | hypothetical protein               | NP_216917.2      | 2                         |
| 40040 | E05           | 256        | Rv1721c  | hypothetical protein               | NP_216237.2      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40039 | E06           | 256        | Rv1560   | hypothetical protein                     | NP_216076.1      | 2                         |
| 40053 | E07           | 259        | Rv3462c  | translation initiation factor IF-1       | NP_217979.1      | 2                         |
| 40044 | E08           | 259        | Rv0300   | hypothetical protein                     | NP_214814.1      | 2.44015444                |
| 40054 | E09           | 262        | Rv0325   | hypothetical protein                     | NP_214839.1      | 2                         |
| 40059 | E10           | 262        | Rv2292c  | hypothetical protein                     | NP_216808.1      | 2.393129771               |
| 10017 | E11           | 262        | Rv2530A  | hypothetical protein                     | NP_217046.1      | -                         |
| 40065 | E12           | 265        | Rv2520c  | hypothetical protein                     | NP_217036.1      | 2.396226415               |
| 40063 | F01           | 265        | Rv1545   | hypothetical protein                     | NP_216061.1      | 2                         |
| 40068 | F02           | 265        | Rv2660c  | hypothetical protein                     | NP_217176.1      | 2                         |
| 40062 | F03           | 265        | Rv1211   | hypothetical protein                     | NP_215727.1      | 2                         |
| 40067 | F04           | 265        | Rv2526   | hypothetical protein                     | NP_217042.1      | 2.411320755               |
| 10066 | F05           | 265        | Rv0609A  | hypothetical protein                     | YP_177628.1      | 1.754716981               |
| 9982  | F06           |            | Rv2614A  | hypothetical protein                     |                  |                           |
| 40071 | F07           | 268        | Rv2132   | hypothetical protein                     | NP_216648.1      | 2                         |
| 10086 | F08           | 268        | Rv1489A  | hypothetical protein                     | YP_177645.1      | 1.757462687               |
| 40077 | F09           | 271        | Rv3739c  | PPE family protein                       | YP_178010.1      | 2                         |
| 40073 | F10           | 271        | Rv0239   | hypothetical protein                     | NP_214753.1      | 1.79704797                |
| 40074 | F11           | 271        | Rv0709   | 50S ribosomal protein L29                | NP_215223.1      | 2                         |
| 10104 | F12           | 271        | Rv2063   | hypothetical protein                     | YP_177657.1      | 2.597785978               |
| 40086 | G01           | 274        | Rv1535   | hypothetical protein                     | NP_216051.1      | 2                         |
| 40084 | G02           | 274        | Rv1055   | hypothetical protein                     | NP_215571.2      | 2.755474453               |
| 40082 | G03           | 274        | Rv0599c  | hypothetical protein                     | NP_215113.1      | 1.981751825               |
| 40085 | G04           | 274        | Rv1134   | hypothetical protein                     | NP_215650.1      | 2.270072993               |
| 40087 | G05           | 274        | Rv2058c  | 50S ribosomal protein L28                | NP_216574.1      | 2                         |
| 10038 | G06           | 274        | Rv0500A  | hypothetical protein                     | YP_177624.1      | 2.448905109               |
| 40089 | G07           | 277        | Rv0460   | hypothetical protein                     | NP_214974.1      | 2                         |
| 40091 | G08           | 277        | Rv1590   | hypothetical protein                     | NP_216106.1      | 1.63898917                |
| 9945  | G09           | 277        | Rv0787A  | phosphoribosylformylglycinamide synthase | YP_177755.1      | 1.815884477               |
| 40099 | G10           | 280        | Rv2302   | hypothetical protein                     | NP_216818.1      | 1.642857143               |
| 40101 | G11           | 280        | Rv2908c  | hypothetical protein                     | NP_217424.1      | 2.439285714               |
| 40096 | G12           | 280        | Rv1734c  | hypothetical protein                     | NP_216250.1      | 2                         |
| 40097 | H01           | 280        | Rv2009   | hypothetical protein                     | NP_216525.1      | 2                         |
| 40095 | H02           | 280        | Rv1298   | 50S ribosomal protein L31                | NP_215814.1      | 2                         |
| 40100 | H03           | 280        | Rv2635   | hypothetical protein                     | NP_217151.1      | 2                         |
| 40094 | H04           | 280        | Rv0615   | integral membrane protein                | NP_215129.1      | 2                         |
| 10042 | H05           | 280        | Rv3724A  | cutinase precursor                       | YP_178007.1      | 1.628571429               |
| 40110 | H06           | 283        | Rv1305   | F0F1 ATP synthase subunit C              | NP_215821.1      | 2                         |
| 40107 | H07           | 283        | Rv0660c  | hypothetical protein                     | NP_215174.1      | 2.745583039               |
| 40111 | H08           | 283        | Rv2550c  | hypothetical protein                     | NP_217066.1      | 2                         |
| 40125 | H09           | 286        | Rv3374   | enoyl-CoA hydratase                      | YP_177966.1      | 2                         |
| 40124 | H10           | 286        | Rv2960c  | hypothetical protein                     | NP_217476.1      | 2.374125874               |
| 40123 | H11           | 286        | Rv2722   | hypothetical protein                     | NP_217238.1      | 1.629370629               |
| 40121 | H12           | 286        | Rv2708c  | hypothetical protein                     | NP_217224.1      | 2                         |

Table 12: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 12 (ZMTLB), NR-19648

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                    | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40120 | A01           | 286        | Rv1741   | hypothetical protein                       | NP_216257.1      | 2                         |
| 40128 | A02           | 289        | Rv2517c  | hypothetical protein                       | NP_217033.1      | 2                         |
| 40126 | A03           | 289        | Rv1960c  | hypothetical protein                       | NP_216476.1      | 2                         |
| 40127 | A04           | 289        | Rv2076c  | hypothetical protein                       | NP_216592.1      | 2                         |
| 40129 | A05           | 289        | Rv3112   | molybdenum cofactor biosynthesis protein D | YP_177928.1      | 1.626297578               |
| 10046 | A06           | 289        | Rv2094c  | twin arginine translocase protein A        | NP_216610.1      | 4.166089965               |
| 9950  | A07           | 289        | Rv0634A  | hypothetical protein                       | YP_177629.1      | 1.775086505               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40131 | A08           | 292        | Rv0623   | hypothetical protein                               | NP_215137.1      | 2                         |
| 40130 | A09           | 292        | Rv0055   | 30S ribosomal protein S18                          | YP_177688.1      | 2                         |
| 40134 | A10           | 292        | Rv2104c  | hypothetical protein                               | NP_216620.1      | 2                         |
| 40139 | A11           | 292        | Rv3219   | transcriptional regulatory protein WHIB-like WHIB1 | NP_217735.1      | 2                         |
| 40133 | A12           |            | Rv0689c  | CLONE IS INVALID                                   |                  |                           |
| 40136 | B01           | 292        | Rv2664   | hypothetical protein Rv2664                        | NP_217180.1      | 2.284246575               |
| 9952  | B02           | 292        | Rv3198A  | ATP-dependent DNA helicase II UVRD2                | NP_217714.1      | 2.657534247               |
| 10092 | B03           | 292        | Rv0590A  | MCE family-like protein                            | YP_177627.1      | 2.366438356               |
| 40146 | B04           | 295        | Rv1107c  | exodeoxyribonuclease VII small subunit             | NP_215623.1      | 2                         |
| 40162 | B05           | 295        | Rv3358   | hypothetical protein                               | NP_217875.1      | 2                         |
| 40159 | B06           | 295        | Rv2871   | hypothetical protein                               | NP_217387.1      | 2.379661017               |
| 40150 | B07           | 295        | Rv1831   | hypothetical protein                               | NP_216347.1      | 1.983050847               |
| 40156 | B08           | 295        | Rv2706c  | hypothetical protein                               | NP_217222.1      | 2.644067797               |
| 40143 | B09           | 295        | Rv0596c  | hypothetical protein                               | NP_215110.1      | 1.610169492               |
| 40157 | B10           | 295        | Rv2808   | hypothetical protein                               | NP_217324.1      | 2                         |
| 40153 | B11           |            | Rv2547   | hypothetical protein                               |                  |                           |
| 40161 | B12           | 295        | Rv3346c  | hypothetical protein                               | NP_217863.1      | 2.613559322               |
| 10122 | C01           | 295        | Rv1638A  | hypothetical protein                               | YP_177650.1      | 2.762711864               |
| 40167 | C02           | 298        | Rv2657c  | phiRv2 prophage protein                            | NP_217173.1      | 2                         |
| 40163 | C03           | 298        | Rv0626   | hypothetical protein                               | NP_215141.1      | 2                         |
| 40165 | C04           | 298        | Rv2412   | 30S ribosomal protein S20                          | NP_216928.1      | 2                         |
| 40164 | C05           | 298        | Rv1241   | hypothetical protein                               | NP_215757.1      | 2                         |
| 40166 | C06           | 298        | Rv2441c  | 50S ribosomal protein L27                          | NP_216957.1      | 2                         |
| 40173 | C07           | 301        | Rv2866   | hypothetical protein                               | NP_217382.1      | 2                         |
| 40169 | C08           | 301        | Rv0476   | transmembrane protein                              | NP_214990.1      | 2                         |
| 40170 | C09           | 301        | Rv0898c  | hypothetical protein                               | NP_215413.1      | 3.485049834               |
| 40172 | C10           | 301        | Rv1839c  | hypothetical protein                               | NP_216355.1      | 2                         |
| 40168 | C11           | 301        | Rv0033   | acyl carrier protein AcpA                          | NP_214547.1      | 2                         |
| 40177 | C12           | 304        | Rv1083   | hypothetical protein                               | NP_215599.1      | 3.289473684               |
| 40178 | D01           | 304        | Rv2055c  | 30S ribosomal protein S18                          | NP_216571.1      | 2                         |
| 40174 | D02           | 304        | Rv0550c  | hypothetical protein                               | NP_215064.1      | 2                         |
| 40175 | D03           | 304        | Rv0569   | hypothetical protein                               | NP_215083.1      | 2                         |
| 40176 | D04           | 304        | Rv0616c  | hypothetical protein                               | NP_215130.1      | 2                         |
| 40179 | D05           | 304        | Rv2758c  | hypothetical protein                               | NP_217274.1      | 1.644736842               |
| 9946  | D06           | 304        | Rv3566A  | hypothetical protein                               | YP_177990.1      | 3.161184211               |
| 40185 | D07           | 307        | Rv3260c  | transcriptional regulatory protein WHIB-like WHIB2 | NP_217777.1      | 2                         |
| 40181 | D08           | 307        | Rv1519   | hypothetical protein                               | NP_216035.1      | 2                         |
| 40182 | D09           | 307        | Rv2312   | hypothetical protein                               | NP_216828.1      | 2                         |
| 40180 | D10           | 307        | Rv1247c  | hypothetical protein                               | NP_215763.1      | 1.993485342               |
| 40184 | D11           | 307        | Rv2785c  | 30S ribosomal protein S15                          | NP_217301.1      | 2                         |
| 40183 | D12           | 307        | Rv2760c  | hypothetical protein                               | NP_217276.1      | 2                         |
| 40186 | E01           | 310        | Rv0664   | hypothetical protein                               | NP_215178.1      | 2.396774194               |
| 40192 | E02           | 310        | Rv3904c  | hypothetical protein                               | NP_218421.1      | 2                         |
| 40191 | E03           | 310        | Rv3769   | hypothetical protein                               | NP_218286.1      | 2                         |
| 40190 | E04           | 310        | Rv2662   | hypothetical protein                               | NP_217178.1      | 2                         |
| 40189 | E05           | 310        | Rv2422   | hypothetical protein                               | NP_216938.1      | 2                         |
| 40187 | E06           | 310        | Rv1580c  | phiRv1 phage protein                               | NP_216096.1      | 2                         |
| 40188 | E07           | 310        | Rv1993c  | hypothetical protein                               | NP_216509.1      | 2                         |
| 10007 | E08           | 310        | Rv3208A  | hypothetical protein                               | YP_177943.1      | -                         |
| 40194 | E09           | 313        | Rv0879c  | transmembrane protein                              | NP_215394.1      | 3.083067093               |
| 40195 | E10           | 313        | Rv1053c  | hypothetical protein                               | NP_215569.1      | 3.562300319               |
| 40193 | E11           | 313        | Rv0424c  | hypothetical protein                               | NP_214938.1      | 2                         |
| 40198 | E12           | 313        | Rv3357   | hypothetical protein                               | NP_217874.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 40197 | F01           | 313        | Rv2755c  | type I restriction/modification system specificity determinant HsdS     | YP_177904.1      | 2                         |
| 40200 | F02           | 316        | Rv0544c  | transmembrane protein   | NP_215058.1      | 2.379746835               |
| 40202 | F03           | 316        | Rv0942   | hypothetical protein  | NP_215457.1      | 2                         |
| 40203 | F04           | 316        | Rv2545   | hypothetical protein  | NP_217061.1      | 2                         |
| 40201 | F05           | 316        | Rv0868c  | molybdenum cofactor biosynthesis protein D                              | NP_215383.1      | 2                         |
| 9985  | F06           | 316        | Rv2438A  | hypothetical protein  | YP_177671.1      | -                         |
| 9964  | F07           | 316        | Rv3197A  | transcriptional regulatory protein WHIB-like WHIB7                      | YP_177940.1      | 3.155063291               |
| 40213 | F08           | 319        | Rv2865   | hypothetical protein  | NP_217381.1      | 2                         |
| 40205 | F09           | 319        | Rv0705   | 30S ribosomal protein S19   | NP_215219.1      | 2                         |
| 40210 | F10           | 319        | Rv2632c  | hypothetical protein  | NP_217148.1      | 2                         |
| 40206 | F11           | 319        | Rv0863   | hypothetical protein  | NP_215378.1      | 2                         |
| 40214 | F12           | 319        | Rv3269   | hypothetical protein  | NP_217786.1      | 2                         |
| 40207 | G01           | 319        | Rv1335   | 9.5 kDa culture filtrate antigen CFP10A                                 | NP_215851.1      | 2                         |
| 40209 | G02           | 319        | Rv2122c  | phosphoribosyl-ATP pyrophosphatase                                      | YP_177860.1      | 2.344827586               |
| 40204 | G03           | 319        | Rv0011c  | putative septation inhibitor protein                                    | NP_214525.1      | 2.482758621               |
| 9959  | G04           | 319        | Rv2922A  | Acylphosphatase   | YP_177679.1      | 2                         |
| 40222 | G05           | 322        | Rv1793   | putative ESAT-6 like protein ESXN (ESAT-6 like protein 5)               | YP_177838.1      | 2                         |
| 40220 | G06           | 322        | Rv1567c  | hypothetical protein  | NP_216083.1      | 2                         |
| 40221 | G07           | 322        | Rv1738   | hypothetical protein  | NP_216254.1      | 2                         |
| 40219 | G08           | 322        | Rv1198   | putative ESAT-6 like protein ESXL (ESAT-6 like protein 4)               | NP_215714.1      | 2                         |
| 40216 | G09           | 322        | Rv0105c  | 50S ribosomal protein L28   | YP_177691.1      | 1.605590062               |
| 10056 | G10           | 322        | Rv1159A  | pterin-4-alpha-carbinolamine dehydratase                                | YP_177641.1      | 4.335403727               |
| 10090 | G11           | 325        | Rv2309A  | hypothetical protein  | YP_177668.1      | 4.033846154               |
| 9954  | G12           | 325        | Rv2601A  | hypothetical protein  | YP_177673.1      | 2.593846154               |
| 10100 | H01           | 337        | Rv2077A  | transmembrane protein   | NP_216593.1      | 2.584569733               |
| 10130 | H02           | 343        | Rv3221A  | putative acetyl-CoA carboxylase biotin carboxyl carrier protein subunit | NP_217737.1      | 3.174927114               |
| 40328 | H03           | 349        | Rv1574   | phiRV1 phage related protein  | NP_216090.1      | 2                         |
| 10080 | H04           | 349        | Rv3312A  | secreted protein antigen  | YP_177957.1      | 3.277936963               |
| 40342 | H05           | 352        | Rv0741   | transposase   | NP_215255.1      | 2                         |
| 40350 | H06           | 352        | Rv3126c  | hypothetical protein  | NP_217642.1      | 2                         |
| 40349 | H07           | 352        | Rv2876   | transmembrane protein   | NP_217392.1      | 2                         |
| 40344 | H08           | 352        | Rv1849   | urease subunit beta   | NP_216365.1      | 2                         |
| 40348 | H09           | 352        | Rv2749   | hypothetical protein  | NP_217265.1      | 2                         |
| 40347 | H10           | 352        | Rv2442c  | 50S ribosomal protein L21   | NP_216958.1      | 2                         |
| 40346 | H11           | 352        | Rv2078   | hypothetical protein  | NP_216594.1      | 2                         |
| 40343 | H12           | 352        | Rv1579c  | phiRV1 phage protein  | NP_216095.1      | 2                         |

Table 13: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 13 (ZMTLC), NR-19649

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---------------------------|------------------|---------------------------|
| 10112 | A01           | 352        | Rv1290A  | hypothetical protein      | NP_215806.1      | 3.005681818               |
| 10098 | A02           | 352        | Rv3022A  | PPE family protein        | YP_177684.1      | 4.022727273               |
| 40352 | A03           | 355        | Rv0027   | hypothetical protein      | NP_214541.1      | 2.695774648               |
| 40361 | A04           | 355        | Rv2274c  | hypothetical protein      | NP_216790.1      | 2                         |
| 40356 | A05           | 355        | Rv1495   | hypothetical protein      | NP_216011.1      | 2.205633803               |
| 40362 | A06           | 355        | Rv2375   | hypothetical protein      | NP_216891.1      | 2                         |
| 40354 | A07           | 355        | Rv0715   | 50S ribosomal protein L24 | NP_215229.1      | 2                         |
| 40353 | A08           | 355        | Rv0531   | hypothetical protein      | NP_215045.1      | 2                         |
| 40358 | A09           | 355        | Rv2044c  | hypothetical protein      | NP_216560.1      | 3.171830986               |
| 40364 | A10           | 355        | Rv3592   | hypothetical protein      | NP_218109.1      | 1.892957746               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 40355 | A11           | 355        | Rv0948c  | hypothetical protein                          | NP_215463.1      | 2                         |
| 40363 | A12           | 355        | Rv2644c  | hypothetical protein                          | NP_217160.1      | 2                         |
| 40365 | B01           | 358        | Rv1103c  | hypothetical protein                          | NP_215619.1      | 2                         |
| 40368 | B02           | 358        | Rv3706c  | proline rich protein                          | NP_218223.1      | 3.268156425               |
| 40366 | B03           | 358        | Rv1344   | acyl carrier protein                          | NP_215860.1      | 2                         |
| 10124 | B04           | 358        | Rv1087A  | hypothetical protein                          | YP_177637.1      | 3.156424581               |
| 40369 | B05           | 361        | Rv0257c  | CLONE IS INVALID                              |                  | 2                         |
| 40375 | B06           | 361        | Rv3488   | hypothetical protein                          | NP_218005.1      | 2                         |
| 40376 | B07           | 361        | Rv3891c  | ESAT-6 like protein EsxD                      | NP_218408.1      | 2                         |
| 40370 | B08           | 361        | Rv1117   | hypothetical protein                          | NP_215633.1      | 2                         |
| 40373 | B09           | 361        | Rv2653c  | phiRv2 prophage protein                       | NP_217169.1      | 2                         |
| 40372 | B10           | 361        | Rv2481c  | hypothetical protein                          | NP_216997.1      | 1.900277008               |
| 40371 | B11           | 361        | Rv2034   | ArsR-type repressor protein                   | NP_216550.1      | 2                         |
| 40374 | B12           | 361        | Rv3065   | multidrug-transport integral membrane protein | YP_177922.1      | 2                         |
| 40400 | C01           | 364        | Rv3381c  | transposase                                   | NP_217898.1      | 2.315934066               |
| 40386 | C02           | 364        | Rv1804c  | hypothetical protein                          | NP_216320.1      | 2                         |
| 40394 | C03           | 364        | Rv2798c  | hypothetical protein                          | NP_217314.1      | 2                         |
| 40381 | C04           | 364        | Rv1177   | ferredoxin FdxC                               | NP_215693.1      | 2                         |
| 40398 | C05           | 364        | Rv3325   | transposase                                   | NP_217842.1      | 3.302197802               |
| 40389 | C06           | 364        | Rv2278   | transposase                                   | NP_216794.1      | 2                         |
| 40402 | C07           | 364        | Rv3474   | transposase IS6110                            | NP_217991.1      | 2                         |
| 40384 | C08           | 364        | Rv1757c  | putative transposase                          | NP_216273.1      | 2                         |
| 40383 | C09           | 364        | Rv1489c  | hypothetical protein                          | YP_177646.1      | -                         |
| 40385 | C10           | 364        | Rv1763   | putative transposase                          | NP_216279.1      | 2                         |
| 40392 | C11           | 364        | Rv2480c  | transposase                                   | NP_216996.1      | 2                         |
| 40395 | C12           | 364        | Rv2815c  | transposase                                   | NP_217331.1      | 3.318681319               |
| 40382 | D01           | 364        | Rv1370c  | transposase                                   | NP_215886.1      | 2                         |
| 40393 | D02           | 364        | Rv2648   | transposase IS6110                            | NP_217164.1      | 2                         |
| 40378 | D03           | 364        | Rv0795   | transposase IS6110                            | NP_215310.1      | 1.60989011                |
| 40390 | D04           | 364        | Rv2348c  | hypothetical protein                          | NP_216864.1      | 2                         |
| 40397 | D05           | 364        | Rv3186   | transposase                                   | NP_217702.1      | 2                         |
| 40396 | D06           | 364        | Rv3184   | transposase                                   | NP_217700.1      | 2                         |
| 40388 | D07           | 364        | Rv2168c  | transposase                                   | NP_216684.1      | 2                         |
| 40391 | D08           | 364        | Rv2354   | transposase                                   | NP_216870.1      | 2                         |
| 40387 | D09           | 364        | Rv2105   | transposase                                   | NP_216621.1      | 1.612637363               |
| 40412 | D10           | 367        | Rv1942c  | hypothetical protein                          | NP_216458.1      | 2                         |
| 40413 | D11           | 367        | Rv2273   | transmembrane protein                         | NP_216789.1      | 2                         |
| 40416 | D12           | 367        | Rv3612c  | hypothetical protein                          | NP_218129.1      | 2                         |
| 40409 | E01           | 367        | Rv0692   | hypothetical protein                          | NP_215206.1      | -                         |
| 40411 | E02           | 367        | Rv1351   | hypothetical protein                          | NP_215867.1      | 2.689373297               |
| 40415 | E03           | 367        | Rv3183   | transcriptional regulatory protein            | NP_217699.1      | 1.662125341               |
| 40432 | E04           | 370        | Rv3686c  | hypothetical protein                          | NP_218203.1      | 2                         |
| 40418 | E05           | 370        | Rv0759c  | hypothetical protein                          | NP_215273.1      | 2                         |
| 40424 | E06           | 370        | Rv1390   | DNA-directed RNA polymerase subunit omega     | NP_215906.1      | 2                         |
| 40433 | E07           | 370        | Rv3898c  | hypothetical protein                          | NP_218415.1      | 2                         |
| 40426 | E08           | 370        | Rv2639c  | hypothetical protein                          | NP_217155.1      | 2                         |
| 40422 | E09           | 370        | Rv1174c  | low molecular weight T-cell antigen TB8.4     | NP_215690.1      | 2                         |
| 40417 | E10           | 370        | Rv0156   | NAD(P) transhydrogenase subunit alpha         | NP_214670.1      | 2                         |
| 40427 | E11           |            | Rv3129   | CLONE IS INVALID                              |                  |                           |
| 40431 | E12           | 370        | Rv3453   | transmembrane protein                         | NP_217970.1      | 2                         |
| 40419 | F01           | 370        | Rv0850   | transposase                                   | NP_215365.1      | 2                         |
| 40425 | F02           | 370        | Rv2269c  | hypothetical protein                          | NP_216785.1      | 1.905405405               |
| 40420 | F03           | 370        | Rv0991c  | putative serine rich protein                  | NP_215506.1      | 3.594594595               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                          | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40423 | F04           | 370        | Rv1214c  | PE family protein                                | YP_177797.1      | 2                         |
| 40429 | F05           |            | Rv3216   | CLONE IS INVALID                                 |                  |                           |
| 40437 | F06           | 373        | Rv3819   | hypothetical protein                             | NP_218336.1      | 2                         |
| 40434 | F07           | 373        | Rv1291c  | hypothetical protein                             | NP_215807.1      | 3.292225201               |
| 40435 | F08           | 373        | Rv2050   | hypothetical protein                             | NP_216566.1      | 2                         |
| 40436 | F09           | 373        | Rv3746c  | PE family protein                                | YP_178011.1      | 2                         |
| 10070 | F10           | 373        | Rv1990A  | transcriptional regulatory protein               | NP_216506.1      | 2.975871314               |
| 40441 | F11           | 376        | Rv2745c  | transcriptional regulatory protein               | NP_217261.1      | 2                         |
| 40442 | F12           | 376        | Rv2919c  | nitrogen regulatory protein P-II GLNB            | NP_217435.1      | 2                         |
| 40440 | G01           | 376        | Rv1036c  | truncated IS1560 transposase                     | NP_215552.1      | 2                         |
| 40443 | G02           | 376        | Rv3004   | low molecular weight protein antigen 6 (CFP-6)   | NP_217520.1      | 2                         |
| 40438 | G03           | 376        | Rv0559c  | hypothetical protein                             | NP_215073.1      | 2                         |
| 40444 | G04           | 376        | Rv3316   | succinate dehydrogenase cytochrome B-556 subunit | NP_217833.1      | 2                         |
| 40439 | G05           | 376        | Rv0665   | hypothetical protein                             | NP_215179.1      | 2                         |
| 40445 | G06           | 376        | Rv3597c  | iron-regulated LSR2 protein precursor            | NP_218114.1      | 2                         |
| 40446 | G07           | 379        | Rv0572c  | hypothetical protein                             | NP_215086.1      | 2                         |
| 40450 | G08           | 379        | Rv2365c  | hypothetical protein                             | NP_216881.1      | 2                         |
| 40451 | G09           | 379        | Rv2816c  | hypothetical protein                             | NP_217332.1      | 2                         |
| 40449 | G10           | 379        | Rv1990c  | dehydrogenase                                    | YP_177656.1      | 2                         |
| 40448 | G11           | 379        | Rv1271c  | hypothetical protein                             | NP_215787.1      | 2                         |
| 40447 | G12           | 379        | Rv1136   | enoyl-CoA hydratase                              | NP_215652.1      | 2                         |
| 40452 | H01           | 379        | Rv2904c  | 50S ribosomal protein L19                        | NP_217420.1      | 2                         |
| 10075 | H02           | 379        | Rv2160c  | hypothetical protein                             | NP_216676.1      | 2                         |
| 40458 | H03           | 382        | Rv3182   | hypothetical protein                             | NP_217698.1      | 2                         |
| 40454 | H04           | 382        | Rv1991c  | hypothetical protein                             | NP_216507.1      | 2                         |
| 40460 | H05           | 382        | Rv3632   | hypothetical protein                             | NP_218149.1      | 2                         |
| 40453 | H06           | 382        | Rv0081   | transcriptional regulatory protein               | NP_214595.1      | 2                         |
| 40455 | H07           | 382        | Rv2007c  | ferredoxin FDXA                                  | NP_216523.1      | 2                         |
| 40459 | H08           | 382        | Rv3353c  | hypothetical protein                             | NP_217870.2      | 2                         |
| 40461 | H09           | 385        | Rv0039c  | transmembrane protein                            | NP_214553.1      | 1.981818182               |
| 40473 | H10           | 385        | Rv3636   | transposase                                      | NP_218153.1      | 2                         |
| 40467 | H11           | 385        | Rv1606   | phosphoribosyl-AMP cyclohydrolase                | NP_216638.2      | 2                         |
| 40469 | H12           | 385        | Rv1805c  | hypothetical protein                             | NP_216321.1      | 2                         |

Table 14: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 14 (ZMTLD), NR-19650

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40472 | A01           | 385        | Rv3188   | hypothetical protein Rv3188                        | NP_217704.1      | 2                         |
| 40468 | A02           | 385        | Rv1670   | hypothetical protein Rv1670                        | NP_216186.1      | 2.2                       |
| 40465 | A03           |            | Rv1466   | CLONE IS INVALID                                   |                  |                           |
| 40464 | A04           | 385        | Rv0961   | integral membrane protein                          | NP_215476.1      | 2                         |
| 40470 | A05           | 385        | Rv2244   | acyl carrier protein                               | NP_216760.1      | 2                         |
| 40471 | A06           | 385        | Rv2588c  | preprotein translocase subunit YajC                | NP_217104.1      | 2                         |
| 40477 | A07           | 388        | Rv0520   | hypothetical protein Rv0520                        | NP_215034.1      | 2                         |
| 40480 | A08           | 388        | Rv3862c  | transcriptional regulatory protein WHIB-like WHIB6 | NP_218379.1      | 2                         |
| 40478 | A09           | 388        | Rv1717   | hypothetical protein Rv1717                        | NP_216233.1      | 2                         |
| 40479 | A10           | 388        | Rv1948c  | hypothetical protein Rv1948c                       | NP_216464.1      | 2                         |
| 40476 | A11           | 388        | Rv0454   | hypothetical protein Rv0454                        | NP_214968.1      | 2                         |
| 40481 | A12           | 388        | Rv3914   | thioredoxin trxC (TRX) (MPT46)                     | NP_218431.1      | 3.208762887               |
| 40488 | B01           | 391        | Rv2767c  | hypothetical protein Rv2767c                       | NP_217283.1      | 2                         |
| 40483 | B02           | 391        | Rv1440   | preprotein translocase subunit SecG                | NP_215956.2      | 2                         |
| 40498 | B03           | 394        | Rv3073c  | hypothetical protein Rv3073c                       | NP_217589.1      | 2                         |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 40491 | B04           | 394        | Rv1810   | hypothetical protein Rv1810   | NP_216326.1      | 2                         |
| 40497 | B05           | 394        | Rv2801c  | hypothetical protein Rv2801c  | NP_217317.1      | 2                         |
| 40495 | B06           | 394        | Rv2204c  | hypothetical protein Rv2204c  | NP_216720.1      | 2.583756345               |
| 40494 | B07           | 394        | Rv2144c  | transmembrane protein   | NP_216660.1      | 2                         |
| 40492 | B08           | 394        | Rv1889c  | hypothetical protein Rv1889c  | NP_216405.1      | 2                         |
| 40493 | B09           | 394        | Rv1994c  | transcriptional regulatory protein  | NP_216510.1      | 2                         |
| 40504 | B10           | 397        | Rv2640c  | ArsR family transcriptional regulator   | NP_217156.1      | 1.914357683               |
| 40499 | B11           | 397        | Rv0967   | hypothetical protein Rv0967   | NP_215482.1      | 2                         |
| 40505 | B12           | 397        | Rv3178   | hypothetical protein Rv3178   | NP_217694.1      | 2.586901763               |
| 40510 | C01           | 397        | Rv3845   | hypothetical protein Rv3845   | NP_218362.1      | 2.652392947               |
| 40506 | C02           | 397        | Rv3748   | hypothetical protein Rv3748   | NP_218265.1      | 2                         |
| 40518 | C03           | 400        | Rv1342c  | hypothetical protein Rv1342c  | YP_177800.1      | 2.1175                    |
| 40526 | C04           |            | Rv3424c  | CLONE IS INVALID  |                  |                           |
| 40520 | C05           | 400        | Rv2628   | hypothetical protein Rv2628   | NP_217144.1      | 2                         |
| 40529 | C06           |            | Rv3922c  | CLONE IS INVALID  |                  |                           |
| 40528 | C07           | 400        | Rv3744   | transcriptional regulatory protein ArsR-family                                      | NP_218261.1      | 3.19                      |
| 40519 | C08           | 400        | Rv1669   | hypothetical protein Rv1669   | NP_216185.1      | 2                         |
| 40516 | C09           | 400        | Rv1171   | hypothetical protein Rv1171   | NP_215687.2      | 2.595                     |
| 40511 | C10           |            | Rv0025   | CLONE IS INVALID  |                  |                           |
| 10034 | C11           | 400        | Rv1508A  | hypothetical protein Rv1508c  | NP_216024.1      | 3.01                      |
| 40534 | C12           | 403        | Rv1824   | hypothetical protein Rv1824   | NP_216340.1      | 2                         |
| 40537 | D01           | 403        | Rv3789   | integral membrane protein   | NP_218306.1      | 2                         |
| 40531 | D02           | 403        | Rv1152   | transcriptional regulatory protein  | NP_215668.1      | 3.29528536                |
| 40552 | D03           | 406        | Rv2063c  |   |                  | 2.581280788               |
| 40539 | D04           | 406        | Rv0123   | hypothetical protein Rv0123   | NP_214637.1      | 2                         |
| 40555 | D05           | 406        | Rv2647   | hypothetical protein Rv2647   | NP_217163.1      | 2                         |
| 40540 | D06           | 406        | Rv0397   | 13E12 repeat family protein   | NP_214911.1      | 2                         |
| 40550 | D07           | 406        | Rv1209   | hypothetical protein Rv1209   | NP_215725.1      | 2.586206897               |
| 40556 | D08           | 406        | Rv2694c  | hypothetical protein Rv2694c  | NP_217210.1      | 2                         |
| 40557 | D09           | 406        | Rv3360   | hypothetical protein Rv3360   | NP_217877.1      | 2                         |
| 40558 | D10           | 406        | Rv3363c  | hypothetical protein Rv3363c  | NP_217880.1      | 2                         |
| 40541 | D11           | 406        | Rv0521c  | hypothetical protein Rv0521   | YP_177626.1      | 2                         |
| 40538 | D12           | 406        | Rv0122   | hypothetical protein Rv0122   | NP_214636.1      | 2                         |
| 40554 | E01           | 406        | Rv2272   | transmembrane protein   | NP_216788.1      | 3.221674877               |
| 40547 | E02           | 406        | Rv0720   | 50S ribosomal protein L18   | NP_215234.1      | 2.669950739               |
| 40548 | E03           | 406        | Rv1137c  | hypothetical protein Rv1137c  | NP_215653.1      | 2                         |
| 40559 | E04           | 406        | Rv3687c  | anti-anti-sigma factor RSFB (anti-sigma factor antagonist) (regulator of sigma F B) | NP_218204.1      | 2                         |
| 40564 | E05           | 409        | Rv1471   | thioredoxin TRXB1   | YP_177815.1      | 3.273838631               |
| 40562 | E06           | 409        | Rv1352   | hypothetical protein Rv1352   | NP_215868.1      | 2                         |
| 40566 | E07           | 409        | Rv2446c  | integral membrane protein   | NP_216962.1      | 2.836185819               |
| 40568 | E08           | 409        | Rv3352c  | Oxidoreductase  | NP_217869.1      | 2.589242054               |
| 40575 | E09           | 412        | Rv1470   | thioredoxin TRXA  | NP_215986.1      | 2                         |
| 40581 | E10           | 412        | Rv3460c  | 30S ribosomal protein S13   | NP_217977.1      | 2                         |
| 40579 | E11           | 412        | Rv2822c  | hypothetical protein Rv2822c  | NP_217338.1      | 2.650485437               |
| 40573 | E12           | 412        | Rv1114   | hypothetical protein Rv1114   | NP_215630.1      | 2                         |
| 40574 | F01           | 412        | Rv1269c  | hypothetical protein Rv1269c  | NP_215785.1      | 2                         |
| 40572 | F02           | 412        | Rv0682   | 30S ribosomal protein S12   | NP_215196.1      | 2                         |
| 40569 | F03           | 412        | Rv0333   | hypothetical protein Rv0333   | NP_214847.1      | 2                         |
| 40580 | F04           | 412        | Rv3046c  | hypothetical protein Rv3046c  | NP_217562.1      | 2                         |
| 40586 | F05           | 415        | Rv1974   | hypothetical protein Rv1974   | NP_216490.1      | 2                         |
| 40590 | F06           | 415        | Rv3289c  | transmembrane protein   | NP_217806.1      | 2                         |
| 40595 | F07           | 415        | Rv3675   | hypothetical protein Rv3675   | NP_218192.1      | 2                         |
| 40584 | F08           | 415        | Rv1555   | fumarate reductase subunit D  | NP_216071.1      | 2.178313253               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 40589 | F09           | 415        | Rv2548   | hypothetical protein Rv2548   | NP_217064.1      | 1.985542169               |
| 40596 | F10           | 415        | Rv3923c  | ribonuclease P  | NP_218440.2      | 2.937349398               |
| 40585 | F11           | 415        | Rv1943c  | hypothetical protein Rv1943c  | NP_216459.1      | 2                         |
| 40604 | F12           | 418        | Rv2420c  | hypothetical protein Rv2420c  | NP_216936.1      | 2                         |
| 40601 | G01           |            | Rv1554   | CLONE IS INVALID  |                  |                           |
| 40606 | G02           | 418        | Rv3070   | camphor resistance protein CrcB   | NP_217586.1      | -                         |
| 40605 | G03           | 418        | Rv2642   | ArsR family transcriptional regulator   | NP_217158.1      | 2.980861244               |
| 40599 | G04           | 418        | Rv0353   | HEAT shock protein transcriptional repressor HspR                                   | NP_214867.1      | 2                         |
| 40598 | G05           | 418        | Rv0140   | hypothetical protein Rv0140   | NP_214654.1      | 2.655502392               |
| 40600 | G06           | 418        | Rv1343c  | lipoprotein LprD  | NP_215859.1      | 2                         |
| 40603 | G07           | 418        | Rv1924c  | hypothetical protein Rv1924c  | NP_216440.1      | 2                         |
| 40607 | G08           |            | Rv2863   | CLONE IS INVALID  |                  |                           |
| 40612 | G09           | 421        | Rv0960   | hypothetical protein Rv0960   | NP_215475.1      | 3.163895487               |
| 40610 | G10           | 421        | Rv0656c  | hypothetical protein Rv0656c  | NP_215170.1      | 2                         |
| 40618 | G11           | 421        | Rv3747   | hypothetical protein Rv3747   | NP_218264.1      | 1.895486936               |
| 40609 | G12           | 421        | Rv0611c  | hypothetical protein Rv0611c  | NP_215125.1      | 2.190023753               |
| 40614 | H01           | 421        | Rv1690   | lipoprotein LprJ  | NP_216206.1      | 2.593824228               |
| 40619 | H02           | 424        | Rv0313   | hypothetical protein Rv0313   | NP_214827.1      | 2                         |
| 40623 | H03           | 424        | Rv1365c  | anti-anti-sigma factor RSFA (anti-sigma factor antagonist) (regulator of sigma F A) | NP_215881.1      | 2.570754717               |
| 40628 | H04           | 424        | Rv3145   | NADH dehydrogenase subunit A  | NP_217661.1      | 2.655660377               |
| 40626 | H05           |            | Rv2898c  | CLONE IS INVALID  |                  |                           |
| 40624 | H06           | 424        | Rv2331   | hypothetical protein Rv2331   | NP_216847.1      | 2                         |
| 40622 | H07           | 424        | Rv0607   | hypothetical protein Rv0607   | NP_215121.1      | 2                         |
| 40625 | H08           | 424        | Rv2470   | globin GlbO   | NP_216986.1      | 2                         |
| 40621 | H09           |            | Rv0546c  | CLONE IS INVALID  |                  |                           |
| 40650 | H10           |            | Rv2570   | CLONE IS INVALID  |                  |                           |
| 40635 | H11           | 427        | Rv0807   | hypothetical protein Rv0807   | NP_215322.1      | 1.592505855               |
| 40653 | H12           | 427        | Rv2961   | transposase   | NP_217477.1      | 2                         |

Table 15: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 15 (ZMTLE), NR-19651

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------------|------------------|---------------------------|
| 40645 | A01           | 427        | Rv1871c  | hypothetical protein Rv1871c       | NP_216387.1      | 2                         |
| 40637 | A02           | 427        | Rv0870c  | hypothetical protein Rv0870c       | NP_215385.1      | 2                         |
| 40656 | A03           | 427        | Rv3541c  | hypothetical protein Rv3541c       | NP_218058.1      | 1.5971897                 |
| 40642 | A04           | 427        | Rv1643   | 50S ribosomal protein L20          | NP_216159.1      | 2                         |
| 40639 | A05           | 427        | Rv1034c  | transposase                        | NP_215550.1      | 2.20140515                |
| 40651 | A06           | 427        | Rv2661c  | hypothetical protein Rv2661c       | NP_217177.1      | 2                         |
| 40654 | A07           | 427        | Rv3354   | hypothetical protein Rv3354        | NP_217871.1      | 2                         |
| 40646 | A08           | 427        | Rv2186c  | hypothetical protein Rv2186c       | NP_216702.1      | 2                         |
| 40647 | A09           | 427        | Rv2556c  | hypothetical protein Rv2556c       | NP_217072.1      | 2.56206089                |
| 40630 | A10           | 427        | Rv0076c  | hypothetical protein Rv0076c       | NP_214590.1      | 2.57142857                |
| 40644 | A11           | 427        | Rv1720c  | hypothetical protein Rv1720c       | NP_216236.1      | 2.60421546                |
| 40648 | A12           | 427        | Rv2562   | hypothetical protein Rv2562        | NP_217078.1      | 2                         |
| 40634 | B01           | 427        | Rv0786c  | hypothetical protein Rv0786c       | NP_215300.1      | 3.05854801                |
| 40652 | B02           | 427        | Rv2705c  | hypothetical protein Rv2705c       | NP_217221.1      | 2                         |
| 9966  | B03           |            | Rv3705A  | hypothetical protein Rv3705c       | NP_218222.1      |                           |
| 40664 | B04           | 430        | Rv1671   | hypothetical protein Rv1671        | NP_216187.1      | 2.57209302                |
| 40658 | B05           | 430        | Rv0396   | hypothetical protein Rv0396        | NP_214910.1      | 3.24418605                |
| 40666 | B06           | 430        | Rv2523c  | 4'-phosphopantetheinyl transferase | NP_217039.1      | 2                         |
| 40659 | B07           | 430        | Rv0595c  | hypothetical protein Rv0595c       | NP_215109.1      | 2                         |
| 40662 | B08           | 430        | Rv0847   | lipoprotein LpqS                   | NP_215362.1      | 2.9                       |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                             | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 40665 | B09           | 430        | Rv2359   | ferric uptake regulation protein FURB               | NP_216875.1      | 2                         |
| 40660 | B10           | 430        | Rv0652   | 50S ribosomal protein L7/L12                        | NP_215166.1      | 3.44651163                |
| 40661 | B11           | 430        | Rv0827c  | transcriptional regulatory protein                  | NP_215342.1      | 2                         |
| 40674 | B12           | 430        | Rv3750c  | excisionase   | NP_218267.1      | 2.92325581                |
| 40673 | C01           | 430        | Rv3384c  | hypothetical protein Rv3384c                        | NP_217901.1      | 3.05116279                |
| 40671 | C02           |            | Rv3364c  | hypothetical protein Rv3364c                        | NP_217881.1      |                           |
| 40689 | C03           | 433        | Rv2759c  | hypothetical protein Rv2759c                        | NP_217275.1      | 2                         |
| 40682 | C04           | 433        | Rv1066   | hypothetical protein Rv1066                         | NP_215582.1      | 2                         |
| 40676 | C05           | 433        | Rv0034   | hypothetical protein Rv0034                         | NP_214548.1      | 3.18013857                |
| 40683 | C06           | 433        | Rv1224   | sec-independent translocase                         | NP_215740.1      | 2                         |
| 40690 | C07           | 433        | Rv3110   | pterin-4- $\alpha$ -carbinolamine dehydratase MoaB1 | YP_177926.1      | 2.4665127                 |
| 40691 | C08           | 433        | Rv3742c  | oxidoreductase                                      | NP_218259.1      | 2                         |
| 40685 | C09           |            | Rv1581c  | phiRv1 phage protein                                |                  |                           |
| 40686 | C10           | 433        | Rv1838c  | hypothetical protein Rv1838c                        | NP_216354.1      | 2                         |
| 40680 | C11           | 433        | Rv0624   | hypothetical protein Rv0624                         | NP_215138.1      | 2.59122402                |
| 40687 | C12           | 433        | Rv2183c  | hypothetical protein Rv2183c                        | NP_216699.1      | -                         |
| 40688 | D01           | 433        | Rv2549c  | hypothetical protein Rv2549c                        | NP_217065.1      | 2                         |
| 40697 | D02           | 436        | Rv2451   | hypothetical protein Rv2451                         | NP_216967.1      | 2                         |
| 40695 | D03           | 436        | Rv1616   | hypothetical protein Rv1616                         | NP_216132.1      | 2                         |
| 40696 | D04           | 436        | Rv2010   | hypothetical protein Rv2010                         | NP_216526.1      | 2                         |
| 40692 | D05           | 436        | Rv0718   | 30S ribosomal protein S8                            | NP_215232.1      | 2                         |
| 40698 | D06           | 436        | Rv3069   | camphor resistance protein CrcB                     | NP_217585.1      | 2                         |
| 40700 | D07           | 436        | Rv3135   | PPE family protein                                  | YP_177934.1      | 2.5733945                 |
| 40728 | D08           | 439        | Rv3716c  | hypothetical protein Rv3716c                        | NP_218233.1      | 2.65831435                |
| 40711 | D09           | 439        | Rv1414   | hypothetical protein Rv1414                         | NP_215930.1      | 2                         |
| 40712 | D10           | 439        | Rv1744c  | hypothetical protein Rv1744c                        | NP_216260.1      | 2                         |
| 40704 | D11           |            | Rv0065   | hypothetical protein Rv0065                         | NP_214579.1      |                           |
| 40718 | D12           | 439        | Rv2600   | integral membrane protein                           | NP_217116.1      | 3.14578588                |
| 40713 | E01           | 439        | Rv1947   | hypothetical protein Rv1947                         | NP_216463.1      | 2                         |
| 40707 | E02           |            | Rv0617   | hypothetical protein Rv0617                         | NP_215131.1      |                           |
| 40716 | E03           | 439        | Rv2527   | hypothetical protein Rv2527                         | NP_217043.1      | 2                         |
| 40726 | E04           | 439        | Rv3607c  | dihydroneopterin aldolase FolB                      | YP_177996.1      | 2.58997722                |
| 40721 | E05           | 439        | Rv3078   | hydroxylaminobenzene mutase HAB                     | NP_217594.1      | 2                         |
| 40706 | E06           | 439        | Rv0609   | hypothetical protein Rv0609                         | NP_215123.1      | 2.59453303                |
| 40717 | E07           | 439        | Rv2532c  | hypothetical protein Rv2532c                        | NP_217048.1      | -                         |
| 40722 | E08           | 439        | Rv3143   | response regulator                                  | NP_217659.1      | 2                         |
| 40732 | E09           | 442        | Rv1826   | glycine cleavage system protein H                   | NP_216342.1      | 2                         |
| 40737 | E10           | 442        | Rv2774c  | hypothetical protein Rv2774c                        | NP_217290.1      | 2                         |
| 40735 | E11           | 442        | Rv2169c  | transmembrane protein                               | NP_216685.1      | 2                         |
| 40740 | E12           | 442        | Rv3852   | histone-like protein HNS                            | NP_218369.1      | 2                         |
| 40730 | F01           | 442        | Rv0856   | hypothetical protein Rv0856                         | NP_215371.1      | 2                         |
| 40734 | F02           | 442        | Rv2061c  | hypothetical protein Rv2061c                        | NP_216577.1      | 2                         |
| 40733 | F03           | 442        | Rv1903   | hypothetical protein Rv1903                         | NP_216419.1      | 3.57239819                |
| 40736 | F04           | 442        | Rv2596   | hypothetical protein Rv2596                         | NP_217112.1      | 2                         |
| 40729 | F05           | 442        | Rv0395   | hypothetical protein Rv0395                         | NP_214909.1      | 2                         |
| 40731 | F06           | 442        | Rv1561   | hypothetical protein Rv1561                         | NP_216077.1      | 2                         |
| 40750 | F07           | 445        | Rv1976c  | hypothetical protein Rv1976c                        | NP_216492.1      | 2                         |
| 40753 | F08           | 445        | Rv2358   | ArsR family transcriptional regulator               | NP_216874.1      | 3.51235955                |
| 40745 | F09           | 445        | Rv1042c  | IS like-2 transposase                               | NP_215558.1      | 2.15955056                |
| 40743 | F10           | 445        | Rv0871   | cold shock-like protein B CspB                      | NP_215386.1      | 2                         |
| 40749 | F11           | 445        | Rv1962c  | hypothetical protein Rv1962c                        | NP_216478.1      | 2.18651685                |
| 40746 | F12           | 445        | Rv1149   | transposase   | NP_215665.1      | 2                         |
| 40748 | G01           | 445        | Rv1914c  | hypothetical protein Rv1914c                        | NP_216430.1      | 2                         |
| 40747 | G02           | 445        | Rv1891   | hypothetical protein Rv1891                         | NP_216407.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------------|------------------|---------------------------|
| 40752 | G03           | 445        | Rv2233   | hypothetical protein Rv2232        | NP_216748.2      | 3.16629213                |
| 40741 | G04           | 445        | Rv0582   | hypothetical protein Rv0582        | NP_215096.1      | 2.57303371                |
| 40742 | G05           | 445        | Rv0627   | hypothetical protein Rv0628c       | NP_215142.1      | 2                         |
| 40766 | G06           | 448        | Rv1444c  | hypothetical protein Rv1444c       | NP_215960.1      | 2                         |
| 40773 | G07           | 448        | Rv2445c  | nucleoside diphosphate kinase      | NP_216961.1      | 2                         |
| 40775 | G08           | 448        | Rv3067   | hypothetical protein Rv3067        | NP_217583.1      | 2                         |
| 40774 | G09           | 448        | Rv2674   | hypothetical protein Rv2674        | NP_217190.1      | 2                         |
| 40767 | G10           | 448        | Rv1542c  | hemoglobin glbN                    | NP_216058.1      | 2                         |
| 40772 | G11           | 448        | Rv2432c  | hypothetical protein Rv2432c       | NP_216948.1      | 2                         |
| 40769 | G12           | 448        | Rv1573   | phiRV1 phage protein               | NP_216089.1      | 3.20089286                |
| 40763 | H01           | 448        | Rv0420c  | transmembrane protein              | NP_214934.1      | 2                         |
| 40778 | H02           | 448        | Rv3412   | hypothetical protein Rv3412        | NP_217929.1      | 2                         |
| 40757 | H03           | 448        | Rv0141c  | hypothetical protein Rv0141c       | NP_214655.1      | 2.59151786                |
| 40756 | H04           | 448        | Rv0095c  | hypothetical protein Rv0095c       | NP_214609.1      | 2                         |
| 40781 | H05           | 451        | Rv0549c  | hypothetical protein Rv0549c       | NP_215063.1      | 2.57871397                |
| 40787 | H06           | 451        | Rv2137c  | hypothetical protein Rv2137c       | NP_216653.1      | 2                         |
| 40782 | H07           | 451        | Rv0598c  | hypothetical protein Rv0598c       | NP_215112.1      | 2                         |
| 40791 | H08           | 451        | Rv2923c  | hypothetical protein Rv2923c       | NP_217439.1      | 3.23281596                |
| 40786 | H09           | 451        | Rv2074   | hypothetical protein Rv2074        | NP_216590.1      | 3.09534368                |
| 40792 | H10           | 451        | Rv3288c  | hypothetical protein Rv3288c       | NP_217805.1      | 2                         |
| 40796 | H11           | 451        | Rv3840   | transcriptional regulatory protein | NP_218357.1      | 3.10864745                |
| 40805 | H12           | 454        | Rv2757c  | hypothetical protein Rv2757c       | NP_217273.1      | 3.22907489                |

Table 16: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 16 (ZMTLF), NR-19652

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40804 | A01           | 454        | Rv2475c  | hypothetical protein                               | NP_216991.1      | 2                         |
| 40799 | A02           | 454        | Rv0841c  | transmembrane protein                              | YP_177634.1      | 3.169603524               |
| 40797 | A03           | 454        | Rv0708   | 50S ribosomal protein L16                          | NP_215222.1      | 2                         |
| 40814 | A04           | 457        | Rv2199c  | integral membrane protein                          | NP_216715.1      | 2                         |
| 40808 | A05           | 457        | Rv0760c  | hypothetical protein                               | NP_215274.1      | 2                         |
| 40821 | A06           | 457        | Rv2887   | transcriptional regulatory protein                 | NP_217403.1      | 2                         |
| 40815 | A07           | 457        | Rv2341   | lipoprotein LppQ                                   | NP_216857.1      | 2                         |
| 40813 | A08           | 457        | Rv1982c  | hypothetical protein                               | NP_216498.1      | 1.98249453                |
| 40807 | A09           | 457        | Rv0022c  | transcriptional regulatory protein WHIB-like WHIB5 | NP_214536.1      | 2                         |
| 40820 | A10           | 457        | Rv2762c  | hypothetical protein                               | NP_217278.1      | 2                         |
| 40819 | A11           | 457        | Rv2551c  | hypothetical protein                               | NP_217067.1      | 2                         |
| 40817 | A12           | 457        | Rv2437   | hypothetical protein                               | NP_216953.1      | 1.81619256                |
| 40809 | B01           | 457        | Rv0965c  | hypothetical protein                               | NP_215480.1      | 2                         |
| 40810 | B02           | 457        | Rv1064c  | lipoprotein LpqV                                   | NP_215580.1      | 1.93654267                |
| 40822 | B03           | 457        | Rv3259   | hypothetical protein                               | NP_217776.1      | 2                         |
| 40825 | B04           | 457        | Rv3601c  | aspartate alpha-decarboxylase                      | NP_218118.1      | 2                         |
| 40818 | B05           | 457        | Rv2530c  | hypothetical protein                               | YP_177672.1      | 2                         |
| 40829 | B06           | 460        | Rv0474   | transcriptional regulatory protein                 | NP_214988.1      | 2.104347826               |
| 40833 | B07           | 460        | Rv1847   | hypothetical protein                               | NP_216363.1      | 2                         |
| 40827 | B08           | 460        | Rv0451c  | membrane protein                                   | NP_214965.1      | 2                         |
| 40830 | B09           | 460        | Rv0816c  | thioredoxin ThiX                                   | NP_215331.1      | -                         |
| 40834 | B10           | 460        | Rv1881c  | lipoprotein LppE                                   | NP_216397.1      | 2                         |
| 40836 | B11           | 460        | Rv2513   | hypothetical protein                               | NP_217029.1      | 2                         |
| 40826 | B12           | 460        | Rv0390   | hypothetical protein                               | NP_214904.1      | 2                         |
| 40835 | C01           | 460        | Rv2261c  | hypothetical protein                               | NP_216777.1      | 2                         |
| 10040 | C02           | 460        | Rv2219A  | hypothetical protein                               | YP_177661.1      | 3.906521739               |
| 40850 | C03           | 463        | Rv2620c  | transmembrane protein                              | NP_217136.1      | 3.177105832               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40852 | C04           | 463        | Rv3064c  | integral membrane protein  | NP_217580.1      | 2                         |
| 40845 | C05           | 463        | Rv0866   | molybdenum cofactor biosynthesis protein E2                      | NP_215381.1      | 2                         |
| 40846 | C06           | 463        | Rv1160   | 7,8-dihydro-8-oxoguanine-triphosphatase                          | NP_215676.1      | 2                         |
| 40849 | C07           | 463        | Rv2494   | hypothetical protein   | NP_217010.1      | 2                         |
| 40847 | C08           |            | Rv1439c  | hypothetical protein   | NP_215955.1      |                           |
| 40839 | C09           | 463        | Rv0061   | hypothetical protein   | NP_214575.1      | 2                         |
| 40862 | C10           | 466        | Rv0749   | hypothetical protein   | NP_215263.1      | 2                         |
| 40861 | C11           | 466        | Rv0677c  | hypothetical protein   | NP_215191.1      | 2                         |
| 40857 | C12           | 466        | Rv0441c  | hypothetical protein   | NP_214955.1      | 3.096566524               |
| 40870 | D01           | 466        | Rv3320c  | hypothetical protein   | NP_217837.1      | 2                         |
| 40867 | D02           | 466        | Rv2406c  | hypothetical protein   | NP_216922.1      | 3.072961373               |
| 40854 | D03           | 466        | Rv0277c  | hypothetical protein   | NP_214791.1      | 2.650214592               |
| 40868 | D04           | 466        | Rv2704   | hypothetical protein   | NP_217220.1      | 2                         |
| 40869 | D05           | 466        | Rv3142c  | hypothetical protein   | NP_217658.1      | -                         |
| 40863 | D06           | 466        | Rv1987   | chitinase  | NP_216503.1      | 2                         |
| 40855 | D07           | 466        | Rv0403c  | membrane protein   | NP_214917.1      | 2                         |
| 40858 | D08           | 466        | Rv0636   | (3R)-hydroxyacyl-ACP dehydratase subunit HadB                    | NP_215150.1      | 2                         |
| 40874 | D09           | 469        | Rv1242   | hypothetical protein   | NP_215758.1      | 2                         |
| 40881 | D10           | 469        | Rv2166c  | cell division protein MraZ                                       | NP_216682.1      | 2                         |
| 40883 | D11           | 469        | Rv2599   | hypothetical protein   | NP_217115.1      | 3.085287846               |
| 40877 | D12           | 469        | Rv1897c  | D-tyrosyl-tRNA(Tyr) deacylase                                    | NP_216413.1      | 2                         |
| 40886 | E01           | 469        | Rv2645   | hypothetical protein   | NP_217161.1      | 2.569296375               |
| 40872 | E02           | 469        | Rv0880   | MarR family transcriptional regulator                            | NP_215395.1      | 2                         |
| 40888 | E03           | 469        | Rv3217c  | integral membrane protein  | NP_217733.1      | 3.232409382               |
| 40878 | E04           | 469        | Rv1904   | hypothetical protein   | NP_216420.1      | 2                         |
| 40875 | E05           | 469        | Rv1546   | hypothetical protein   | NP_216062.1      | 2                         |
| 40871 | E06           | 469        | Rv0188   | transmembrane protein  | NP_214702.1      | 2                         |
| 40884 | E07           | 469        | Rv2626c  | hypothetical protein   | NP_217142.1      | 2                         |
| 40873 | E08           | 469        | Rv0997   | hypothetical protein   | NP_215512.1      | 2                         |
| 40876 | E09           | 469        | Rv1813c  | hypothetical protein   | NP_216329.1      | 2.33901919                |
| 40880 | E10           | 469        | Rv2011c  | hypothetical protein   | NP_216527.1      | 3.221748401               |
| 9956  | E11           | 469        | Rv2307B  | glycine rich protein   | YP_177666.1      | 3.752665245               |
| 40895 | E12           | 472        | Rv1081c  | hypothetical protein   | NP_215597.1      | 2                         |
| 40899 | F01           | 472        | Rv1487   | hypothetical protein   | NP_216003.1      | 2                         |
| 40903 | F02           | 472        | Rv2185c  | hypothetical protein   | NP_216701.1      | 3.569915254               |
| 40897 | F03           | 472        | Rv1088   | PE family protein  | YP_177784.1      | 3.163135593               |
| 40901 | F04           | 472        | Rv2031c  | heat shock protein hspX  | NP_216547.1      | 2                         |
| 40898 | F05           | 472        | Rv1262c  | HIT-like protein   | NP_215778.1      | 2                         |
| 40906 | F06           | 472        | Rv3369   | hypothetical protein   | NP_217886.1      | 2                         |
| 40905 | F07           | 472        | Rv3317   | succinate dehydrogenase hydrophobic membrane anchor subunit SdhD | NP_217834.1      | 2                         |
| 40904 | F08           | 472        | Rv3180c  | hypothetical protein   | NP_217696.1      | 2                         |
| 40900 | F09           | 472        | Rv1532c  | hypothetical protein   | NP_216048.1      | 2                         |
| 40902 | F10           | 472        | Rv2103c  | hypothetical protein   | NP_216619.1      | 2                         |
| 40894 | F11           | 472        | Rv0910   | hypothetical protein   | NP_215425.1      | 2                         |
| 40893 | F12           | 472        | Rv0771   | 4-carboxymuconolactone decarboxylase                             | NP_215285.1      | 2                         |
| 10044 | G01           | 472        | Rv2306B  | hypothetical protein   | YP_177664.1      | 3.186440678               |
| 40915 | G02           | 475        | Rv3697c  | hypothetical protein   | NP_218214.1      | 2.932631579               |
| 40911 | G03           | 475        | Rv0661c  | hypothetical protein   | NP_215175.1      | 3.193684211               |
| 40914 | G04           | 475        | Rv3162c  | integral membrane protein  | NP_217678.1      | 1.593684211               |
| 40913 | G05           | 475        | Rv3103c  | hypothetical protein   | NP_217619.1      | 2                         |
| 40907 | G06           | 475        | Rv0008c  | hypothetical protein   | NP_214522.1      | 2                         |
| 40909 | G07           | 475        | Rv0360c  | hypothetical protein   | NP_214874.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)               | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---------------------------------------|------------------|---------------------------|
| 40912 | G08           | 475        | Rv1873   | hypothetical protein                  | NP_216389.1      | 2                         |
| 40908 | G09           | 475        | Rv0240   | hypothetical protein                  | NP_214754.1      | 2                         |
| 40918 | G10           | 478        | Rv1334   | hypothetical protein                  | NP_215850.1      | 2                         |
| 40916 | G11           | 478        | Rv0723   | 50S ribosomal protein L15             | NP_215237.1      | 3.487447699               |
| 40919 | G12           | 478        | Rv1615   | hypothetical protein                  | NP_216131.1      | 2                         |
| 40925 | H01           | 478        | Rv2617c  | hypothetical protein                  | NP_217133.1      | 2                         |
| 40920 | H02           | 478        | Rv1636   | hypothetical protein                  | NP_216152.1      | 2                         |
| 40927 | H03           | 478        | Rv3334   | MerR family transcriptional regulator | NP_217851.1      | 2                         |
| 40926 | H04           | 478        | Rv3108   | hypothetical protein                  | NP_217624.1      | 2                         |
| 40924 | H05           | 478        | Rv2602   | hypothetical protein                  | NP_217118.1      | 2                         |
| 40923 | H06           | 478        | Rv2175c  | putative regulatory protein           | NP_216691.1      | 1.966527197               |
| 10005 | H07           | 478        | Rv0470A  | mycolic acid synthase pcaA            | YP_177730.1      | 2                         |
| 40928 | H08           | 481        | Rv0426c  | hypothetical protein                  | NP_214940.1      | 1.98960499                |
| 40932 | H09           | 481        | Rv0854   | hypothetical protein                  | NP_215369.1      | 2.565488565               |
| 40939 | H10           | 481        | Rv2537c  | 3-dehydroquinate dehydratase          | NP_217053.1      | 2                         |
| 40935 | H11           |            | Rv1312   | hypothetical protein                  | NP_215828.1      |                           |
| 40940 | H12           | 481        | Rv2872   | hypothetical protein                  | NP_217388.1      | 2                         |

Table 17: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 17 (ZMTLG), NR-19653

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 40933 | A01           | 481        | Rv1155   | hypothetical protein                         | NP_215671.1      | 2                         |
| 40930 | A02           | 481        | Rv0506   | membrane protein                             | NP_215020.1      | 2.584199584               |
| 40936 | A03           | 481        | Rv1632c  | hypothetical protein                         | NP_216148.1      | 1.98960499                |
| 40941 | A04           | 481        | Rv2910c  | hypothetical protein                         | NP_217426.1      | 2                         |
| 40945 | A05           | 481        | Rv3718c  | hypothetical protein                         | NP_218235.1      | 2                         |
| 40944 | A06           | 481        | Rv3443c  | 50S ribosomal protein L13                    | NP_217960.1      | 2.74012474                |
| 40942 | A07           | 481        | Rv3119   | molybdenum cofactor biosynthesis protein E   | YP_177931.1      | 2                         |
| 40947 | A08           | 484        | Rv0477   | hypothetical protein                         | NP_214991.1      | 2                         |
| 40946 | A09           | 484        | Rv0455c  | hypothetical protein                         | NP_214969.1      | -                         |
| 40952 | A10           | 484        | Rv2324   | AsnC family transcriptional regulator        | NP_216840.1      | 2                         |
| 40954 | A11           | 484        | Rv2709   | transmembrane protein                        | NP_217225.1      | 2                         |
| 40953 | A12           | 484        | Rv2638   | hypothetical protein                         | NP_217154.1      | 1.989669421               |
| 40951 | B01           | 484        | Rv1558   | hypothetical protein                         | NP_216074.1      | 3.185950413               |
| 40958 | B02           | 487        | Rv1752   | hypothetical protein                         | NP_216268.1      | 3.106776181               |
| 40956 | B03           | 487        | Rv1261c  | hypothetical protein                         | NP_215777.1      | 2                         |
| 40967 | B04           | 487        | Rv3527   | hypothetical protein                         | NP_218044.1      | 2                         |
| 40955 | B05           | 487        | Rv0912   | transmembrane protein                        | NP_215427.1      | 2                         |
| 40963 | B06           | 487        | Rv2740   | hypothetical protein                         | NP_217256.1      | 3.151950719               |
| 40960 | B07           | 487        | Rv1778c  | hypothetical protein                         | NP_216294.1      | 3.156057495               |
| 40966 | B08           | 487        | Rv3486   | hypothetical protein                         | NP_218003.1      | 2                         |
| 40968 | B09           | 487        | Rv3901c  | hypothetical protein                         | NP_218418.1      | 2                         |
| 40961 | B10           | 487        | Rv1956   | transcriptional regulatory protein           | NP_216472.1      | 2                         |
| 40971 | B11           | 490        | Rv2297   | hypothetical protein                         | NP_216813.1      | 2                         |
| 40976 | B12           | 490        | Rv3291c  | AsnC family transcriptional regulator        | NP_217808.1      | 2.589795918               |
| 40969 | C01           | 490        | Rv1909c  | ferric uptake regulation protein furA (fur)  | NP_216425.1      | 2                         |
| 40973 | C02           | 490        | Rv3052c  | ribonucleotide reductase stimulatory protein | NP_217568.1      | 2                         |
| 40975 | C03           | 490        | Rv3181c  | hypothetical protein                         | NP_217697.1      | 2                         |
| 40972 | C04           | 490        | Rv2771c  | hypothetical protein                         | NP_217287.1      | 2                         |
| 40974 | C05           | 490        | Rv3098c  | hypothetical protein                         | NP_217614.1      | 2                         |
| 40970 | C06           | 490        | Rv1946c  | lipoprotein                                  | NP_216462.1      | 2                         |
| 40983 | C07           | 493        | Rv3547   | hypothetical protein                         | NP_218064.1      | 2                         |
| 10068 | C08           | 496        | Rv1322A  | hypothetical protein                         | YP_177643.1      | 2.889112903               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 10116 | C09           | 505        | Rv2803   | hypothetical protein   | YP_177678.1      | 3.099009901               |
| 9948  | C10           | 523        | Rv0164   | hypothetical protein   | YP_177617.1      | 2.738049713               |
| 41062 | C11           | 526        | Rv1465   | nitrogen fixation related protein  | NP_215981.1      | 2                         |
| 41063 | C12           | 526        | Rv1827   | hypothetical protein   | NP_216343.1      | 2                         |
| 41068 | D01           | 526        | Rv3583c  | transcription factor   | NP_218100.1      | 2                         |
| 41067 | D02           | 526        | Rv2909c  | 30S ribosomal protein S16  | NP_217425.1      | 1.990494297               |
| 41069 | D03           | 526        | Rv3628   | inorganic pyrophosphatase  | NP_218145.1      | 2                         |
| 41061 | D04           | 526        | Rv0875c  | hypothetical protein   | NP_215390.1      | 3.133079848               |
| 41059 | D05           | 526        | Rv0471c  | hypothetical protein   | NP_214985.1      | 2                         |
| 41087 | D06           | 529        | Rv3258c  | hypothetical protein   | NP_217775.1      | 3.132325142               |
| 41081 | D07           | 529        | Rv1628c  | hypothetical protein   | NP_216144.1      | 2.631379962               |
| 41078 | D08           | 529        | Rv0580c  | hypothetical protein   | NP_215094.1      | 2.139886578               |
| 41090 | D09           | 529        | Rv3844   | transposase  | NP_218361.1      | 3.172022684               |
| 41089 | D10           | 529        | Rv3348   | transposase  | NP_217865.1      | 3.13610586                |
| 41076 | D11           | 529        | Rv0566c  | putative nucleotide-binding protein  | NP_215080.1      | 2                         |
| 41073 | D12           | 529        | Rv0310c  | hypothetical protein   | NP_214824.1      | 2                         |
| 41079 | E01           | 529        | Rv1284   | hypothetical protein   | NP_215800.1      | 2                         |
| 41082 | E02           | 529        | Rv2234   | phosphotyrosine protein phosphatase PTPA (protein-tyrosine-phosphatase) (PTPase) (LMW phosphatase) | NP_216750.1      | 2                         |
| 41085 | E03           | 529        | Rv2991   | hypothetical protein   | NP_217507.1      | 2                         |
| 41092 | E04           | 532        | Rv0054   | single-stranded DNA-binding protein  | NP_214568.1      | 3.065789474               |
| 41095 | E05           | 532        | Rv1080c  | transcription elongation factor GreA   | NP_215596.1      | 2                         |
| 41099 | E06           | 532        | Rv1961   | hypothetical protein   | NP_216477.1      | 2                         |
| 41101 | E07           | 532        | Rv2598   | hypothetical protein   | NP_217114.1      | 2                         |
| 41102 | E08           | 532        | Rv2717c  | hypothetical protein   | NP_217233.1      | 2                         |
| 41097 | E09           | 532        | Rv1120c  | hypothetical protein   | NP_215636.1      | 2.114661654               |
| 41100 | E10           | 532        | Rv2012   | hypothetical protein   | NP_216528.1      | 2                         |
| 41098 | E11           | 532        | Rv1829   | hypothetical protein   | NP_216345.1      | 2                         |
| 41110 | E12           | 535        | Rv1382   | export or membrane protein   | NP_215898.1      | 2                         |
| 41120 | F01           | 535        | Rv3807c  | transmembrane protein  | NP_218324.1      | 2                         |
| 41115 | F02           | 535        | Rv1932   | thiol peroxidase   | NP_216448.1      | 3.153271028               |
| 41109 | F03           | 535        | Rv1316c  | methylated-DNA--protein-cysteine methyltransferase   | NP_215832.1      | 2                         |
| 41111 | F04           | 535        | Rv1528c  | polyketide synthase associated protein   | NP_216044.1      | 2                         |
| 41117 | F05           |            | Rv2683   | hypothetical protein   | NP_217199.1      |                           |
| 41108 | F06           | 535        | Rv0737   | transcriptional regulatory protein   | NP_215251.1      | 2                         |
| 41105 | F07           | 535        | Rv0678   | hypothetical protein   | NP_215192.1      | 2.895327103               |
| 41107 | F08           | 535        | Rv0679c  | putative threonine rich protein  | NP_215193.1      | 3.138317757               |
| 41121 | F09           | 538        | Rv0637   | (3R)-hydroxyacyl-ACP dehydratase subunit   | NP_215151.1      | 2                         |
| 41130 | F10           | 538        | Rv3637   | transposase  | NP_218154.1      | 1.879182156               |
| 41131 | F11           | 538        | Rv3733c  | hypothetical protein   | NP_218250.1      | 2                         |
| 41123 | F12           | 538        | Rv0919   | hypothetical protein   | NP_215434.1      | 2.412639405               |
| 41124 | G01           | 538        | Rv1139c  | hypothetical protein   | NP_215655.1      | 2                         |
| 9980  | G02           | 538        | Rv0504c  | hypothetical protein   | NP_215018.1      | 5.408921933               |
| 41141 | G03           | 541        | Rv2468c  | hypothetical protein   | NP_216984.1      | 3.284658041               |
| 41137 | G04           | 541        | Rv0864   | molybdenum cofactor biosynthesis protein C   | NP_215379.1      | 2                         |
| 41134 | G05           | 541        | Rv0138   | hypothetical protein   | NP_214652.1      | 2                         |
| 41138 | G06           | 541        | Rv2253   | hypothetical protein   | NP_216769.1      | 4.38077634                |
| 9968  | G07           | 541        | Rv1507A  | hypothetical protein   | NP_216023.1      | 4.184842884               |
| 41145 | G08           | 544        | Rv0744c  | transcriptional regulatory protein   | NP_215258.1      | 3.439338235               |
| 41149 | G09           | 544        | Rv3002c  | acetolactate synthase 3 regulatory subunit   | NP_217518.1      | 2                         |
| 41148 | G10           | 544        | Rv2376c  | low molecular weight antigen CFP2 (low molecular weight protein antigen 2) (CFP-2)                 | NP_216892.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                    | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41150 | G11           | 544        | Rv3422c  | hypothetical protein                       | NP_217939.1      | 2                         |
| 41158 | G12           | 547        | Rv3749c  | hypothetical protein                       | NP_218266.1      | 3.462522852               |
| 41156 | H01           | 547        | Rv3231c  | hypothetical protein                       | NP_217748.1      | 2                         |
| 41153 | H02           | 547        | Rv0185   | hypothetical protein                       | NP_214699.1      | 2                         |
| 41154 | H03           | 547        | Rv0268c  | hypothetical protein                       | NP_214782.1      | 2                         |
| 41155 | H04           | 547        | Rv1571   | hypothetical protein                       | NP_216087.1      | 2                         |
| 41165 | H05           | 550        | Rv2554c  | Holliday junction resolvase-like protein   | NP_217070.1      | 2                         |
| 41164 | H06           | 550        | Rv1955   | hypothetical protein                       | NP_216471.1      | 4.296363636               |
| 41161 | H07           | 550        | Rv1577c  | phiRv1 phage protein                       | NP_216093.1      | 2                         |
| 41166 | H08           | 550        | Rv3111   | molybdenum cofactor biosynthesis protein C | YP_177927.1      | 2                         |
| 41162 | H09           | 550        | Rv1657   | arginine repressor                         | NP_216173.1      | 2                         |
| 41173 | H10           | 553        | Rv1413   | hypothetical protein                       | NP_215929.1      | 2                         |
| 41168 | H11           | 553        | Rv0369c  | membrane oxidoreductase                    | NP_214883.1      | 2                         |
| 41179 | H12           | 553        | Rv2779c  | transcriptional regulatory protein         | NP_217295.2      | 2                         |

Table 18: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 18 (ZMTLH), NR-19654

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41177 | A01           | 553        | Rv1939   | oxidoreductase  | NP_216455.1      | 3.508137432               |
| 41172 | A02           | 553        | Rv1306   | F0F1 ATP synthase subunit B   | NP_215822.1      | 2                         |
| 41175 | A03           | 553        | Rv1585c  | phiRv1 phage protein  | NP_216101.1      | 3.128390597               |
| 41167 | A04           | 553        | Rv0335c  | PE family protein   | YP_177717.1      | 2                         |
| 41178 | A05           | 553        | Rv2290   | lipoprotein lppO  | NP_216806.1      | 2                         |
| 41171 | A06           | 553        | Rv0556   | transmembrane protein   | NP_215070.1      | 2                         |
| 41170 | A07           | 553        | Rv0443   | hypothetical protein  | NP_214957.1      | 3.927667269               |
| 41185 | A08           | 556        | Rv3278c  | transmembrane protein   | NP_217795.1      | 3.877697842               |
| 41187 | A09           | 556        | Rv3669   | transmembrane protein   | NP_218186.1      | 3.888489209               |
| 41188 | A10           | 559        | Rv0057   | hypothetical protein  | NP_214571.1      | 2                         |
| 41191 | A11           | 559        | Rv2668   | hypothetical protein  | NP_217184.1      | 2                         |
| 41190 | A12           | 559        | Rv1954c  | hypothetical protein  | NP_216470.1      | 3.799642218               |
| 41192 | B01           | 559        | Rv2878c  | soluble secreted antigen MPT53 precursor                                | NP_217394.1      | 2                         |
| 41204 | B02           | 562        | Rv3072c  | hypothetical protein  | NP_217588.1      | 2                         |
| 41206 | B03           | 562        | Rv3275c  | phosphoribosylaminoimidazole carboxylase catalytic subunit              | NP_217792.1      | 4.268683274               |
| 41201 | B04           | 562        | Rv2311   | hypothetical protein  | NP_216827.1      | 4.259786477               |
| 41200 | B05           | 562        | Rv1930c  | hypothetical protein  | NP_216446.1      | 3.003558719               |
| 41195 | B06           | 562        | Rv0254c  | bifunctional cobinamide kinase/cobinamide phosphate guanylyltransferase | NP_214768.1      | 2                         |
| 41198 | B07           | 562        | Rv0481c  | hypothetical protein  | NP_214995.1      | 2                         |
| 41199 | B08           | 562        | Rv1758   | cutinase Cut1   | NP_216274.1      | 2                         |
| 41203 | B09           | 562        | Rv2747   | N-acetylglutamate synthase  | NP_217263.1      | 3.886120996               |
| 41207 | B10           | 562        | Rv3525c  | siderophore-binding protein   | NP_218042.1      | 2                         |
| 41196 | B11           | 562        | Rv0461   | hypothetical protein  | NP_214975.1      | 4.544483986               |
| 41214 | B12           | 565        | Rv0901   | hypothetical protein  | NP_215416.1      | 3.49380531                |
| 41212 | C01           | 565        | Rv0745   | hypothetical protein  | NP_215259.1      | 2                         |
| 41215 | C02           | 565        | Rv1234   | hypothetical protein  | NP_215750.1      | 2                         |
| 41220 | C03           | 565        | Rv2270   | lipoprotein lppN  | NP_216786.1      | 2                         |
| 41209 | C04           | 565        | Rv0740   | hypothetical protein  | NP_215254.1      | 4.325663717               |
| 41221 | C05           | 565        | Rv2330c  | lipoprotein LppP  | NP_216846.1      | 2                         |
| 41232 | C06           | 568        | Rv3902c  | hypothetical protein  | NP_218419.1      | 3.913732394               |
| 41225 | C07           | 568        | Rv2539c  | shikimate kinase  | NP_217055.1      | 2                         |
| 41227 | C08           | 568        | Rv3114   | hypothetical protein  | NP_217630.1      | 2                         |
| 41226 | C09           | 568        | Rv2907c  | 16S rRNA-processing protein RimM  | NP_217423.1      | 2                         |
| 41230 | C10           | 568        | Rv3572   | hypothetical protein  | NP_218089.1      | 2                         |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41223 | C11           | 568        | Rv1884c  | resuscitation-promoting factor RpfC                    | NP_216400.1      | 2                         |
| 41224 | C12           | 568        | Rv2140c  | hypothetical protein                                   | NP_216656.1      | 2                         |
| 41222 | D01           | 568        | Rv1000   | CLONE IS INVALID                                       |                  | 2                         |
| 9986  | D02           | 568        | Rv2943A  | transposase  | YP_177680.1      | 4.146126761               |
| 41239 | D03           | 571        | Rv3281   | hypothetical protein                                   | NP_217798.1      | 3.098073555               |
| 41233 | D04           | 571        | Rv0735   | RNA polymerase sigma factor SigL                       | NP_215249.1      | 2                         |
| 41235 | D05           | 571        | Rv2256c  | hypothetical protein                                   | NP_216772.1      | 2                         |
| 41238 | D06           | 571        | Rv2651c  | phiRv2 prophage protease                               | NP_217167.1      | 2                         |
| 41241 | D07           | 571        | Rv3471c  | hypothetical protein                                   | NP_217988.1      | 2                         |
| 41242 | D08           | 571        | Rv3847   | hypothetical protein                                   | NP_218364.1      | 2                         |
| 41240 | D09           | 571        | Rv3324c  | molybdenum cofactor biosynthesis protein C             | NP_217841.2      | 2                         |
| 41234 | D10           | 571        | Rv1227c  | hypothetical protein                                   | NP_215743.1      | 2                         |
| 41247 | D11           | 574        | Rv3429   | PPE family protein                                     | YP_177973.1      | 2                         |
| 41248 | D12           | 574        | Rv3780   | hypothetical protein                                   | NP_218297.1      | 2                         |
| 41246 | E01           | 574        | Rv0651   | 50S ribosomal protein L10                              | NP_215165.1      | 3.893728223               |
| 41250 | E02           | 577        | Rv0382c  | orotate phosphoribosyltransferase                      | YP_177723.1      | 4.372616984               |
| 41253 | E03           | 577        | Rv1988   | methyltransferase                                      |                  | 3.760831889               |
| 41255 | E04           | 577        | Rv2630   | hypothetical protein                                   | NP_217146.1      | 4.285961872               |
| 41252 | E05           | 577        | Rv0719   | 50S ribosomal protein L6                               | NP_215233.1      | 2                         |
| 41249 | E06           | 577        | Rv0340   | hypothetical protein                                   | NP_214854.1      | 2                         |
| 41261 | E07           | 580        | Rv1231c  | hypothetical protein                                   | NP_215747.1      | 2                         |
| 41264 | E08           | 580        | Rv3456c  | CLONE IS INVALID                                       |                  | 3.482758621               |
| 41256 | E09           | 580        | Rv0047c  | hypothetical protein                                   | NP_214561.1      | 2                         |
| 41259 | E10           |            | Rv1105   | CLONE IS INVALID                                       |                  |                           |
| 41263 | E11           | 580        | Rv1275   | lipoprotein LprC                                       | NP_215791.1      | 2.644827586               |
| 41273 | E12           | 583        | Rv2321c  | ornithine aminotransferase                             | NP_216837.1      | 2                         |
| 41271 | F01           | 583        | Rv0984   | pterin-4-alpha-carbinolamine dehydratase MoaB2         | NP_215499.1      | 2                         |
| 41267 | F02           |            | Rv0619   | CLONE IS INVALID                                       |                  |                           |
| 41277 | F03           | 583        | Rv2843   | hypothetical protein                                   | NP_217359.1      | 3.159519726               |
| 41270 | F04           | 583        | Rv0762c  | hypothetical protein                                   | NP_215276.1      | 2                         |
| 41280 | F05           | 583        | Rv3841   | bacterioferritin BfrB                                  | NP_218358.1      | 2                         |
| 41265 | F06           | 583        | Rv0262c  | aminoglycoside 2'-N-acetyltransferase AAC (AAC(2')-IC) | NP_214776.1      | 2                         |
| 41272 | F07           | 583        | Rv1957   | hypothetical protein                                   | NP_216473.1      | 2                         |
| 41290 | F08           | 586        | Rv1677   | lipoprotein DsbF                                       | NP_216193.1      | 4.327645051               |
| 41292 | F09           | 586        | Rv2367c  | putative metalloprotease                               | NP_216883.1      | 2                         |
| 41286 | F10           | 586        | Rv0738   | hypothetical protein                                   | NP_215252.1      | 1.796928328               |
| 41294 | F11           | 586        | Rv3584   | lipoprotein LpqE                                       | NP_218101.1      | 2                         |
| 41293 | F12           | 586        | Rv3033   | hypothetical protein                                   | NP_217549.1      | 2                         |
| 41291 | G01           | 586        | Rv1732c  | hypothetical protein                                   | NP_216248.1      | 2                         |
| 41283 | G02           | 586        | Rv0137c  | methionine sulfoxide reductase A                       | NP_214651.1      | 2                         |
| 41282 | G03           | 586        | Rv0009   | iron-regulated peptidyl-prolyl cis-trans isomerase A   | NP_214523.1      | 3.109215017               |
| 41284 | G04           | 586        | Rv0219   | transmembrane protein                                  | NP_214733.1      | 2                         |
| 41287 | G05           |            | Rv1503c  | CLONE IS INVALID                                       |                  |                           |
| 41285 | G06           | 586        | Rv0513   | transmembrane protein                                  | NP_215027.1      | 2.537542662               |
| 41305 | G07           | 589        | Rv3222c  | hypothetical protein                                   | NP_217738.1      | 2                         |
| 41307 | G08           | 589        | Rv3867   | hypothetical protein                                   | NP_218384.1      | 2                         |
| 41306 | G09           | 589        | Rv3361c  | hypothetical protein                                   | NP_217878.1      | 2                         |
| 41303 | G10           | 589        | Rv2838c  | ribosome-binding factor A                              | NP_217354.1      | 2                         |
| 41304 | G11           | 589        | Rv2842c  | hypothetical protein                                   | NP_217358.1      | 2                         |
| 41296 | G12           | 589        | Rv0098   | hypothetical protein                                   | NP_214612.1      | 2.36672326                |
| 41311 | H01           | 592        | Rv3614c  | hypothetical protein                                   | NP_218131.1      | 2                         |
| 41308 | H02           | 592        | Rv0177   | MCE associated protein                                 | NP_214691.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------|------------------|---------------------------|
| 41310 | H03           | 592        | Rv3146   | NADH dehydrogenase subunit B | NP_217662.1      | 2                         |
| 41309 | H04           | 592        | Rv3054c  | hypothetical protein         | NP_217570.1      | 2                         |
| 41320 | H05           | 595        | Rv2390c  | hypothetical protein         | NP_216906.1      | 3.173109244               |
| 41324 | H06           | 595        | Rv2882c  | ribosome recycling factor    | NP_217398.1      | 3.287394958               |
| 41321 | H07           |            | Rv2499c  | CLONE IS INVALID             |                  |                           |
| 41314 | H08           | 595        | Rv1274   | lipoprotein LprB             | NP_215790.1      | 2                         |
| 41313 | H09           | 595        | Rv1228   | lipoprotein LpqX             | NP_215744.1      | 2                         |
| 41316 | H10           | 595        | Rv1749c  | integral membrane protein    | NP_216265.1      | 1.83697479                |
| 41312 | H11           | 595        | Rv0743c  | hypothetical protein         | NP_215257.1      | 2                         |
| 41331 | H12           | 598        | Rv1989c  | CLONE IS INVALID             | NP_216505.1      | 1.941471572               |

Table 19: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 19 (ZMTLI), NR-19655

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41329 | A01           | 598        | Rv1776c  | transcriptional regulatory protein   | NP_216292.1      | 2                         |
| 41335 | A02           | 598        | Rv3209   | hypothetical protein   | NP_217725.1      | 3.548494983               |
| 41332 | A03           | 598        | Rv2043c  | pyrazinamidase/nicotinamidase PNCA (PZase)                                 | NP_216559.1      | 3.852842809               |
| 41325 | A04           |            | Rv0344c  | CLONE IS INVALID   |                  |                           |
| 41330 | A05           | 598        | Rv1888c  | transmembrane protein  | NP_216404.1      | 2                         |
| 41340 | A06           | 601        | Rv1205   | hypothetical protein   | NP_215721.1      | 4.364392679               |
| 41351 | A07           | 601        | Rv3920c  | hypothetical protein   | NP_218437.1      | 2                         |
| 41345 | A08           | 601        | Rv2080   | lipoprotein LppJ   | NP_216596.1      | 2                         |
| 41349 | A09           | 601        | Rv3567c  | Oxidoreductase   | NP_218084.1      | 1.856905158               |
| 41350 | A10           | 601        | Rv3724   | cutinase   | NP_216817        | 2                         |
| 41337 | A11           | 601        | Rv0052   | hypothetical protein   | NP_214566.1      | 2                         |
| 41346 | A12           | 601        | Rv2534c  | elongation factor P  | NP_217050.1      | 2                         |
| 41344 | B01           | 601        | Rv1780   | hypothetical protein   | NP_216296.1      | 2                         |
| 41338 | B02           | 601        | Rv0445c  | RNA polymerase sigma factor SigK   | NP_214959.1      | 2                         |
| 41339 | B03           | 601        | Rv0716   | 50S ribosomal protein L5   | NP_215230.1      | 2                         |
| 41336 | B04           | 601        | Rv0004   | hypothetical protein   | NP_214518.1      | 2                         |
| 41360 | B05           | 604        | Rv3606c  | 2-amino-4-hydroxy-6-hydroxy-methylidihydropteridine pyrophosphokinase FolK | NP_218123.1      | 4.245033113               |
| 41353 | B06           | 604        | Rv1065   | hypothetical protein   | NP_215581.1      | 4.223509934               |
| 41361 | B07           | 604        | Rv3639c  | hypothetical protein   | NP_218156.1      | 2                         |
| 41358 | B08           | 604        | Rv3405c  | transcriptional regulatory protein   | NP_217922.1      | 2                         |
| 41356 | B09           | 604        | Rv2594c  | Holliday junction resolvase  | NP_217110.1      | 2                         |
| 41357 | B10           | 604        | Rv2966c  | methyltransferase (methylase)  | NP_217482.1      | 2                         |
| 41369 | B11           | 607        | Rv2405   | hypothetical protein   | NP_216921.1      | 2                         |
| 41368 | B12           | 607        | Rv2116   | No growth on plate   | NP_216632.1      | 2                         |
| 41364 | C01           | 607        | Rv1176c  | hypothetical protein   | NP_215692.1      | 4.439868204               |
| 41363 | C02           | 607        | Rv1031   | potassium-transporting ATPase subunit C                                    | NP_215547.1      | 2                         |
| 41362 | C03           | 607        | Rv0067c  | TetR family transcriptional regulator                                      | NP_214581.1      | 2                         |
| 41374 | C04           | 610        | Rv0464c  | hypothetical protein   | NP_214978.1      | 2                         |
| 41373 | C05           | 610        | Rv0321   | deoxycytidine triphosphate deaminase                                       | NP_214836.1      | 2                         |
| 41372 | C06           | 610        | Rv0114   | D-alpha,beta-D-heptose-1,7-biphosphate phosphatase                         | NP_214628.1      | 2                         |
| 41379 | C07           | 613        | Rv2016   | hypothetical protein   | NP_216532.1      | 2                         |
| 41381 | C08           |            | Rv3770c  | CLONE IS INVALID   |                  |                           |
| 41380 | C09           | 613        | Rv3657c  | hypothetical protein   | NP_218174.1      | 3.314845024               |
| 41377 | C10           | 613        | Rv1014c  | peptidyl-tRNA hydrolase  | NP_215530.1      | 2                         |
| 41383 | C11           | 613        | Rv3832c  | hypothetical protein   | NP_218349.1      | 2                         |
| 41378 | C12           | 613        | Rv1972   | mce associated membrane protein  | NP_216488.1      | 2                         |
| 41384 | D01           | 616        | Rv3491   | hypothetical protein   | NP_218008.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                     | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41393 | D02           | 619        | Rv2792c  | resolvase   | NP_217308.1      | 3.134087237               |
| 41394 | D03           | 619        | Rv2875   | major secreted immunogenic protein MPT70                    | NP_217391.1      | 2                         |
| 41387 | D04           | 619        | Rv0274   | hypothetical protein  | NP_214788.1      | 2                         |
| 41388 | D05           | 619        | Rv0921   | resolvase   | NP_215436.1      | 2                         |
| 41389 | D06           | 619        | Rv1314c  | hypothetical protein  | NP_215830.1      | 3.224555735               |
| 41396 | D07           | 619        | Rv3362c  | ATP/GTP-binding protein                                     | NP_217879.1      | 2.337641357               |
| 41404 | D08           | 622        | Rv3773c  | hypothetical protein  | NP_218290.1      | 2.856913183               |
| 41400 | D09           | 622        | Rv2430c  | PPE family protein  | YP_177881.1      | 2                         |
| 41399 | D10           | 622        | Rv1203c  | hypothetical protein  | NP_215719.1      | 2                         |
| 41403 | D11           | 622        | Rv2979c  | resolvase   | NP_217495.1      | 2                         |
| 41398 | D12           | 622        | Rv0196   | transcriptional regulatory protein                          | NP_214710.1      | 3.135048232               |
| 41412 | E01           | 625        | Rv2613c  | hypothetical protein  | NP_217129.1      | 2                         |
| 41410 | E02           | 625        | Rv2428   | alkyl hydroperoxide reductase subunit C                     | NP_216944.1      | 3.5664                    |
| 41413 | E03           | 625        | Rv2912c  | TetR family transcriptional regulator                       | NP_217428.1      | 2                         |
| 41408 | E04           | 625        | Rv1624c  | hypothetical protein  | NP_216140.1      | 4.1248                    |
| 41406 | E05           | 625        | Rv1156   | hypothetical protein  | NP_215672.1      | 1.7168                    |
| 41409 | E06           | 625        | Rv2134c  | hypothetical protein  | NP_216650.1      | 2                         |
| 41419 | E07           | 628        | Rv2593c  | Holliday junction DNA helicase RuvA                         | NP_217109.1      | 2                         |
| 41418 | E08           | 628        | Rv1944c  | hypothetical protein  | NP_216460.1      | 2                         |
| 41415 | E09           | 628        | Rv0113   | phosphoheptose isomerase                                    | NP_214627.1      | 3.109872611               |
| 41420 | E10           | 628        | Rv3233c  | hypothetical protein  | NP_217750.1      | 2                         |
| 41417 | E11           | 628        | Rv1703c  | catechol-o-methyltransferase                                | NP_216219.1      | 2                         |
| 41416 | E12           | 628        | Rv0681   | TetR family transcriptional regulator                       | NP_215195.1      | 2                         |
| 41422 | F01           | 631        | Rv0089   | methyltransferase/methylase                                 | NP_214603.1      | 3.050713154               |
| 41424 | F02           | 631        | Rv0371c  | hypothetical protein  | NP_214885.1      | 2                         |
| 41428 | F03           | 631        | Rv0992c  | hypothetical protein  | NP_215507.1      | 2                         |
| 41431 | F04           | 631        | Rv1541c  | lipoprotein LprI  | NP_216057.1      | 3.846275753               |
| 41432 | F05           | 631        | Rv1910c  | hypothetical protein  | NP_216426.1      | 2                         |
| 41427 | F06           | 631        | Rv0706   | 50S ribosomal protein L22                                   | NP_215220.1      | 2                         |
| 41429 | F07           | 631        | Rv1019   | TetR family transcriptional regulator                       | NP_215535.1      | 2                         |
| 41426 | F08           |            | Rv0429c  | CLONE IS INVALID  |                  |                           |
| 41423 | F09           | 631        | Rv0366c  | hypothetical protein  | NP_214880.1      | 2                         |
| 10111 | F10           | 631        | Rv0078A  | hypothetical protein  | YP_177616.1      | 5.199683043               |
| 9991  | F11           | 631        | Rv2306A  | hypothetical protein  | YP_177663.1      | 2                         |
| 41436 | F12           | 634        | Rv2604c  | glutamine amidotransferase subunit PdxT                     | NP_217120.1      | 2                         |
| 41435 | G01           | 634        | Rv1233c  | hypothetical protein  | NP_215749.1      | 2                         |
| 41434 | G02           | 634        | Rv0691c  | transcriptional regulatory protein                          | NP_215205.1      | 3.105678233               |
| 41442 | G03           | 637        | Rv1885c  | chorismate mutase   | NP_216401.1      | 3.466248038               |
| 41445 | G04           | 637        | Rv3574   | transcriptional regulatory protein TetR-family              | NP_218091.1      | 2                         |
| 41443 | G05           | 637        | Rv1986   | integral membrane protein                                   | NP_216502.1      | 2                         |
| 41439 | G06           | 637        | Rv0789c  | hypothetical protein  | NP_215304.1      | 4.185243328               |
| 41440 | G07           | 637        | Rv1504c  | hypothetical protein  | NP_216020.1      | 2                         |
| 41446 | G08           | 637        | Rv3755c  | hypothetical protein  | NP_218272.1      | 2                         |
| 41437 | G09           | 637        | Rv0475   | iron-regulated heparin binding hemagglutinin hbhA (adhesin) | NP_214989.1      | 2                         |
| 41444 | G10           | 637        | Rv2949c  | hypothetical protein  | NP_217465.1      | 2                         |
| 41451 | G11           | 640        | Rv2461c  | ATP-dependent Clp protease proteolytic subunit              | YP_177883.1      | 4.2625                    |
| 41447 | G12           | 640        | Rv0328   | TetR/AcrR family transcriptional regulator                  | NP_214842.1      | 2                         |
| 41449 | H01           | 640        | Rv1401   | hypothetical protein  | NP_215917.1      | 3.090625                  |
| 41452 | H02           | 640        | Rv3120   | hypothetical protein  | NP_217636.1      | 2                         |
| 41454 | H03           | 640        | Rv3173c  | TetR/ACRR family transcriptional regulator                  | NP_217689.1      | 3.0921875                 |
| 41455 | H04           | 640        | Rv3557c  | TetR family transcriptional regulator                       | NP_218074.1      | 2                         |
| 41466 | H05           | 643        | Rv1167c  | transcriptional regulatory protein                          | NP_215683.1      | 2                         |
| 41475 | H06           | 643        | Rv3458c  | 30S ribosomal protein S4                                    | NP_217975.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41474 | H07           | 643        | Rv2453c  | molybdopterin-guanine dinucleotide biosynthesis protein A | NP_216969.1      | 2                         |
| 41457 | H08           | 643        | Rv0133   | acetyltransferase   | NP_214647.1      | 2                         |
| 41467 | H09           | 643        | Rv1412   | riboflavin synthase subunit alpha                         | NP_215928.1      | 2                         |
| 41464 | H10           | 643        | Rv1126c  | hypothetical protein                                      | NP_215642.1      | 2                         |
| 41465 | H11           | 643        | Rv1163   | respiratory nitrate reductase subunit delta NarJ          | NP_215679.1      | 2                         |
| 41468 | H12           |            | Rv1641   | CLONE IS INVALID  |                  |                           |

Table 20: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 20 (ZMTLJ), NR-19656

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41456 | A01           | 643        | Rv0078   | transcriptional regulatory protein                        | NP_214592.1      | 2                         |
| 41471 | A02           | 643        | Rv1911c  | lipoprotein LppC  | NP_216427.1      | 3.833592535               |
| 41479 | A03           | 646        | Rv0525   | hypothetical protein                                      | NP_215039.1      | 4.27244582                |
| 41490 | A04           | 646        | Rv3609c  | GTP cyclohydrolase I                                      | NP_218126.1      | 2                         |
| 41484 | A05           | 646        | Rv1539   | lipoprotein signal peptidase                              | NP_216055.1      | 2                         |
| 41481 | A06           | 646        | Rv1252c  | lipoprotein LprE  | NP_215768.1      | 2                         |
| 41485 | A07           | 646        | Rv1556   | regulatory protein  | NP_216072.1      | 4.255417957               |
| 41482 | A08           | 646        | Rv1255c  | transcriptional regulatory protein                        | NP_215771.1      | 2                         |
| 41483 | A09           | 646        | Rv1435c  | proline, glycine, valine-rich secreted protein            | NP_215951.1      | 2                         |
| 41489 | A10           | 646        | Rv3465   | dTDP-4-dehydrorhamnose 3,5-epimerase RmlC                 | NP_217982.1      | 2                         |
| 41487 | A11           | 646        | Rv2811   | hypothetical protein                                      | NP_217327.1      | 2                         |
| 41480 | A12           | 646        | Rv0605   | resolvase   | NP_215119.1      | 2                         |
| 41488 | B01           | 646        | Rv3066   | DeoR family transcriptional regulator                     | NP_217582.1      | 2                         |
| 41498 | B02           | 649        | Rv1890c  | hypothetical protein                                      | NP_216406.1      | 2                         |
| 41495 | B03           | 649        | Rv1688   | 3-methyladenine DNA glycosylase                           | NP_216204.1      | 2                         |
| 41501 | B04           | 649        | Rv3715c  | recombination protein RecR                                | NP_218232.1      | 2                         |
| 41492 | B05           | 649        | Rv0698   | hypothetical protein                                      | NP_215212.1      | 4.235747304               |
| 41502 | B06           | 649        | Rv3828c  | resolvase   | NP_218345.1      | 2                         |
| 41500 | B07           | 649        | Rv3214   | acid phosphatase  | YP_177944.1      | 2                         |
| 41499 | B08           | 649        | Rv2193   | cytochrome C oxidase subunit III                          | NP_216709.1      | 2                         |
| 41497 | B09           | 649        | Rv1745c  | isopentenyl-diphosphate delta-isomerase                   | NP_216261.1      | 3.1201849                 |
| 41510 | B10           | 652        | Rv2732c  | transmembrane protein                                     | NP_217248.1      | 2                         |
| 41504 | B11           | 652        | Rv0238   | TetR family transcriptional regulator                     | NP_214752.1      | 4.225460123               |
| 41509 | B12           | 652        | Rv1958c  | hypothetical protein                                      | NP_216474.1      | 2                         |
| 41508 | C01           | 652        | Rv1341   | putative deoxyribonucleotide triphosphate pyrophosphatase | NP_215857.1      | 3.685582822               |
| 41505 | C02           | 652        | Rv0316   | muconolactone isomerase                                   | NP_214830.1      | 2                         |
| 41515 | C03           | 652        | Rv3322c  | methyltransferase   | YP_177958.1      | 2                         |
| 41511 | C04           | 652        | Rv3007c  | oxidoreductase  | NP_217523.1      | 4.306748466               |
| 41518 | C05           | 655        | Rv1626   | two-component system transcriptional regulator            | NP_216142.1      | 2                         |
| 41517 | C06           | 655        | Rv1498c  | hypothetical protein                                      | YP_177647.1      | 3.838167939               |
| 41524 | C07           | 658        | Rv2597   | hypothetical protein                                      | NP_217113.1      | 1.995440729               |
| 41523 | C08           | 658        | Rv2170   | hypothetical protein                                      | NP_216686.1      | 2                         |
| 41522 | C09           | 658        | Rv1602   | imidazole glycerol phosphate synthase subunit HisH        | NP_216118.1      | 2                         |
| 41519 | C10           | 658        | Rv0273c  | transcriptional regulatory protein                        | NP_214787.1      | 2                         |
| 41542 | C11           | 661        | Rv3588c  | carbonic anhydrase  | NP_218105.1      | 3.838124054               |
| 41539 | C12           | 661        | Rv3008   | hypothetical protein                                      | NP_217524.1      | 2                         |
| 41527 | D01           | 661        | Rv0600c  | two component sensor kinase                               | NP_215114.2      | 2                         |
| 41533 | D02           | 661        | Rv2114   | hypothetical protein                                      | NP_216630.1      | 2                         |
| 41537 | D03           | 661        | Rv2849c  | cob(I)yrinic acid a,c-diamide adenosyltransferase         | YP_177908.1      | 4.220877458               |
| 41534 | D04           | 661        | Rv2466c  | hypothetical protein                                      | NP_216982.1      | 2                         |
| 41540 | D05           | 661        | Rv3309c  | uracil phosphoribosyltransferase                          | NP_217826.1      | 4.248108926               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41532 | D06           | 661        | Rv1700   | hypothetical protein   | NP_216216.1      | 2                         |
| 41538 | D07           | 661        | Rv2926c  | hypothetical protein   | NP_217442.1      | 2                         |
| 41544 | D08           | 661        | Rv3846   | superoxide dismutase   | NP_218363.1      | 2.515885023               |
| 41529 | D09           | 661        | Rv1044   | hypothetical protein   | NP_215560.1      | 2                         |
| 41528 | D10           | 661        | Rv0775   | hypothetical protein   | NP_215289.1      | 2                         |
| 41535 | D11           | 661        | Rv2491   | hypothetical protein   | NP_217007.1      | 2                         |
| 41545 | D12           | 664        | Rv0042c  | MarR family transcriptional regulator                              | NP_214556.1      | 2                         |
| 41546 | E01           | 664        | Rv0329c  | hypothetical protein   | NP_214843.1      | 2                         |
| 41553 | E02           | 664        | Rv2652c  | phiRv2 prophage protein  | NP_217168.1      | 2                         |
| 41554 | E03           | 664        | Rv3167c  | TetR family transcriptional regulator                              | NP_217683.1      | 2                         |
| 41551 | E04           | 664        | Rv2065   | precorrin-8X methylmutase  | NP_216581.1      | 2                         |
| 41548 | E05           | 664        | Rv1389   | guanylate kinase   | NP_215905.1      | 3.826807229               |
| 41549 | E06           | 664        | Rv1853   | urease accessory protein ureD                                      | NP_216369.1      | 3.832831325               |
| 41552 | E07           | 664        | Rv2306c  | hypothetical protein   | NP_216823.1      | 2                         |
| 10033 | E08           | 664        | Rv3395A  | hypothetical protein   | NP_217912.2      | 2                         |
| 41558 | E09           | 667        | Rv1822   | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase | NP_216338.1      | 2                         |
| 41563 | E10           | 667        | Rv3016   | lipoprotein LpqA   | NP_217532.1      | 2                         |
| 41556 | E11           |            | Rv0804   | hypothetical protein   | NP_215319.1      |                           |
| 41555 | E12           | 667        | Rv0421c  | hypothetical protein   | NP_214935.1      | 2                         |
| 41559 | F01           | 667        | Rv2746c  | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase | NP_217262.1      | 2                         |
| 41562 | F02           | 667        | Rv2804c  | hypothetical protein   | NP_217320.1      | 4.24137931                |
| 41560 | F03           | 667        | Rv2799   | hypothetical protein   | NP_217315.1      | 2                         |
| 41564 | F04           | 667        | Rv3830c  | transcriptional regulatory protein TetR-family                     | NP_218347.1      | 4.217391304               |
| 41572 | F05           | 670        | Rv1601   | imidazoleglycerol-phosphate dehydratase                            | NP_216117.1      | 2                         |
| 41565 | F06           | 670        | Rv0264c  | hypothetical protein   | NP_214778.1      | 2                         |
| 41578 | F07           | 670        | Rv3897c  | hypothetical protein   | NP_218414.1      | 2                         |
| 41567 | F08           | 670        | Rv0539   | dolichyl-phosphate sugar synthase                                  | NP_215053.1      | 2                         |
| 41577 | F09           | 670        | Rv2968c  | integral membrane protein  | NP_217484.1      | 2                         |
| 41574 | F10           | 670        | Rv1733c  | transmembrane protein  | NP_216249.1      | 4.219402985               |
| 41566 | F11           | 670        | Rv0302   | TetR/ACRR family transcriptional regulator                         | NP_214816.1      | 2                         |
| 41570 | F12           | 670        | Rv1289   | hypothetical protein   | NP_215805.1      | 2                         |
| 41569 | G01           | 670        | Rv0970   | integral membrane protein  | NP_215485.1      | 4.228358209               |
| 41571 | G02           | 670        | Rv1347c  | hypothetical protein   | NP_215863.1      | 2                         |
| 41584 | G03           | 673        | Rv2421c  | nicotinic acid mononucleotide adenyltransferase                    | NP_216937.1      | 3.50371471                |
| 41583 | G04           | 673        | Rv2260   | hypothetical protein   | NP_216776.1      | 1.891530461               |
| 41590 | G05           | 673        | Rv3421c  | hypothetical protein   | NP_217938.1      | 2                         |
| 41591 | G06           | 673        | Rv3641c  | cell filamentation protein FIC                                     | NP_218158.1      | 2                         |
| 41581 | G07           | 673        | Rv1870c  | hypothetical protein   | NP_216386.1      | 2                         |
| 41580 | G08           | 673        | Rv1851   | urease accessory protein uref                                      | NP_216367.1      | 2                         |
| 41579 | G09           | 673        | Rv0195   | two component transcriptional regulatory protein                   | NP_214709.1      | -                         |
| 41588 | G10           | 673        | Rv3249c  | TetR family transcriptional regulator                              | NP_217766.1      | 2                         |
| 41589 | G11           | 673        | Rv3294   | INVALID CLONE  |                  | 2                         |
| 41596 | G12           | 676        | Rv1377c  | putative transferase   | NP_215893.1      | 2.044378698               |
| 41593 | H01           | 676        | Rv1109c  | hypothetical protein   | NP_215625.1      | 2.221893491               |
| 41597 | H02           | 676        | Rv2295   | hypothetical protein   | NP_216811.1      | 3.125739645               |
| 41594 | H03           | 676        | Rv1219c  | transcriptional regulatory protein                                 | NP_215735.1      | 2                         |
| 41600 | H04           | 676        | Rv3414c  | RNA polymerase sigma factor SigD                                   | NP_217931.1      | 2.202662722               |
| 41610 | H05           | 679        | Rv3160c  | TetR family transcriptional regulator                              | NP_217676.1      | 2                         |
| 41603 | H06           | 679        | Rv0398c  | hypothetical protein   | NP_214912.1      | 2                         |
| 41604 | H07           | 679        | Rv0767c  | hypothetical protein   | NP_215281.1      | 4.762886598               |
| 41606 | H08           | 679        | Rv0821c  | phosphate transport regulator                                      | NP_215336.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name) | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------|------------------|---------------------------|
| 41607 | H09           | 679        | Rv0825c  | hypothetical protein    | NP_215340.1      | 2                         |
| 41613 | H10           | 679        | Rv3242c  | hypothetical protein    | NP_217759.1      | 2.223858616               |
| 41611 | H11           | 679        | Rv3235   | hypothetical protein    | NP_217752.1      | 3.430044183               |
| 41608 | H12           | 679        | Rv1154c  | hypothetical protein    | NP_215670.1      | 2                         |

Table 21: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 21 (ZMTLK), NR-19657

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41614 | A01           | 679        | Rv3373   | enoyl-CoA hydratase  | NP_217890.1      | 2                         |
| 41609 | A02           | 679        | Rv2036   | hypothetical protein Rv2036                                      | NP_216552.1      | 2                         |
| 41616 | A03           | 682        | Rv0356c  | hypothetical protein Rv0356c                                     | NP_214870.1      | 2                         |
| 41627 | A04           | 682        | Rv3247c  | thymidylate kinase   | NP_217764.1      | 3.850439883               |
| 41629 | A05           | 682        | Rv3338   | hypothetical protein Rv3338                                      | NP_217855.1      | 2                         |
| 41617 | A06           | 682        | Rv0835   | lipoprotein LpqQ   | NP_215350.1      | 2                         |
| 41620 | A07           | 682        | Rv2197c  | transmembrane protein  | NP_216713.1      | 2                         |
| 41633 | A08           | 682        | Rv3705c  | proline rich protein   | YP_178006.1      | 2.19941349                |
| 41626 | A09           | 682        | Rv3241c  | hypothetical protein Rv3241c                                     | NP_217758.1      | 2                         |
| 41631 | A10           | 682        | Rv3368c  | oxidoreductase   | NP_217885.1      | 2.394428152               |
| 41621 | A11           | 682        | Rv2460c  | ATP-dependent Clp protease proteolytic subunit                   | NP_216976.1      | 2                         |
| 41615 | A12           | 682        | Rv0158   | TetR family transcriptional regulator                            | NP_214672.1      | 2                         |
| 41642 | B01           |            | Rv1907c  | CLONE IS INVALID   | NP_216423.1      |                           |
| 41647 | B02           | 685        | Rv2825c  | hypothetical protein Rv2825c                                     | NP_217341.1      | 4.081751825               |
| 41638 | B03           | 685        | Rv1015c  | 50S ribosomal protein L25/general stress protein Ctc             | NP_215531.1      | 3.861313869               |
| 41646 | B04           | 685        | Rv2511   | oligoribonuclease  | NP_217027.1      | 3.835036496               |
| 41649 | B05           | 688        | Rv0844c  | nitrate/nitrite response transcriptional regulatory protein NarL | NP_215359.1      | 2                         |
| 41654 | B06           | 688        | Rv3223c  | RNA polymerase sigma factor RpoE                                 | NP_217739.1      | 2                         |
| 41656 | B07           | 688        | Rv3855   | transcriptional regulatory repressor protein (TETR-family) ETHR  | NP_218372.1      | 2                         |
| 41653 | B08           | 688        | Rv3058c  | TetR family transcriptional regulator                            | NP_217574.1      | 2                         |
| 41655 | B09           | 688        | Rv3624c  | hypoxanthine-guanine phosphoribosyltransferase                   | NP_218141.1      | 2                         |
| 41652 | B10           | 688        | Rv2700   | secreted alanine rich protein                                    | NP_217216.1      | 2                         |
| 41648 | B11           | 688        | Rv0526   | thioredoxin protein  | NP_215040.1      | 2                         |
| 41664 | B12           | 691        | Rv1301   | hypothetical protein Rv1301                                      | NP_215817.1      | 2                         |
| 41659 | C01           | 691        | Rv0413   | 7,8-dihydro-8-oxoguanine-triphosphatase                          | NP_214927.1      | 3.269175109               |
| 41668 | C02           | 691        | Rv1984c  | cutinase precursor CFP21   | NP_216500.1      | 2                         |
| 41663 | C03           | 691        | Rv0836c  | hypothetical protein Rv0836c                                     | NP_215351.1      | 2                         |
| 41675 | C04           | 691        | Rv3133c  | two component transcriptional regulatory protein                 | NP_217649.1      | 2                         |
| 41679 | C05           | 691        | Rv3690   | hypothetical protein Rv3690                                      | NP_218207.1      | 2                         |
| 41667 | C06           | 691        | Rv1667c  | macrolide-transport ATP-binding protein ABC transporter          | NP_216183.1      | 2                         |
| 41676 | C07           | 691        | Rv3376   | hypothetical protein Rv3376                                      | NP_217893.1      | 2                         |
| 41674 | C08           | 691        | Rv2720   | LexA repressor   | NP_217236.1      | 2                         |
| 41671 | C09           | 691        | Rv2474c  | hypothetical protein Rv2474c                                     | NP_216990.1      | 2                         |
| 41661 | C10           | 691        | Rv0434   | hypothetical protein Rv0434                                      | NP_214948.1      | 2                         |
| 41662 | C11           | 691        | Rv0701   | 50S ribosomal protein L3   | NP_215215.1      | 2                         |
| 41693 | C12           | 694        | Rv3013   | hypothetical protein Rv3013                                      | NP_217529.1      | 2                         |
| 41690 | D01           | 694        | Rv2503c  | succinyl-CoA:3-ketoacid-coenzyme A transferase subunit beta ScoB | NP_217019.1      | 3.005763689               |
| 41695 | D02           | 694        | Rv3850   | hypothetical protein Rv3850                                      | NP_218367.1      | 2                         |
| 41689 | D03           | 694        | Rv2046   | lipoprotein lppI   | NP_216562.1      | 2.061959654               |
| 41694 | D04           | 694        | Rv3513c  | fatty-acid-CoA ligase  | NP_218030.1      | 2                         |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41684 | D05           | 694        | Rv0990c  | hypothetical protein Rv0990c                       | NP_215505.1      | 2                         |
| 41683 | D06           | 694        | Rv0802c  | hypothetical protein Rv0802c                       | NP_215317.1      | 2                         |
| 41682 | D07           | 694        | Rv0727c  | L-fucose-phosphate aldolase                        | NP_215241.1      | 2                         |
| 41687 | D08           | 694        | Rv1674c  | transcriptional regulatory protein                 | NP_216190.1      | 2                         |
| 41697 | D09           | 697        | Rv0349   | hypothetical protein Rv0349                        | NP_214863.1      | 2                         |
| 41699 | D10           | 697        | Rv2250c  | transcriptional regulator                          | NP_216766.2      | 2.444763271               |
| 41696 | D11           | 697        | Rv0199   | hypothetical protein Rv0199                        | NP_214713.1      | 2                         |
| 41708 | D12           | 700        | Rv0187   | O-methyltransferase                                | NP_214701.1      | 2                         |
| 41706 | E01           |            | Rv0085   | CLONE IS INVALID                                   | NP_214600.1      |                           |
| 41710 | E02           | 700        | Rv0320   | hypothetical protein Rv0320                        | NP_214834.1      | 3.837142857               |
| 41714 | E03           | 700        | Rv0721   | 30S ribosomal protein S5                           | NP_215235.1      | 2                         |
| 41721 | E04           | 700        | Rv3483c  | hypothetical protein Rv3483c                       | NP_218000.1      | 2                         |
| 41717 | E05           | 700        | Rv2544   | lipoprotein LppB                                   | NP_217060.1      | 4.26                      |
| 41709 | E06           | 700        | Rv0314c  | hypothetical protein Rv0314c                       | NP_214828.1      | 2                         |
| 41720 | E07           | 700        | Rv2873   | cell surface lipoprotein mpt83 (lipoprotein P23)   | NP_217389.1      | 2                         |
| 41719 | E08           | 700        | Rv2692   | TRK system potassium uptake protein CEOC           | YP_177901.1      | 2.39                      |
| 41725 | E09           | 703        | Rv1815   | hypothetical protein Rv1815                        | NP_216331.1      | 4.226173542               |
| 41722 | E10           | 703        | Rv0448c  | hypothetical protein Rv0448c                       | NP_214962.1      | 3.20625889                |
| 41731 | E11           | 703        | Rv3295   | TetR family transcriptional regulator              | NP_217812.1      | 4.105263158               |
| 41727 | E12           | 703        | Rv1975   | hypothetical protein Rv1975                        | NP_216491.1      | -                         |
| 41728 | F01           | 703        | Rv2177c  | transposase  | NP_216693.1      | 4.216216216               |
| 41732 | F02           | 703        | Rv3301c  | phosphate transporter PhoU                         | NP_217818.1      | 1.992887624               |
| 41723 | F03           | 703        | Rv1505c  | hypothetical protein Rv1505c                       | NP_216021.1      | 1.991465149               |
| 41730 | F04           | 703        | Rv2322c  | ornithine aminotransferase                         | NP_216838.1      | 2.691322902               |
| 41724 | F05           | 703        | Rv1591   | hypothetical protein Rv1591                        | NP_216107.1      | 1.991465149               |
| 41736 | F06           | 706        | Rv0414c  | thiamine-phosphate pyrophosphorylase               | NP_214928.1      | 4                         |
| 41735 | F07           | 706        | Rv0319   | pyrrolidone-carboxylate peptidase                  | NP_214833.1      | 3.827195467               |
| 41742 | F08           | 706        | Rv3113   | phosphatase  | NP_217629.1      | 2                         |
| 41737 | F09           | 706        | Rv1588c  | REP13E12 repeat-containing protein                 | NP_216104.1      | 1.994334278               |
| 41744 | F10           | 706        | Rv3282   | Maf-like protein                                   | NP_217799.1      | 1.992917847               |
| 41745 | F11           | 706        | Rv3466   | hypothetical protein Rv3466                        | NP_217983.1      | 2                         |
| 41741 | F12           | 706        | Rv2469c  | hypothetical protein Rv2469c                       | NP_216985.1      | 2.253541076               |
| 41743 | G01           | 706        | Rv3271c  | integral membrane protein                          | NP_217788.1      | 1.992917847               |
| 41753 | G02           | 709        | Rv2419c  | phosphoglycerate mutase (phosphoglyceromutase)     | NP_216935.1      | 1.992947814               |
| 41750 | G03           | 709        | Rv0323c  | hypothetical protein Rv0323c                       | NP_214837.1      | 4.235543018               |
| 41756 | G04           | 709        | Rv2693c  | integral membrane alanine and leucine rich protein | NP_217209.1      | 2                         |
| 41752 | G05           | 709        | Rv0702   | 50S ribosomal protein L4                           | NP_215216.1      | 4.231311707               |
| 41749 | G06           | 709        | Rv0306   | putative oxidoreductase                            | NP_214820.1      | 2.047954866               |
| 41754 | G07           | 709        | Rv2584c  | adenine phosphoribosyltransferase                  | NP_217100.1      | 4.221438646               |
| 41765 | G08           | 712        | Rv1852   | urease accessory protein ureG                      | NP_216368.1      | 2                         |
| 41771 | G09           | 712        | Rv2621c  | transcriptional regulatory protein                 | NP_217137.1      | 3.233146067               |
| 41768 | G10           | 712        | Rv2581c  | glyoxalase II                                      | NP_217097.1      | 1.990168539               |
| 41761 | G11           | 712        | Rv0788   | phosphoribosylformylglycinamide synthase I         | NP_215303.1      | 1.992977528               |
| 41775 | G12           | 712        | Rv3741c  | oxidoreductase                                     | NP_218258.1      | 1.992977528               |
| 41773 | H01           |            | Rv3676   | CLONE IS INVALID                                   | NP_218193.1      |                           |
| 41758 | H02           | 712        | Rv0478   | deoxyribose-phosphate aldolase                     | NP_214992.1      | 2                         |
| 41764 | H03           | 712        | Rv1216c  | integral membrane protein                          | NP_215732.1      | 2                         |
| 41772 | H04           | 712        | Rv3203   | lipase LipV  | NP_217719.1      | 3.231741573               |
| 41757 | H05           | 712        | Rv0088   | hypothetical protein Rv0088                        | NP_214602.1      | 2                         |
| 41776 | H06           | 712        | Rv3919c  | 16S rRNA methyltransferase GidB                    | NP_218436.1      | 4.247191011               |
| 41783 | H07           | 715        | Rv2636   | hypothetical protein Rv2636                        | NP_217152.1      | 3.620979021               |
| 41781 | H08           | 715        | Rv1856c  | short chain dehydrogenase                          | NP_216372.1      | 3.586013986               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)     | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-----------------------------|------------------|---------------------------|
| 41780 | H09           | 715        | Rv1830   | hypothetical protein Rv1830 | NP_216346.1      | 1.993006993               |
| 41784 | H10           | 715        | Rv3387   | transposase                 | NP_217904.1      | 2                         |
| 41782 | H11           | 715        | Rv2618   | hypothetical protein Rv2618 | NP_217134.1      | 1.991608392               |
| 41791 | H12           | 718        | Rv1027c  |                             | NP_215543.1      | 1.991643454               |

Table 22: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 22 (ZMTLL), NR-19658

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41796 | A01           | 718        | Rv1686c  | integral membrane protein ABC transporter   | NP_216202.1      | 4.229805014               |
| 41793 | A02           | 718        | Rv1321   | hypothetical protein Rv1321   | NP_215837.1      | 2                         |
| 41788 | A03           | 718        | Rv0813c  | hypothetical protein Rv0813c  | NP_215328.1      | 2.823119777               |
| 41787 | A04           | 718        | Rv0324   | ArsR family transcriptional regulator   | NP_214838.1      | 4.181058496               |
| 41800 | A05           | 718        | Rv3674c  | endonuclease III  | NP_218191.2      | 4.181058496               |
| 41792 | A06           | 718        | Rv1265   | hypothetical protein Rv1265   | NP_215781.1      | 4.157381616               |
| 41808 | A07           | 721        | Rv2794c  | hypothetical protein Rv2794c  | NP_217310.1      | 2.056865465               |
| 41810 | A08           | 721        | Rv3036c  | hypothetical protein Rv3036c  | NP_217552.1      | 2.685159501               |
| 41801 | A09           | 721        | Rv0364   | transmembrane protein   | NP_214878.1      | 2                         |
| 41806 | A10           | 721        | Rv2691   | TRK system potassium uptake protein CEOB  | YP_177900.1      | 2                         |
| 41803 | A11           | 721        | Rv1158c  | hypothetical protein Rv1158c  | NP_215674.1      | 3.198335645               |
| 41811 | A12           | 721        | Rv3673c  | membrane-anchored thioredoxin-like protein  | NP_218190.1      | 4.056865465               |
| 41809 | B01           | 721        | Rv2976c  | uracil-DNA glycosylase  | NP_217492.1      | 2                         |
| 41802 | B02           | 721        | Rv0491   | two component sensory transduction protein RegX3  | NP_215005.1      | 1.993065187               |
| 41821 | B03           | 724        | Rv3208   | TetR family transcriptional regulator   | NP_217724.1      | 1.990331492               |
| 41820 | B04           | 724        | Rv2788   | transcriptional repressor SIRR  | NP_217304.1      | 1.991712707               |
| 41822 | B05           | 724        | Rv3246c  | two component sensory transduction transcriptional regulatory protein MTRA  | NP_217763.1      | 1.991712707               |
| 41816 | B06           | 724        | Rv1418   | lipoprotein LprH  | NP_215934.1      | 1.991712707               |
| 41819 | B07           | 724        | Rv2716   | hypothetical protein Rv2716   | NP_217232.1      | 1.995856354               |
| 41812 | B08           | 724        | Rv0583c  | lipoprotein LpqN  | NP_215097.1      | 1.993093923               |
| 41815 | B09           | 724        | Rv1035c  | transposase   | NP_215551.1      | 3.832872928               |
| 41817 | B10           | 724        | Rv1874   | hypothetical protein Rv1874   | NP_216390.1      | 3.821823204               |
| 41818 | B11           | 724        | Rv1980c  | immunogenic protein MPT64 (antigen MPT64/MPB64)   | NP_216496.1      | 2                         |
| 41813 | B12           | 724        | Rv0784   | hypothetical protein Rv0784   | NP_215298.1      | 3.827348066               |
| 41814 | C01           | 724        | Rv1024   | hypothetical protein Rv1024   | NP_215540.1      | 1.990331492               |
| 41824 | C02           | 727        | Rv0232   | TetR/ACRR family transcriptional regulator  | NP_214746.1      | 1.991746905               |
| 41823 | C03           | 727        | Rv0200   | transmembrane protein   | NP_214714.1      | 4.127922971               |
| 41833 | C04           | 727        | Rv3766   | hypothetical protein Rv3766   | NP_218283.1      | 1.993122421               |
| 41832 | C05           | 727        | Rv3757c  | osmoprotectant (glycine betaine/carnitine/choline/L-proline) transport integral membrane protein ABC transporter    | NP_218274.1      | 1.994497937               |
| 41831 | C06           | 727        | Rv3481c  | integral membrane protein   | NP_217998.1      | 2                         |
| 41828 | C07           | 727        | Rv3102c  | putative cell division ATP-binding protein FTSE (septation component-transport ATP-binding protein ABC transporter) | NP_217618.1      | 1.993122421               |
| 41826 | C08           | 727        | Rv1104   | hypothetical protein Rv1104   | NP_215620.1      | 1.980742779               |
| 41827 | C09           | 727        | Rv2335   | serine acetyltransferase CysE   | NP_216851.1      | 2                         |
| 41846 | C10           | 730        | Rv2217   | lipoyltransferase   | NP_216733.1      | 4.212328767               |
| 41848 | C11           | 730        | Rv2536   | transmembrane protein   | NP_217052.1      | 2                         |
| 41849 | C12           | 730        | Rv2711   | IRON-dependent repressor and activator IDER   | NP_217227.1      | 4.195890411               |
| 41847 | D01           | 730        | Rv2286c  | hypothetical protein Rv2286c  | NP_216802.1      | 2                         |
| 41850 | D02           | 730        | Rv2906c  | tRNA (guanine-N(1)-)-methyltransferase  | NP_217422.1      | 4.209589041               |
| 41845 | D03           | 730        | Rv2203   | hypothetical protein Rv2203   | NP_216719.1      | 2.221917808               |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 41839 | D04           | 730        | Rv0981   | two component response transcriptional regulatory protein MprA | NP_215496.1      | 1.989041096               |
| 41836 | D05           | 730        | Rv0966c  | hypothetical protein Rv0966c                                   | NP_215481.2      | 4.205479452               |
| 41843 | D06           | 730        | Rv1712   | cytidylate kinase  | NP_216228.1      | 2.201369863               |
| 41857 | D07           | 733        | Rv0653c  | TetR family transcriptional regulator                          | NP_215167.1      | 4.233287858               |
| 41863 | D08           | 733        | Rv3210c  | hypothetical protein Rv3210c                                   | NP_217726.1      | 4.218281037               |
| 41853 | D09           | 733        | Rv0518   | hypothetical protein Rv0518                                    | NP_215032.1      | 2                         |
| 41865 | D10           | 733        | Rv3582c  | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase         | NP_218099.1      | 2                         |
| 41861 | D11           | 733        | Rv2676c  | hypothetical protein Rv2676c                                   | NP_217192.1      | 1.989085948               |
| 41854 | D12           | 733        | Rv0618   | galactose-1-phosphate uridylyltransferase galTa                | YP_177741.1      | 4.203274216               |
| 41862 | E01           | 733        | Rv2728c  | hypothetical protein Rv2728c                                   | NP_217244.1      | 4.241473397               |
| 41851 | E02           |            | Rv0437c  | CLONE IS INVALID   | NP_214951.1      |                           |
| 41867 | E03           | 733        | Rv3713   | cobyric acid synthase CobQ2                                    | NP_218230.1      | 2.556616644               |
| 41856 | E04           | 733        | Rv0632c  | hypothetical protein Rv0632c                                   | NP_215147.1      | 3.181446112               |
| 41858 | E05           | 733        | Rv1507c  | hypothetical protein Rv1507A                                   | YP_177648.1      | 2.233287858               |
| 41877 | E06           | 736        | Rv3837c  | phosphoglycerate mutase  | NP_218354.1      | 3.502717391               |
| 41872 | E07           | 736        | Rv1115   | hypothetical protein Rv1115                                    | NP_215631.1      | 1.991847826               |
| 41873 | E08           | 736        | Rv1268c  | hypothetical protein Rv1268c                                   | NP_215784.1      | 1.991847826               |
| 41876 | E09           | 736        | Rv3668c  | protease   | NP_218185.1      | 2                         |
| 41875 | E10           | 736        | Rv3426   | PPE family protein   | YP_177972.1      | 1.993206522               |
| 41874 | E11           | 736        | Rv1408   | ribulose-phosphate 3-epimerase                                 | NP_215924.1      | 2                         |
| 41888 | E12           | 739        | Rv3699   | hypothetical protein Rv3699                                    | NP_218216.1      | 2.219215156               |
| 41885 | F01           | 739        | Rv2989   | transcriptional regulatory protein                             | NP_217505.1      | 3.427604871               |
| 41884 | F02           | 739        | Rv2945c  | lipoprotein LppX   | NP_217461.1      | 2                         |
| 41878 | F03           | 739        | Rv1100   | hypothetical protein Rv1100                                    | NP_215616.1      | 4.220568336               |
| 41890 | F04           | 739        | Rv3702c  | hypothetical protein Rv3702c                                   | NP_218219.1      | 1.700947226               |
| 41893 | F05           | 742        | Rv1676   | hypothetical protein Rv1676                                    | NP_216192.1      | 1.991913747               |
| 41892 | F06           | 742        | Rv0558   | ubiquinone/menaquinone biosynthesis methyltransferase          | YP_177738.1      | 1.991913747               |
| 41895 | F07           | 742        | Rv1816   | transcriptional regulatory protein                             | NP_216332.1      | 2                         |
| 41891 | F08           | 742        | Rv0472c  | TetR family transcriptional regulator                          | NP_214986.1      | 2                         |
| 41894 | F09           | 742        | Rv1811   | Mg <sup>2+</sup> transport P-type ATPase C                     | NP_216327.1      | 1.993261456               |
| 41897 | F10           | 742        | Rv3404c  | hypothetical protein Rv3404c                                   | NP_217921.1      | 2                         |
| 41896 | F11           | 742        | Rv3386   | transposase  | NP_217903.1      | 1.989218329               |
| 41902 | F12           | 745        | Rv0641   | 50S ribosomal protein L1                                       | NP_215155.1      | 1.987919463               |
| 41901 | G01           | 745        | Rv0351   | GRPE protein (HSP-70 cofactor)                                 | NP_214865.1      | 1.991946309               |
| 41900 | G02           | 745        | Rv0071   | maturase   | NP_214585.1      | 1.991946309               |
| 41905 | G03           | 745        | Rv2695   | hypothetical protein Rv2695                                    | NP_217211.1      | 4.253691275               |
| 41903 | G04           | 745        | Rv1610   | hypothetical protein Rv1610                                    | NP_216126.1      | 4.177181208               |
| 41907 | G05           | 745        | Rv3174   | short chain dehydrogenase                                      | NP_217690.1      | 1.991946309               |
| 41918 | G06           | 748        | Rv2821c  | hypothetical protein Rv2821c                                   | NP_217337.1      | 1.994652406               |
| 41910 | G07           | 748        | Rv0781   | oligopeptidase B   | NP_215296.2      | 2.113636364               |
| 41908 | G08           | 748        | Rv0452   | transcriptional regulatory protein                             | NP_214966.1      | 1.993315508               |
| 41912 | G09           | 748        | Rv1411c  | lipoprotein LprG   | NP_215927.1      | 3.252673797               |
| 41914 | G10           | 748        | Rv1725c  | hypothetical protein Rv1725c                                   | NP_216241.1      | 2                         |
| 41917 | G11           | 748        | Rv2558   | hypothetical protein Rv2558                                    | NP_217074.1      | 4.20855615                |
| 41919 | G12           | 748        | Rv3147   | NADH dehydrogenase subunit C                                   | NP_217663.1      | 4.219251337               |
| 41920 | H01           | 748        | Rv3390   | lipoprotein LpqD   | NP_217907.1      | 1.99197861                |
| 41911 | H02           | 748        | Rv0903c  | two component response transcriptional regulatory protein PRRA | NP_215418.1      | 1.99197861                |
| 41913 | H03           | 748        | Rv1593c  | hypothetical protein Rv1593c                                   | NP_216109.1      | 1.99197861                |
| 41930 | H04           | 751        | Rv3528c  | hypothetical protein Rv3528c                                   | NP_218045.1      | 1.986684421               |
| 41923 | H05           | 751        | Rv0634c  | Glyoxalase II GlxII  | NP_215148.1      | 4.215712383               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41926 | H06           | 751        | Rv2687c  | Integral membrane protein ABC transporter | NP_217203.1      | 4.215712383               |
| 41931 | H07           | 751        | Rv3576   | lipoprotein LppH                          | YP_177991.1      | 1.994673768               |
| 41929 | H08           | 751        | Rv3434c  | transmembrane protein                     | NP_217951.1      | 2.427430093               |
| 41925 | H09           | 751        | Rv2054   | hypothetical protein Rv2054               | NP_216570.1      | 2                         |
| 41924 | H10           | 751        | Rv1151c  | NAD-dependent deacetylase                 | NP_215667.1      | 1.99334221                |
| 41928 | H11           | 751        | Rv2972c  | hypothetical protein Rv2972c              | NP_217488.1      | 2                         |
| 41932 | H12           | 751        | Rv3821   | integral membrane protein                 | NP_218338.1      | 2                         |

Table 23: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 23 (ZMTLM), NR-19659

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41940 | A01           | 754        | Rv2308   | hypothetical protein Rv2308   | NP_216824.1      | 1.99204244                |
| 41941 | A02           | 754        | Rv2473   | alanine and proline rich membrane protein   | NP_216989.1      | 4.194960212               |
| 41937 | A03           | 754        | Rv0658c  | integral membrane protein   | NP_215172.1      | 2                         |
| 41939 | A04           | 754        | Rv2102   | hypothetical protein Rv2102   | NP_216618.1      | 2.031830239               |
| 41942 | A05           | 754        | Rv2944   | IS1533 transposase  | NP_217460.1      | 1.9933687                 |
| 41945 | A06           | 757        | Rv2018   | hypothetical protein Rv2018   | NP_216534.1      | 3.200792602               |
| 41943 | A07           | 757        | Rv0394c  | hypothetical protein Rv0394c  | NP_214908.1      | 2                         |
| 41946 | A08           | 757        | Rv2408   | PE family protein   | YP_177880.1      | 4.190224571               |
| 41947 | A09           | 757        | Rv2993c  | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase   | NP_217509.1      | 1.992073976               |
| 41944 | A10           | 757        | Rv1046c  | hypothetical protein Rv1046c  | NP_215562.2      | 4.169088507               |
| 41948 | A11           | 757        | Rv3756c  | osmoprotectant (glycine betaine/carnitine/choline/L-proline) transport integral membrane protein ABC transporter PROZ | NP_218273.1      | 1.989431968               |
| 41955 | A12           |            | Rv2525c  | CLONE IS INVALID  |                  |                           |
| 41951 | B01           | 760        | Rv0674   | hypothetical protein Rv0674   | NP_215188.1      | 2                         |
| 41957 | B02           | 760        | Rv2925c  | ribonuclease III  | NP_217441.1      | 1.992105263               |
| 41950 | B03           | 760        | Rv0586   | GntR family transcriptional regulator   | NP_215100.1      | 1.993421053               |
| 41958 | B04           | 760        | Rv3623   | lipoprotein LpqG  | NP_218140.1      | 1.994736842               |
| 41949 | B05           | 760        | Rv0432   | periplasmic superoxide dismutase  | NP_214946.1      | 2.981578947               |
| 41954 | B06           | 760        | Rv1337   | integral membrane protein   | NP_215853.1      | 2                         |
| 41963 | B07           | 763        | Rv0756c  | hypothetical protein Rv0756c  | NP_215270.1      | 2.70904325                |
| 41969 | B08           | 763        | Rv3717   | hypothetical protein Rv3717   | NP_218234.1      | 1.994757536               |
| 41965 | B09           | 763        | Rv2147c  | hypothetical protein Rv2147c  | NP_216663.1      | 4.592398427               |
| 41967 | B10           | 763        | Rv2954c  | hypothetical protein Rv2954c  | NP_217470.1      | 2                         |
| 41968 | B11           | 763        | Rv3631   | transferase   | NP_218148.1      | 1.296199214               |
| 41964 | B12           | 763        | Rv1478   | invasion protein  | NP_215994.1      | 1.998689384               |
| 41972 | C01           | 766        | Rv0730   | hypothetical protein Rv0730   | NP_215244.1      | 1.994778068               |
| 41971 | C02           | 766        | Rv0207c  | hypothetical protein Rv0207c  | NP_214721.1      | 1.983028721               |
| 41974 | C03           | 766        | Rv1085c  | hemolysin-like protein  | NP_215601.1      | 3.578328982               |
| 41977 | C04           | 766        | Rv3493c  | Mce associated alanine and valine rich protein  | NP_218010.1      | 1.996083551               |
| 41973 | C05           | 766        | Rv0790c  | hypothetical protein Rv0790c  | NP_215305.1      | 1.98694517                |
| 41978 | C06           | 769        | Rv0905   | enoyl-CoA hydratase   | NP_215420.1      | 4.390117035               |
| 41980 | C07           | 769        | Rv1513   | hypothetical protein Rv1513   | NP_216029.1      | 1.988296489               |
| 41983 | C08           | 769        | Rv2108   | PPE family protein  | YP_177859.1      | 3.804941482               |
| 41985 | C09           | 769        | Rv3342   | methyltransferase (methylase)   | NP_217859.1      | 3.091027308               |
| 41979 | C10           | 769        | Rv1022   | lipoprotein LpqU  | NP_215538.1      | 1.992197659               |
| 41984 | C11           | 769        | Rv2956   | hypothetical protein Rv2956   | NP_217472.1      | 1.993498049               |
| 41986 | C12           | 772        | Rv0043c  | GntR family transcriptional regulator   | NP_214557.1      | 1.993523316               |
| 41989 | D01           | 772        | Rv0181c  | hypothetical protein Rv0181c  | NP_214695.1      | 1.99611399                |
| 41996 | D02           | 772        | Rv2091c  | hypothetical protein Rv2091c  | NP_216607.1      | 1.806994819               |
| 41992 | D03           | 772        | Rv1270c  | lipoprotein LprA  | NP_215786.1      | 1.992227979               |
| 41997 | D04           | 772        | Rv3238c  | integral membrane protein   | NP_217755.1      | 1.99611399                |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 41993 | D05           | 772        | Rv1675c  | transcriptional regulatory protein                                | NP_216191.1      | 1.993523316               |
| 41994 | D06           | 772        | Rv2070c  | cobalt-precocorrin-6x reductase                                   | NP_216586.1      | 3.791450777               |
| 41988 | D07           | 772        | Rv0178   | mce associated membrane protein                                   | NP_214692.1      | 2.090673575               |
| 41998 | D08           | 772        | Rv3916c  | hypothetical protein Rv3916c                                      | NP_218433.1      | 2                         |
| 41999 | D09           | 775        | Rv0925c  | hypothetical protein Rv0925c                                      | NP_215440.1      | 1.99483871                |
| 42007 | D10           | 775        | Rv2927c  | hypothetical protein Rv2927c                                      | NP_217443.1      | 1.993548387               |
| 42008 | D11           | 775        | Rv2959c  | methyltransferase (methylase)                                     | NP_217475.1      | 2                         |
| 42002 | D12           | 775        | Rv1742   | hypothetical protein Rv1742                                       | NP_216258.1      | 1.99483871                |
| 42003 | E01           | 775        | Rv2229c  | hypothetical protein Rv2229c                                      | NP_216745.1      | 4.131612903               |
| 42005 | E02           | 775        | Rv2765   | hypothetical protein Rv2765                                       | NP_217281.1      | 1.909677419               |
| 42006 | E03           | 775        | Rv2773c  | dihydrodipicolinate reductase                                     | NP_217289.1      | 1.993548387               |
| 42012 | E04           |            | Rv0625c  | CLONE IS INVALID  | NP_215140.1      |                           |
| 42020 | E05           | 778        | Rv3050c  | AsnC family transcriptional regulator                             | NP_217566.1      | 1.992287918               |
| 42011 | E06           | 778        | Rv0330c  | hypothetical protein Rv0330c                                      | NP_214844.1      | 1.992287918               |
| 42014 | E07           |            | Rv1164   | CLONE IS INVALID  |                  |                           |
| 42021 | E08           | 778        | Rv3349c  | transposase   | NP_217866.1      | 4.242930591               |
| 42019 | E09           | 778        | Rv3027c  | hypothetical protein Rv3027c                                      | NP_217543.1      | 1.992287918               |
| 42016 | E10           | 778        | Rv2293c  | hypothetical protein Rv2293c                                      | NP_216809.1      | 2                         |
| 42034 | E11           | 781        | Rv1828   | hypothetical protein Rv1828                                       | NP_216344.1      | 4.206145967               |
| 42040 | E12           |            | Rv3550   | CLONE IS INVALID  |                  |                           |
| 42022 | F01           | 781        | Rv0259c  | hypothetical protein Rv0259c                                      | NP_214773.1      | 4.213828425               |
| 42035 | F02           | 781        | Rv2182c  | 1-acylglycerol-3-phosphate O-acyltransferase                      | NP_216698.1      | 1.996158771               |
| 42031 | F03           | 781        | Rv1483   | 3-oxoacyl-  | NP_215999.1      | 1.973111396               |
| 42052 | F04           | 784        | Rv3908   | hypothetical protein Rv3908                                       | NP_218425.1      | 2.840561224               |
| 42049 | F05           | 784        | Rv2109c  | proteasome (alpha subunit) PrcA                                   | NP_216625.1      | 2                         |
| 42050 | F06           | 784        | Rv2504c  | succinyl-CoA:3-ketoacid-coenzyme A transferase subunit alpha ScoA | NP_217020.1      | 4.204081633               |
| 42046 | F07           | 784        | Rv0986   | adhesion component transport ATP-binding protein ABC transporter  | NP_215501.1      | 4.18877551                |
| 42051 | F08           | 784        | Rv3638   | transposase   | NP_218155.1      | 1.992346939               |
| 42048 | F09           | 784        | Rv1773c  | transcriptional regulatory protein                                | NP_216289.1      | 2.168367347               |
| 42064 | F10           | 787        | Rv2831   | enoyl-CoA hydratase   | NP_217347.1      | 4.074968234               |
| 42053 | F11           | 787        | Rv0110   | integral membrane protein   | NP_214624.1      | 2                         |
| 42056 | F12           | 787        | Rv0489   | phosphoglyceromutase  | YP_177731.1      | 1.992376112               |
| 42059 | G01           | 787        | Rv2073c  | shortchain dehydrogenase  | NP_216589.1      | 4.229987294               |
| 42066 | G02           | 787        | Rv2891   | hypothetical protein Rv2891                                       | NP_217407.1      | 1.99364676                |
| 42080 | G03           | 790        | Rv3552   | CoA-transferase subunit beta                                      | NP_218069.1      | 2                         |
| 42071 | G04           | 790        | Rv1359   | transcriptional regulatory protein                                | NP_215875.1      | 1.992405063               |
| 42067 | G05           | 790        | Rv0736   | hypothetical protein Rv0736                                       | NP_215250.1      | 1.994936709               |
| 42075 | G06           | 790        | Rv2001   | hypothetical protein Rv2001                                       | NP_216517.1      | 1.993670886               |
| 42079 | G07           | 790        | Rv2675c  | hypothetical protein Rv2675c                                      | NP_217191.1      | 1.993670886               |
| 42072 | G08           | 790        | Rv1691   | hypothetical protein Rv1691                                       | NP_216207.1      | 4.174683544               |
| 42074 | G09           | 790        | Rv1913   | hypothetical protein Rv1913                                       | NP_216429.1      | 4.203797468               |
| 42078 | G10           | 790        | Rv2492   | hypothetical protein Rv2492                                       | NP_217008.1      | 2                         |
| 42070 | G11           | 790        | Rv1304   | F0F1 ATP synthase subunit A                                       | NP_215820.1      | 1.992405063               |
| 42077 | G12           | 790        | Rv2219   | transmembrane protein   | NP_216735.1      | 1.992405063               |
| 42076 | H01           | 790        | Rv2149c  | hypothetical protein Rv2149c                                      | NP_216665.1      | 4.439240506               |
| 10115 | H02           | 790        | Rv2754c  | FAD-dependent thymidylate synthase                                | NP_217270.1      | 2                         |
| 42083 | H03           | 793        | Rv0372c  | hypothetical protein Rv0372c                                      | NP_214886.1      | 4.460277427               |
| 42095 | H04           | 793        | Rv3427c  | transposase   | NP_217944.1      | 1.99369483                |
| 42089 | H05           | 793        | Rv1864c  | hypothetical protein Rv1864c                                      | NP_216380.1      | 4.228247163               |
| 42098 | H06           | 793        | Rv3817   | phosphotransferase  | NP_218334.1      | 1.996216898               |
| 42097 | H07           | 793        | Rv3815c  | acyltransferase   | NP_218332.1      | 2.134930643               |
| 42085 | H08           | 793        | Rv0484c  | short-chain type oxidoreductase                                   | NP_214998.1      | 2.076923077               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 42094 | H09           | 793        | Rv2603c  | hypothetical protein Rv2603c           | NP_217119.1      | 4.192938209               |
| 42088 | H10           | 793        | Rv1051c  | hypothetical protein Rv1051c           | NP_215567.1      | 2.195460277               |
| 42091 | H11           | 793        | Rv2071c  | precorrin-4 C11-methyltransferase CobM | NP_216587.1      | 4.195460277               |
| 42086 | H12           | 793        | Rv0695   | hypothetical protein Rv0695            | NP_215209.1      | 3.232030265               |

Table 24: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 24 (ZMTLN), NR-19660

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 42101 | A01           | 796        | Rv0579   | hypothetical protein Rv0579                                       | NP_215093.1      | 2.07160804                |
| 42112 | A02           | 796        | Rv2884   | transcriptional regulatory protein                                | NP_217400.1      | 4.197236181               |
| 42110 | A03           | 796        | Rv2686c  | antibiotic ABC transporter transmembrane protein                  | NP_217203.1      | 4.210062893               |
| 42102 | A04           | 796        | Rv0670   | endonuclease IV   | NP_215184.1      | 4.236180905               |
| 42107 | A05           | 796        | Rv1597   | hypothetical protein Rv1597                                       | NP_216113.1      | 3.806532663               |
| 42099 | A06           | 796        | Rv0417   | thiazole synthase   | NP_214931.1      | 1.993718593               |
| 42113 | A07           | 796        | Rv3149   | NADH dehydrogenase subunit E                                      | NP_217665.1      | 3.198492462               |
| 42114 | A08           | 796        | Rv3226c  | hypothetical protein Rv3226c                                      | NP_217743.1      | 2                         |
| 42115 | A09           | 799        | Rv0602c  | two component DNA binding transcriptional regulatory protein TCRA | NP_215116.1      | 4.143929912               |
| 42116 | A10           | 799        | Rv0883c  | hypothetical protein Rv0883c                                      | NP_215398.1      | 4.097622028               |
| 42117 | A11           | 799        | Rv0945   | short chain dehydrogenase   | NP_215460.1      | 1.993742178               |
| 42123 | A12           |            | Rv1517   | CLONE IS INVALID  | NP_216033.1      |                           |
| 42134 | B01           | 802        | Rv3912   | hypothetical protein Rv3912                                       | NP_218429.1      | 4.184538653               |
| 42133 | B02           | 802        | Rv3791   | short chain dehydrogenase   | NP_218308.1      | 1.483790524               |
| 42120 | B03           | 802        | Rv0224c  | methyltransferase (methylase)                                     | NP_214738.1      | 3.233167082               |
| 42128 | B04           | 802        | Rv3501c  | integral membrane protein YrbE4a                                  | NP_218018.1      | 4.183291771               |
| 42121 | B05           |            | Rv1056   | CLONE IS INVALID  |                  |                           |
| 42126 | B06           | 802        | Rv2392   | phosphoadenosine phosphosulfate reductase                         | NP_216908.1      | 3.230673317               |
| 42125 | B07           | 802        | Rv1711   | hypothetical protein Rv1711                                       | NP_216227.1      | 1.995012469               |
| 42127 | B08           | 802        | Rv3039c  | enoyl-CoA hydratase   | NP_217555.1      | 4.180798005               |
| 42140 | B09           | 805        | Rv1995   | hypothetical protein Rv1995                                       | NP_216511.1      | 2                         |
| 42143 | B10           | 805        | Rv2969c  | hypothetical protein Rv2969c                                      | NP_217485.1      | 1.99378882                |
| 42138 | B11           | 805        | Rv1687c  | ABC transporter ATP-binding protein                               | NP_216203.1      | 1.990062112               |
| 42139 | B12           | 805        | Rv1928c  | short chain dehydrogenase   | NP_216444.1      | 1.990062112               |
| 42137 | C01           | 805        | Rv0818   | transcriptional regulatory protein                                | NP_215333.1      | 4.11552795                |
| 42146 | C02           | 808        | Rv0023   | transcriptional regulatory protein                                | NP_214537.1      | 4.225247525               |
| 42154 | C03           | 808        | Rv1863c  | integral membrane protein   | NP_216379.1      | 1.992574257               |
| 42155 | C04           | 808        | Rv1941   | short-chain type dehydrogenase/reductase                          | NP_216457.1      | 4.232673267               |
| 42153 | C05           | 808        | Rv1728c  | hypothetical protein Rv1728c                                      | NP_216244.1      | 1.992574257               |
| 42148 | C06           | 808        | Rv0317c  | glycerophosphoryl diester phosphodiesterase                       | NP_214831.1      | 4.57549505                |
| 42160 | C07           |            | Rv3455c  | CLONE IS INVALID  | NP_217973.1      |                           |
| 42147 | C08           | 808        | Rv0090   | hypothetical protein Rv0090                                       | NP_214604.1      | 2.219059406               |
| 42171 | C09           | 811        | Rv1927   | hypothetical protein Rv1927                                       | NP_216443.1      | 1.992601726               |
| 42174 | C10           | 811        | Rv3591c  | hydrolase   | NP_218108.1      | 3.180024661               |
| 42168 | C11           | 811        | Rv1033c  | two component transcriptional regulator TRCR                      | NP_215549.1      | 2                         |
| 42166 | C12           | 811        | Rv0911   | hypothetical protein Rv0911                                       | NP_215426.1      | 1.997533909               |
| 42169 | D01           | 811        | Rv1070c  | enoyl-CoA hydratase   | NP_215586.1      | 1.993834772               |
| 42170 | D02           | 811        | Rv1221   | RNA polymerase sigma factor SigE                                  | NP_215737.1      | 2                         |
| 42167 | D03           | 811        | Rv0941c  | hypothetical protein Rv0941c                                      | NP_215456.1      | 1.996300863               |
| 42177 | D04           | 814        | Rv1998c  | hypothetical protein Rv1998c                                      | NP_216514.1      | 2                         |
| 42179 | D05           | 814        | Rv2671   | hypothetical protein Rv2671                                       | NP_217187.1      | 4.214987715               |
| 42180 | D06           | 814        | Rv2857c  | short chain dehydrogenase   | NP_217373.1      | 4.196560197               |
| 42176 | D07           | 814        | Rv0820   | phosphate ABC transporter ATP-binding protein                     | NP_215335.1      | 2                         |
| 42178 | D08           | 814        | Rv2148c  | hypothetical protein Rv2148c                                      | NP_216664.1      | 1.992628993               |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 42194 | D09           | 817        | Rv3816c  | acyltransferase   | NP_218333.1      | 4.303549572               |
| 42188 | D10           | 817        | Rv1340   | ribonuclease PH   | NP_215856.1      | 1.993880049               |
| 42193 | D11           | 817        | Rv3549c  | short chain dehydrogenase   | NP_218066.1      | 1.987760098               |
| 42184 | D12           | 817        | Rv0359   | integral membrane protein   | NP_214873.1      | 1.993880049               |
| 42183 | E01           | 817        | Rv0128   | transmembrane protein   | NP_214642.1      | 2                         |
| 42190 | E02           | 817        | Rv1931c  | transcriptional regulatory protein                                  | NP_216447.1      | 4.190942472               |
| 42185 | E03           | 817        | Rv0527   | cytochrome C-type biogenesis protein CcdA                           | YP_177735.1      | 3.833537332               |
| 42192 | E04           | 817        | Rv2696c  | hypothetical protein Rv2696c  | NP_217212.1      | 2.1750306                 |
| 42189 | E05           | 817        | Rv1719   | transcriptional regulatory protein                                  | NP_216235.1      | 1.99877601                |
| 42203 | E06           | 820        | Rv3530c  | short chain dehydrogenase   | NP_218047.1      | 1.992682927               |
| 42200 | E07           | 820        | Rv3137   | monophosphatase   | NP_217653.1      | 1.992682927               |
| 42198 | E08           | 820        | Rv2289   | CDP-diacylglycerol pyrophosphatase                                  | NP_216805.1      | 1.990243902               |
| 42196 | E09           | 820        | Rv2002   | 20-beta-hydroxysteroid dehydrogenase                                | NP_216518.1      | 4.215853659               |
| 42197 | E10           | 820        | Rv2145c  | hypothetical protein Rv2145c  | NP_216661.1      | 1.995121951               |
| 42199 | E11           | 820        | Rv2766c  | 3-ketoacyl-(acyl-carrier-protein) reductase                         | YP_177905.1      | 4.379268293               |
| 42195 | E12           | 820        | Rv1644   | 23S rRNA methyltransferase TsnR                                     | NP_216160.1      | 1.990243902               |
| 42206 | F01           | 823        | Rv0577   | hypothetical protein Rv0577   | NP_215091.1      | 1.993924666               |
| 42210 | F02           | 823        | Rv1438   | triosephosphate isomerase   | NP_215954.1      | 4.165249089               |
| 42223 | F03           | 823        | Rv3814c  | acyltransferase   | NP_218331.1      | 1.989064399               |
| 42207 | F04           | 823        | Rv1353c  | transcriptional regulatory protein                                  | NP_215869.1      | 2                         |
| 42208 | F05           | 823        | Rv1363c  | hypothetical protein Rv1363c  | NP_215879.1      | 1.992709599               |
| 42214 | F06           | 823        | Rv1857   | molybdate-binding lipoprotein                                       | NP_216373.1      | 2                         |
| 42209 | F07           | 823        | Rv1368   | lipoprotein LprF  | NP_215884.1      | 2                         |
| 42215 | F08           | 823        | Rv2883c  | uridylylate kinase  | NP_217399.1      | 3.179829891               |
| 42222 | F09           | 823        | Rv3536c  | hydratase   | NP_218053.1      | 1.993924666               |
| 42205 | F10           | 823        | Rv0332   | hypothetical protein Rv0332   | NP_214846.1      | 1.987849332               |
| 42212 | F11           | 823        | Rv1457c  | unidentified antibiotic-transport integral membrane ABC transporter | NP_215973.1      | 4.194410693               |
| 42204 | F12           | 823        | Rv0294   | trans-aconitate methyltransferase tam                               | NP_214808.1      | 3.832320778               |
| 42213 | G01           | 823        | Rv1525   | rhamnosyl transferase WbbL2   | NP_216041.1      | 1.993924666               |
| 42228 | G02           | 826        | Rv0877   | hypothetical protein Rv0877   | NP_215392.1      | 1.992736077               |
| 42239 | G03           |            | Rv3559c  | CLONE IS INVALID  |                  |                           |
| 42237 | G04           | 826        | Rv3154   | NADH dehydrogenase subunit J  | NP_217670.1      | 4.180387409               |
| 42227 | G05           | 826        | Rv0554   | peroxidase BpoC   | NP_215068.1      | 4.190072639               |
| 42231 | G06           | 826        | Rv1249c  | hypothetical protein Rv1249c  | NP_215765.1      | 4.179176755               |
| 42236 | G07           | 826        | Rv2372c  | 16S ribosomal RNA methyltransferase RsmE                            | NP_216888.1      | 1.995157385               |
| 42234 | G08           | 826        | Rv1762c  | hypothetical protein Rv1762c  | NP_216278.1      | 1.996368039               |
| 42226 | G09           | 826        | Rv0222   | enoyl-CoA hydratase   | NP_214736.1      | 1.99031477                |
| 42235 | G10           | 826        | Rv2133c  | hypothetical protein Rv2133c  | NP_216649.1      | 3.180387409               |
| 42224 | G11           | 826        | Rv0012   | hypothetical protein Rv0012   | NP_214526.1      | 4.198547216               |
| 42233 | G12           | 826        | Rv1514c  | hypothetical protein Rv1514c  | NP_216030.1      | 2                         |
| 42238 | H01           | 826        | Rv3400   | hydrolase   | NP_217917.1      | 1.996368039               |
| 42248 | H02           | 829        | Rv3319   | succinate dehydrogenase iron-sulfur subunit                         | NP_217836.1      | 2.108564536               |
| 42246 | H03           | 829        | Rv2764c  | thymidylate synthase  | NP_217280.1      | 2                         |
| 42241 | H04           | 829        | Rv0208c  | tRNA (guanine-N(7)-)-methyltransferase                              | NP_214722.1      | 2                         |
| 42244 | H05           | 829        | Rv0927c  | short chain dehydrogenase   | NP_215442.1      | 4.194209891               |
| 42242 | H06           |            | Rv0675   | CLONE IS INVALID  | YP_177745.1      |                           |
| 42245 | H07           | 829        | Rv1356c  | hypothetical protein Rv1356c  | NP_215872.1      | 3.189384801               |
| 42253 | H08           | 832        | Rv0044c  | oxidoreductase  | NP_214558.1      | 2.186298077               |
| 42255 | H09           | 832        | Rv03183  | integral membrane protein   | YP_177716.1      | 2                         |
| 42266 | H10           | 832        | Rv3587c  | hypothetical protein Rv3587c  | NP_218104.1      | 2                         |
| 42262 | H11           | 832        | Rv1858   | molbdenum-transport integral membrane protein ABC transporter       | NP_216374.1      | 4.177884615               |
| 42254 | H12           | 832        | Rv0165c  | GntR family transcriptional regulator                               | YP_177700.1      | 4.1875                    |

Table 25: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 25 (ZMTLO), NR-29661

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                            | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 42258 | A01           | 832        | Rv0535   | 5'-methylthioadenosine phosphorylase               | NP_215049.1      | 2                         |
| 42267 | A02           | 832        | Rv3677c  | hydrolase  | NP_218194.1      | 4.169471154               |
| 42261 | A03           | 832        | Rv1637c  | hypothetical protein Rv1637c                       | NP_216153.1      | 2                         |
| 42263 | A04           | 832        | Rv2902c  | ribonuclease HII                                   | NP_217418.1      | 1.997596154               |
| 42274 | A05           | 835        | Rv0798c  | 29 kDa antigen CFP29                               | NP_215313.1      | 4.20239521                |
| 42269 | A06           | 835        | Rv0167   | integral membrane protein YRBE1A                   | NP_214681.1      | 2                         |
| 42273 | A07           | 835        | Rv0686   | hypothetical protein Rv0686                        | NP_215200.1      | 2                         |
| 42277 | A08           | 835        | Rv2042c  | hypothetical protein Rv2042c                       | NP_216558.1      | 4.182035928               |
| 42278 | A09           | 835        | Rv2240c  | hypothetical protein Rv2240c                       | NP_216756.1      | 1.994011976               |
| 42270 | A10           | 835        | Rv0422c  | phosphomethylpyrimidine kinase                     | NP_214936.1      | 2                         |
| 42272 | A11           | 835        | Rv0587   | integral membrane protein YrbE2a                   | NP_215101.1      | 2.901796407               |
| 42284 | A12           |            | Rv2631   | CLONE IS INVALID                                   |                  |                           |
| 42294 | B01           | 838        | Rv3658c  | transmembrane protein                              | NP_218175.1      | 1.973747017               |
| 42287 | B02           | 838        | Rv1463   | ABC transporter ATP-binding protein                | NP_215979.1      | 4.118138425               |
| 42285 | B03           | 838        | Rv0734   | methionine aminopeptidase                          | YP_177748.1      | 4.094272076               |
| 42290 | B04           |            | Rv3213c  | CLONE IS INVALID                                   |                  |                           |
| 42288 | B05           | 838        | Rv3029c  | electron transfer flavoprotein subunit beta        | NP_217545.1      | 3.798329356               |
| 42293 | B06           | 838        | Rv3279c  | biotin--protein ligase                             | NP_217796.1      | 2.064439141               |
| 42286 | B07           | 838        | Rv0963c  | hypothetical protein Rv0963c                       | NP_215478.1      | 2                         |
| 42304 | B08           | 841        | Rv2666   | truncated IS1081 transposase                       | NP_217182.1      | 2                         |
| 42297 | B09           | 841        | Rv0295c  | hypothetical protein Rv0295c                       | NP_214809.1      | 1.996432818               |
| 42301 | B10           | 841        | Rv1605   | imidazole glycerol phosphate synthase subunit HisF | NP_216121.1      | 1.346016647               |
| 42299 | B11           | 841        | Rv1544   | ketoacyl reductase                                 | NP_216060.1      | 2.093935791               |
| 42305 | B12           | 844        | Rv0739   | hypothetical protein Rv0739                        | NP_215253.1      | 4.079383886               |
| 42314 | C01           | 844        | Rv2509   | short-chain type dehydrogenase/reductase           | NP_217025.1      | 2                         |
| 42315 | C02           | 844        | Rv3134c  | hypothetical protein Rv3134c                       | NP_217650.1      | 2                         |
| 42310 | C03           | 844        | Rv1648   | transmembrane protein                              | NP_216164.1      | 2.187203791               |
| 42308 | C04           | 844        | Rv1142c  | enoyl-CoA hydratase                                | NP_215658.1      | 4.197867299               |
| 42311 | C05           | 844        | Rv1694   | cytotoxin/hemolysin TlyA                           | NP_216210.1      | 2                         |
| 42321 | C06           | 847        | Rv1484   | enoyl-(acyl carrier protein) reductase             | NP_216000.1      | 1.997638725               |
| 42322 | C07           | 847        | Rv2552c  | shikimate 5-dehydrogenase                          | NP_217068.1      | 1.983471074               |
| 42318 | C08           | 847        | Rv0792c  | GntR family transcriptional regulator              | NP_215307.1      | 4.146399055               |
| 10031 | C09           | 847        | Rv3294c  | hypothetical protein Rv3294c                       | YP_177954.1      | 2                         |
| 42334 | C10           | 850        | Rv2744c  | hypothetical protein Rv2744c                       | YP_177903.1      | 4.112941176               |
| 42337 | C11           | 850        | Rv2952   | methyltransferase (methylase)                      | NP_217468.1      | 4.148235294               |
| 42327 | C12           | 850        | Rv1604   | inositol-monophosphatase                           | NP_216120.1      | 2.355294118               |
| 42323 | D01           | 850        | Rv0817c  | hypothetical protein Rv0817c                       | NP_215332.1      | 2                         |
| 42332 | D02           | 850        | Rv2743c  | hypothetical protein Rv2743c                       | NP_217259.1      | 4.182352941               |
| 42339 | D03           | 853        | Rv1338   | glutamate racemase                                 | NP_215854.1      | 3.13950762                |
| 42343 | D04           | 853        | Rv2248   | hypothetical protein Rv2248                        | NP_216764.1      | 4.137162954               |
| 42346 | D05           | 853        | Rv3234c  | hypothetical protein Rv3234c                       | NP_217751.1      | 3.105509965               |
| 42340 | D06           | 853        | Rv1433   | hypothetical protein Rv1433                        | NP_215949.1      | 4.093786635               |
| 42342 | D07           | 853        | Rv2235   | transmembrane protein                              | NP_216751.1      | 3.76084408                |
| 42338 | D08           | 853        | Rv0831c  | hypothetical protein Rv0831c                       | NP_215346.1      | 3.751465416               |
| 42345 | D09           | 853        | Rv2889c  | elongation factor Ts                               | NP_217405.1      | 2.098475967               |
| 42341 | D10           | 853        | Rv1965   | integral membrane protein YrbE3b                   | NP_216481.1      | 4.120750293               |
| 42353 | D11           | 856        | Rv2257c  | hypothetical protein Rv2257c                       | NP_216773.1      | 3.841121495               |
| 42348 | D12           | 856        | Rv1611   | indole-3-glycerol-phosphate synthase               | NP_216127.1      | 4.019859813               |
| 42349 | E01           |            | Rv1718   | CLONE IS INVALID                                   |                  |                           |
| 42347 | E02           | 856        | Rv0406c  | beta lactamase like protein                        | NP_214920.1      | 3.697429907               |
| 42356 | E03           | 856        | Rv2624c  | hypothetical protein Rv2624c                       | NP_217140.1      | 1.931074766               |
| 42358 | E04           | 856        | Rv3277   | transmembrane protein                              | NP_217794.1      | 4.002336449               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 42357 | E05           | 856        | Rv2750   | 3-ketoacyl-(acyl-carrier-protein) reductase                                      | NP_217266.1      | 3.137850467               |
| 42352 | E06           | 856        | Rv1775   | hypothetical protein Rv1775  | NP_216291.1      | 1.96728972                |
| 42371 | E07           | 859        | Rv2407   | ribonuclease Z   | NP_216923.1      | 1.835855646               |
| 42375 | E08           | 859        | Rv2507   | proline rich membrane protein  | NP_217023.1      | 2.642607683               |
| 42365 | E09           | 859        | Rv0937c  | hypothetical protein Rv0937c   | NP_215452.1      | 1.940628638               |
| 42373 | E10           | 859        | Rv2498c  | citrate (Pro-3S)-lyase beta subunit  | NP_217014.1      | 2.636786962               |
| 42369 | E11           | 859        | Rv1501   | hypothetical protein Rv1501  | NP_216017.1      | 4.132712456               |
| 42381 | E12           | 859        | Rv3813c  | hypothetical protein Rv3813c   | NP_218330.1      | 3.431897555               |
| 42378 | F01           | 859        | Rv3672c  | hypothetical protein Rv3672c   | NP_218189.1      | 3.124563446               |
| 42368 | F02           | 859        | Rv1366   | hypothetical protein Rv1366  | NP_215882.1      | 4.121071013               |
| 42380 | F03           | 859        | Rv3781   | o-antigen/lipopolysaccharide transport ATP-binding protein ABC transporter RfbE  | NP_218298.1      | 1.88242142                |
| 42389 | F04           | 862        | Rv1405c  | putative methyltransferase   | NP_215921.1      | 4.075406032               |
| 42391 | F05           | 862        | Rv1680   | hypothetical protein Rv1680  | NP_216196.1      | 2.151972158               |
| 42396 | F06           | 862        | Rv3842c  | glycerophosphoryl diester phosphodiesterase                                      | NP_218359.1      | 4.16937355                |
| 42382 | F07           | 862        | Rv0707   | 30S ribosomal protein S3   | NP_215221.1      | 2.77262181                |
| 42386 | F08           | 862        | Rv1385   | orotidine 5'-phosphate decarboxylase   | NP_215901.1      | 3.660092807               |
| 42395 | F09           | 862        | Rv3774   | enoyl-CoA hydratase  | NP_218291.1      | 4.03712297                |
| 42392 | F10           | 862        | Rv2317   | sugar-transport integral membrane protein ABC transporter UspB                   | YP_177866.1      | 4.069605568               |
| 42416 | F11           | 865        | Rv3079c  | hypothetical protein Rv3079c   | NP_217595.1      | 3.028901734               |
| 42402 | F12           | 865        | Rv0851c  | short chain dehydrogenase  | NP_215366.1      | 4.001156069               |
| 42408 | G01           | 865        | Rv1428c  | hypothetical protein Rv1428c   | NP_215944.1      | 4.048554913               |
| 42414 | G02           |            | Rv2957   | CLONE IS INVALID   |                  |                           |
| 42401 | G03           | 865        | Rv0765c  | short chain dehydrogenase  | NP_215279.1      | 3.149132948               |
| 42406 | G04           | 865        | Rv1192   | hypothetical protein Rv1192  | NP_215708.1      | 3.478612717               |
| 42418 | G05           | 865        | Rv3594   | hypothetical protein Rv3594  | NP_218111.1      | 3.142196532               |
| 42417 | G06           | 865        | Rv3415c  | hypothetical protein Rv3415c   | NP_217932.1      | 3.168786127               |
| 42399 | G07           |            | Rv0687   | CLONE IS INVALID   |                  |                           |
| 42413 | G08           | 865        | Rv2880c  | hypothetical protein Rv2880c   | NP_217396.1      | 3.298265896               |
| 42398 | G09           | 865        | Rv0590   | MCE-family protein MCE2B   | NP_215104.1      | 3.615028902               |
| 42405 | G10           | 865        | Rv1094   | acyl-  | NP_215610.1      | 1.878612717               |
| 42411 | G11           | 865        | Rv2834c  | sn-glycerol-3-phosphate transport integral membrane protein ABC transporter UGPE | NP_217350.1      | 3.098265896               |
| 42397 | G12           | 865        | Rv0361   | hypothetical protein Rv0361  | NP_214875.1      | 4.106358382               |
| 42426 | H01           |            | Rv2136c  | CLONE IS INVALID   |                  |                           |
| 42422 | H02           | 868        | Rv0933   | phosphate ABC transporter ATP-binding protein                                    | NP_215448.1      | 3.612903226               |
| 42419 | H03           | 868        | Rv0077c  | oxidoreductase   | NP_214591.1      | 3.169354839               |
| 42425 | H04           | 868        | Rv1716   | hypothetical protein Rv1716  | NP_216232.1      | 4.093317972               |
| 42433 | H05           | 868        | Rv3085   | short-chain type dehydrogenase/reductase   | NP_217601.1      | 3.124423963               |
| 42434 | H06           | 868        | Rv3889c  | hypothetical protein Rv3889c   | NP_218406.1      | 3.944700461               |
| 42424 | H07           | 868        | Rv1245c  | short-chain type dehydrogenase/reductase   | NP_215761.1      | 3.996543779               |
| 42423 | H08           | 868        | Rv1225c  | hypothetical protein Rv1225c   | NP_215741.1      | 4.061059908               |
| 42430 | H09           | 868        | Rv2899c  | formate dehydrogenase accessory protein  | NP_217415.1      | 4.065668203               |
| 42438 | H10           | 871        | Rv3117   | thiosulfate sulfurtransferase CysA3  | NP_217633.1      | 4.075774971               |
| 42435 | H11           | 871        | Rv0815c  | thiosulfate sulfurtransferase CysA2  | NP_215330.1      | 4.112514351               |
| 42436 | H12           | 871        | Rv1882c  | short chain dehydrogenase  | NP_216398.1      | 4.106773823               |

Table 26: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 26 (ZMTLP), NR-19662

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------|------------------|---------------------------|
| 42437 | A01           | 871        | Rv2742c  | hypothetical protein Rv2742c | NP_217258.1      | 4.063145809               |
| 42445 | A02           | 874        | Rv1709   | hypothetical protein Rv1709  | NP_216225.1      | 4.060640732               |
| 42448 | A03           | 874        | Rv3510c  | hypothetical protein Rv3510c | NP_218027.1      | 4.09610984                |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 42441 | A04           | 874        | Rv0852   | fatty-acid-CoA ligase  | NP_215367.1      | 4.04576659                |
| 42444 | A05           |            | Rv1460   | CLONE IS INVALID   |                  |                           |
| 42443 | A06           | 874        | Rv1072   | transmembrane protein  | NP_215588.1      | 3.964530892               |
| 42455 | A07           | 877        | Rv3517   | hypothetical protein Rv3517  | NP_218034.1      | 4.054732041               |
| 42453 | A08           | 877        | Rv3005c  | hypothetical protein Rv3005c   | NP_217521.1      | 4.061573546               |
| 42449 | A09           | 877        | Rv0633c  | glyoxalase II  | NP_215148.1      | 3.122006842               |
| 42450 | A10           | 877        | Rv2028c  | hypothetical protein Rv2028c   | NP_216544.1      | 4.114025086               |
| 42471 | A11           |            | Rv3438   | CLONE IS INVALID   |                  |                           |
| 42456 | A12           | 880        | Rv0144   | TetR family transcriptional regulator  | NP_214658.1      | 4.064772727               |
| 42460 | B01           | 880        | Rv0704   | 50S ribosomal protein L2   | NP_215218.1      | 4.035227273               |
| 42466 | B02           | 880        | Rv2118c  | RNA methyltransferase  | NP_216634.1      | 3.189772727               |
| 42468 | B03           | 880        | Rv2417c  | hypothetical protein Rv2417c   | NP_216933.1      | 4.040909091               |
| 42458 | B04           | 880        | Rv0498   | hypothetical protein Rv0498  | NP_215012.1      | 4.078409091               |
| 42473 | B05           | 880        | Rv3500c  | integral membrane protein YrbE4b   | NP_218017.1      | 4.082954545               |
| 42465 | B06           | 880        | Rv2039c  | sugar-transport integral membrane protein ABC transporter                                    | NP_216555.1      | 3.714772727               |
| 42477 | B07           |            | Rv3878   | CLONE IS INVALID   |                  |                           |
| 42459 | B08           | 880        | Rv0671   | lipoprotein LpqP   | NP_215185.1      | 3.886363636               |
| 42474 | B09           | 880        | Rv3608c  | dihydropteroate synthase   | YP_177997.1      | 4.046590909               |
| 42467 | B10           | 880        | Rv2194   | ubiquinol-cytochrome C reductase QcrC(cytochrome C subunit)                                  | NP_216710.1      | 3.264772727               |
| 42457 | B11           | 880        | Rv0241c  | hypothetical protein Rv0241c   | NP_214755.1      | 3.646590909               |
| 42483 | B12           | 883        | Rv2393   | hypothetical protein Rv2393  | NP_216909.1      | 3.038505096               |
| 42481 | C01           | 883        | Rv2225   | 3-methyl-2-oxobutanoate hydroxymethyltransferase   | NP_216741.1      | 3.678369196               |
| 42490 | C02           | 883        | Rv3431c  | hypothetical protein Rv3431c   | NP_217948.1      | 3.404303511               |
| 42484 | C03           |            | Rv2605c  | CLONE IS INVALID   |                  |                           |
| 42488 | C04           | 883        | Rv3356c  | bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase | NP_217873.1      | 4.087202718               |
| 42482 | C05           | 883        | Rv2307c  |  |                  | 4.073612684               |
| 42479 | C06           | 883        | Rv0024   | putative secreted protein P60-related protein  | NP_214538.1      | 3.653454134               |
| 42495 | C07           | 886        | Rv1153c  | O-methyltransferase  | NP_215669.1      | 3.967268623               |
| 42492 | C08           | 886        | Rv0093c  | hypothetical protein Rv0093c   | NP_214607.1      | 1.60496614                |
| 42499 | C09           | 886        | Rv2971   | oxidoreductase   | NP_217487.1      | 4.046275395               |
| 42500 | C10           | 886        | Rv3224   | short chain dehydrogenase  | NP_217740.1      | 3.089164786               |
| 42493 | C11           | 886        | Rv0953c  | oxidoreductase   | NP_215468.1      | 3.098194131               |
| 42494 | C12           | 886        | Rv1140   | integral membrane protein  | NP_215656.1      | 4.051918736               |
| 42498 | D01           | 886        | Rv2325c  | hypothetical protein Rv2325c   | NP_216841.1      | 4.071106095               |
| 42506 | D02           | 889        | Rv3866   | hypothetical protein Rv3866  | NP_218383.1      | 4.071991001               |
| 42501 | D03           | 889        | Rv1073   | hypothetical protein Rv1073  | NP_215589.1      | 1.970753656               |
| 42505 | D04           | 889        | Rv3099c  | hypothetical protein Rv3099c   | NP_217615.1      | 2.239595051               |
| 42502 | D05           | 889        | Rv2399c  | sulfate-transport integral membrane protein  | NP_216915.1      | 1.968503937               |
| 42503 | D06           | 889        | Rv2895c  | mycobactin utilization protein ViuB  | NP_217411.1      | 4.061867267               |
| 42512 | D07           | 892        | Rv2734   | hypothetical protein Rv2734  | NP_217250.1      | 3.125560538               |
| 42507 | D08           | 892        | Rv0383c  | hypothetical protein Rv0383c   | NP_214897.1      | 4.007847534               |
| 42509 | D09           | 892        | Rv2291   | thiosulfate sulfurtransferase SseB   | NP_216807.1      | 3.65470852                |
| 42514 | D10           | 892        | Rv2867c  | hypothetical protein Rv2867c   | NP_217383.1      | 2.298206278               |
| 42508 | D11           | 892        | Rv2121c  | ATP phosphoribosyltransferase  | NP_216637.1      | 4.127802691               |
| 42520 | D12           | 895        | Rv1003   | hypothetical protein Rv1003  | NP_215519.1      | 4.12849162                |
| 42526 | E01           | 895        | Rv2003c  | hypothetical protein Rv2003c   | NP_216519.1      | 3.176536313               |
| 42527 | E02           | 895        | Rv2861c  | methionine aminopeptidase  | YP_177911.1      | 4.108379888               |
| 42525 | E03           | 895        | Rv1596   | nicotinate-nucleotide pyrophosphorylase  | NP_216112.1      | 4.10726257                |
| 42519 | E04           | 895        | Rv0891c  | transcriptional regulatory protein   | NP_215406.1      | 3.987709497               |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 42529 | E05           | 895        | Rv3463   | hypothetical protein Rv3463  | NP_217980.1      | 3.925139665               |
| 42528 | E06           | 895        | Rv3207c  | hypothetical protein Rv3207c   | NP_217723.1      | 4.011173184               |
| 42541 | E07           | 898        | Rv0645c  | methoxy mycolic acid synthase  | NP_215159.1      | 4.040089087               |
| 42538 | E08           | 898        | Rv0469   | mycolic acid synthase  | YP_177729.1      | 4.08908686                |
| 42540 | E09           | 898        | Rv0563   | heat shock protein HtpX  | NP_215077.1      | 2.469933185               |
| 42550 | E10           | 898        | Rv2990c  | hypothetical protein Rv2990c   | NP_217506.1      | 2.708240535               |
| 42542 | E11           | 898        | Rv0840c  | proline iminopeptidase   | NP_215355.1      | 4.079064588               |
| 42551 | E12           | 898        | Rv3177   | peroxidase   | NP_217693.1      | 4.069042316               |
| 42537 | F01           | 898        | Rv0468   | 3-hydroxybutyryl-CoA dehydrogenase   | NP_214982.1      | 3.042316258               |
| 42548 | F02           | 898        | Rv1865c  | short chain dehydrogenase  | NP_216381.1      | 3.937639198               |
| 42547 | F03           | 898        | Rv1833c  | haloalkane dehalogenase  | NP_216349.1      | 4.002227171               |
| 42531 | F04           | 898        | Rv0148   | short-chain type dehydrogenase/reductase   | NP_214662.1      | 4.071269488               |
| 42552 | F05           | 898        | Rv3538   | dehydrogenase  | YP_177986.1      | 3.762806236               |
| 42569 | F06           | 901        | Rv3392c  | cyclopropane-fatty-acyl-phospholipid synthase 1 CMAA1 (cyclopropane fatty acid synthase) (CFA synthase) (cyclopropane mycolic acid synthase 1) | NP_217909.1      | 4.147613762               |
| 42556 | F07           | 901        | Rv1041c  | IS like-2 transposase  | NP_215557.1      | 4.029966704               |
| 42555 | F08           | 901        | Rv0644c  | methoxy mycolic acid synthase  | NP_215158.1      | 1.86681465                |
| 42566 | F09           | 901        | Rv3041c  | ABC transporter ATP-binding protein  | NP_217557.1      | 3.318534961               |
| 42565 | F10           | 901        | Rv2890c  | 30S ribosomal protein S2   | NP_217406.1      | 2.096559378               |
| 42557 | F11           | 901        | Rv1061   | hypothetical protein Rv1061  | NP_215577.1      | 3.953385128               |
| 42570 | F12           | 901        | Rv3661   | hypothetical protein Rv3661  | NP_218178.1      | 4.00554939                |
| 42575 | G01           | 904        | Rv1082   | Mycothiol conjugate amidase Mca (Mycothiol S-conjugate amidase)  | NP_215598.1      | 4.058628319               |
| 42571 | G02           | 904        | Rv0334   | alpha-D-glucose-1-phosphate thymidyltransferase RmlA   | NP_214848.1      | 2.956858407               |
| 42579 | G03           | 904        | Rv3040c  | hypothetical protein Rv3040c   | NP_217556.1      | 4.01880531                |
| 42580 | G04           | 904        | Rv3577   | hypothetical protein Rv3577  | NP_218094.1      | 3.629424779               |
| 42576 | G05           | 904        | Rv1834   | hydrolase  | NP_216350.1      | 3.94579646                |
| 42574 | G06           | 904        | Rv0940c  | oxidoreductase   | NP_215455.1      | 3.94579646                |
| 42581 | G07           | 907        | Rv0048c  | hypothetical protein Rv0048c   | NP_214562.1      | 4.014332966               |
| 42586 | G08           | 907        | Rv0812   | 4-amino-4-deoxychorismate lyase  | YP_177757.1      | 1.934950386               |
| 42584 | G09           | 907        | Rv0168   | integral membrane protein YRBE1B   | NP_214682.1      | 1.696802646               |
| 42582 | G10           | 907        | Rv0097   | oxidoreductase   | NP_214611.1      | 4.040793826               |
| 42589 | G11           | 907        | Rv2726c  | diaminopimelate epimerase  | NP_217242.1      | 3.958103638               |
| 42594 | G12           | 907        | Rv3124   | transcriptional regulatory protein   | NP_217640.1      | 3.952590959               |
| 42592 | H01           |            | Rv2937   | CLONE IS INVALID   |                  |                           |
| 42600 | H02           |            | Rv1282c  | CLONE IS INVALID   |                  |                           |
| 42604 | H03           | 910        | Rv2701c  | extragenic suppressor protein SuhB   | NP_217217.1      | 3.981318681               |
| 42605 | H04           | 910        | Rv3389c  | dehydrogenase  | NP_217906.1      | 3.637362637               |
| 42603 | H05           | 910        | Rv2316   | sugar-transport integral membrane protein ABC transporter UspA   | NP_216832.1      | 3.652747253               |
| 42606 | H06           | 913        | Rv0427c  | exodeoxyribonuclease III protein   | NP_214941.1      | 3.993428258               |
| 42610 | H07           | 913        | Rv2110c  | proteasome (beta subunit) PrcB   | NP_216626.1      | 1.360350493               |
| 42617 | H08           | 913        | Rv3633   | hypothetical protein Rv3633  | NP_218150.1      | 4.021905805               |
| 42607 | H09           | 913        | Rv0499   | hypothetical protein Rv0499  | NP_215013.1      | 3.969331873               |
| 42612 | H10           | 913        | Rv2426c  | hypothetical protein Rv2426c   | NP_216942.1      | 2.60788609                |
| 42616 | H11           | 913        | Rv3569c  | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase BphD   | NP_218086.1      | 2.143483023               |
| 42608 | H12           | 913        | Rv1096   | glycosyl hydrolase   | NP_215612.1      | 3.899233297               |

Table 27: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 27 (ZMTLQ), NR-19663

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 42623 | A01           | 916        | Rv2319c  | hypothetical protein Rv2319c  | NP_216835.1      | 3.996724891               |
| 42622 | A02           | 916        | Rv2125   | hypothetical protein Rv2125   | NP_216641.1      | 3.624454148               |
| 42618 | A03           |            | Rv0534c  | CLONE IS INVALID  |                  |                           |
| 42621 | A04           | 916        | Rv1825   | hypothetical protein Rv1825   | NP_216341.1      | 3.986899563               |
| 42620 | A05           | 916        | Rv1190   | hypothetical protein Rv1190   | NP_215706.1      | 4.022925764               |
| 42624 | A06           | 916        | Rv3205c  | hypothetical protein Rv3205c  | NP_217721.1      | 4.010917031               |
| 42625 | A07           | 916        | Rv3551   | CoA-transferase subunit alpha   | NP_218068.1      | 3.990174672               |
| 42630 | A08           | 919        | Rv1509   | hypothetical protein Rv1509   | NP_216025.1      | 4                         |
| 42632 | A09           | 919        | Rv2575   | hypothetical protein Rv2575   | NP_217091.1      | 3.9390642                 |
| 42629 | A10           | 919        | Rv1097c  | hypothetical protein Rv1097c  | NP_215613.1      | 3.784548422               |
| 42628 | A11           | 919        | Rv1045   | hypothetical protein Rv1045   | NP_215561.1      | 3.048966268               |
| 42631 | A12           | 919        | Rv2129c  | short chain dehydrogenase   | NP_216645.1      | 4.011969532               |
| 42634 | B01           | 922        | Rv0547c  | short chain dehydrogenase   | NP_215061.1      | 3.984815618               |
| 42642 | B02           | 922        | Rv1764   | putative transposase  | NP_216280.1      | 3.990238612               |
| 42643 | B03           |            | Rv2026c  | CLONE IS INVALID  |                  |                           |
| 42646 | B04           | 922        | Rv2903c  | signal peptidase I LepB   | NP_217419.1      | 4.056399132               |
| 42641 | B05           | 922        | Rv1756c  | putative transposase  | NP_216272.1      | 3.96637744                |
| 42640 | B06           | 922        | Rv1654   | acetylglutamate kinase  | NP_216170.1      | 3.594360087               |
| 42633 | B07           | 922        | Rv0315   | beta-1,3-glucanase precursor  | NP_214829.1      | 3.918655098               |
| 42645 | B08           | 922        | Rv2826c  | hypothetical protein Rv2826c  | NP_217342.1      | 3.865509761               |
| 42659 | B09           | 925        | Rv2827c  | hypothetical protein Rv2827c  | NP_217343.1      | 3.966486486               |
| 42665 | B10           | 925        | Rv3406   | Dioxygenase   | NP_217923.1      | 4.00972973                |
| 42662 | B11           | 925        | Rv3090   | hypothetical protein Rv3090   | NP_217606.1      | 4.033513514               |
| 42658 | B12           | 925        | Rv2180c  | integral membrane protein   | NP_216696.1      | 3.690810811               |
| 42655 | C01           | 925        | Rv0588   | integral membrane protein YrbE2b  | NP_215102.1      | 4.078918919               |
| 42653 | C02           | 925        | Rv0500   | pyrroline-5-carboxylate reductase   | NP_215014.1      | 4.059459459               |
| 42656 | C03           | 925        | Rv0770   | dehydrogenase/reductase   | NP_215284.1      | 3.938378378               |
| 42657 | C04           | 925        | Rv2005c  | hypothetical protein Rv2005c  | NP_216521.1      | 3.887567568               |
| 42671 | C05           | 928        | Rv3378c  | hypothetical protein Rv3378c  | NP_217895.1      | 2.169181034               |
| 42672 | C06           | 928        | Rv3714c  | hypothetical protein Rv3714c  | NP_218231.1      | 4.023706897               |
| 42668 | C07           | 928        | Rv2361c  | long (C50) chain Z-isoprenyl diphosphate synthase (Z-decaprenyl diphosphate synthase)                         | NP_216877.1      | 4.03125                   |
| 42679 | C08           | 931        | Rv3101c  | putative cell division protein FTSX (septation component-transport integral membrane protein ABC transporter) | NP_217617.1      | 3.880773362               |
| 42673 | C09           | 931        | Rv0780   | phosphoribosylaminoimidazole-succinocarboxamide synthase  | NP_215294.1      | 4.010741139               |
| 42678 | C10           | 931        | Rv2623   | hypothetical protein Rv2623   | NP_217139.1      | 3.934479055               |
| 42680 | C11           | 931        | Rv3283   | thiosulfate sulfurtransferase SseA  | NP_217800.1      | 3.968850698               |
| 42681 | C12           | 934        | Rv0045c  | Hydrolase   | NP_214559.1      | 3.867237687               |
| 42683 | D01           | 934        | Rv1515c  | hypothetical protein Rv1515c  | NP_216031.1      | 3.903640257               |
| 42686 | D02           | 934        | Rv2894c  | site-specific tyrosine recombinase XerC   | NP_217410.1      | 3.952890792               |
| 42682 | D03           | 934        | Rv0370c  | Oxidoreductase  | NP_214884.1      | 3.970021413               |
| 42688 | D04           | 937        | Rv0712   | hypothetical protein Rv0712   | NP_215226.1      | 2.093916756               |
| 42691 | D05           | 937        | Rv1502   | hypothetical protein Rv1502   | NP_216018.1      | 3.966915688               |
| 42693 | D06           | 937        | Rv2198c  | membrane protein  | NP_216714.1      | 1.404482391               |
| 42698 | D07           | 937        | Rv3310   | acid phosphatase  | NP_217827.1      | 3.933831377               |
| 42699 | D08           | 937        | Rv3413c  | hypothetical protein Rv3413c  | NP_217930.1      | 3.512273212               |
| 42697 | D09           | 937        | Rv3196   | hypothetical protein Rv3196   | NP_217712.1      | 3.469583778               |
| 42694 | D10           | 937        | Rv2606c  | pyridoxal biosynthesis lyase PdxS   | NP_217122.1      | 3.921024546               |
| 42716 | D11           | 940        | Rv2753c  | dihydrodipicolinate synthase  | NP_217269.1      | 2.011702128               |
| 42707 | D12           | 940        | Rv1678   | integral membrane protein   | NP_216194.1      | 3.985106383               |
| 42705 | E01           | 940        | Rv0519c  | hypothetical protein Rv0519c  | NP_215033.1      | 3.974468085               |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 42709 | E02           | 940        | Rv1814   | membrane-bound C-5 sterol desaturase erg3 (sterol-c5-desaturase)  | NP_216330.1      | 3.953191489               |
| 42718 | E03           | 940        | Rv3568c  | biphenyl-2,3-diol 1,2-dioxygenase   | NP_218085.1      | 3.915957447               |
| 42710 | E04           | 940        | Rv2040c  | sugar-transport integral membrane protein ABC transporter   | NP_216556.1      | 3.990425532               |
| 42712 | E05           | 940        | Rv2364c  | GTP-binding protein Era   | YP_177873.1      | 3.964893617               |
| 42702 | E06           | 940        | Rv0134   | epoxide hydrolase EphF  | NP_214648.1      | 3.524468085               |
| 42704 | E07           | 940        | Rv0263c  | hypothetical protein Rv0263c  | NP_214777.1      | 2.079787234               |
| 42708 | E08           | 940        | Rv1794   | hypothetical protein Rv1794   | NP_216310.1      | 3.861702128               |
| 42706 | E09           | 940        | Rv1618   | acyl-CoA thioesterase II TesB1  | NP_216134.1      | 3.869148936               |
| 42717 | E10           | 940        | Rv3034c  | Transferase   | NP_217550.1      | 3.044680851               |
| 42711 | E11           | 940        | Rv2296   | haloalkane dehalogenase   | NP_216812.1      | 3.946808511               |
| 42725 | E12           | 943        | Rv1050   | Oxidoreductase  | NP_215566.1      | 3.920466596               |
| 42721 | F01           | 943        | Rv0725c  | hypothetical protein Rv0725c  | NP_215239.1      | 3.575821845               |
| 42734 | F02           | 943        | Rv3265c  | dTDP-RHA:A-D-GlcNAc-diphosphoryl polyprenol   | YP_177952.1      | 3.885471898               |
| 42733 | F03           | 943        | Rv2729c  | hypothetical protein Rv2729c  | NP_217245.1      | 3.937433722               |
| 42730 | F04           | 943        | Rv2277c  | glycerolphosphodiesterase   | NP_216793.1      | 3.868504772               |
| 42732 | F05           | 943        | Rv2688c  | antibiotic ABC transporter ATP-binding protein  | NP_217204.1      | 2.559915164               |
| 42723 | F06           |            | Rv0936   | CLONE IS INVALID  |                  |                           |
| 42729 | F07           | 943        | Rv2216   | hypothetical protein Rv2216   | NP_216732.1      | 2.056203606               |
| 42726 | F08           | 943        | Rv1421   | hypothetical protein Rv1421   | NP_215937.1      | 3.054082715               |
| 42720 | F09           | 943        | Rv0646c  | lipase/esterase LipG  | NP_215160.1      | 3.938494168               |
| 42719 | F10           | 943        | Rv0642c  | methoxy mycolic acid synthase   | NP_215156.1      | 3.970307529               |
| 42722 | F11           | 943        | Rv0830   | hypothetical protein Rv0830   | NP_215345.1      | 3.945917285               |
| 42727 | F12           | 943        | Rv2172c  | hypothetical protein Rv2172c  | NP_216688.1      | 3.906680806               |
| 42742 | G01           | 946        | Rv0303   | dehydrogenase/reductase   | NP_214817.1      | 1.801268499               |
| 42760 | G02           | 946        | Rv3848   | transmembrane protein   | NP_218365.1      | 3.877378436               |
| 42743 | G03           | 946        | Rv0381c  | hypothetical protein Rv0381c  | NP_214895.1      | 3.846723044               |
| 42737 | G04           | 946        | Rv0217c  | esterase LipW   | NP_214731.1      | 2.950317125               |
| 42759 | G05           | 946        | Rv3806c  | phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase  | NP_218323.1      | 3.984143763               |
| 42746 | G06           | 946        | Rv0503c  | cyclopropane-fatty-acyl-phospholipid synthase 2 CMAA2 (cyclopropane fatty acid synthase) (CFA synthase) (cyclopropane mycolic acid synthase 2) (mycolic acid trans-cyclopropane synthetase) | NP_215017.1      | 3.921775899               |
| 42761 | G07           | 946        | Rv3896c  | hypothetical protein Rv3896c  | NP_218413.1      | 3.984143763               |
| 42758 | G08           | 946        | Rv3397c  | phytoene synthase   | NP_217914.1      | 3.791754757               |
| 42754 | G09           | 946        | Rv2323c  | hypothetical protein Rv2323c  | NP_216839.1      | 3.956659619               |
| 42749 | G10           | 946        | Rv1123c  | peroxidase BpoB   | NP_215639.1      | 3.746300211               |
| 42757 | G11           | 946        | Rv2820c  | hypothetical protein Rv2820c  | NP_217336.1      | 3.820295983               |
| 42766 | G12           | 949        | Rv1145   | transmembrane transport protein Mmpl13A   | NP_215661.1      | 3.030558483               |
| 42765 | H01           | 949        | Rv0954   | transmembrane protein   | NP_215469.1      | 2.147523709               |
| 42775 | H02           | 949        | Rv3521   | hypothetical protein Rv3521   | NP_218038.1      | 2.72918862                |
| 42778 | H03           | 949        | Rv3603c  | hypothetical protein Rv3603c  | NP_218120.1      | 1.939936776               |
| 42776 | H04           | 949        | Rv3535c  | acetaldehyde dehydrogenase  | NP_218052.1      | 4.038988409               |
| 42770 | H05           | 949        | Rv1896c  | hypothetical protein Rv1896c  | NP_216412.1      | 3.291886196               |
| 42769 | H06           | 949        | Rv1446c  | putative OXPP cycle protein OPCA  | NP_215962.1      | 3.915700738               |
| 42762 | H07           | 949        | Rv0068   | short chain dehydrogenase   | NP_214582.1      | 3.836670179               |
| 42763 | H08           | 949        | Rv0952   | succinyl-CoA synthetase subunit alpha   | NP_215467.1      | 3.816649104               |
| 42794 | H09           | 952        | Rv3266c  | dTDP-6-deoxy-L-lyxo-4-hexulose reductase RmlD   | NP_217783.1      | 3.881302521               |
| 42798 | H10           | 952        | Rv3589   | adenine glycosylase MutY  | NP_218106.1      | 3.949579832               |
| 42779 | H11           | 952        | Rv0007   | hypothetical protein Rv0007   | NP_214521.1      | 3.572478992               |
| 42787 | H12           | 952        | Rv1191   | hypothetical protein Rv1191   | NP_215707.1      | 3.942226891               |

Table 28: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 28 (ZMLTR), NR-19664

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 42797 | A01           | 952        | Rv3548c  | short chain dehydrogenase   | NP_218065.1      | 3.06407563                |
| 42791 | A02           | 952        | Rv2436   | ribokinase RBSK   | NP_216952.1      | 3.021008403               |
| 42790 | A03           | 952        | Rv1715   | 3-hydroxybutyryl-CoA dehydrogenase FADB3                            | YP_177829.1      | 3.963235294               |
| 42782 | A04           | 952        | Rv0456c  | enoyl-CoA hydratase   | NP_214970.1      | 2.478991597               |
| 42800 | A05           | 952        | Rv3782   | L-rhamnosyltransferase  | YP_178014.1      | 2.790966387               |
| 42801 | A06           | 955        | Rv1309   | F0F1 ATP synthase subunit gamma                                     | NP_215825.1      | 3.966492147               |
| 42802 | A07           | 955        | Rv1682   | coiled-coil structural protein                                      | NP_216198.1      | 3.986387435               |
| 42810 | A08           | 958        | Rv2385   | putative acetyl hydrolase MBTJ                                      | YP_177876.1      | 3.910229645               |
| 42807 | A09           | 958        | Rv0993   | UTP--glucose-1-phosphate uridylyltransferase                        | NP_215508.1      | 3.954070981               |
| 42811 | A10           | 958        | Rv2528c  | restriction system protein mrr                                      | NP_217044.1      | 3.019832985               |
| 42813 | A11           | 958        | Rv3092c  | integral membrane protein   | NP_217608.1      | 3.896659708               |
| 42812 | A12           | 958        | Rv2881c  | integral membrane phosphatidate cytidylyltransferase CdsA           | NP_217397.1      | 3.86743215                |
| 42823 | B01           | 961        | Rv2068c  | class A BETA-lactamase BLAC   | NP_216584.1      | 3.905306972               |
| 42818 | B02           | 961        | Rv1695   | inorganic polyphosphate/ATP-NAD kinase                              | NP_216211.1      | 3.927159209               |
| 42815 | B03           | 961        | Rv1357c  | hypothetical protein Rv1357c  | NP_215873.1      | 3.906347555               |
| 42814 | B04           | 961        | Rv1236   | sugar-transport integral membrane protein ABC transporter SugA      | NP_215752.1      | 3.936524454               |
| 42820 | B05           | 961        | Rv1823   | hypothetical protein Rv1823   | NP_216339.1      | 4.017689906               |
| 42830 | B06           | 964        | Rv1172c  | PE family protein   | YP_177793.1      | 3.503112033               |
| 42846 | B07           | 964        | Rv3787c  | hypothetical protein Rv3787c  | NP_218304.1      | 1.553941909               |
| 42834 | B08           | 964        | Rv2093c  | Sec-independent protein translocase transmembrane protein tatC      | NP_216609.1      | 3.81120332                |
| 42836 | B09           | 964        | Rv2859c  | amidotransferase  | NP_217375.1      | 3.859958506               |
| 42838 | B10           | 964        | Rv3104c  | transmembrane protein   | NP_217620.1      | 3.899377593               |
| 42835 | B11           | 964        | Rv2582   | peptidyl-prolyl cis-trans isomerase B                               | NP_217098.1      | 3.900414938               |
| 42833 | B12           | 964        | Rv1540   | hypothetical protein Rv1540   | NP_216056.1      | 3.911825726               |
| 42837 | C01           | 964        | Rv3084   | acetyl-hydrolase/esterase LipR                                      | NP_217600.1      | 3.976141079               |
| 42848 | C02           | 967        | Rv0510   | porphobilinogen deaminase   | NP_215024.1      | 2.405377456               |
| 42853 | C03           | 967        | Rv3602c  | pantoate--beta-alanine ligase                                       | NP_218119.1      | 3.192347466               |
| 42854 | C04           | 967        | Rv3725   | oxidoreductase  | NP_218242.1      | 3.521199586               |
| 42867 | C05           | 970        | Rv2964   | formyltetrahydrofolate deformylase                                  | NP_217480.1      | 3.874226804               |
| 42862 | C06           | 970        | Rv1673c  | hypothetical protein Rv1673c  | NP_216189.1      | 3.587628866               |
| 42864 | C07           | 970        | Rv2300c  | hypothetical protein Rv2300c  | NP_216816.1      | 3.882474227               |
| 42860 | C08           | 970        | Rv1456c  | unidentified antibiotic-transport integral membrane ABC transporter | NP_215972.1      | 2.153608247               |
| 42858 | C09           | 970        | Rv0497   | transmembrane protein   | NP_215011.1      | 3.769072165               |
| 42857 | C10           | 970        | Rv0146   | hypothetical protein Rv0146   | NP_214660.1      | 3.8                       |
| 42861 | C11           | 970        | Rv1646   | PE family protein   | YP_177825.1      | 3.869072165               |
| 42871 | C12           | 973        | Rv1218c  | tetronasin-transport ATP-binding protein ABC transporter            | NP_215734.1      | 4.024665982               |
| 42875 | D01           | 973        | Rv3900c  | hypothetical protein Rv3900c  | NP_218417.1      | 1.877697842               |
| 42870 | D02           | 973        | Rv0439c  | short chain dehydrogenase   | NP_214953.1      | 1.841726619               |
| 42874 | D03           | 973        | Rv3542c  | hypothetical protein Rv3542c  | NP_218059.1      | 1.818088386               |
| 42873 | D04           | 973        | Rv2218   | lipoyl synthase   | NP_216734.1      | 1.807810894               |
| 42872 | D05           | 973        | Rv1701   | site-specific tyrosine recombinase XerD                             | NP_216217.1      | 1.798561151               |
| 42883 | D06           | 976        | Rv1729c  | hypothetical protein Rv1729c  | NP_216245.1      | 3.893442623               |
| 42877 | D07           | 976        | Rv0774c  | hypothetical protein Rv0774c  | NP_215288.2      | 3.618852459               |
| 42889 | D08           |            | Rv2282c  | CLONE IS INVALID  |                  |                           |
| 42876 | D09           | 976        | Rv0673   | enoyl-CoA hydratase   | NP_215187.1      | 4.014344262               |
| 42882 | D10           | 976        | Rv1406   | methionyl-tRNA formyltransferase                                    | NP_215922.1      | 1.780737705               |
| 42901 | D11           | 976        | Rv3328c  | RNA polymerase sigma factor SigJ                                    | NP_217845.1      | 3.868852459               |
| 42903 | D12           | 979        | Rv0713   | transmembrane protein   | NP_215227.1      | 3.915219612               |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 42904 | E01           | 979        | Rv1458c  | unidentified antibiotic-transport ATP-binding protein ABC transporter  | NP_215974.1      | 3.986721144               |
| 42907 | E02           | 979        | Rv3199c  | NADH pyrophosphatase   | NP_217715.1      | 3.284984678               |
| 42905 | E03           |            | Rv2236c  | CLONE IS INVALID   | NP_216752.1      |                           |
| 42914 | E04           | 982        | Rv1698   | hypothetical protein Rv1698  | NP_216214.1      | 1.701629328               |
| 42926 | E05           | 982        | Rv3634c  | UDP-glucose 4-epimerase GALE1 (galactowaldenase) (UDP-galactose 4-epimerase) (uridine diphosphate galactose 4-epimerase) (uridine diphospho-galactose 4-epimerase) | NP_215015.2      | 1.787169043               |
| 42913 | E06           | 982        | Rv1075c  | hypothetical protein Rv1075c   | NP_215591.1      | 3.899185336               |
| 42912 | E07           | 982        | Rv0548c  | naphthoate synthase  | NP_215062.1      | 1.721995927               |
| 42909 | E08           | 982        | Rv0117   | oxidative stress response regulatory protein OXYS  | NP_214631.1      | 3.953156823               |
| 42915 | E09           | 982        | Rv2083   | hypothetical protein Rv2083  | NP_216599.1      | 3.952138493               |
| 42917 | E10           | 982        | Rv2569c  | hypothetical protein Rv2569c   | NP_217085.1      | 3.569246436               |
| 42916 | E11           | 982        | Rv2151c  | cell division protein FtsQ   | NP_216667.1      | 3.975560081               |
| 42931 | E12           | 985        | Rv3759c  | osmoprotectant (glycine betaine/carnitine /choline/L-proline) binding lipoprotein PROX   | NP_218276.1      | 3.944162437               |
| 42929 | F01           | 985        | Rv0819   | hypothetical protein Rv0819  | NP_215334.1      | 3.25786802                |
| 42930 | F02           | 985        | Rv3738c  | PPE family protein   | YP_178009.1      | 3.015228426               |
| 42938 | F03           | 988        | Rv1647   | hypothetical protein Rv1647  | NP_216163.1      | 3.139676113               |
| 42932 | F04           | 988        | Rv0084   | formate hydrogenlyase HYCD   | NP_214598.1      | 3.468623482               |
| 42935 | F05           | 988        | Rv1124   | epoxide hydrolase EphC   | NP_215640.1      | 3.950404858               |
| 42945 | F06           | 988        | Rv2611c  | lipid A biosynthesis lauroyl acyltransferase   | NP_217127.1      | 1.824898785               |
| 42941 | F07           | 988        | Rv2095c  | hypothetical protein Rv2095c   | NP_216611.1      | 3.946356275               |
| 42948 | F08           | 991        | Rv1010   | dimethyladenosine transferase  | NP_215526.1      | 2.796165489               |
| 42954 | F09           |            | Rv2985   | CLONE IS INVALID   |                  |                           |
| 42952 | F10           | 991        | Rv1996   | hypothetical protein Rv1996  | NP_216512.1      | 1.746720484               |
| 42951 | F11           | 991        | Rv1480   | hypothetical protein Rv1480  | NP_215996.1      | 3.827447023               |
| 42949 | F12           |            | Rv1201c  | CLONE IS INVALID   |                  |                           |
| 42958 | G01           | 991        | Rv3502c  | 3-ketoacyl-(acyl-carrier-protein) reductase  | NP_218019.1      | 3.93037336                |
| 42953 | G02           | 991        | Rv2263   | short chain dehydrogenase  | NP_216779.1      | 3.97073663                |
| 42947 | G03           | 991        | Rv0145   | hypothetical protein Rv0145  | NP_214659.1      | 3.960645812               |
| 42946 | G04           | 991        | Rv0094c  | hypothetical protein Rv0094c   | NP_214608.1      | 1.835519677               |
| 42962 | G05           | 994        | Rv1207   | dihydropteroate synthase 2 FolP2   | NP_215723.1      | 3.998993964               |
| 42960 | G06           | 994        | Rv0731c  | hypothetical protein Rv0731c   | NP_215245.1      | 3.979879276               |
| 42961 | G07           | 994        | Rv0805   | hypothetical protein Rv0805  | NP_215320.1      | 3.959758551               |
| 42966 | G08           | 994        | Rv2338c  | hypothetical protein Rv2338c   | NP_216854.1      | 3.974849095               |
| 42967 | G09           | 994        | Rv3028c  | electron transfer flavoprotein subunit alpha   | NP_217544.1      | 3.904426559               |
| 42970 | G10           | 994        | Rv3564   | acyl-CoA dehydrogenase FADE33  | NP_218081.1      | 2.699195171               |
| 42959 | G11           | 994        | Rv0112   | GDP-mannose 4,6-dehydratase  | NP_214626.1      | 3.081488934               |
| 42963 | G12           | 994        | Rv1708   | putative initiation inhibitor protein  | NP_216224.1      | 1.769617706               |
| 42964 | H01           | 994        | Rv1935c  | enoyl-CoA hydratase  | NP_216451.1      | 3.976861167               |
| 42974 | H02           | 997        | Rv1380   | aspartate carbamoyltransferase catalytic subunit   | NP_215896.1      | 3.646940822               |
| 42977 | H03           | 997        | Rv1518   | hypothetical protein Rv1518  | NP_216034.1      | 3.979939819               |
| 42980 | H04           | 997        | Rv3166c  | hypothetical protein Rv3166c   | NP_217682.1      | 3.976930792               |
| 42978 | H05           |            | Rv1949c  | CLONE IS INVALID   |                  |                           |
| 42981 | H06           | 997        | Rv3563   | acyl-CoA dehydrogenase FADE32  | NP_218080.1      | 3.932798395               |
| 42973 | H07           | 997        | Rv1026   | hypothetical protein Rv1026  |                  | 3.879638917               |
| 42987 | H08           | 1000       | Rv3164c  | methanol dehydrogenase transcriptional regulatory protein MoxR3  | NP_217680.1      | 3.749                     |
| 42986 | H09           | 1000       | Rv1905c  | D-amino acid oxidase   | NP_216421.1      | 3.906                     |
| 42988 | H10           | 1003       | Rv0377   | LysR family transcriptional regulator  | NP_214891.1      | 3.974077767               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------|------------------|---------------------------|
| 42992 | H11           | 1003       | Rv3701c  | hypothetical protein Rv3701c | NP_218218.1      | 3.875373878               |
| 42993 | H12           | 1003       | Rv3838c  | prephenate dehydratase       | NP_218355.1      | 3.939182453               |

Table 29: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 29 (ZMTLS), NR-19665

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 42990 | A01           | 1003       | Rv2999   | lipoprotein LppY  | NP_217515.1      | 3.838484546               |
| 42991 | A02           | 1003       | Rv3218   | hypothetical protein Rv3218   | NP_217734.1      | 3.937188435               |
| 42989 | A03           | 1003       | Rv2955c  | hypothetical protein Rv2955c  | NP_217471.1      | 3.923230309               |
| 43002 | A04           | 1006       | Rv3579c  | tRNA/rRNA methyltransferase   | NP_218096.1      | 3.05666004                |
| 42996 | A05           | 1006       | Rv0176   | mce associated transmembrane protein  | NP_214690.1      | 3.855864811               |
| 42994 | A06           | 1006       | Rv0021c  | hypothetical protein Rv0021c  | NP_214535.1      | 3.767395626               |
| 43003 | A07           | 1006       | Rv3617   | epoxide hydrolase EphA  | NP_218134.1      | 3.852882704               |
| 43000 | A08           |            | Rv1981c  | CLONE IS INVALID  | YP_177853.1      |                           |
| 43001 | A09           | 1006       | Rv2336   | hypothetical protein Rv2336   | NP_216852.1      | 3.219681909               |
| 42998 | A10           | 1006       | Rv1512   | nucleotide-sugar epimerase epiA   | NP_216028.1      | 1.881709742               |
| 42995 | A11           | 1006       | Rv0149   | quinone oxidoreductase  | NP_214663.1      | 1.815109344               |
| 43011 | A12           | 1009       | Rv2710   | RNA polymerase sigma factor SigB  | NP_217226.1      | 1.754212091               |
| 43012 | B01           | 1009       | Rv3141   | NADPH quinone oxidoreductase  | NP_217657.1      | 3.933597621               |
| 43004 | B02           | 1009       | Rv0183   | lysophospholipase   | NP_214697.2      | 3.82160555                |
| 43005 | B03           | 1009       | Rv0212c  | transcriptional regulatory protein NadR   | NP_214726.1      | 3.774033697               |
| 43009 | B04           | 1009       | Rv2077c  | hypothetical protein Rv2077A  | YP_177658.1      | 3.816650149               |
| 43010 | B05           | 1009       | Rv2298   | hypothetical protein Rv2298   | NP_216814.1      | 3.870168484               |
| 43015 | B06           |            | Rv1283c  | CLONE IS INVALID  | NP_215799.1      |                           |
| 43017 | B07           | 1012       | Rv0529   | cytochrome C-type biogenesis protein CcsA   | NP_215041.2      | 3.877470356               |
| 43021 | B08           | 1012       | Rv2037c  | transmembrane protein   | NP_216553.1      | 3.91798419                |
| 43024 | B09           | 1012       | Rv2707   | hypothetical protein Rv2707   | NP_217223.1      | 3.937747036               |
| 43023 | B10           | 1012       | Rv2202c  | carbohydrate kinase CbhK  | NP_216718.1      | 3.90513834                |
| 43020 | B11           | 1012       | Rv1208   | putative glucosyl-3-phosphoglycerate synthase   | NP_215724.1      | 3.883399209               |
| 43019 | B12           | 1012       | Rv0929   | phosphate ABC transporter transmembrane protein   | NP_215444.1      | 3.899209486               |
| 43028 | C01           | 1012       | Rv3048c  | ribonucleotide-diphosphate reductase subunit beta   | YP_177921.1      | 3.513833992               |
| 43027 | C02           | 1012       | Rv2795c  | hypothetical protein Rv2795c  | NP_217311.1      | 3.846837945               |
| 43029 | C03           | 1015       | Rv0893c  | hypothetical protein Rv0893c  | NP_215408.1      | 3.418719212               |
| 43030 | C04           | 1015       | Rv0989c  | polyprenyl-diphosphate synthase   | NP_215504.1      | 1.695566502               |
| 43040 | C05           | 1015       | Rv2560   | hypothetical protein Rv2560   | NP_217076.1      | 3.852216749               |
| 43034 | C06           | 1015       | Rv1423   | transcriptional regulatory protein WHIA   | NP_215939.1      | 3.909359606               |
| 43038 | C07           | 1015       | Rv1886c  | secreted antigen 85-B fbpB (85B) (antigen 85 complex B) (Mycolyl transferase 85B) (fibronectin-binding protein B) | NP_216402.1      | 2.200985222               |
| 43039 | C08           | 1015       | Rv2410c  | hypothetical protein Rv2410c  | NP_216926.1      | 3.878817734               |
| 43031 | C09           | 1015       | Rv1021   | nucleoside triphosphate pyrophosphohydrolase  | NP_215537.1      | 3.890640394               |
| 43044 | C10           | 1018       | Rv0553   | O-succinylbenzoate synthase   | NP_215067.1      | 3.942043222               |
| 43049 | C11           | 1018       | Rv1017c  | ribose-phosphate pyrophosphokinase  | NP_215533.1      | 2.158153242               |
| 43053 | C12           | 1018       | Rv3784   | dTDP-glucose 4,6-dehydratase  | YP_178015.1      | 3.73280943                |
| 43043 | D01           | 1018       | Rv0230c  | phosphotriesterase  | NP_214744.1      | 3.84675835                |
| 43050 | D02           | 1018       | Rv1373   | glycolipid sulfotransferase   | NP_215889.1      | 3.86345776                |
| 43047 | D03           | 1018       | Rv0899   | outer membrane protein A OMPA   | NP_215414.1      | 1.764243615               |
| 43045 | D04           | 1018       | Rv0728c  | D-3-phosphoglycerate dehydrogenase  | NP_215242.1      | 3.197445973               |
| 43054 | D05           | 1021       | Rv3038c  | hypothetical protein Rv3038c  | NP_217554.1      | 3.858961802               |
| 43057 | D06           | 1024       | Rv0347   | hypothetical protein Rv0347   | NP_214861.1      | 3.833007813               |
| 43063 | D07           |            | Rv2649   | CLONE IS INVALID  | NP_217166.1      |                           |
| 43059 | D08           | 1024       | Rv0496   | hypothetical protein Rv0496   | NP_215010.1      | 3.80859375                |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43064 | D09           | 1024       | Rv3777   | oxidoreductase  | NP_218294.1      | 3.760742188               |
| 43058 | D10           | 1024       | Rv0411c  | glutamine-binding lipoprotein   | NP_214925.1      | 2.51953125                |
| 43060 | D11           | 1024       | Rv1099c  | fructose 1,6-bisphosphatase II  | NP_215615.1      | 3.850585938               |
| 43061 | D12           | 1024       | Rv1454c  | quinone reductase   | NP_215970.1      | 3.876953125               |
| 43072 | E01           | 1027       | Rv3711c  | DNA polymerase III subunit epsilon  | NP_218228.1      | 3.486854917               |
| 43065 | E02           | 1027       | Rv0493c  | hypothetical protein Rv0493c  | NP_215007.1      | 3.679649464               |
| 43069 | E03           | 1027       | Rv1240   | malate dehydrogenase  | NP_215756.1      | 3.919182084               |
| 43066 | E04           | 1027       | Rv0512   | delta-aminolevulinic acid dehydratase   | NP_215026.1      | 3.003894839               |
| 43078 | E05           | 1030       | Rv2564   | glutamine-transport ATP-binding protein ABC transporter GlnQ                      | NP_217080.1      | 3.852427184               |
| 43075 | E06           | 1030       | Rv0614   | hypothetical protein Rv0614   | NP_215128.1      | 3.80776699                |
| 43079 | E07           | 1030       | Rv2735c  | hypothetical protein Rv2735c  | NP_217251.1      | 3.787378641               |
| 43080 | E08           | 1030       | Rv3228   | hypothetical protein Rv3228   | NP_217745.1      | 3.739805825               |
| 43074 | E09           | 1030       | Rv0265c  | periplasmic IRON-transport lipoprotein  | YP_177705.1      | 3.708737864               |
| 43073 | E10           | 1030       | Rv0073   | glutamine-transport ATP-binding protein   | NP_214587.1      | 3.62815534                |
| 43086 | E11           | 1033       | Rv2032   | hypothetical protein Rv2032   | NP_216548.1      | 3.546950629               |
| 43088 | E12           | 1033       | Rv2936   | daunorubicin-DIM-transport ATP-binding protein ABC transporter DrrA               | NP_217452.1      | 3.900290416               |
| 43083 | F01           | 1033       | Rv0292   | transmembrane protein   | NP_214806.1      | 3.869312682               |
| 43087 | F02           | 1033       | Rv2786c  | bifunctional riboflavin kinase/FMN adenylyltransferase                            | NP_217302.1      | 3.826718296               |
| 43097 | F03           | 1036       | Rv2025c  | hypothetical protein Rv2025c  | NP_216541.1      | 1.546332046               |
| 43100 | F04           | 1036       | Rv3131   | hypothetical protein Rv3131   | NP_217647.1      | 3.803088803               |
| 43099 | F05           | 1036       | Rv2646   | integrase   | NP_217162.1      | 1.741312741               |
| 43094 | F06           | 1036       | Rv0950c  | hypothetical protein Rv0950c  | NP_215465.1      | 1.88996139                |
| 43098 | F07           | 1036       | Rv2096c  | hypothetical protein Rv2096c  | NP_216612.1      | 3.142857143               |
| 43103 | F08           | 1039       | Rv0998   | hypothetical protein Rv0998   | NP_215513.1      | 4.613089509               |
| 10023 | F09           | 1039       | Rv2977c  | thiamine monophosphate kinase   | NP_217493.1      | 1.75360924                |
| 43113 | F10           |            | Rv1912c  | CLONE IS INVALID  |                  |                           |
| 43115 | F11           | 1042       | Rv3093c  | oxidoreductase  | NP_217609.1      | 4.448176583               |
| 43114 | F12           | 1042       | Rv2982c  | NAD(P)H-dependent glycerol-3-phosphate dehydrogenase                              | NP_217498.1      | 4.854126679               |
| 43110 | G01           | 1042       | Rv0843   | dehydrogenase   | NP_215358.1      | 4.928982726               |
| 43111 | G02           | 1042       | Rv1496   | arginine/ornithine transport system ATPase  | NP_216012.1      | 4.977927063               |
| 43119 | G03           | 1045       | Rv1110   | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase                                | YP_177788.1      | 4.645933014               |
| 43122 | G04           | 1045       | Rv3913   | thioredoxin reductase TRXB2   | NP_218430.1      | 4.663157895               |
| 43116 | G05           | 1045       | Rv0533c  | 3-oxoacyl-(acyl carrier protein) synthase III                                     | NP_215047.1      | 4.978947368               |
| 43117 | G06           | 1045       | Rv0562   | polyprenyl-diphosphate synthase   | NP_215076.1      | 4.419138756               |
| 43121 | G07           | 1045       | Rv3856c  | hypothetical protein Rv3856c  | NP_218373.1      | 4.90430622                |
| 43120 | G08           | 1045       | Rv1481   | hypothetical protein Rv1481   | NP_215997.1      | 4.954066986               |
| 43118 | G09           | 1045       | Rv0799c  | hypothetical protein Rv0799c  | NP_215314.1      | 4.891866029               |
| 43123 | G10           | 1048       | Rv0407   | F420-dependent glucose-6-phosphate dehydrogenase                                  | NP_214921.1      | 4.041984733               |
| 43126 | G11           | 1048       | Rv2995c  | 3-isopropylmalate dehydrogenase   | NP_217511.1      | 4.757633588               |
| 43128 | G12           | 1048       | Rv3469c  | 4-hydroxy-2-ketovalerate aldolase   | NP_217986.1      | 4.719465649               |
| 43127 | H01           | 1048       | Rv3336c  | tryptophanyl-tRNA synthetase  | NP_217853.1      | 4.922709924               |
| 43125 | H02           | 1048       | Rv2837c  | hypothetical protein Rv2837c  | NP_217353.1      | 3.033396947               |
| 43129 | H03           | 1048       | Rv3707c  | hypothetical protein Rv3707c  | NP_218224.1      | 4.607824427               |
| 43130 | H04           | 1048       | Rv3802c  | hypothetical protein Rv3802c  | NP_218319.1      | 4.979007634               |
| 43132 | H05           | 1051       | Rv3015c  | hypothetical protein Rv3015c  | NP_217531.1      | 4.990485252               |
| 43131 | H06           | 1051       | Rv0216   | hypothetical protein Rv0216   | NP_214730.1      | 4.8905804                 |
| 43138 | H07           | 1054       | Rv3804c  | secreted antigen 85-A FBPA (fibronectin-binding protein A) (antigen 85 complex A) | NP_218321.1      | 3.016129032               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 43134 | H08           | 1054       | Rv0935   | phosphate ABC transporter transmembrane protein  | YP_177771.1      | 4.886148008               |
| 43136 | H09           | 1054       | Rv2817c  | hypothetical protein Rv2817c   | NP_217333.1      | 4.815939279               |
| 43133 | H10           | 1054       | Rv0824c  | acyl-  | YP_177758.1      | 1.617647059               |
| 43135 | H11           | 1054       | Rv1138c  | oxidoreductase   | NP_215654.1      | 4.756166983               |
| 43140 | H12           | 1057       | Rv1409   | bifunctional diaminohydroxyphosphoribosyl-aminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino) uracil reductase | NP_215925.1      | 4.860927152               |

Table 30: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 30 (ZMTLT), NR-19666

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 43146 | A01           | 1057       | Rv3544c  | acyl-CoA dehydrogenase FADE28                                      | NP_218061.1      | 4.072847682               |
| 43145 | A02           | 1057       | Rv2029c  | phosphofruktokinase PfkB (phosphohexokinase)                       | NP_216545.1      | 2.821192053               |
| 43139 | A03           | 1057       | Rv0567   | methyltransferase/methylase  | NP_215081.1      | 4.482497635               |
| 43143 | A04           | 1057       | Rv1482c  | hypothetical protein Rv1482c                                       | NP_215998.2      | 4.940397351               |
| 43142 | A05           | 1057       | Rv1436   | glyceraldehyde-3-phosphate dehydrogenase                           | NP_215952.1      | 4.92526017                |
| 43166 | A06           | 1060       | Rv3679   | anion transporter ATPase   | NP_218196.1      | 4.60754717                |
| 43149 | A07           | 1060       | Rv0139   | Oxidoreductase   | NP_214653.1      | 4.50754717                |
| 43156 | A08           | 1060       | Rv1122   | 6-phosphogluconate dehydrogenase-like protein                      | NP_215638.1      | 3.667924528               |
| 43159 | A09           | 1060       | Rv1511   | GDP-D-mannose dehydratase gmdA (GDP-mannose 4,6 dehydratase) (GMD) | NP_216027.1      | 4.818867925               |
| 43151 | A10           | 1060       | Rv0415   | thiamine biosynthesis oxidoreductase ThiO                          | NP_214929.1      | 2.263207547               |
| 43158 | A11           | 1060       | Rv1360   | Oxidoreductase   | NP_215876.1      | 4.576415094               |
| 43161 | A12           | 1060       | Rv2578c  | hypothetical protein Rv2578c                                       | NP_217094.1      | 2.348113208               |
| 43163 | B01           | 1060       | Rv3082c  | virulence-regulating transcriptional regulator VirS                | NP_217598.1      | 2.49245283                |
| 43167 | B02           |            | Rv2568c  | CLONE IS INVALID   |                  |                           |
| 43172 | B03           |            | Rv1043c  | CLONE IS INVALID   |                  |                           |
| 43174 | B04           | 1063       | Rv1543   | fatty acyl-CoA reductase   | NP_216059.1      | 4.522107244               |
| 43175 | B05           | 1063       | Rv1649   | phenylalanyl-tRNA synthetase subunit alpha                         | NP_216165.1      | 4.841015992               |
| 43170 | B06           | 1063       | Rv0622   | hypothetical protein Rv0622  | NP_215136.2      | 4.757290687               |
| 43169 | B07           | 1063       | Rv0564c  | NAD(P)H-dependent glycerol-3-phosphate dehydrogenase               | NP_215078.1      | 4.445907808               |
| 43177 | B08           | 1063       | Rv2715   | Hydrolase  | NP_217231.1      | 4.831608655               |
| 43179 | B09           | 1063       | Rv3888c  | hypothetical protein Rv3888c                                       | NP_218405.1      | 4.8579492                 |
| 43186 | B10           | 1066       | Rv3843c  | transmembrane protein  | NP_218360.1      | 4.891181989               |
| 43181 | B11           | 1066       | Rv0837c  | hypothetical protein Rv0837c                                       | NP_215352.1      | 3.380863039               |
| 43182 | B12           | 1066       | Rv1422   | hypothetical protein Rv1422  | NP_215938.1      | 4.894934334               |
| 43183 | C01           | 1066       | Rv1500   | Glycosyltransferase  | NP_216016.1      | 4.838649156               |
| 43185 | C02           | 1066       | Rv1967   | MCE-family protein MCE3B   | NP_216483.1      | 2.058161351               |
| 43192 | C03           | 1069       | Rv3524   | hypothetical protein Rv3524  | NP_218041.1      | 3.242282507               |
| 43191 | C04           | 1069       | Rv3010c  | 6-phosphofruktokinase  | NP_217526.1      | 4.762394761               |
| 43190 | C05           | 1069       | Rv2374c  | heat-inducible transcription repressor                             | NP_216890.1      | 4.720299345               |
| 43197 | C06           |            | Rv2592c  | CLONE IS INVALID   |                  |                           |
| 43194 | C07           | 1072       | Rv1333   | Hydrolase  | NP_215849.1      | 4.554104478               |
| 43199 | C08           | 1072       | Rv2781c  | alanine rich oxidoreductase  | NP_217297.1      | 4.569029851               |
| 43201 | C09           | 1072       | Rv3191c  | Transposase  | NP_217707.1      | 4.564365672               |
| 43204 | C10           | 1072       | Rv3917c  | chromosome partitioning protein ParB                               | NP_218435.2      | 4.588619403               |
| 43196 | C11           | 1072       | Rv2159c  | hypothetical protein Rv2159c                                       | NP_216675.1      | 4.858208955               |
| 43193 | C12           | 1072       | Rv0363c  | fructose-bisphosphate aldolase                                     | NP_214877.1      | 3.489738806               |
| 43200 | D01           | 1072       | Rv3127   | hypothetical protein Rv3127  | NP_217643.1      | 4.681902985               |
| 43195 | D02           | 1072       | Rv1485   | Ferrocyclase   | NP_216001.1      | 4.541044776               |
| 43208 | D03           | 1075       | Rv3651   | hypothetical protein Rv3651  | NP_218168.1      | 4.486511628               |
| 43205 | D04           | 1075       | Rv1071c  | enoyl-CoA hydratase  | NP_215587.1      | 3.993488372               |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                     | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43210 | D05           | 1075       | Rv3708c  | aspartate-semialdehyde dehydrogenase                        | NP_218225.1      | 4.489302326               |
| 43227 | D06           | 1078       | Rv2854   | hypothetical protein Rv2854                                 | NP_217370.1      | 4.849721707               |
| 43238 | D07           | 1078       | Rv3730c  | hypothetical protein Rv3730c                                | NP_218247.1      | 4.56864564                |
| 43215 | D08           |            | Rv1168c  | CLONE IS INVALID  |                  |                           |
| 43221 | D09           | 1078       | Rv1862   | alcohol dehydrogenase AdhA                                  | NP_216378.1      | 4.919294991               |
| 43222 | D10           | 1078       | Rv2017   | transcriptional regulatory protein                          | NP_216533.1      | 4.577922078               |
| 43214 | D11           | 1078       | Rv0943c  | Monooxygenase   | NP_215458.1      | 4.563079777               |
| 43237 | D12           | 1078       | Rv3684   | Lyase   | NP_218201.1      | 3.003710575               |
| 43228 | E01           | 1078       | Rv3045   | NADP-dependent alcohol dehydrogenase ADHC                   | NP_217561.1      | 4.856215213               |
| 43235 | E02           | 1078       | Rv3534c  | 4-hydroxy-2-ketovaleate aldolase                            | NP_218051.1      | 4.30890538                |
| 43211 | E03           | 1078       | Rv0170   | MCE-family protein MCE1B                                    | NP_214684.1      | 4.598330241               |
| 43243 | E04           | 1081       | Rv2802c  | hypothetical protein Rv2802c                                | NP_217318.1      | 4.888066605               |
| 43247 | E05           | 1081       | Rv3520c  | coenzyme F420-dependent oxidoreductase                      | NP_218037.1      | 3.237742831               |
| 43245 | E06           | 1081       | Rv3457c  | DNA-directed RNA polymerase subunit alpha                   | NP_217974.1      | 3.781683626               |
| 43248 | E07           | 1081       | Rv3918c  | chromosome partitioning protein ParA                        | NP_218434.2      | 4.62719704                |
| 43244 | E08           | 1081       | Rv2841c  | transcription elongation factor NusA                        | NP_217357.1      | 4.335800185               |
| 43251 | E09           | 1084       | Rv2423   | hypothetical protein Rv2423                                 | NP_216939.1      | 4.922509225               |
| 43250 | E10           | 1084       | Rv1977   | hypothetical protein Rv1977                                 | NP_216493.1      | 4.884686347               |
| 43249 | E11           | 1084       | Rv0479c  | hypothetical protein Rv0479c                                | NP_214993.1      | 4.880073801               |
| 43260 | E12           | 1087       | Rv1589   | biotin synthase   | NP_216105.1      | 4.840846366               |
| 43262 | F01           | 1087       | Rv2563   | glutamine-transport transmembrane protein ABC transporter   | NP_217079.1      | 4.805887764               |
| 43261 | F02           | 1087       | Rv1594   | quinolinate synthetase                                      | NP_216110.1      | 4.7700092                 |
| 43256 | F03           |            | Rv0072   | CLONE IS INVALID  |                  |                           |
| 43267 | F04           | 1090       | Rv3660c  | hypothetical protein Rv3660c                                | NP_218177.1      | 4.496330275               |
| 43264 | F05           | 1090       | Rv3383c  | polyprenyl synthetase ldsB                                  | NP_217900.1      | 4.832110092               |
| 43266 | F06           | 1090       | Rv3626c  | hypothetical protein Rv3626c                                | NP_218143.1      | 4.821100917               |
| 43263 | F07           | 1090       | Rv1790   | PPE family protein  | YP_177836.1      | 4.865137615               |
| 43265 | F08           | 1090       | Rv3498c  | MCE-family protein MCE4B                                    | NP_218015.1      | 4.580733945               |
| 43271 | F09           | 1093       | Rv2609c  | hypothetical protein Rv2609c                                | NP_217125.1      | 4.576395242               |
| 43272 | F10           | 1093       | Rv3761c  | acyl-CoA dehydrogenase                                      | NP_218278.1      | 4.565416285               |
| 43268 | F11           | 1093       | Rv0826   | hypothetical protein Rv0826                                 | NP_215341.1      | 4.81610247                |
| 43270 | F12           | 1093       | Rv2397c  | sulfate-transport ATP-binding protein ABC transporter CysA1 | YP_177879.1      | 4.836230558               |
| 43269 | G01           | 1093       | Rv1645c  | hypothetical protein Rv1645c                                | NP_216161.1      | 4.805123513               |
| 43278 | G02           | 1096       | Rv2173   | geranylgeranyl pyrophosphate synthetase                     | NP_216689.1      | 3.09580292                |
| 43276 | G03           | 1096       | Rv2143   | hypothetical protein Rv2143                                 | NP_216659.1      | 4.497262774               |
| 43273 | G04           | 1096       | Rv0060   | hypothetical protein Rv0060                                 | NP_214574.1      | 4.801094891               |
| 43281 | G05           | 1096       | Rv2712c  | hypothetical protein Rv2712c                                | NP_217228.1      | 4.298357664               |
| 43287 | G06           | 1099       | Rv1665   | chalcone synthase   | NP_216181.1      | 4.832575068               |
| 43294 | G07           | 1099       | Rv3772   | putative aminotransferase                                   | NP_218289.1      | 2.54322111                |
| 43286 | G08           | 1099       | Rv1660   | chalcone synthase   | NP_216176.1      | 4.801637853               |
| 43292 | G09           | 1099       | Rv3736   | transcriptional regulatory protein AraC/XylS-family         | NP_218253.1      | 4.74522293                |
| 43288 | G10           | 1099       | Rv1692   | Phosphatase   | NP_216208.1      | 4.702456779               |
| 43291 | G11           | 1099       | Rv2258c  | transcriptional regulator                                   | NP_216774.1      | 4.713375796               |
| 43297 | G12           | 1102       | Rv0923c  | hypothetical protein Rv0923c                                | NP_215438.1      | 5.097096189               |
| 43298 | H01           | 1102       | Rv1059   | hypothetical protein Rv1059                                 | NP_215575.1      | 4.505444646               |
| 43300 | H02           | 1102       | Rv2353c  | PPE family protein  | YP_177871.1      | 1.593466425               |
| 43301 | H03           | 1102       | Rv3522   | lipid-transfer protein                                      | NP_218039.1      | 4.296733212               |
| 43299 | H04           | 1102       | Rv1202   | succinyl-diaminopimelate desuccinylase                      | YP_177796.1      | 4.827586207               |
| 43307 | H05           | 1105       | Rv3553   | Oxidoreductase  | NP_218070.1      | 4.469683258               |
| 43306 | H06           | 1105       | Rv3200c  | transmembrane cation transporter                            | NP_217716.1      | 4.757466063               |
| 43309 | H07           | 1108       | Rv2400c  | sulfate-binding lipoprotein                                 | NP_216916.1      | 4.731949458               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                             | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43308 | H08           | 1108       | Rv1938   | epoxide hydrolase EphB                              | NP_216454.1      | 4.739169675               |
| 43312 | H09           | 1111       | Rv0215c  | acyl-CoA dehydrogenase FADE3                        | NP_214729.1      | 2.915391539               |
| 43321 | H10           | 1111       | Rv3785   | hypothetical protein Rv3785                         | NP_218302.1      | 4.739873987               |
| 43315 | H11           | 1111       | Rv2038c  | sugar-transport ATP-binding protein ABC transporter | NP_216554.1      | 4.747974797               |
| 43317 | H12           | 1111       | Rv2139   | dihydroorotate dehydrogenase 2                      | NP_216655.1      | 2.702970297               |

Table 31: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 31 (ZMTLU), NR-19667

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 43313 | A01           | 1111       | Rv1112   | GTP-dependent nucleic acid-binding protein EngD  | NP_215628.1      | 4.720072007               |
| 43320 | A02           | 1111       | Rv3497c  | MCE-family protein MCE4C   | NP_218014.1      | 4.747074707               |
| 43314 | A03           | 1111       | Rv1299   | peptide chain release factor 1   | NP_215815.1      | 3.936993699               |
| 43324 | A04           | 1114       | Rv0926c  | hypothetical protein Rv0926c   | NP_215441.1      | 2.859964093               |
| 43331 | A05           | 1114       | Rv3571   | hemoglobine-like protein   | NP_218088.1      | 3.961400359               |
| 43336 | A06           | 1114       | Rv3731   | ATP-dependent DNA ligase   | NP_218248.1      | 3.946140036               |
| 43327 | A07           | 1114       | Rv2138   | lipoprotein LppL   | NP_216654.1      | 4.772890485               |
| 43334 | A08           |            | Rv3692   | CLONE IS INVALID   | NP_218209.1      |                           |
| 43330 | A09           | 1114       | Rv3037c  | hypothetical protein Rv3037c   | NP_217553.1      | 4.438061041               |
| 43322 | A10           | 1114       | Rv0502   | hypothetical protein Rv0502  | NP_215016.1      | 4.745960503               |
| 43338 | A11           | 1117       | Rv0855   | fatty-acid-CoA racemase  | NP_215370.1      | 4.692927484               |
| 43346 | A12           | 1117       | Rv3264c  | D-alpha-D-mannose-1-phosphate guanylyltransferase MANB (D-alpha-D-heptose-1-phosphate guanylyltransferase) | YP_177951.1      | 4.642793196               |
| 43337 | B01           | 1117       | Rv0655   | ribonucleotide ABC transporter ATP-binding protein   | NP_215169.1      | 4.736794987               |
| 43345 | B02           | 1117       | Rv3109   | molybdenum cofactor biosynthesis protein A   | YP_177925.1      | 4.000895255               |
| 43347 | B03           | 1117       | Rv3398c  | multifunctional dimethylallyltransferase/farnesyl diphosphate synthetase/farnesyltranstransferase          | YP_177970.1      | 4.742166517               |
| 43356 | B04           | 1120       | Rv1295   | threonine synthase   | NP_215811.1      | 4.733928571               |
| 43354 | B05           | 1120       | Rv1143   | alpha-methylacyl-CoA racemase  | NP_215659.1      | 2.122321429               |
| 43357 | B06           | 1120       | Rv1607   | ionic transporter integral membrane protein chaA   | NP_216123.1      | 3.132142857               |
| 43353 | B07           | 1120       | Rv1063c  | hypothetical protein Rv1063c   | NP_215579.1      | 3.86875                   |
| 43350 | B08           | 1120       | Rv0132c  | putative f420-dependent glucose-6-phosphate dehydrogenase Fgd2   | NP_214646.1      | 4.11875                   |
| 43359 | B09           | 1120       | Rv2832c  | sn-glycerol-3-phosphate transport ATP-binding protein ABC transporter UGPC                                 | NP_217348.1      | 4.727678571               |
| 43358 | B10           | 1120       | Rv2262c  | hypothetical protein Rv2262c   | NP_216778.1      | 4.73125                   |
| 43363 | B11           | 1123       | Rv2207   | nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase                                     | NP_216723.1      | 4.750667854               |
| 43362 | B12           | 1123       | Rv0209   | hypothetical protein Rv0209  | NP_214723.1      | 3.960819234               |
| 43374 | C01           | 1126       | Rv3138   | pyruvate formate lyase activating protein PflA   | NP_217654.1      | 4.431616341               |
| 43370 | C02           | 1126       | Rv1009   | resuscitation-promoting factor rpfB  | NP_215525.1      | 4.719360568               |
| 43372 | C03           | 1126       | Rv1178   | N-succinyldiaminopimelate aminotransferase   | NP_215694.1      | 4.414742451               |
| 43373 | C04           | 1126       | Rv2538c  | 3-dehydroquinase synthase  | NP_217054.1      | 4.379218472               |
| 43379 | C05           | 1129       | Rv2064   | cobalamin biosynthesis protein CobG  | NP_216580.1      | 4.715677591               |
| 43380 | C06           | 1129       | Rv2200c  | transmembrane cytochrome C oxidase subunit II CtaC   | NP_216716.1      | 4.389725421               |
| 43377 | C07           | 1129       | Rv1933c  | acyl-CoA dehydrogenase FADE18  | NP_216449.1      | 4.729849424               |
| 43384 | C08           | 1132       | Rv0809   | phosphoribosylaminoimidazole synthetase  | NP_215324.1      | 4.71819788                |
| 43383 | C09           | 1132       | Rv0797   | IS1547 transposase   | NP_215312.1      | 2.479681979               |
| 43388 | C10           | 1132       | Rv2761c  | type I restriction/modification system specificity determinant HsdS  | NP_217277.1      | 4.696996466               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43385 | C11           | 1132       | Rv2228c  | bifunctional RNase H/acid phosphatase   | NP_216744.1      | 4.720848057               |
| 43395 | C12           | 1135       | Rv3313c  | adenosine deaminase   | NP_217830.1      | 3.856387665               |
| 43391 | D01           | 1135       | Rv0029   | hypothetical protein Rv0029   | NP_214543.1      | 4.672246696               |
| 43392 | D02           | 1135       | Rv1765c  | transposase   | YP_177652.1      | 4.626431718               |
| 43397 | D03           | 1135       | Rv3629c  | hypothetical protein Rv3629c  | NP_218146.1      | 4.678414097               |
| 43399 | D04           | 1138       | Rv0192   | hypothetical protein Rv0192   | NP_214706.1      | 4.699472759               |
| 43401 | D05           | 1138       | Rv1239c  | magnesium/cobalt transporter CorA   | NP_215755.1      | 4.731107206               |
| 43398 | D06           | 1138       | Rv0155   | NAD(P) transhydrogenase subunit alpha   | NP_214669.1      | 4.69771529                |
| 43415 | D07           | 1141       | Rv3024c  | tRNA-specific 2-thiouridylase MnmA  | NP_217540.1      | 2.914110429               |
| 43410 | D08           | 1141       | Rv1915   | isocitrate lyase  | NP_216431.1      | 4.695004382               |
| 43408 | D09           | 1141       | Rv0726c  | hypothetical protein Rv0726c  | NP_215240.1      | 4.695880806               |
| 43405 | D10           | 1141       | Rv0046c  | myo-inositol-1-phosphate synthase INO1 (inositol 1-phosphate synthetase) (D-glucose 6-phosphate cycloaldolase) (glucose 6-phosphate cyclase) (glucocycloaldolase) | NP_214560.1      | 2.406660824               |
| 43413 | D11           | 1141       | Rv2497c  | pyruvate dehydrogenase E1 component alpha subunit PdhA  | NP_217013.1      | 2.412795793               |
| 43409 | D12           | 1141       | Rv1530   | alcohol dehydrogenase adh   | NP_216046.1      | 3.586327783               |
| 43416 | E01           | 1144       | Rv0811c  | hypothetical protein Rv0811c  | NP_215326.1      | 4.666958042               |
| 43418 | E02           | 1144       | Rv2210c  | branched-chain amino acid aminotransferase  | NP_216726.1      | 3.19493007                |
| 43421 | E03           | 1144       | Rv3873   | PPE family protein  | YP_178022.1      | 4.692307692               |
| 43426 | E04           | 1147       | Rv1859   | molybdenum ABC transporter ATP-binding protein  | NP_216375.1      | 3.934612031               |
| 43430 | E05           | 1147       | Rv2670c  | hypothetical protein Rv2670c  | NP_217186.1      | 2.66695728                |
| 43425 | E06           | 1147       | Rv0482   | UDP-N-acetylenolpyruvoylglucosamine reductase   | NP_214996.1      | 4.667829119               |
| 43423 | E07           | 1147       | Rv0179c  | lipoprotein LprO  | NP_214693.1      | 4.669572799               |
| 43431 | E08           | 1147       | Rv3071   | hypothetical protein Rv3071   | NP_217587.1      | 4.316477768               |
| 43439 | E09           | 1150       | Rv2915c  | hypothetical protein Rv2915c  | NP_217431.1      | 4.606086957               |
| 43438 | E10           | 1150       | Rv2192c  | anthranilate phosphoribosyltransferase  | NP_216708.1      | 3.524347826               |
| 43434 | E11           | 1150       | Rv0932c  | periplasmic phosphate-binding lipoprotein PSTS2 (PBP-2) (PSTS2)   | YP_177769.1      | 4.335652174               |
| 43435 | E12           | 1150       | Rv1106c  | cholesterol dehydrogenase   | NP_215622.1      | 3.897391304               |
| 43432 | F01           | 1150       | Rv0182c  | RNA polymerase factor sigma-70  | NP_214696.1      | 4.675652174               |
| 43433 | F02           | 1150       | Rv0928   | periplasmic phosphate-binding lipoprotein secreted L-alanine dehydrogenase (40 kDa antigen) (TB43)  | NP_217296.1      | 4.671292281               |
| 43441 | F04           | 1153       | Rv1048c  | hypothetical protein Rv1048c  | NP_215564.1      | 4.13876843                |
| 43444 | F05           | 1153       | Rv1922   | lipoprotein   | NP_216438.1      | 4.522983521               |
| 43450 | F06           | 1156       | Rv1668c  | macrolide-transport ATP-binding protein ABC transporter   | NP_216184.1      | 4.621107266               |
| 43448 | F07           | 1156       | Rv0906   | hypothetical protein Rv0906   | NP_215421.1      | 4.288062284               |
| 43452 | F08           |            | Rv2535c  | CLONE IS INVALID  |                  |                           |
| 43446 | F09           | 1156       | Rv0848   | cysteine synthase A CysK2   | YP_177762.1      | 4.666089965               |
| 43451 | F10           | 1156       | Rv2337c  | hypothetical protein Rv2337c  | NP_216853.1      | 4.393598616               |
| 43456 | F11           | 1156       | Rv3215   | isochorismate synthase  | NP_217731.1      | 4.686851211               |
| 43449 | F12           | 1156       | Rv1260   | hypothetical protein Rv1260   | NP_215776.1      | 4.670415225               |
| 43462 | G01           | 1159       | Rv1679   | acyl-CoA dehydrogenase  | NP_216195.1      | 4.664365833               |
| 43459 | G02           | 1159       | Rv1448c  | transaldolase   | NP_215964.1      | 3.868852459               |
| 43457 | G03           | 1159       | Rv0505c  | phosphoserine phosphatase   | YP_177732.1      | 4.331320104               |
| 43458 | G04           | 1159       | Rv0889c  | citrate synthase 2  | NP_215404.1      | 4.581535807               |
| 43466 | G05           | 1159       | Rv2981c  | D-alanyl-alanine synthetase A   | NP_217497.1      | 2.584987058               |
| 43468 | G06           | 1159       | Rv3505   | acyl-CoA dehydrogenase FADE27   | NP_218022.1      | 4.661777394               |
| 43467 | G07           | 1159       | Rv3006   | lipoprotein LppZ  | NP_217522.1      | 4.686798965               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43463 | G08           | 1159       | Rv2454c  | 2-oxoglutarate ferredoxin oxidoreductase subunit beta           | NP_216970.1      | 4.681622088               |
| 43470 | G09           | 1162       | Rv2629   | hypothetical protein Rv2629                                     | NP_217145.1      | 4.683304647               |
| 43471 | G10           | 1162       | Rv3169   | hypothetical protein Rv3169                                     | NP_217685.1      | 4.674698795               |
| 43469 | G11           | 1162       | Rv0934   | periplasmic phosphate-binding lipoprotein PSTS1 (PBP-1) (PSTS1) | YP_177770.1      | 4.669535284               |
| 43477 | G12           | 1165       | Rv2388c  | coproporphyrinogen III oxidase                                  | NP_216904.1      | 3.164806867               |
| 43474 | H01           |            | Rv2089c  | CLONE IS INVALID  |                  |                           |
| 43484 | H02           | 1165       | Rv3531c  | hypothetical protein Rv3531c                                    | NP_218048.1      | 3.065236052               |
| 43485 | H03           | 1165       | Rv3796   | hypothetical protein Rv3796                                     | YP_178016.1      | 3.644635193               |
| 43472 | H04           | 1165       | Rv0761c  | zinc-containing alcohol dehydrogenase NAD dependent ADHB        | YP_177754.1      | 4.497854077               |
| 43480 | H05           | 1165       | Rv2819c  | hypothetical protein Rv2819c                                    | NP_217335.1      | 4.150214592               |
| 43478 | H06           | 1165       | Rv2659c  | phiRv2 prophage integrase                                       | NP_217175.1      | 4.652360515               |
| 43473 | H07           | 1165       | Rv1533   | hypothetical protein Rv1533                                     | NP_216049.1      | 4.681545064               |
| 43497 | H08           | 1168       | Rv2970c  | hypothetical protein Rv2970A                                    | YP_177681.1      | 3.988013699               |
| 43498 | H09           | 1168       | Rv3094c  | hypothetical protein Rv3094c                                    | NP_217610.1      | 4.667808219               |
| 43486 | H10           | 1168       | Rv0365c  | hypothetical protein Rv0365c                                    | NP_214879.1      | 4.080479452               |
| 43494 | H11           | 1168       | Rv1894c  | hypothetical protein Rv1894c                                    | NP_216410.1      | 3.659246575               |
| 43491 | H12           | 1168       | Rv0884c  | phosphoserine aminotransferase                                  | NP_215399.1      | 4.659246575               |

Table 32: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 32 (ZMTLV), NR-19668

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43499 | A01           | 1168       | Rv3758c  | osmoprotectant (glycine betaine/carnitine/choline/L-proline) transport ATP-binding protein ABC transporter PROV | NP_218275.1      | 4.628424658               |
| 43492 | A02           | 1168       | Rv1383   | carbamoyl phosphate synthase small subunit  | NP_215899.1      | 4.315068493               |
| 43490 | A03           | 1168       | Rv0501   | UDP-glucose 4-epimerase   | NP_215050.2      | 2.344178082               |
| 43500 | A04           | 1171       | Rv0272c  | hypothetical protein Rv0272c  | NP_214786.1      | 4.096498719               |
| 43504 | A05           | 1171       | Rv1970   | MCE-family lipoprotein LprM   | NP_216486.1      | 4.667805295               |
| 43501 | A06           | 1171       | Rv1367c  | hypothetical protein Rv1367c  | NP_215883.1      | 4.64560205                |
| 43511 | A07           | 1174       | Rv2084   | hypothetical protein Rv2084   | NP_216600.1      | 4.65758092                |
| 43515 | A08           | 1174       | Rv3168   | hypothetical protein Rv3168   | NP_217684.1      | 3.074105622               |
| 43512 | A09           | 1174       | Rv2212   | hypothetical protein Rv2212   | NP_216728.1      | 4.597103918               |
| 43514 | A10           | 1174       | Rv3105c  | peptide chain release factor 2  | NP_217621.1      | 4.556218058               |
| 43513 | A11           | 1174       | Rv2610c  | alpha-mannosyltransferase PIMA  | NP_217126.1      | 4.626064736               |
| 43522 | A12           | 1177       | Rv3096   | hypothetical protein Rv3096   | NP_217612.1      | 4.644859813               |
| 43520 | B01           | 1177       | Rv2211c  | glycine cleavage system aminomethyltransferase  | NP_216727.1      | 4.663551402               |
| 43524 | B02           |            | Rv3341   | CLONE IS INVALID  | NP_217858.1      |                           |
| 43521 | B03           | 1177       | Rv2230c  | hypothetical protein Rv2230c  | NP_216746.1      | 4.635514019               |
| 43529 | B04           | 1180       | Rv1600   | histidinol-phosphate aminotransferase   | YP_177823.1      | 4.055932203               |
| 43527 | B05           | 1180       | Rv0376c  | hypothetical protein Rv0376c  | NP_214890.1      | 4.36779661                |
| 43532 | B06           | 1180       | Rv3230c  | oxidoreductase  | NP_217747.1      | 4.600847458               |
| 43528 | B07           | 1180       | Rv0574c  | hypothetical protein Rv0574c  | NP_215088.1      | 4.539830508               |
| 43531 | B08           | 1180       | Rv3136   | PPE family protein  | YP_177935.1      | 4.606779661               |
| 43530 | B09           | 1180       | Rv1887   | hypothetical protein Rv1887   | NP_216403.1      | 4.599152542               |
| 43535 | B10           | 1183       | Rv1488   | hypothetical protein Rv1488   | NP_216004.1      | 3.351648352               |
| 43536 | B11           |            | Rv2951c  | CLONE IS INVALID  |                  |                           |
| 43533 | B12           | 1183       | Rv0260c  | bifunctional uroporphyrinogen-III synthetase/response regulator domain protein                                  | NP_214774.1      | 3.35249366                |
| 43538 | C01           | 1186       | Rv0975c  | acyl-CoA dehydrogenase FADE13   | NP_215490.1      | 3.857504216               |
| 43539 | C02           | 1186       | Rv2328   | PE family protein   | YP_177867.1      | 4.58010118                |
| 43540 | C03           | 1186       | Rv2373c  | chaperone protein DnaJ2   | NP_216889.1      | 4.63153457                |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 43541 | C04           | 1186       | Rv2818c  | hypothetical protein Rv2818c                             | NP_217334.1      | 4.623946037               |
| 43545 | C05           | 1189       | Rv0162c  | zinc-type alcohol dehydrogenase E subunit                | YP_177699.1      | 2.17746005                |
| 43548 | C06           | 1189       | Rv1254   | acyltransferase  | NP_215770.1      | 4.064760303               |
| 43555 | C07           | 1192       | Rv2807   | hypothetical protein Rv2807                              | NP_217323.1      | 4.604026846               |
| 43552 | C08           | 1192       | Rv1895   | dehydrogenase  | NP_216411.1      | 4.645973154               |
| 43558 | C09           | 1192       | Rv3529c  | hypothetical protein Rv3529c                             | NP_218046.1      | 4.637583893               |
| 43553 | C10           |            | Rv2164c  | CLONE IS INVALID   |                  |                           |
| 43551 | C11           | 1192       | Rv0225   | hypothetical protein Rv0225                              | NP_214739.1      | 3.033557047               |
| 43560 | C12           | 1195       | Rv0003   | recombination protein F                                  | NP_214517.1      | 4.433472803               |
| 43569 | D01           | 1195       | Rv3236c  | integral membrane transport protein                      | YP_177949.1      | 4.577405858               |
| 43570 | D02           | 1195       | Rv3560c  | acyl-CoA dehydrogenase FADE30                            | NP_218077.1      | 4.548117155               |
| 43563 | D03           | 1195       | Rv0610c  | hypothetical protein Rv0610c                             | NP_215124.1      | 4.482008368               |
| 43564 | D04           | 1195       | Rv1101c  | hypothetical protein Rv1101c                             | NP_215617.1      | 4.551464435               |
| 43574 | D05           | 1198       | Rv0874c  | hypothetical protein Rv0874c                             | NP_215389.1      | 1.57345576                |
| 43580 | D06           | 1198       | Rv2724c  | acyl-CoA dehydrogenase FADE20                            | NP_217240.1      | 4.598497496               |
| 43581 | D07           | 1198       | Rv3526   | oxidoreductase   | NP_218043.1      | 4.311352254               |
| 43577 | D08           | 1198       | Rv1346   | acyl-CoA dehydrogenase                                   | NP_215862.1      | 2.072621035               |
| 43575 | D09           | 1198       | Rv0988   | hypothetical protein Rv0988                              | NP_215503.1      | 4.560100167               |
| 43593 | D10           | 1201       | Rv3543c  | acyl-CoA dehydrogenase FADE29                            | NP_218060.1      | 3.838467943               |
| 43589 | D11           | 1201       | Rv1212c  | putative glycosyl transferase                            | NP_215728.1      | 4.572855953               |
| 43588 | D12           | 1201       | Rv0951   | succinyl-CoA synthetase subunit beta                     | NP_215466.1      | 3.92173189                |
| 43592 | E01           | 1201       | Rv3430c  | transposase  | NP_217947.1      | 4.575353872               |
| 43603 | E02           | 1204       | Rv2267c  | hypothetical protein Rv2267c                             | NP_216783.1      | 4.563122924               |
| 43597 | E03           | 1204       | Rv0575c  | hypothetical protein Rv0575c                             | NP_215089.1      | 4.573089701               |
| 43599 | E04           | 1204       | Rv0972c  | acyl-CoA dehydrogenase FADE12                            | NP_215487.1      | 2.75                      |
| 43607 | E05           | 1204       | Rv3565   | aspartate aminotransferase                               | NP_218082.1      | 3.214285714               |
| 43600 | E06           | 1204       | Rv1079   | cystathionine gamma-synthase                             | NP_215595.1      | 4.568106312               |
| 43602 | E07           | 1204       | Rv1267c  | transcriptional regulatory protein EMBR                  | NP_215783.1      | 2.681893688               |
| 43594 | E08           | 1204       | Rv0237   | lipoprotein LpqI   | YP_177702.1      | 4.303986711               |
| 43610 | E09           | 1207       | Rv1323   | acetyl-CoA acetyltransferase                             | NP_215839.1      | 4.634631317               |
| 43613 | E10           | 1207       | Rv3116   | molybdenum cofactor biosynthesis protein MoeB            | YP_177929.1      | 4.607290804               |
| 43614 | E11           | 1207       | Rv3274c  | acyl-CoA dehydrogenase FADE25                            | NP_217791.1      | 3.526926263               |
| 43625 | E12           | 1210       | Rv1229c  | MRP family ATP-binding protein                           | NP_215745.1      | 4.60661157                |
| 43618 | F01           | 1210       | Rv0075   | aminotransferase   | NP_214589.1      | 4.60661157                |
| 43619 | F02           | 1210       | Rv0173   | MCE-family lipoprotein LprK                              | NP_214687.1      | 4.09338843                |
| 43621 | F03           |            | Rv0385   | CLONE IS INVALID   | NP_214899.1      |                           |
| 43624 | F04           | 1210       | Rv0752c  | acyl-CoA dehydrogenase FADE9                             | NP_215266.1      | 1.633884298               |
| 43637 | F05           | 1213       | Rv2352c  | PPE family protein                                       | YP_177870.1      | 4.586150041               |
| 43633 | F06           | 1213       | Rv0693   | coenzyme PQQ synthesis protein E                         | NP_215207.1      | 2.637262984               |
| 43635 | F07           |            | Rv1196   | CLONE IS INVALID   |                  |                           |
| 43634 | F08           | 1213       | Rv1039c  | PPE family protein                                       | YP_177778.1      | 3.765045342               |
| 43639 | F09           | 1213       | Rv3125c  | PPE family protein                                       | YP_177932.1      | 2.829348722               |
| 43640 | F10           | 1213       | Rv3372   | trehalose 6-phosphate phosphatase                        | NP_217889.1      | 4.273701566               |
| 43644 | F11           | 1216       | Rv3616c  | hypothetical protein Rv3616c                             | NP_218133.1      | 4.610197368               |
| 43645 | F12           | 1216       | Rv3863   | hypothetical protein Rv3863                              | NP_218380.1      | 4.59375                   |
| 43643 | G01           | 1216       | Rv3206c  | molybdopterin biosynthesis-like protein MoeZ             | YP_177942.1      | 3.532072368               |
| 43652 | G02           | 1219       | Rv1238   | sugar-transport ATP-binding protein ABC transporter SugC | NP_215754.1      | 4.596390484               |
| 43646 | G03           | 1219       | Rv0894   | LuxR family transcriptional regulator                    | NP_215409.1      | 4.053322395               |
| 43655 | G04           | 1219       | Rv1697   | hypothetical protein Rv1697                              | NP_216213.1      | 4.580803938               |
| 43659 | G05           | 1219       | Rv2090   | 5'-3' exonuclease  | NP_216606.1      | 3.806398687               |
| 43662 | G06           | 1219       | Rv2625c  | hypothetical protein Rv2625c                             | NP_217141.1      | 4.552912223               |
| 43664 | G07           | 1219       | Rv3025c  | cysteine desulfurase IscS                                | NP_217541.1      | 3.312551272               |
| 43658 | G08           | 1219       | Rv1789   | PPE family protein                                       | YP_177835.1      | 4.304347826               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|------------------------------|------------------|---------------------------|
| 43675 | G09           | 1222       | Rv3523   | acetyl-CoA acetyltransferase | NP_218040.1      | 4.302782324               |
| 43667 | G10           | 1222       | Rv1706c  | hypothetical protein Rv1706A | YP_177651.1      | 4.582651391               |
| 43671 | G11           | 1222       | Rv2768c  | PPE family protein           | YP_177906.1      | 3.779050737               |
| 43668 | G12           | 1222       | Rv2463   | esterase/lipase LipP         | NP_216979.1      | 4.585924714               |
| 43676 | H01           | 1222       | Rv3570c  | oxidoreductase               | NP_218087.1      | 4.547463175               |
| 43672 | H02           | 1222       | Rv3272   | hypothetical protein Rv3272  | NP_217789.1      | 3.876432079               |
| 43669 | H03           |            | Rv2500c  | CLONE IS INVALID             |                  |                           |
| 43677 | H04           | 1225       | Rv0352   | chaperone protein DnaJ1      | YP_177719.1      | 3.822857143               |
| 43692 | H05           | 1228       | Rv3359   | oxidoreductase               | NP_217876.1      | 4.578990228               |

Table 33: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 33 (ZMTLW), NR-19669

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43698 | A01           | 1231       | Rv1462   | hypothetical protein Rv1462   | NP_215978.1      | 4.581640942               |
| 43705 | A02           | 1231       | Rv3671c  | membrane-associated serine protease   | NP_218188.1      | 4.595450853               |
| 43695 | A03           | 1231       | Rv0858c  | aminotransferase  | NP_215373.1      | 4.581640942               |
| 43712 | A04           | 1234       | Rv1916   | isocitrate lyase  | NP_216432.1      | 1.378444084               |
| 43711 | A05           | 1234       | Rv1658   | argininosuccinate synthase  | NP_216174.1      | 1.824149109               |
| 43713 | A06           | 1234       | Rv3518c  | cytochrome P450 monooxygenase 142   | NP_218035.1      | 4.513776337               |
| 43708 | A07           | 1234       | Rv0106   | hypothetical protein Rv0106   | NP_214620.1      | 4.508103728               |
| 43720 | A08           | 1237       | Rv3892c  | PPE family protein  | YP_178024.1      | 4.500404204               |
| 43716 | A09           | 1237       | Rv2176   | transmembrane serine/threonine-protein kinase L                                   | NP_216692.1      | 3.503637833               |
| 43719 | A10           | 1237       | Rv3809c  | UDP-galactopyranose mutase Glf  | NP_218326.1      | 4.535974131               |
| 43726 | A11           | 1240       | Rv3499c  | MCE-family protein MCE4A  | YP_177977.1      | 4.540322581               |
| 43721 | A12           | 1240       | Rv0293c  | hypothetical protein Rv0293c  | NP_214807.1      | 4.284677419               |
| 43722 | B01           | 1240       | Rv1655   | acetylornithine aminotransferase  | NP_216171.1      | 4.546774194               |
| 43725 | B02           | 1240       | Rv3121   | cytochrome P450 141   | NP_217637.1      | 4.535483871               |
| 43727 | B03           | 1240       | Rv3504   | acyl-CoA dehydrogenase FADE26   | NP_218021.1      | 4.488709677               |
| 43732 | B04           |            | Rv3644c  | CLONE IS INVALID  | NP_218162.1      |                           |
| 43730 | B05           | 1243       | Rv2790c  | lipid-transfer protein  | NP_217306.1      | 4.549477072               |
| 43731 | B06           | 1243       | Rv3140   | acyl-CoA dehydrogenase FADE23   | NP_217656.1      | 3.780370072               |
| 43742 | B07           | 1246       | Rv2770c  | PPE family protein  | YP_177677.1      | 4.014446228               |
| 43737 | B08           | 1246       | Rv0766c  | cytochrome P450 123   | NP_215280.1      | 3.186195827               |
| 43734 | B09           | 1246       | Rv0002   | DNA polymerase III subunit beta   | NP_214516.1      | 4.52247191                |
| 43743 | B10           | 1246       | Rv3864   | hypothetical protein Rv3864   | NP_218381.1      | 4.510433387               |
| 43746 | B11           | 1249       | Rv0368c  | hypothetical protein Rv0368c  | NP_214882.1      | 3.955164131               |
| 43748 | B12           | 1249       | Rv1392   | S-adenosylmethionine synthetase   | NP_215908.1      | 4.42113691                |
| 43745 | C01           | 1249       | Rv0220   | esterase LipC   | NP_214734.1      | 4.527622098               |
| 43744 | C02           | 1249       | Rv0154c  | acyl-CoA dehydrogenase FADE2  | NP_214668.1      | 4.231385108               |
| 43747 | C03           | 1249       | Rv0859   | acetyl-CoA acetyltransferase  | NP_215374.1      | 4.533226581               |
| 43750 | C04           |            | Rv2542   | CLONE IS INVALID  |                  |                           |
| 43749 | C05           | 1249       | Rv1807   | PPE family protein  | YP_177653.1      | 4.530024019               |
| 43761 | C06           | 1252       | Rv3822   | hypothetical protein Rv3822   | NP_218339.1      | 4.539936102               |
| 43753 | C07           | 1252       | Rv1213   | glucose-1-phosphate adenyllyltransferase  | NP_215729.1      | 4.256389776               |
| 43758 | C08           | 1252       | Rv2869c  | transmembrane protein   | NP_217385.1      | 4.53115016                |
| 43752 | C09           | 1252       | Rv0589   | MCE-family protein MCE2A  | YP_177740.1      | 2.132587859               |
| 43759 | C10           | 1252       | Rv3446c  | hypothetical protein Rv3446c  | NP_217963.1      | 3.166134185               |
| 43771 | C11           | 1255       | Rv2847c  | multifunctional uroporphyrinogen III methylase/precorrin-2 oxidase/ferrochelatase | NP_215025.2      | 3.429482072               |
| 43762 | C12           | 1255       | Rv0438c  | molybdopterin biosynthesis protein MoeA2  | YP_177725.1      | 3.998406375               |
| 43779 | D01           | 1258       | Rv1963c  | transcriptional repressor (probably TETR-family) MCE3R                            | NP_216479.1      | 4.011923688               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                              | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 43782 | D02           | 1258       | Rv3915   | hydrolase  | YP_178027.1      | 4.539745628               |
| 43780 | D03           | 1258       | Rv2963   | integral membrane protein                            | NP_217479.1      | 4.500794913               |
| 43777 | D04           | 1258       | Rv0688   | putative ferredoxin reductase                        | NP_215202.1      | 2.617647059               |
| 43774 | D05           | 1258       | Rv0391   | O-succinylhomoserine sulfhydrylase                   | NP_214905.1      | 4.447535771               |
| 43778 | D06           | 1258       | Rv1797   | hypothetical protein Rv1797                          | NP_216313.1      | 4.526232114               |
| 43781 | D07           | 1258       | Rv3532   | PPE family protein                                   | YP_177984.1      | 4.563593005               |
| 43793 | D08           | 1261       | Rv3212   | hypothetical protein Rv3212                          | NP_217728.1      | 4.529738303               |
| 43788 | D09           | 1261       | Rv1631   | dephospho-CoA kinase/unknown domain fusion protein   | NP_216147.1      | 1.973830293               |
| 43801 | D10           | 1264       | Rv3255c  | mannose-6-phosphate isomerase                        | NP_217772.1      | 4.353639241               |
| 43806 | D11           | 1264       | Rv3827c  | transposase  | NP_218344.1      | 3.453322785               |
| 43796 | D12           | 1264       | Rv0561c  | oxidoreductase                                       | NP_215075.1      | 4.094936709               |
| 43803 | E01           | 1264       | Rv3423c  | alanine racemase                                     | NP_217940.1      | 4.124208861               |
| 43800 | E02           | 1264       | Rv2892c  | PPE family protein                                   | YP_177913.1      | 4.355221519               |
| 43797 | E03           | 1264       | Rv2416c  | hypothetical protein Rv2416c                         | NP_216932.2      | 4.445411392               |
| 43804 | E04           | 1264       | Rv3722c  | hypothetical protein Rv3722c                         | NP_218239.2      | 4.421677215               |
| 43810 | E05           |            | Rv1808   | CLONE IS INVALID                                     | YP_177844.1      |                           |
| 43808 | E06           | 1267       | Rv0399c  | lipoprotein LpqK                                     | NP_214913.1      | 3.498816101               |
| 43815 | E07           | 1267       | Rv3042c  | phosphoserine phosphatase                            | NP_217558.1      | 3.502762431               |
| 43807 | E08           | 1267       | Rv0311   | hypothetical protein Rv0311                          | NP_214825.1      | 4.093922652               |
| 43813 | E09           | 1267       | Rv2265   | integral membrane protein                            | NP_216781.1      | 3.63851618                |
| 43818 | E10           | 1267       | Rv3339c  | isocitrate dehydrogenase                             | NP_217856.1      | 4.302288871               |
| 43816 | E11           |            | Rv3144c  | CLONE IS INVALID                                     | YP_177936.1      |                           |
| 43812 | E12           | 1267       | Rv1934c  | acyl-CoA dehydrogenase FADE17                        | NP_216450.1      | 4.355958958               |
| 43827 | F01           | 1270       | Rv2789c  | acyl-CoA dehydrogenase FADE21                        | NP_217305.1      | 4.530708661               |
| 43821 | F02           | 1270       | Rv0490   | putative two component sensor histidine kinase SENX3 | NP_215004.1      | 4.522047244               |
| 43829 | F03           | 1270       | Rv3428c  | transposase  | NP_217945.1      | 4.222047244               |
| 43822 | F04           | 1270       | Rv1612   | tryptophan synthase subunit beta                     | NP_216128.1      | 4.537007874               |
| 43828 | F05           | 1270       | Rv3152   | NADH dehydrogenase subunit H                         | NP_217668.1      | 3.754330709               |
| 43832 | F06           | 1273       | Rv0074   | hypothetical protein Rv0074                          | NP_214588.1      | 4.153181461               |
| 43835 | F07           | 1273       | Rv1230c  | hypothetical protein Rv1230c                         | NP_215746.1      | 4.461901021               |
| 43836 | F08           | 1273       | Rv1869c  | reductase  | NP_216385.1      | 4.503534957               |
| 43844 | F09           | 1276       | Rv3081   | hypothetical protein Rv3081                          | NP_217597.1      | 2.782915361               |
| 43841 | F10           | 1276       | Rv1437   | phosphoglycerate kinase                              | NP_215953.1      | 4.40830721                |
| 43845 | F11           | 1276       | Rv3402c  | hypothetical protein Rv3402c                         | NP_217919.1      | 4.412225705               |
| 43846 | F12           | 1279       | Rv0191   | integral membrane protein                            | NP_214705.1      | 3.268960125               |
| 43848 | G01           | 1279       | Rv2340c  | PE-PGRS family protein                               | YP_177869.1      | 4.317435496               |
| 43864 | G02           |            | Rv1872c  | CLONE IS INVALID                                     |                  |                           |
| 43866 | G03           | 1282       | Rv2130c  | cysteinyl-tRNA synthetase                            | NP_216646.1      | 4.388455538               |
| 43860 | G04           | 1282       | Rv1125   | hypothetical protein Rv1125                          | NP_215641.1      | 4.351014041               |
| 43867 | G05           | 1282       | Rv2242   | hypothetical protein Rv2242                          | NP_216758.1      | 4.281591264               |
| 43863 | G06           | 1282       | Rv1769   | hypothetical protein Rv1769                          | NP_216285.1      | 4.310452418               |
| 43859 | G07           | 1282       | Rv0778   | cytochrome P450 126                                  | NP_215292.1      | 4.361154446               |
| 43868 | G08           | 1282       | Rv3032   | transferase  | NP_217548.1      | 3.762870515               |
| 43871 | G09           | 1285       | Rv1108c  | exodeoxyribonuclease VII large subunit               | NP_215624.1      | 4.322178988               |
| 43878 | G10           | 1285       | Rv2515c  | hypothetical protein Rv2515c                         | NP_217031.1      | 3.657587549               |
| 43877 | G11           | 1285       | Rv2512c  | IS1081 transposase                                   | NP_217028.1      | 2.06848249                |
| 43873 | G12           | 1285       | Rv1199c  | transposase  | NP_215715.1      | 2.4                       |
| 43881 | H01           | 1285       | Rv3115   | transposase  | NP_217631.1      | 4.500389105               |
| 43870 | H02           | 1285       | Rv1047   | transposase  | NP_215563.1      | 2.038132296               |
| 43882 | H03           | 1285       | Rv3292   | hypothetical protein Rv3292                          | NP_217809.1      | 3.99844358                |
| 43875 | H04           | 1285       | Rv2427c  | gamma-glutamyl phosphate reductase                   | NP_216943.1      | 3.996108949               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                           | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43874 | H05           | 1285       | Rv1723   | hydrolase   | NP_216239.1      | 4.805447471               |
| 43885 | H06           | 1288       | Rv2245   | 3-oxoacyl-(acyl carrier protein) synthase II      | NP_216761.1      | 4.429347826               |
| 10050 | H07           | 1288       | Rv3252c  | transmembrane alkane 1-monooxygenase AlkB         | NP_217769.1      | 5.49068323                |
| 43890 | H08           | 1291       | Rv1464   | cysteine desulfurase                              | NP_215980.1      | 4.330751356               |
| 43891 | H09           | 1291       | Rv2387   | hypothetical protein Rv2387                       | NP_216903.1      | 4.46630519                |
| 43894 | H10           | 1294       | Rv1315   | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | NP_215831.1      | 4.50927357                |
| 43897 | H11           | 1294       | Rv2015c  | hypothetical protein Rv2015c                      | NP_216531.1      | 4.482225657               |
| 43900 | H12           | 1294       | Rv2953   | hypothetical protein Rv2953                       | NP_217469.1      | 4.491499227               |

Table 34: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 34 (ZMTLX), NR-19670

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 43896 | A01           | 1294       | Rv1625c  | membrane-anchored adenylyl cyclase, Cya (ATP pyrophosphate-lyase) (adenylate cyclase) | NP_216141.2      | 4.501545595               |
| 43899 | A02           | 1294       | Rv2456c  | integral membrane transport protein   | NP_216972.1      | 4.515455951               |
| 43895 | A03           | 1294       | Rv1391   | bifunctional phosphopantothenoylecysteine decarboxylase/phosphopantothenate synthase  | NP_215907.1      | 4.469088099               |
| 43902 | A04           | 1297       | Rv0849   | integral membrane transport protein   | NP_215364.1      | 4.418658443               |
| 43905 | A05           | 1297       | Rv1258c  | integral membrane transport protein   | NP_215774.1      | 4.411719352               |
| 43906 | A06           | 1297       | Rv2449c  | hypothetical protein Rv2449c  | NP_216965.1      | 1.353122591               |
| 43901 | A07           | 1297       | Rv0389   | phosphoribosylglycinamide formyltransferase 2   | NP_214903.1      | 4.482652274               |
| 43907 | A08           | 1297       | Rv3834c  | seryl-tRNA synthetase   | NP_218351.1      | 4.515034695               |
| 43912 | A09           | 1300       | Rv3720   | fatty acid synthase   |                  | 2.998461538               |
| 43910 | A10           | 1300       | Rv3311   | hypothetical protein Rv3311   | NP_217828.1      | 1.544615385               |
| 43915 | A11           | 1303       | Rv1194c  | hypothetical protein Rv1194c  | NP_215710.1      | 4.463545664               |
| 43921 | A12           | 1303       | Rv3709c  | aspartate kinase  | NP_218226.1      | 2.435917114               |
| 43924 | B01           | 1306       | Rv1902c  | sialic acid-transport integral membrane protein, NanT                                 | NP_216418.1      | 4.343797856               |
| 43925 | B02           | 1306       | Rv2921c  | cell division protein FtsY  | NP_217437.1      | 4.398162328               |
| 43928 | B03           | 1306       | Rv3454   | integral membrane protein   | NP_217971.1      | 4.483154671               |
| 43927 | B04           | 1306       | Rv2939   | acyltransferase PapA5   | NP_217455.1      | 4.482388974               |
| 43923 | B05           | 1306       | Rv1429   | hypothetical protein Rv1429   | NP_215945.1      | 1.483920368               |
| 43922 | B06           | 1306       | Rv0772   | phosphoribosylamine--glycine ligase   | NP_215286.1      | 4.532159265               |
| 43934 | B07           | 1309       | Rv2580c  | histidyl-tRNA synthetase  | NP_217096.1      | 4.459893048               |
| 43931 | B08           | 1309       | Rv1801   | PPE family protein  | YP_177840.1      | 4.378915202               |
| 43935 | B09           | 1309       | Rv3163c  | hypothetical protein Rv3163c  | NP_217679.1      | 4.404125286               |
| 43932 | B10           | 1309       | Rv1921c  | lipoprotein LppF  | NP_216437.1      | 4.372039725               |
| 43939 | B11           | 1312       | Rv3074   | hypothetical protein Rv3074   | NP_217590.1      | 4.304878049               |
| 43938 | B12           | 1312       | Rv1689   | tyrosyl-tRNA synthetase   | NP_216205.1      | 4.429115854               |
| 43950 | C01           | 1315       | Rv3703c  | hypothetical protein Rv3703c  | NP_218220.1      | 4.323954373               |
| 43945 | C02           | 1315       | Rv1415   | bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II      | NP_215931.1      | 2.450190114               |
| 43941 | C03           | 1315       | Rv0070c  | serine hydroxymethyltransferase   | NP_214584.1      | 2.842585551               |
| 43943 | C04           | 1315       | Rv1200   | integral membrane transport protein   | NP_215716.1      | 4.450190114               |
| 43942 | C05           | 1315       | Rv0845   | two component sensor kinase   | NP_215360.1      | 4.428897338               |
| 43947 | C06           | 1315       | Rv1966   | MCE-family protein MCE3A  | YP_177852.1      | 2.778707224               |
| 43954 | C07           | 1318       | Rv2457c  | ATP-dependent protease ATP-binding subunit ClpX                                       | NP_216973.1      | 4.391502276               |
| 43951 | C08           | 1318       | Rv0994   | molybdopterin biosynthesis protein MoeA1  | YP_177776.1      | 4.42185129                |
| 43953 | C09           | 1318       | Rv1526c  | glycosyltransferase   | NP_216042.1      | 3.852048558               |
| 43952 | C10           | 1318       | Rv1093   | serine hydroxymethyltransferase   | YP_177787.1      | 3.805766313               |
| 43960 | C11           | 1321       | Rv3314c  | thymidine phosphorylase   | NP_217831.1      | 4.397426192               |
| 43959 | C12           | 1321       | Rv3229c  | linoleoyl-CoA desaturase  | YP_177948.1      | 4.443603331               |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 43955 | D01           | 1321       | Rv0447c  | cyclopropane-fatty-acyl-phospholipid synthase  | NP_214961.1      | 4.390613172               |
| 43964 | D02           | 1324       | Rv1770   | hypothetical protein Rv1770  | NP_216286.1      | 1.493202417               |
| 43969 | D03           | 1324       | Rv2685   | arsenic-transport integral membrane protein, ArsB1   | YP_177899.1      | 4.456193353               |
| 43961 | D04           | 1324       | Rv0467   | isocitrate lyase   | YP_177728.1      | 4.36858006                |
| 43970 | D05           | 1324       | Rv2958c  | glycosyl transferase   | NP_217474.1      | 4.435045317               |
| 43962 | D06           | 1324       | Rv0924c  | manganese transport protein, MntH  | YP_177767.1      | 4.415407855               |
| 43974 | D07           | 1327       | Rv1559   | threonine dehydratase  | NP_216075.1      | 4.313489073               |
| 43976 | D08           | 1327       | Rv2305   | hypothetical protein Rv2305  | NP_216821.1      | 3.476262246               |
| 43980 | D09           | 1327       | Rv3276c  | phosphoribosylaminoimidazole carboxylase ATPase subunit  | NP_217793.1      | 3.661642803               |
| 43971 | D10           | 1327       | Rv0337c  | aminotransferase AlaT  | NP_214851.1      | 4.404672193               |
| 43972 | D11           | 1327       | Rv1023   | phosphopyruvate hydratase  | NP_215539.1      | 4.351168048               |
| 43973 | D12           | 1327       | Rv1497   | esterase LipL  | NP_216013.1      | 4.438583271               |
| 43979 | E01           | 1327       | Rv3179   | hypothetical protein Rv3179  | NP_217695.1      | 4.403918613               |
| 43975 | E02           | 1327       | Rv2195   | Rieske iron-sulfur protein, QcrA   | NP_216711.1      | 4.391107762               |
| 43978 | E03           | 1327       | Rv2684   | arsenic-transport integral membrane protein, ArsA  | NP_217200.1      | 4.379804069               |
| 43982 | E04           | 1330       | Rv1381   | dihydroorotase   | NP_215897.1      | 4.430827068               |
| 43984 | E05           | 1330       | Rv1666c  | cytochrome P450 139, CYP139  | NP_216182.1      | 4.401503759               |
| 43981 | E06           | 1330       | Rv0842   | integral membrane protein  | NP_215357.1      | 4.301503759               |
| 43985 | E07           | 1330       | Rv1901   | competence damage-inducible protein A  | NP_216417.1      | 4.305263158               |
| 43986 | E08           | 1333       | Rv0015c  | transmembrane serine/threonine-protein kinase A PKNA (protein kinase A) (STPK A)   | NP_214529.1      | 4.315828957               |
| 43992 | E09           | 1333       | Rv2344c  | deoxyguanosinetriphosphate triphosphohydrolase-like protein  | NP_216860.1      | 2.973743436               |
| 43991 | E10           | 1333       | Rv2284   | esterase LipM  | NP_216800.1      | 4.423105776               |
| 43988 | E11           |            | Rv0896   | CLONE IS INVALID   | 215411.1         |                           |
| 43995 | E12           | 1333       | Rv3630   | integral membrane protein  | NP_218147.1      | 4.401350338               |
| 43990 | F01           | 1333       | Rv1159   | mannosyltransferase  | NP_215675.1      | 4.438109527               |
| 43994 | F02           | 1333       | Rv2378c  | lysine-N-oxygenase MBTG (L-lysine 6-monooxygenase) (lysine N6-hydroxylase)   | NP_216894.1      | 4.376594149               |
| 43997 | F03           | 1336       | Rv1453   | transcriptional activator protein  | NP_215969.2      | 4.408682635               |
| 44000 | F04           | 1336       | Rv3704c  | glutamate--cysteine ligase gshA (gamma-glutamylcysteine synthetase) (gamma-ECS) (GCS) (gamma-glutamyl-L-cysteine synthetase) | NP_218221.1      | 4.383982036               |
| 43996 | F05           | 1336       | Rv0357c  | adenylosuccinate synthetase  | NP_214871.1      | 3.804640719               |
| 44002 | F06           | 1339       | Rv0800   | putative aminopeptidase 2  | NP_215315.1      | 4.389843167               |
| 44012 | F07           | 1342       | Rv1777   | cytochrome p450 144, CYP144  | NP_216293.1      | 1.937406855               |
| 9974  | F08           | 1342       | Rv0522   | GABA permease, GabP  | YP_177734.1      | 6.189269747               |
| 44022 | F09           | 1345       | Rv2366c  | transmembrane protein  | NP_216882.1      | 4.328624535               |
| 44019 | F10           | 1345       | Rv1490   | hypothetical protein Rv1490  | NP_216006.1      | 4.005204461               |
| 44027 | F11           | 1348       | Rv2833c  | sn-glycerol-3-phosphate-binding lipoprotein, UGPB  | NP_217349.1      | 3.965133531               |
| 44026 | F12           | 1348       | Rv0517   | membrane acyltransferase   | NP_215031.1      | 1.837537092               |
| 44028 | G01           | 1348       | Rv2870c  | 1-deoxy-D-xylulose 5-phosphate reductoisomerase  | NP_217386.2      | 4.098664688               |
| 44024 | G02           | 1348       | Rv0246   | integral membrane protein  | NP_214760.1      | 3.695103858               |
| 44029 | G03           | 1351       | Rv0213c  | methyltransferase (methylase)  | NP_214727.1      | 4.382679497               |
| 44034 | G04           | 1351       | Rv2370c  | hypothetical protein Rv2370c   | NP_216886.1      | 4.387120651               |
| 44035 | G05           | 1351       | Rv3097c  | triacylglycerol lipase   | YP_177924.1      | 4.36565507                |
| 44037 | G06           | 1354       | Rv1599   | histidinol dehydrogenase   | NP_216115.1      | 4.352289513               |
| 44038 | G07           | 1354       | Rv1880c  | cytochrome p450 140, CYP140  | NP_216396.1      | 1.342688331               |
| 44044 | G08           | 1354       | Rv3329   | hypothetical protein Rv3329  | NP_217846.1      | 3.578286558               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)             | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------------------|------------------|---------------------------|
| 44036 | G09           | 1354       | Rv0485   | transcriptional regulatory protein  | NP_214999.1      | 1.430576071               |
| 44043 | G10           | 1354       | Rv2782c  | zinc protease PEPR                  | NP_217298.1      | 4.389217134               |
| 44045 | G11           | 1357       | Rv0412c  | hypothetical protein Rv0412c        | NP_214926.1      | 4.413411938               |
| 44049 | G12           | 1357       | Rv1375   | hypothetical protein Rv1375         | NP_215891.1      | 4.087693441               |
| 44048 | H01           | 1357       | Rv0920c  | transposase                         | NP_215435.1      | 4.339719971               |
| 44058 | H02           | 1360       | Rv1999c  | integral membrane protein           | NP_216515.1      | 4.324264706               |
| 44062 | H03           | 1360       | Rv3148   | NADH dehydrogenase subunit D        | NP_217664.1      | 3.294117647               |
| 44057 | H04           | 1360       | Rv0243   | acetyl-CoA acetyltransferase        | NP_214757.1      | 2.522058824               |
| 44067 | H05           | 1363       | Rv0136   | cytochrome P450 138                 | NP_214650.1      | 2.240645635               |
| 44073 | H06           | 1363       | Rv2008c  | hypothetical protein Rv2008c        | NP_216524.1      | 4.400586941               |
| 44070 | H07           | 1363       | Rv0732   | preprotein translocase subunit SecY | NP_215246.1      | 4.32355099                |
| 44065 | H08           | 1363       | Rv0037c  | integral membrane protein           | NP_214551.1      | 4.396184886               |
| 44072 | H09           | 1363       | Rv1294   | homoserine dehydrogenase            | NP_215810.1      | 3.410858401               |
| 44077 | H10           | 1366       | Rv2586c  | preprotein translocase subunit SecF | NP_217102.1      | 2.67715959                |
| 44079 | H11           | 1369       | Rv0571c  | hypothetical protein Rv0571c        | NP_215085.1      | 3.365960555               |
| 44078 | H12           | 1369       | Rv0322   | UDP-glucose 6-dehydrogenase UdgA    | NP_214836.1      | 4.064280496               |

Table 35: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 35 (ZMTLY), NR-19671

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                    | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 44080 | A01           | 1369       | Rv0878c  | PPE family protein   | YP_177764.1      | 4.042366691               |
| 44083 | A02           | 1372       | Rv1313c  | transposase  | NP_215829.1      | 4.352769679               |
| 44085 | A03           | 1372       | Rv3798   | transposase  | NP_218315.1      | 4.331632653               |
| 44084 | A04           | 1372       | Rv2382c  | polyketide synthetase MBTC (polyketide synthase)           | NP_216898.1      | 4.344752187               |
| 44091 | A05           | 1375       | Rv3150   | NADH dehydrogenase I chain F                               | NP_217666.1      | 3.794181818               |
| 44090 | A06           | 1375       | Rv2994   | integral membrane protein                                  | NP_217510.1      | 4.344                     |
| 44088 | A07           |            | Rv2508c  | CLONE IS INVALID   |                  |                           |
| 44098 | A08           | 1378       | Rv1923   | lipase LIPD  | NP_216439.1      | 4.314949202               |
| 44099 | A09           | 1378       | Rv2222c  | glutamine synthetase                                       | NP_216738.1      | 4.335994194               |
| 44096 | A10           | 1378       | Rv1592c  | hypothetical protein Rv1592c                               | NP_216108.1      | 4.375181422               |
| 44097 | A11           | 1378       | Rv1774   | oxidoreductase   | NP_216290.1      | 4.377358491               |
| 44095 | A12           | 1378       | Rv1307   | F0F1 ATP synthase subunit delta                            | NP_215823.1      | 1.945573295               |
| 44106 | B01           | 1381       | Rv1293   | diaminopimelate decarboxylase LysA                         | NP_215809.1      | 2.640115858               |
| 44107 | B02           | 1381       | Rv3197   | ABC transporter ATP-binding protein                        | NP_217713.1      | 4.310644461               |
| 44109 | B03           | 1384       | Rv0729   | D-xylulose kinase XylB                                     | NP_215243.1      | 4.265895954               |
| 44110 | B04           | 1384       | Rv2141c  | hypothetical protein Rv2141c                               | YP_177864.1      | 4.26300578                |
| 44112 | B05           | 1384       | Rv3170   | flavin-containing monoamine oxidase                        | NP_217686.1      | 1.836705202               |
| 44113 | B06           | 1384       | Rv3262   | F420-0--gamma-glutamyl ligase                              | NP_217779.1      | 3.998554913               |
| 44108 | B07           | 1384       | Rv0026   | hypothetical protein Rv0026                                | NP_214540.1      | 4.302745665               |
| 44114 | B08           | 1384       | Rv3441c  | phospho-sugar mutase / MRSA protein                        | NP_217958.1      | 4                         |
| 44115 | B09           | 1384       | Rv3740c  | hypothetical protein Rv3740c                               | NP_218257.1      | 2.831647399               |
| 44117 | B10           | 1387       | Rv0161   | oxidoreductase   | NP_214675.1      | 1.902667628               |
| 44120 | B11           | 1387       | Rv0541c  | integral membrane protein                                  | NP_215055.1      | 3.775054074               |
| 44123 | B12           | 1387       | Rv3290c  | L-lysine aminotransferase                                  | NP_217807.1      | 4.218457102               |
| 44125 | C01           | 1387       | Rv3476c  | dicarboxylic acid transport integral membrane protein KgtP | NP_217993.1      | 3.744051911               |
| 44122 | C02           | 1387       | Rv2962c  | glycosyl transferase                                       | NP_217478.1      | 4.281903389               |
| 44121 | C03           | 1387       | Rv2589   | 4-aminobutyrate aminotransferase                           | NP_217105.1      | 4.211968277               |
| 44124 | C04           | 1387       | Rv3340   | O-acetylhomoserine aminocarboxypropyltransferase           | NP_217857.1      | 4.187454939               |
| 44118 | C05           | 1387       | Rv0327c  | cytochrome P450 135A1                                      | NP_214841.1      | 4.226387888               |
| 44128 | C06           | 1390       | Rv1878   | glutamine synthetase                                       | NP_216394.1      | 4.248920863               |
| 44133 | C07           | 1390       | Rv3227   | 3-phosphoshikimate 1-carboxyvinyltransferase               | NP_217744.1      | 4.158273381               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 44129 | C08           | 1390       | Rv2386c  | salicylate synthase MbtI   | YP_177877.1      | 4.285611511               |
| 44138 | C09           | 1393       | Rv3496c  | MCE-family protein MCE4D   | NP_218013.1      | 4.312993539               |
| 44139 | C10           | 1393       | Rv3689   | transmembrane protein  | NP_218206.1      | 4.274946159               |
| 44137 | C11           | 1393       | Rv1128c  | hypothetical protein Rv1128c                                       | NP_215644.1      | 3.765254846               |
| 44134 | C12           | 1393       | Rv0483   | lipoprotein LprQ   | NP_214997.1      | 4.231155779               |
| 44141 | D01           | 1396       | Rv3593   | lipoprotein LpqF   | NP_218110.1      | 4.246418338               |
| 44140 | D02           | 1396       | Rv2559c  | recombination factor protein RarA                                  | NP_217075.1      | 3.53008596                |
| 10085 | D03           | 1396       | Rv2097c  | hypothetical protein Rv2097c                                       | NP_216613.1      | 1.377507163               |
| 10095 | D04           | 1396       | Rv0180c  | transmembrane protein  | NP_214694.1      | 1.388968481               |
| 10049 | D05           | 1402       | Rv1945   | hypothetical protein Rv1945  | NP_216461.1      | 7.45149786                |
| 10088 | D06           | 1402       | Rv3734c  | hypothetical protein Rv3734c                                       | NP_218251.1      | 7.538516405               |
| 10028 | D07           | 1402       | Rv0242c  | 3-ketoacyl-(acyl-carrier-protein) reductase                        | NP_214756.1      | 6.813837375               |
| 10058 | D08           | 1402       | Rv0169   | MCE-family protein MCE1A   | YP_177701.1      | 6.44721826                |
| 9998  | D09           | 1402       | Rv1702c  | hypothetical protein Rv1702c                                       | NP_216218.1      | 6.728245364               |
| 10306 | D10           | 1405       | Rv3449   | membrane-anchored mycosin  | NP_217966.1      | 7.392882562               |
| 10244 | D11           | 1405       | Rv0127   | hypothetical protein Rv0127  | NP_214641.1      | 6.985765125               |
| 10169 | D12           | 1405       | Rv2858c  | aldehyde dehydrogenase   | NP_217374.1      | 1.471886121               |
| 10212 | E01           | 1405       | Rv1842c  | hypothetical protein Rv1842c                                       | NP_216358.1      | 7.257651246               |
| 10202 | E02           | 1408       | Rv3106   | NADPH:adrenodoxin oxidoreductase FPRA (NADPH-ferredoxin reductase) | NP_217622.1      | 7.219460227               |
| 10184 | E03           | 1408       | Rv1288   | hypothetical protein Rv1288  | NP_215804.1      | 6.966619318               |
| 10221 | E04           | 1408       | Rv0473   | transmembrane protein  | NP_214987.1      | 1.365056818               |
| 10240 | E05           | 1411       | Rv2848c  | cobyrinic acid a,c-diamide synthase                                | NP_217364.1      | 6.936924167               |
| 10180 | E06           | 1411       | Rv2860c  | glutamine synthetase   | NP_217376.1      | 7.055988661               |
| 10161 | E07           | 1411       | Rv1407   | Fmu protein (SUN protein)  | NP_215923.1      | 1.429482636               |
| 10288 | E08           | 1414       | Rv1005c  | aminodeoxychorismate synthase component I                          | NP_215521.1      | 6.465346535               |
| 10298 | E09           | 1417       | Rv2280   | dehydrogenase  | NP_216796.1      | 6.2900494                 |
| 10198 | E10           | 1417       | Rv1425   | hypothetical protein Rv1425  | NP_215941.1      | 7.028934368               |
| 10174 | E11           | 1417       | Rv2978c  | transposase  | NP_217494.1      | 7.607621736               |
| 10167 | E12           | 1417       | Rv2855   | mycothione reductase   | YP_177910.1      | 6.310515173               |
| 10230 | F01           | 1417       | Rv0958   | magnesium chelatase  | NP_215473.1      | 7.330275229               |
| 10280 | F02           | 1420       | Rv3432c  | glutamate decarboxylase GadB                                       | NP_217949.1      | 7.152816901               |
| 10247 | F03           | 1420       | Rv1751   | hypothetical protein Rv1751  | NP_216267.1      | 1.29084507                |
| 10150 | F04           | 1420       | Rv2885c  | transposase  | NP_217401.1      | 7.199295775               |
| 10290 | F05           | 1420       | Rv0362   | Mg <sup>2+</sup> transport transmembrane protein MgtE              | NP_214876.1      | 7.507042254               |
| 10258 | F06           | 1423       | Rv3627c  | hypothetical protein Rv3627c                                       | NP_218144.1      | 7.134926212               |
| 10190 | F07           | 1423       | Rv0291   | membrane-anchored mycosin  | NP_214805.1      | 7.359803233               |
| 10292 | F08           | 1423       | Rv3790   | oxidoreductase   | NP_218307.1      | 7.361911455               |
| 10223 | F09           |            | Rv1726   | CLONE IS INVALID   |                  |                           |
| 10250 | F10           | 1423       | Rv0069c  | L-serine dehydratase SdaA  | NP_214583.1      | 6.817287421               |
| 10285 | F11           | 1423       | Rv1394c  | cytochrome P450 132  | YP_177807.1      | 7.027406887               |
| 10243 | F12           | 1426       | Rv1263   | amidase  | NP_215779.1      | 1.368863955               |
| 10300 | G01           | 1426       | Rv2178c  | 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG          | NP_216694.1      | 7.389200561               |
| 10314 | G02           | 1426       | Rv3254   | hypothetical protein Rv3254  | NP_217771.1      | 7.292426367               |
| 10318 | G03           | 1426       | Rv3882c  | hypothetical protein Rv3882c                                       | NP_218399.1      | 7.561009818               |
| 10282 | G04           | 1426       | Rv0524   | glutamate-1-semialdehyde aminotransferase                          | NP_215038.1      | 7.312061711               |
| 10294 | G05           | 1429       | Rv3130c  | triacylglycerol synthase   | NP_217646.1      | 7.501049685               |
| 10214 | G06           | 1429       | Rv1854c  | NADH dehydrogenase   | NP_216370.1      | 7.491252624               |
| 10262 | G07           | 1429       | Rv0267   | integral membrane nitrite extrusion protein NarU                   | NP_214781.1      | 7.405878237               |
| 10153 | G08           | 1429       | Rv2357c  | glycyl-tRNA synthetase   | NP_216873.1      | 1.371588523               |
| 10159 | G09           | 1429       | Rv1713   | GTP-binding protein EngA   | NP_216229.1      | 1.417074878               |
| 10279 | G10           | 1432       | Rv0462   | dihydrolipoamide dehydrogenase                                     | NP_214976.1      | 6.314944134               |
| 10178 | G11           | 1444       | Rv0509   | glutamyl-tRNA reductase  | NP_215023.1      | 6.808864266               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                      | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 10146 | G12           | 1444       | Rv3139   | acyl-CoA dehydrogenase FADE24                | NP_217655.1      | 5.709141274               |
| 10260 | H01           | 1444       | Rv0159c  | PE family protein                            | YP_177697.1      | 6.263850416               |
| 10316 | H02           | 1444       | Rv1235   | sugar-binding lipoprotein LpqY               | NP_215751.1      | 7.493074792               |
| 10210 | H03           | 1444       | Rv1809   | PPE family protein                           | YP_177845.1      | 6.844875346               |
| 10312 | H04           | 1444       | Rv2713   | soluble pyridine nucleotide transhydrogenase | NP_217229.1      | 5.906509695               |
| 10188 | H05           | 1447       | Rv1586c  | phiRv1 integrase                             | NP_216102.1      | 7.09813407                |
| 10305 | H06           | 1447       | Rv0017c  | cell division protein RodA                   | NP_214531.1      | 6.451278507               |
| 10137 | H07           | 1450       | Rv1659   | argininosuccinate lyase                      | NP_216175.1      | 6.547586207               |
| 10182 | H08           | 1450       | Rv3719   | hypothetical protein Rv3719                  | NP_218236.1      | 6.151034483               |
| 10248 | H09           | 1450       | Rv0696   | membrane sugar transferase                   | NP_215210.1      | 6.937241379               |
| 10272 | H10           | 1450       | Rv1146   | transmembrane transport protein Mmpl13B      | NP_215662.1      | 5.846896552               |
| 10216 | H11           | 1453       | Rv1634   | drug efflux membrane protein                 | NP_216150.1      | 7.052993806               |
| 10177 | H12           | 1453       | Rv1582c  | probable phiRv1 phage protein                | NP_216098.1      | 7.152787337               |

Table 36: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 36 (ZMTLZ), NR-19672

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 10132 | A01           | 1456       | Rv0290   | transmembrane protein  | NP_214804.1      | 6.192994505               |
| 10193 | A02           | 1456       | Rv0777   | adenylosuccinate lyase   | NP_215291.1      | 1.333791209               |
| 10268 | A03           | 1456       | Rv3195   | hypothetical protein Rv3195  | NP_217711.1      | 7.090659341               |
| 10310 | A04           | 1456       | Rv1182   | polyketide synthase associated protein PapA3                                       | NP_215698.1      | 7.06456044                |
| 10254 | A05           | 1456       | Rv1477   | invasion protein   | NP_215993.1      | 5.460164835               |
| 10235 | A06           | 1456       | Rv3087   | hypothetical protein Rv3087  | NP_217603.1      | 1.343406593               |
| 10201 | A07           | 1459       | Rv2247   | acetyl/propionyl-CoA carboxylase beta subunit AccD6                                | NP_216763.1      | 1.32830706                |
| 10457 | A08           | 1459       | Rv1193   | acyl-CoA synthetase  | NP_215709.1      | 1.419465387               |
| 10514 | A09           |            | Rv1576c  | CLONE IS INVALID   |                  |                           |
| 10343 | A10           | 1462       | Rv3225c  | transferase  | NP_217742.1      | 1.358413133               |
| 10330 | A11           | 1462       | Rv3088   | hypothetical protein Rv3088  | NP_217604.1      | 7.432968536               |
| 10428 | A12           | 1462       | Rv0465c  | transcriptional regulatory protein   | NP_214979.1      | 6.645690834               |
| 10334 | B01           | 1465       | Rv0157   | NAD(P) transhydrogenase subunit beta   | NP_214671.1      | 7.521501706               |
| 10452 | B02           | 1465       | Rv1378c  | hypothetical protein Rv1378c   | NP_215894.1      | 7.434812287               |
| 10507 | B03           | 1468       | Rv3685c  | cytochrome P450 137  | NP_218202.1      | 1.360354223               |
| 10418 | B04           | 1468       | Rv2320c  | cationic amino acid transport integral membrane protein RocE                       | NP_216836.1      | 7.271117166               |
| 10375 | B05           | 1468       | Rv1746   | anchored-membrane serine/threonine-protein kinase PKNF (protein kinase F) (STPK F) | NP_216262.1      | 6.669618529               |
| 10388 | B06           | 1471       | Rv0537c  | integral membrane protein  | NP_215051.1      | 7.407205982               |
| 10491 | B07           | 1471       | Rv2920c  | ammonium transporter   | NP_217436.1      | 6.571040109               |
| 10326 | B08           | 1474       | Rv2220   | glutamine synthetase GLNA1 (glutamine synthase) (GS-I)                             | NP_216736.1      | 7.379918589               |
| 10344 | B09           | 1477       | Rv2440c  | GTPase ObgE  | NP_216956.1      | 6.532836831               |
| 10454 | B10           | 1477       | Rv3539   | PPE family protein   | YP_177987.1      | 6.970886933               |
| 10332 | B11           | 1477       | Rv0341   | isoniazid inducible gene protein INIB  | NP_214855.1      | 7.280297901               |
| 10486 | B12           | 1477       | Rv0697   | dehydrogenase  | NP_215211.1      | 7.260663507               |
| 10352 | C01           | 1477       | Rv1843c  | inosine 5-monophosphate dehydrogenase  | NP_216359.1      | 6.773188896               |
| 10405 | C02           | 1477       | Rv2650c  | phage protein  |                  | 1.373053487               |
| 10339 | C03           | 1480       | Rv2997   | alanine rich dehydrogenase   | NP_217513.1      | 1.383783784               |
| 10508 | C04           | 1480       | Rv0486   | mannosyltransferase  | NP_215000.1      | 7.252702703               |
| 10407 | C05           | 1480       | Rv3585   | DNA repair protein RadA  | NP_218102.1      | 7.080405405               |
| 10401 | C06           |            | Rv3907c  | CLONE IS INVALID   |                  |                           |
| 10358 | C07           | 1480       | Rv2205c  | hypothetical protein Rv2205c   | NP_216721.2      | 7.07972973                |
| 10394 | C08           | 1483       | Rv1630   | 30S ribosomal protein S1   | NP_216146.1      | 7.484828051               |
| 10432 | C09           | 1486       | Rv1148c  | hypothetical protein Rv1148c   | NP_215664.1      | 6.664199192               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 10410 | C10           | 1486       | Rv0235c  | transmembrane protein   | NP_214749.1      | 7.345222073               |
| 10439 | C11           | 1492       | Rv2363   | amidase   | NP_216879.1      | 7.105227882               |
| 10480 | C12           | 1495       | Rv1623c  | integral membrane cytochrome D ubiquinol oxidase (subunit I) cydA (cytochrome bd-I oxidase subunit I)         | YP_177824.1      | 6.802675585               |
| 10378 | D01           | 1498       | Rv2155c  | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase  | NP_216671.1      | 7.315754339               |
| 10380 | D02           | 1498       | Rv1310   | F0F1 ATP synthase subunit beta  | NP_215826.1      | 6.335781041               |
| 10350 | D03           | 1498       | Rv0565c  | monooxygenase   | NP_215079.1      | 7.452603471               |
| 10356 | D04           | 1501       | Rv2075c  | hypothetical protein Rv2075c  | NP_216591.1      | 7.38107928                |
| 10336 | D05           | 1501       | Rv0346c  | L-asparagine ABC transporter permease   | YP_177718.1      | 7.43637575                |
| 10500 | D06           | 1501       | Rv0223c  | aldehyde dehydrogenase  | NP_214737.1      | 7.299133911               |
| 10512 | D07           | 1501       | Rv2447c  | folylpolyglutamate synthase protein FolC  | NP_216963.1      | 7.033977348               |
| 10423 | D08           | 1501       | Rv1817   | hypothetical protein Rv1817   | NP_216333.1      | 6.995336442               |
| 10440 | D09           | 1504       | Rv3858c  | glutamate synthase subunit beta   | NP_218375.1      | 7.229388298               |
| 10371 | D10           | 1504       | Rv0086   | possible hydrogenase HycQ   |                  | 1.311170213               |
| 10367 | D11           | 1504       | Rv1180   | polyketide beta-ketoacyl synthase PKS3  | NP_215696.1      | 1.325797872               |
| 10408 | D12           | 1507       | Rv2268c  | cytochrome P450 128   | NP_216784.1      | 7.092236231               |
| 10346 | E01           | 1507       | Rv1371   | hypothetical protein Rv1371   | NP_215887.1      | 7.378898474               |
| 10434 | E02           | 1507       | Rv0768   | aldehyde dehydrogenase NAD dependent AldA   | NP_215282.1      | 7.171201062               |
| 10488 | E03           | 1510       | Rv0888   | hypothetical protein Rv0888   | NP_215403.1      | 7.223178808               |
| 10427 | E04           | 1510       | Rv3060c  | GntR family transcriptional regulator   | NP_217576.1      | 1.228476821               |
| 10402 | E05           | 1510       | Rv1127c  | pyruvate phosphate dikinase   | NP_215643.1      | 7.103311258               |
| 10464 | E06           | 1510       | Rv2992c  | glutamyl-tRNA synthetase  | YP_177915.1      | 7.151655629               |
| 10364 | E07           | 1513       | Rv2443   | C4-dicarboxylate-transport transmembrane protein DctA   | NP_216959.1      | 7.208856576               |
| 10470 | E08           | 1513       | Rv0016c  | penicillin-binding protein PbpA   | NP_214530.1      | 6.77461996                |
| 10448 | E09           | 1513       | Rv2484c  | hypothetical protein Rv2484c  | NP_217000.1      | 7.36483807                |
| 10443 | E10           | 1516       | Rv0210   | hypothetical protein Rv0210   | NP_214724.1      | 1.309366755               |
| 10463 | E11           | 1519       | Rv2852c  | malate:quinone oxidoreductase   | NP_217368.1      | 6.900592495               |
| 10528 | E12           | 1525       | Rv0892   | monooxygenase   | NP_215407.1      | 6.36                      |
| 10568 | F01           |            | Rv3248c  | CLONE IS INVALID  | NP_217765.1      |                           |
| 10702 | F02           | 1525       | Rv1018c  | UDP-N-acetylglucosamine pyrophosphorylase glmU  | NP_215534.1      | 7.203934426               |
| 10578 | F03           | 1525       | Rv3895c  | hypothetical protein Rv3895c  | NP_218412.1      | 7.300327869               |
| 10616 | F04           | 1528       | Rv2947c  | polyketide synthase PKS15   | NP_217463.1      | 7.152486911               |
| 10663 | F05           | 1528       | Rv1317c  | bifunctional methylated-DNA--protein-cysteine methyltransferase/O-6-methylguanine-DNA transcription regulator | NP_215833.1      | 6.352748691               |
| 10570 | F06           | 1534       | Rv2643   | arsenic-transport integral membrane protein   | NP_217159.1      | 7.099739244               |
| 10623 | F07           | 1534       | Rv3267   | hypothetical protein Rv3267   | NP_217784.1      | 6.245110821               |
| 10682 | F08           | 1534       | Rv0419   | lipoprotein peptidase LpqM  | NP_214933.1      | 6.9726206                 |
| 10640 | F09           | 1537       | Rv0794c  | oxidoreductase  | YP_177756.1      | 7.316851008               |
| 10706 | F10           | 1540       | Rv0418   | lipoprotein aminopeptidase LpqL   | NP_214932.1      | 8.116883117               |
| 10544 | F11           | 1543       | Rv3377c  | cyclase   | NP_217894.1      | 8.259235256               |
| 10686 | F12           | 1543       | Rv0654   | dioxygenase   | NP_215168.1      | 8.15683733                |
| 10609 | G01           | 1543       | Rv3220c  | two component sensor kinase   | NP_217736.1      | 1.259883344               |
| 10691 | G02           | 1546       | Rv1663   | polyketide synthase pks17   | NP_216179.1      | 5.598318241               |
| 10525 | G03           | 1546       | Rv0160c  | PE family protein   | YP_177698.1      | 1.309184994               |
| 10520 | G04           | 1546       | Rv0913c  | dioxygenase   | NP_215428.1      | 8.118369987               |
| 10633 | G05           | 1546       | Rv3506   | acyl-CoA synthetase   | NP_218023.1      | 1.307891332               |
| 10538 | G06           | 1546       | Rv1760   | hypothetical protein Rv1760   | NP_216276.1      | 7.714747736               |
| 10692 | G07           | 1549       | Rv2897c  | hypothetical protein Rv2897c  | NP_217413.1      | 8.143963848               |
| 10537 | G08           | 1549       | Rv1795   | hypothetical protein Rv1795   | NP_216311.1      | 1.293092318               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                    | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 10548 | G09           | 1549       | Rv0515   | 13E12 repeat family protein                | NP_215029.1      | 7.487411233               |
| 10612 | G10           | 1549       | Rv1002c  | hypothetical protein Rv1002c               | NP_215518.1      | 7.834086507               |
| 10648 | G11           | 1552       | Rv0104   | hypothetical protein Rv0104                | NP_214618.1      | 7.428479381               |
| 10552 | G12           | 1552       | Rv3812   | PE-PGRS family protein                     | YP_178019.1      | 7.326675258               |
| 10678 | H01           | 1552       | Rv0846c  | oxidase                                    | NP_215361.1      | 8.007087629               |
| 10656 | H02           | 1555       | Rv3598c  | lysyl-tRNA synthetase                      | NP_218115.1      | 8.11318328                |
| 10518 | H03           | 1555       | Rv2315c  | hypothetical protein Rv2315c               | NP_216831.1      | 8.030868167               |
| 10606 | H04           | 1558       | Rv1782   | hypothetical protein Rv1782                | NP_216298.1      | 7.840179718               |
| 10564 | H05           | 1561       | Rv0458   | aldehyde dehydrogenase                     | NP_214972.1      | 8.123638693               |
| 10638 | H06           | 1561       | Rv0001   | chromosomal replication initiation protein | NP_214515.1      | 8.060858424               |
| 10615 | H07           | 1564       | Rv2349c  | phospholipase C 3 PLCC                     | NP_216865.1      | 5.710358056               |
| 10522 | H08           | 1567       | Rv1032c  | two component sensor histidine kinase TRCS | NP_215548.1      | 7.767070836               |
| 10593 | H09           | 1567       | Rv1330c  | nicotinate phosphoribosyltransferase       | NP_215846.2      | 1.25909381                |
| 10694 | H10           | 1570       | Rv0753c  | methylmalonate-semialdehyde dehydrogenase  | NP_215267.1      | 6.902547771               |
| 10660 | H11           | 1573       | Rv3824c  | polyketide synthase associated protein     | NP_218341.1      | 7.268277177               |
| 10566 | H12           | 1573       | Rv3877   | transmembrane protein                      | NP_218394.1      | 6.262555626               |

Table 37: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 37 (ZMTMA), NR-19673

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 10583 | A01           | 1573       | Rv2045c  | carboxylesterase LipT  | NP_216561.1      | 6.824539097               |
| 10602 | A02           | 1576       | Rv3484   | hypothetical protein Rv3484  | NP_218001.1      | 7.066624365               |
| 10670 | A03           | 1576       | Rv2351c  | membrane-associated phospholipase C  | NP_216867.1      | 7.310913706               |
| 10658 | A04           | 1576       | Rv2350c  | membrane-associated phospholipase C  | NP_216866.1      | 7.871192893               |
| 10550 | A05           | 1576       | Rv0773c  | bifunctional cephalosporin acylase/gamma-glutamyltranspeptidase                            | NP_215287.1      | 7.068527919               |
| 10586 | A06           | 1579       | Rv2226   | hypothetical protein Rv2226  | NP_216742.1      | 6.872070931               |
| 10624 | A07           | 1585       | Rv2024c  | hypothetical protein Rv2024c   | NP_216540.1      | 7.137539432               |
| 10654 | A08           | 1588       | Rv2249c  | glycerol-3-phosphate dehydrogenase   | NP_216765.1      | 6.569899244               |
| 10516 | A09           | 1588       | Rv3818   | hypothetical protein Rv3818  | NP_218335.1      | 6.304156171               |
| 10652 | A10           | 1588       | Rv0594   | MCE-family protein MCE2F   | NP_215108.1      | 5.493073048               |
| 10590 | A11           | 1591       | Rv1730c  | penicillin-binding protein   | NP_216246.1      | 5.525455688               |
| 10676 | A12           | 1591       | Rv3696c  | glycerol kinase  | NP_218213.1      | 6.325581395               |
| 10674 | B01           | 1594       | Rv1410c  | aminoglycosides/tetracycline-transport integral membrane protein                           | NP_215926.1      | 7.215809285               |
| 10650 | B02           | 1597       | Rv1007c  | methionyl-tRNA synthetase  | NP_215523.1      | 6.381340013               |
| 10794 | B03           | 1603       | Rv1290c  | hypothetical protein Rv1290A   | YP_177642.1      | 7.149719276               |
| 10867 | B04           | 1609       | Rv0957   | bifunctional phosphoribosylaminoimidazole carboxamide formyltransferase/IMP cyclohydrolase | NP_215472.1      | 5.625233064               |
| 10734 | B05           | 1615       | Rv2916c  | signal recognition particle protein  | NP_217432.1      | 7.064396285               |
| 10724 | B06           | 1615       | Rv3396c  | GMP synthase   | NP_217913.1      | 4.575851393               |
| 10888 | B07           | 1618       | Rv3031   | hypothetical protein Rv3031  | NP_217547.1      | 6.247218789               |
| 10821 | B08           | 1618       | Rv1130   | hypothetical protein Rv1130  | NP_215646.1      | 7.576019778               |
| 10841 | B09           | 1621       | Rv1595   | L-aspartate oxidase  | NP_216111.1      | 7.256631709               |
| 10714 | B10           | 1621       | Rv0808   | amidophosphoribosyltransferase   | NP_215323.1      | 6.906230722               |
| 10861 | B11           | 1621       | Rv3394c  | hypothetical protein Rv3394c   | NP_217911.1      | 6.072794571               |
| 10762 | B12           | 1624       | Rv1279   | dehydrogenase FAD flavoprotein oxidoreductase  | NP_215795.1      | 6.594211823               |
| 10712 | C01           | 1624       | Rv2996c  | D-3-phosphoglycerate dehydrogenase   | YP_177916.1      | 6.891009852               |
| 10834 | C02           | 1624       | Rv1430   | PE family protein  | YP_177810.1      | 7.334359606               |
| 10854 | C03           | 1627       | Rv3411c  | inosine 5'-monophosphate dehydrogenase   | NP_217928.1      | 7.105716042               |
| 10742 | C04           | 1627       | Rv0974c  | acetyl-/propionyl-CoA carboxylase subunit beta   | NP_215489.1      | 7.371850031               |
| 10709 | C05           | 1630       | Rv0172   | MCE-family protein MCE1D   | NP_214686.1      | 5.662576687               |
| 10878 | C06           | 1630       | Rv2846c  | integral membrane efflux protein EfpA  | NP_217362.1      | 7.155828221               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                    | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 10837 | C07           | 1636       | Rv1750c  | acyl-CoA synthetase  | NP_216266.1      | 1.216381418               |
| 10824 | C08           | 1639       | Rv3403c  | hypothetical protein Rv3403c                               | NP_217920.1      | 6.796217206               |
| 10850 | C09           | 1642       | Rv2052c  | hypothetical protein Rv2052c                               | NP_216568.1      | 7.851400731               |
| 10726 | C10           | 1642       | Rv0552   | hypothetical protein Rv0552                                | NP_215066.1      | 6.891595615               |
| 10862 | C11           | 1645       | Rv1319c  | adenylate cyclase  | NP_215835.1      | 6.900911854               |
| 10798 | C12           | 1645       | Rv1427c  | acyl-CoA synthetase  | NP_215943.1      | 6.490577508               |
| 10890 | D01           | 1648       | Rv3829c  | dehydrogenase  | NP_218346.1      | 7.466626214               |
| 10736 | D02           |            | Rv2000   | CLONE IS INVALID   | NP_216516.1      |                           |
| 10884 | D03           | 1651       | Rv0214   | acyl-CoA synthetase  | NP_214728.1      | 6.520896426               |
| 10772 | D04           | 1651       | Rv2333c  | integral membrane transport protein                        | NP_216849.1      | 7.611144761               |
| 10784 | D05           | 1654       | Rv0283   | hypothetical protein Rv0283                                | NP_214797.1      | 6.974002418               |
| 10730 | D06           | 1657       | Rv3417c  | chaperonin GroEL   | NP_217934.1      | 6.754375377               |
| 10817 | D07           | 1660       | Rv0440   | chaperonin GroEL   | NP_214954.1      | 7.677710843               |
| 10828 | D08           | 1660       | Rv0099   | acyl-CoA synthetase  | NP_214613.1      | 7.294578313               |
| 10783 | D09           | 1660       | Rv2756c  | type I restriction/modification system DNA methylase HsdM  | NP_217272.1      | 5.535542169               |
| 10768 | D10           | 1660       | Rv0783c  | multidrug resistance integral membrane efflux protein EmrB | NP_215297.1      | 6.559036145               |
| 10729 | D11           | 1663       | Rv3666c  | periplasmic dipeptide-binding lipoprotein DppA             | NP_218183.1      | 7.12808178                |
| 10770 | D12           | 1663       | Rv1318c  | adenylate cyclase  | NP_215834.1      | 7.288634997               |
| 10710 | E01           | 1666       | Rv1473   | macrolide ABC transporter ATP-binding protein              | NP_215989.1      | 5.456782713               |
| 10864 | E02           | 1669       | Rv1187   | pyrroline-5-carboxylate dehydrogenase ROCA                 | NP_215703.1      | 6.738765728               |
| 10806 | E03           | 1669       | Rv1058   | acyl-CoA synthetase  | NP_215574.1      | 6.039544638               |
| 10722 | E04           |            | Rv1013   | CLONE IS INVALID   |                  |                           |
| 10746 | E05           | 1681       | Rv3068c  | phosphoglucosyltransferase                                 | NP_217584.1      | 7.715645449               |
| 10858 | E06           | 1681       | Rv0423c  | thiamine biosynthesis protein ThiC                         | NP_214937.1      | 7.769185009               |
| 10886 | E07           | 1684       | Rv3663c  | peptide ABC transporter ATP-binding protein                | NP_218180.1      | 7.793349169               |
| 10789 | E08           | 1684       | Rv3515c  | acyl-CoA synthetase  | YP_177983.1      | 1.119952494               |
| 10856 | E09           | 1684       | Rv3280   | propionyl-CoA carboxylase beta chain                       | NP_217797.1      | 7.361638955               |
| 10786 | E10           | 1687       | Rv2196   | ubiquinol-cytochrome C reductase                           | NP_216712.1      | 7.622406639               |
| 10810 | E11           | 1687       | Rv3645   | probable conserved transmembrane protein                   |                  | 7.502667457               |
| 10766 | E12           | 1687       | Rv1223   | serine protease HtrA                                       | NP_215739.2      | 6.819798459               |
| 10898 | F01           | 1687       | Rv1308   | F0F1 ATP synthase subunit alpha                            | NP_215824.1      | 6.39122703                |
| 10740 | F02           | 1690       | Rv0922   | transposase  | NP_215437.1      | 7.205325444               |
| 10797 | F03           | 1690       | Rv1292   | arginyl-tRNA synthetase                                    | NP_215808.1      | 7.641420118               |
| 10716 | F04           | 1690       | Rv3886c  | alanine and proline rich membrane-anchored mycosin         | NP_218403.1      | 7.605325444               |
| 10920 | F05           | 1693       | Rv2411c  | hypothetical protein Rv2411c                               | NP_216927.1      | 5.064382753               |
| 10999 | F06           |            | Rv0782   | CLONE IS INVALID   |                  |                           |
| 10993 | F07           | 1696       | Rv3470c  | acetolactate synthase large subunit                        | NP_217987.1      | 1.188679245               |
| 10978 | F08           | 1696       | Rv3558   | PPE family protein   | YP_177988.1      | 7.102004717               |
| 10930 | F09           | 1699       | Rv3157   | NADH dehydrogenase subunit M                               | NP_217673.1      | 7.260153031               |
| 11010 | F10           | 1699       | Rv3263   | DNA methylase (modification methylase) (methyltransferase) | NP_217780.1      | 6.965862272               |
| 10917 | F11           | 1708       | Rv1635c  | transmembrane protein                                      | NP_216151.1      | 1.159836066               |
| 11023 | F12           | 1708       | Rv1704c  | D-serine/alanine/glycine transporter protein CycA          | NP_216220.1      | 7.6264637                 |
| 10902 | G01           | 1714       | Rv2477c  | putative ABC transporter ATP-binding protein               | NP_216993.1      | 7.779463244               |
| 11046 | G02           | 1714       | Rv1162   | respiratory nitrate reductase subunit beta NarH            | NP_215678.1      | 5.457992999               |
| 10927 | G03           | 1714       | Rv2752c  | hypothetical protein Rv2752c                               | NP_217268.1      | 1.168028005               |
| 10988 | G04           | 1714       | Rv1983   | PE-PGRS family protein                                     | YP_177854.1      | 7.694865811               |
| 10994 | G05           | 1720       | Rv0853c  | pyruvate or indole-3-pyruvate decarboxylase pdc            | NP_215368.1      | 6.439534884               |
| 11021 | G06           | 1720       | Rv1739c  | sulphate-transport transmembrane protein ABC transporter   | NP_216255.1      | 7.074418605               |
| 11014 | G07           | 1720       | Rv0976c  | hypothetical protein Rv0976c                               | NP_215491.1      | 6.597674419               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 10961 | G08           | 1720       | Rv0270   | acyl-CoA synthetase                           | NP_214784.1      | 1.080232558               |
| 11038 | G09           | 1726       | Rv0035   | fatty-acid-CoA ligase                         | YP_177686.1      | 6.582271147               |
| 11012 | G10           | 1726       | Rv2797c  | hypothetical protein Rv2797c                  | NP_217313.1      | 7.629779838               |
| 10972 | G11           | 1726       | Rv1204c  | hypothetical protein Rv1204c                  | NP_215720.1      | 7.281575898               |
| 11074 | G12           | 1729       | Rv1253   | cold-shock DEAD-box protein A                 | NP_215769.1      | 7.322151533               |
| 10912 | H01           | 1729       | Rv2391   | ferredoxin-dependent nitrite reductase NIRA   | NP_216907.1      | 7.326778485               |
| 11002 | H02           | 1729       | Rv3537   | 3-ketosteroid-delta-1-dehydrogenase           | NP_218054.1      | 7.360902256               |
| 11066 | H03           | 1738       | Rv0785   | putative FAD-binding dehydrogenase            | NP_215299.1      | 7.445914845               |
| 10964 | H04           | 1744       | Rv0231   | acyl-CoA dehydrogenase FADE4                  | NP_214745.1      | 7.514908257               |
| 10928 | H05           | 1750       | Rv3327   | transposase                                   | NP_217844.1      | 6.885142857               |
| 11042 | H06           | 1753       | Rv1029   | potassium-transporting ATPase subunit A       | NP_215545.1      | 6.938391329               |
| 11072 | H07           | 1759       | Rv3868   | hypothetical protein Rv3868                   | NP_218385.1      | 6.683342808               |
| 10947 | H08           | 1759       | Rv2587c  | preprotein translocase subunit SecD           | NP_217103.1      | 7.198976691               |
| 11052 | H09           | 1765       | Rv0886   | NADPH:adrenodoxin oxidoreductase FprB         | NP_215401.1      | 7.128045326               |
| 11000 | H10           | 1768       | Rv1132   | hypothetical protein Rv1132                   | NP_215648.1      | 6.846719457               |
| 10940 | H11           | 1771       | Rv1850   | urease subunit alpha                          | NP_216366.1      | 7.451722191               |
| 11082 | H12           | 1774       | Rv3721c  | DNA polymerase III (subunit gamma/tau) dnaZ/X | NP_218238.1      | 6.896279594               |

Table 38: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 38 (ZMTMB), NR-19674

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 11058 | A01           |            | Rv1185c  | CLONE IS INVALID   |                  |                           |
| 11008 | A02           | 1774       | Rv3409c  | cholesterol oxidase precursor  | NP_217926.1      | 7.218714769               |
| 11064 | A03           | 1774       | Rv3132c  | two component sensor histidine kinase DEVS   | NP_217648.1      | 7.399098083               |
| 11068 | A04           | 1777       | Rv1349   | drugs-transport transmembrane ATP-binding protein ABC transporter                                  | NP_215865.1      | 6.949915588               |
| 10976 | A05           | 1780       | Rv2941   | acyl-CoA synthetase  | NP_217457.1      | 7.542696629               |
| 11062 | A06           | 1780       | Rv2483c  | bifunctional putative L-3-phosphoserine phosphatase/1-acyl-SN-glycerol-3-phosphate acyltransferase | NP_216999.1      | 7.308426966               |
| 10967 | A07           | 1780       | Rv1562c  | maltooligosyltrehalose trehalohydrolase TreZ   | YP_177819.1      | 6.698876404               |
| 10911 | A08           | 1780       | Rv2608   | PPE family protein   | YP_177893.1      | 7.162921348               |
| 10952 | A09           | 1786       | Rv1273c  | drugs-transport transmembrane ATP-binding protein ABC transporter                                  | NP_215789.1      | 7.422732363               |
| 10991 | A10           | 1786       | Rv0118c  | putative oxalyl-CoA decarboxylase  | NP_214632.1      | 6.694848824               |
| 10908 | A11           | 1789       | Rv1552   | fumarate reductase flavoprotein subunit  | NP_216068.1      | 8.358300727               |
| 11056 | A12           | 1789       | Rv1521   | acyl-CoA synthetase  | NP_216037.1      | 8.397428731               |
| 10905 | B01           |            | Rv3244c  | CLONE IS INVALID   | NP_217761.1      |                           |
| 10906 | B02           | 1792       | Rv1529   | acyl-CoA synthetase  | NP_216045.1      | 8.267857143               |
| 11088 | B03           | 1792       | Rv0754   | PE-PGRS family protein   | YP_177752.1      | 5.471540179               |
| 11026 | B04           | 1795       | Rv3302c  | glycerol-3-phosphate dehydrogenase   | NP_217819.1      | 8.084122563               |
| 11034 | B05           | 1795       | Rv0404   | acyl-CoA synthetase  | NP_214918.1      | 8.143175487               |
| 11018 | B06           | 1798       | Rv1699   | CTP synthetase   | NP_216215.1      | 7.9243604                 |
| 11006 | B07           | 1801       | Rv1696   | DNA repair protein recN (recombination protein N)  | NP_216212.1      | 6.681288173               |
| 11081 | B08           | 1801       | Rv2787   | hypothetical protein Rv2787  | NP_217303.1      | 8.162687396               |
| 10963 | B09           | 1801       | Rv1069c  | hypothetical protein Rv1069c   | NP_215585.1      | 6.541365908               |
| 10948 | B10           | 1804       | Rv0151c  | PE family protein  | YP_177695.1      | 8.087028825               |
| 11050 | B11           | 1807       | Rv1431   | hypothetical protein Rv1431  | NP_215947.1      | 8.157719978               |
| 11070 | B12           | 1810       | Rv3318   | succinate dehydrogenase flavoprotein subunit   | NP_217835.1      | 8.203867403               |
| 11238 | C01           | 1813       | Rv1459c  | integral membrane protein  | NP_215975.1      | 8.200772201               |
| 11248 | C02           | 1813       | Rv3871   | hypothetical protein Rv3871  | NP_218388.1      | 8.171538886               |
| 11226 | C03           | 1816       | Rv2214c  | short chain dehydrogenase  | NP_216730.1      | 7.883810573               |
| 11277 | C04           | 1816       | Rv2264c  | hypothetical protein Rv2264c   | NP_216780.1      | 7.281387665               |



| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)   | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 11096 | C05           | 1819       | Rv0917   | glycine betaine transport integral membrane protein BetP                                      | NP_215432.1      | 7.73062122                |
| 11160 | C06           | 1819       | Rv3797   | acyl-CoA dehydrogenase FADE35   | NP_218314.1      | 8.213853766               |
| 11170 | C07           | 1831       | Rv1779c  | integral membrane protein   | NP_216295.1      | 8.206990715               |
| 11194 | C08           | 1837       | Rv1508c  | hypothetical protein Rv1508A  | YP_177649.1      | 8.20413718                |
| 11240 | C09           | 1840       | Rv2187   | long-chain-fatty-acid-CoA ligase fadD15 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase) | NP_216703.1      | 7.916304348               |
| 11104 | C10           | 1849       | Rv2864c  | penicillin-binding lipoprotein  | NP_217380.1      | 8.132504056               |
| 11168 | C11           | 1849       | Rv3077   | hydrolase   | YP_177923.1      | 7.979989183               |
| 11206 | C12           | 1858       | Rv0211   | phosphoenolpyruvate carboxykinase   | NP_214725.1      | 7.953175457               |
| 11126 | D01           | 1867       | Rv1467c  | acyl-CoA dehydrogenase FADE15   | NP_215983.1      | 7.893947509               |
| 11230 | D02           | 1870       | Rv1798   | hypothetical protein Rv1798   | NP_216314.1      | 7.826203209               |
| 11251 | D03           | 1882       | Rv1286   | bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein             | NP_215802.1      | 7.876195537               |
| 11258 | D04           | 1885       | Rv0193c  | hypothetical protein Rv0193c  | NP_214707.1      | 7.736870027               |
| 11136 | D05           | 1894       | Rv3003c  | acetolactate synthase 1 catalytic subunit   | YP_177917.1      | 7.623020063               |
| 11192 | D06           | 1897       | Rv2950c  | acyl-CoA synthetase   | NP_217466.2      | 8.024775962               |
| 11262 | D07           | 1900       | Rv0312   | hypothetical protein Rv0312   | NP_214826.1      | 7.921052632               |
| 11215 | D08           | 1909       | Rv1354c  | hypothetical protein Rv1354c  | NP_215870.1      | 7.697223677               |
| 11236 | D09           | 1912       | Rv3436c  | glucosamine--fructose-6-phosphate aminotransferase  | NP_217953.1      | 7.891736402               |
| 11219 | D10           | 1918       | Rv2917   | hypothetical protein Rv2917   | NP_217433.1      | 7.577163712               |
| 11110 | D11           | 1918       | Rv3762c  | hydrolase   | NP_218279.1      | 7.717935349               |
| 11188 | D12           | 1918       | Rv0014c  | transmembrane serine/threonine-protein kinase   | NP_214528.1      | 7.475495308               |
| 11244 | E01           | 1918       | Rv2930   | acyl-CoA synthetase   | NP_217446.2      | 7.927528676               |
| 11178 | E02           | 1924       | Rv1165   | GTP-binding translation elongation factor TypA  | NP_215681.1      | 7.865904366               |
| 11204 | E03           | 1939       | Rv3156   | NADH dehydrogenase subunit L  | NP_217672.1      | 7.401753481               |
| 11200 | E04           | 1945       | Rv1166   | lipoprotein LpqW  | NP_215682.1      | 7.630848329               |
| 11264 | E05           | 1951       | Rv0669c  | hydrolase   | NP_215183.1      | 7.833931317               |
| 11129 | E06           | 1957       | Rv2343c  | DNA primase   | NP_216859.1      | 6.201328564               |
| 11098 | E07           | 1960       | Rv0342   | isoniazid inducible gene protein INIA   | NP_214856.1      | 7.606632653               |
| 11282 | E08           | 1966       | Rv2402   | hypothetical protein Rv2402   | NP_216918.1      | 7.805696846               |
| 11124 | E09           | 1969       | Rv2394   | gamma-glutamyltranspeptidase precursor GgtB   | NP_216910.1      | 7.845606907               |
| 11210 | E10           | 1975       | Rv2191   | hypothetical protein Rv2191   | NP_216707.1      | 7.946329114               |
| 11100 | E11           | 1990       | Rv3391   | short chain dehydrogenase   | NP_217908.1      | 7.214572864               |
| 11167 | E12           | 1990       | Rv0873   | acyl-CoA dehydrogenase FADE10   | NP_215388.1      | 6.363819095               |
| 11222 | F01           | 1996       | Rv2201   | asparagine synthetase AsnB  | NP_216717.1      | 6.596693387               |
| 11150 | F02           | 1996       | Rv2332   | malate dehydrogenase  | NP_216848.2      | 7.644789579               |
| 11122 | F03           | 1999       | Rv2455c  | oxidoreductase alpha subunit  | NP_216971.1      | 7.260630315               |
| 11268 | F04           | 1999       | Rv1364c  | hypothetical protein Rv1364c  | YP_177802.1      | 7.632316158               |
| 11209 | F05           | 1999       | Rv2404c  | GTP-binding protein LepA  | NP_216920.1      | 6.815907954               |
| 11116 | F06           | 2002       | Rv2501c  | acetyl-/propionyl-coenzyme A carboxylase subunit alpha  | NP_217017.1      | 7.664835165               |
| 11162 | F07           | 2005       | Rv1800   | PPE family protein  | YP_177839.1      | 7.607481297               |
| 11120 | F08           | 2005       | Rv1402   | primosome assembly protein PriA   | NP_215918.1      | 6.463341646               |
| 11242 | F09           | 2011       | Rv1469   | cation transporter P-type ATPase D  | NP_215985.1      | 6.860268523               |
| 11165 | F10           | 2011       | Rv2690c  | hypothetical protein Rv2690c  | NP_217206.1      | 7.05619095                |
| 11386 | F11           | 2029       | Rv0198c  | zinc metalloprotease  | NP_214712.1      | 7.521931986               |
| 11288 | F12           | 2032       | Rv1329c  | ATP-dependent helicase DING   | NP_215845.1      | 7.405019685               |
| 11294 | G01           | 2038       | Rv3876   | hypothetical protein Rv3876   | NP_218393.1      | 5.626104024               |
| 11446 | G02           | 2041       | Rv0973c  | acetyl-/propionyl-coenzyme A carboxylase subunit alpha  | NP_215488.1      | 7.955414013               |
| 11473 | G03           | 2062       | Rv1175c  | NADPH dependent 2,4-dienoyl-CoA reductase   | NP_215691.1      | 6.511154219               |
| 11451 | G04           | 2095       | Rv0111   | transmembrane acyltransferase   | NP_214625.1      | 6.988066826               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                                     | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 11296 | G05           | 2119       | Rv3051c  | ribonucleotide-diphosphate reductase subunit alpha          | NP_217567.1      | 6.812175555               |
| 11300 | G06           | 2125       | Rv2874   | integral membrane C-type cytochrome biogenesis protein DipZ | NP_217390.1      | 8.029647059               |
| 11343 | G07           | 2137       | Rv2721c  | hypothetical protein Rv2721c                                | NP_217237.1      | 7.196069256               |
| 11415 | G08           | 2140       | Rv3198c  | glutaredoxin protein  | YP_177941.1      | 6.45                      |
| 11308 | G09           |            | Rv1449c  | CLONE IS INVALID  | NP_215965.1      |                           |
| 11390 | G10           | 2155       | Rv2948c  | acyl-CoA synthetase   | NP_217464.1      | 7.618097448               |
| 11332 | G11           | 2167       | Rv1030   | potassium-transporting ATPase subunit B                     | NP_215546.1      | 8.101522843               |
| 11312 | G12           | 2182       | Rv0005   | DNA gyrase subunit B  | NP_214519.1      | 7.068744271               |
| 11376 | H01           | 2185       | Rv1355c  | hypothetical protein Rv1355c                                | NP_215871.1      | 7.774828375               |
| 11330 | H02           | 2194       | Rv3270   | metal cation-transporting P-type ATPase C CtpC              | NP_217787.1      | 7.783500456               |
| 11362 | H03           | 2200       | Rv0860   | fatty oxidation protein FadB                                | NP_215375.1      | 7.216363636               |
| 11410 | H04           |            | Rv1564c  | CLONE IS INVALID  |                  |                           |
| 11306 | H05           | 2203       | Rv3061c  | acyl-CoA dehydrogenase FADE22                               | NP_217577.1      | 7.856559237               |
| 11403 | H06           | 2230       | Rv2435c  | cyclase   | NP_216951.1      | 7.399103139               |
| 11421 | H07           | 2233       | Rv0271c  | acyl-CoA dehydrogenase FADE6                                | NP_214785.1      | 5.800268697               |
| 11302 | H08           | 2233       | Rv1326c  | glycogen branching enzyme                                   | NP_215842.1      | 7.938199731               |
| 11470 | H09           | 2251       | Rv2973c  | ATP-dependent DNA helicase RecG                             | NP_217489.1      | 7.128387383               |
| 11086 | H10           | 2260       | Rv1908c  | catalase-peroxidase-peroxynitritase T KATG                  | NP_216424.1      | 7.721238938               |
| 11285 | H11           | 2275       | Rv0066c  | isocitrate dehydrogenase                                    | NP_214580.1      | 7.195164835               |
| 11408 | H12           | 2290       | Rv1493   | methylmalonyl-CoA mutase                                    | NP_216009.1      | 7.523580786               |

Table 39: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 39 (ZMTMC), NR-19675

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                           | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 11444 | A01           | 2296       | Rv0103c  | cation-transporter P-type ATPase B                | NP_214617.1      | 7.807926829               |
| 11440 | A02           | 2296       | Rv2783c  | polynucleotide phosphorylase/polyadenylase        | NP_217299.1      | 6.198606272               |
| 11358 | A03           | 2302       | Rv0803   | phosphoribosylformylglycinamide synthase II       | NP_215318.1      | 3.953084275               |
| 11324 | A04           | 2335       | Rv1563c  | maltooligosyltrehalose synthase TreY              | YP_177820.1      | 7.291648822               |
| 11464 | A05           | 2353       | Rv1992c  | metal cation transporter P-type ATPase G CtpG     | NP_216508.1      | 7.819379516               |
| 11454 | A06           | 2368       | Rv3729   | transferase                                       | NP_218246.1      | 8.083192568               |
| 11468 | A07           | 2377       | Rv2900c  | formate dehydrogenase H                           | NP_217416.1      | 7.596129575               |
| 11527 | A08           | 2437       | Rv0373c  | carbon monoxide dehydrogenase large subunit       | NP_214887.1      | 6.924907673               |
| 11570 | A09           | 2446       | Rv3909   | hypothetical protein Rv3909                       | NP_218426.1      | 8.07686018                |
| 11518 | A10           | 2467       | Rv2823c  | hypothetical protein Rv2823c                      | NP_217339.1      | 7.892987434               |
| 11530 | A11           | 2554       | Rv0006   | DNA gyrase subunit A                              | NP_214520.1      | 7.652701644               |
| 11596 | A12           | 2557       | Rv1937   | oxygenase   | NP_216453.1      | 7.380524052               |
| 11664 | B01           | 2584       | Rv0384c  | endopeptidase ATP binding protein                 | NP_214898.1      | 8.087074303               |
| 11632 | B02           |            | Rv0987   | CLONE IS INVALID                                  |                  |                           |
| 11504 | B03           | 2635       | Rv1747   | transmembrane ATP-binding protein ABC transporter | NP_216263.1      | 8.182922201               |
| 11660 | B04           | 2662       | Rv0058   | replicative DNA helicase                          | NP_214572.1      | 8.223891811               |
| 11644 | B05           | 2692       | Rv2567   | hypothetical protein Rv2567                       | NP_217083.1      | 7.604383358               |
| 11540 | B06           |            | Rv2555c  | CLONE IS INVALID                                  | NP_217071.1      |                           |
| 11478 | B07           | 2842       | Rv3646c  | DNA topoisomerase I                               | NP_218163.1      | 7.754750176               |
| 11622 | B08           | 2863       | Rv1832   | glycine dehydrogenase                             | NP_216348.1      | 7.1742927                 |
| 11563 | B09           | 2869       | Rv1475c  | aconitate hydratase                               | NP_215991.1      | 6.112582781               |
| 11492 | B10           | 2887       | Rv3240c  | preprotein translocase subunit SecA               | YP_177950.1      | 8.116383789               |
| 11551 | B11           | 2932       | Rv0676c  | transmembrane transport protein Mmpl5             | NP_215190.1      | 7.303888131               |
| 11511 | B12           | 2938       | Rv0202c  | transmembrane transport protein Mmpl11            | NP_214716.1      | 7.515997277               |
| 11601 | C01           | 2947       | Rv0041   | leucyl-tRNA synthetase                            | NP_214555.1      | 7.543603665               |
| 11612 | C02           | 3016       | Rv3193c  | hypothetical protein Rv3193c                      | NP_217709.1      | 7.952254642               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 11631 | C03           | 3022       | Rv2221c  | glutamate-ammonia-ligase adenylyltransferase<br>GLNE (glutamine-synthetase<br>adenylyltransferase) | NP_216737.1      | 7.176704169               |
| 11508 | C04           | 3091       | Rv1664   | polyketide synthase pks9   | NP_216180.1      | 7.915237787               |
| 11580 | C05           | 3163       | Rv1536   | isoleucyl-tRNA synthetase  | NP_216052.1      | 8.117609864               |
| 11566 | C06           | 3235       | Rv3728   | hypothetical protein Rv3728  | NP_218245.1      | 7.74064915                |
| 11797 | C07           | 3556       | Rv0667   | DNA-directed RNA polymerase subunit beta   | NP_215181.1      | 7.754780652               |

Table 40: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 40 (ZMTMD), NR-19676

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------------|------------------|---------------------------|
| 11825 | A01           | 133        | MT3223   | hypothetical protein MT3223   | NP_337749.1      | -                         |
| 11965 | A02           | 133        | MT2326   | hypothetical protein MT2326   | NP_336794.1      | -                         |
| 11925 | A03           | 136        | MT3156   | hypothetical protein MT3156   | NP_337678.1      | -                         |
| 11833 | A04           |            | MT1342   | CLONE IS INVALID              | NP_335790.1      | -                         |
| 11991 | A05           | 142        | MT0603   | hypothetical protein MT0603   | NP_335012.1      | -                         |
| 11916 | A06           | 145        | MT3536   | hypothetical protein MT3536   | NP_338062.1      | 2                         |
| 11821 | A07           | 145        | MT0506   | hypothetical protein MT0506   | NP_334915.1      | -                         |
| 11951 | A08           | 145        | MT3174.1 | hypothetical protein MT3174.1 | NP_337697.1      | -                         |
| 11949 | A09           |            | MT0827   | CLONE IS INVALID              | NP_335255.1      | -                         |
| 11843 | A10           | 145        | MT0294   | hypothetical protein MT0294   | NP_334704.1      | -                         |
| 11873 | A11           | 145        | MT3436   | hypothetical protein MT3436   | NP_337965.1      | -                         |
| 11909 | A12           | 148        | MT2424   | hypothetical protein MT2424   | NP_336904.1      | -                         |
| 11927 | B01           | 148        | MT3847   | hypothetical protein MT3847   | NP_338397.1      | -                         |
| 11969 | B02           | 151        | MT0416   | hypothetical protein MT0416   | NP_334826.1      | -                         |
| 11869 | B03           | 151        | MT2417   | hypothetical protein MT2417   | NP_336896.1      | -                         |
| 11826 | B04           | 154        | MT0540   | hypothetical protein MT0540   | NP_334949.1      | 2                         |
| 11819 | B05           | 154        | MT2375   | hypothetical protein MT2375   | NP_336854.1      | -                         |
| 11816 | B06           | 154        | MT2895   | hypothetical protein MT2895   | NP_337406.1      | 2                         |
| 11853 | B07           | 154        | MT2083   | hypothetical protein MT2083   | NP_336548.1      | -                         |
| 12003 | B08           | 154        | MT3846   | hypothetical protein MT3846   | NP_338396.1      | -                         |
| 11905 | B09           | 157        | MT1771.1 | hypothetical protein MT1771.1 | NP_336230.1      | -                         |
| 11976 | B10           | 157        | MT0868   | hypothetical protein MT0868   | NP_335297.1      | 1.955414013               |
| 11985 | B11           | 160        | MT2092   | hypothetical protein MT2092   | NP_336557.1      | -                         |
| 11814 | B12           | 160        | MT2115   | hypothetical protein MT2115   | NP_336580.1      | 2                         |
| 11829 | C01           | 160        | MT3290.2 | hypothetical protein MT3290.2 | NP_337819.1      | -                         |
| 11899 | C02           | 160        | MT3767.3 | hypothetical protein MT3767.3 | NP_338320.1      | -                         |
| 11903 | C03           | 160        | MT3580.2 | hypothetical protein MT3580.2 | NP_338125.1      | -                         |
| 11839 | C04           | 163        | MT0116.1 | hypothetical protein MT0116.1 | NP_334525.1      | -                         |
| 11955 | C05           | 163        | MT2369   | hypothetical protein MT2369   | NP_336845.1      | -                         |
| 11913 | C06           | 166        | MT3628   | hypothetical protein MT3628   | NP_338175.1      | -                         |
| 11963 | C07           | 166        | MT2168   | hypothetical protein MT2168   | NP_336637.1      | -                         |
| 11837 | C08           | 166        | MT3994   | hypothetical protein MT3994   | NP_338548.1      | -                         |
| 11961 | C09           | 166        | MT3491.1 | hypothetical protein MT3491.1 | NP_338013.1      | -                         |
| 11941 | C10           | 166        | MT2510   | hypothetical protein MT2510   | NP_336993.1      | -                         |
| 11895 | C11           | 169        | MT2325   | hypothetical protein MT2325   | NP_336793.1      | -                         |
| 11915 | C12           | 169        | MT0740.1 | hypothetical protein MT0740.1 | NP_335158.1      | -                         |
| 11901 | D01           | 169        | MT3876.1 | hypothetical protein MT3876.1 | NP_338427.1      | -                         |
| 12001 | D02           | 169        | MT1578.1 | hypothetical protein MT1578.1 | NP_336031.1      | -                         |
| 11953 | D03           | 172        | MT3362   | hypothetical protein MT3362   | NP_337889.1      | -                         |
| 11882 | D04           | 172        | MT0573.1 | hypothetical protein MT0573.1 | NP_334982.1      | 1.947674419               |
| 11823 | D05           | 175        | MT0773.1 | hypothetical protein MT0773.1 | NP_335200.1      | -                         |
| 11849 | D06           | 175        | MT1070   | hypothetical protein MT1070   | NP_335507.1      | -                         |
| 11939 | D07           | 175        | MT0492   | hypothetical protein MT0492   | NP_334901.1      | -                         |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------------|------------------|---------------------------|
| 11855 | D08           | 178        | MT3972.1 | hypothetical protein MT3972.1 | NP_338526.1      | -                         |
| 11920 | D09           | 178        | MT0991   | hypothetical protein MT0991   | NP_335425.1      | 2                         |
| 11993 | D10           | 178        | MT1098   | hypothetical protein MT1098   | NP_335540.1      | -                         |
| 11929 | D11           | 178        | MT1556.1 | hypothetical protein MT1556.1 | NP_336009.1      | 2                         |
| 11889 | D12           | 181        | MT2960   | hypothetical protein MT2960   | NP_337472.1      | -                         |
| 11831 | E01           | 181        | MT0031   | hypothetical protein MT0031   | NP_334440.1      | -                         |
| 11983 | E02           | 184        | MT1414.1 | hypothetical protein MT1414   | NP_335863.1      | -                         |
| 11865 | E03           | 184        | MT1321   | hypothetical protein MT1321   | NP_335768.1      | -                         |
| 11897 | E04           | 184        | MT3919   | hypothetical protein MT3919   | NP_338471.1      | 2                         |
| 11871 | E05           | 184        | MT0946   | hypothetical protein MT0946   | NP_335379.1      | -                         |
| 11919 | E06           | 184        | MT0910.4 | hypothetical protein MT0910.4 | NP_335342.1      | -                         |
| 11959 | E07           | 187        | MT0910.3 | hypothetical protein MT0910.3 | NP_335341.1      | -                         |
| 11890 | E08           | 187        | MT1122.1 | hypothetical protein MT1122.1 | NP_335566.1      | 1.679144385               |
| 11944 | E09           | 187        | MT2138.1 | hypothetical protein MT2138.1 | NP_336605.1      | 2.85026738                |
| 11986 | E10           | 187        | MT3953   | hypothetical protein MT3953   | NP_338506.1      | 1.743315508               |
| 11863 | E11           | 187        | MT1356   | hypothetical protein MT1356   | NP_335804.1      | -                         |
| 11846 | E12           | 190        | MT1813   | hypothetical protein MT1813   | NP_336270.1      | 1.994736842               |
| 11877 | F01           | 190        | MT1077   | hypothetical protein MT1077   | NP_335515.1      | -                         |
| 12079 | F02           | 190        | MT0431   | hypothetical protein MT0431   | NP_334841.1      | 2                         |
| 12058 | F03           | 190        | MT2554   | hypothetical protein MT2554   | NP_337042.1      | 2                         |
| 12026 | F04           | 190        | MT1288   | hypothetical protein MT1288   | NP_335732.1      | 2                         |
| 12117 | F05           | 193        | MT0576   | hypothetical protein MT0576   | NP_334985.1      | 2                         |
| 12032 | F06           | 193        | MT1178   | hypothetical protein MT1178   | NP_335623.1      | 2                         |
| 12067 | F07           | 193        | MT0910.1 | hypothetical protein MT0910.1 | NP_335339.1      | -                         |
| 12094 | F08           | 196        | MT1497.2 | hypothetical protein MT1497.2 | NP_335947.1      | 1.964285714               |
| 12185 | F09           | 199        | MT0196   | hypothetical protein MT0196   | NP_334602.1      | -                         |
| 12167 | F10           | 199        | MT3780   | hypothetical protein MT3780   | NP_338333.1      | 2                         |
| 12129 | F11           | 199        | MT0069   | hypothetical protein MT0069   | NP_334479.1      | -                         |
| 12187 | F12           | 199        | MT3275.1 | hypothetical protein MT3275.1 | NP_337802.1      | 2                         |
| 12031 | G01           | 199        | MT0553   | hypothetical protein MT0553   | NP_334962.1      | -                         |
| 12011 | G02           | 202        | MT2467   | hypothetical protein MT2467   | NP_336948.1      | 2                         |
| 12072 | G03           | 202        | MT1746.1 | hypothetical protein MT1746.1 | NP_336202.1      | 2                         |
| 12015 | G04           | 202        | MT2370.2 | hypothetical protein MT2370.2 | NP_336848.1      | -                         |
| 12119 | G05           | 205        | MT1585.1 | hypothetical protein MT1585.1 | NP_336038.1      | 2                         |
| 12155 | G06           | 205        | MT0600   | hypothetical protein MT0600   | NP_335009.1      | 2                         |
| 12056 | G07           | 205        | MT2370   | hypothetical protein MT2370   | NP_336846.1      | 2                         |
| 12052 | G08           | 205        | MT0663   | 50S ribosomal protein L33     | NP_335074.1      | 2                         |
| 12170 | G09           | 208        | MT0853   | hypothetical protein MT0853   | NP_335280.1      | 2                         |
| 12077 | G10           | 208        | MT3671.2 | hypothetical protein MT3671.2 | NP_338216.1      | -                         |
| 12115 | G11           | 208        | MT2396   | hypothetical protein MT2396   | NP_336874.1      | -                         |
| 12121 | G12           | 208        | MT3412   | hypothetical protein MT3412   | NP_337941.1      | -                         |
| 12087 | H01           | 208        | MT3014   | hypothetical protein MT3014   | NP_337527.1      | -                         |
| 12163 | H02           | 211        | MT0638.1 | hypothetical protein MT0638.1 | NP_335047.1      | -                         |
| 12180 | H03           | 211        | MT0290   | hypothetical protein MT0290   | NP_334696.1      | 2                         |
| 12152 | H04           | 211        | MT1266   | hypothetical protein MT1266   | NP_335710.1      | 2                         |
| 12005 | H05           | 214        | MT1054.1 | hypothetical protein MT1054.1 | NP_335492.1      | -                         |
| 12195 | H06           | 214        | MT3103   | hypothetical protein MT3103   | NP_337618.1      | -                         |
| 12183 | H07           | 217        | MT3959   | hypothetical protein MT3959   | NP_338512.1      | -                         |
| 12176 | H08           | 217        | MT3268   | hypothetical protein MT3268   | NP_337793.1      | 2                         |
| 12149 | H09           | 220        | MT3149.1 | hypothetical protein MT3149.1 | NP_337669.1      | -                         |
| 12061 | H10           | 220        | MT2365.2 | hypothetical protein MT2365.2 | NP_336840.1      | -                         |
| 12045 | H11           | 220        | MT1121   | hypothetical protein MT1121   | NP_335564.1      | 2                         |
| 12125 | H12           | 223        | MT2588   | hypothetical protein MT2588   | NP_337079.1      | 2                         |

Table 41: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 41 (ZMTME), NR-19677

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)         | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---------------------------------|------------------|---------------------------|
| 12133 | A01           | 223        | MT3280   | hypothetical protein MT3280     | NP_337807.1      | 2                         |
| 12173 | A02           | 226        | MT0859   | hypothetical protein MT0859     | NP_335288.1      | -                         |
| 12169 | A03           | 226        | MT0719.1 | hypothetical protein MT0719.1   | NP_335133.1      | -                         |
| 12151 | A04           | 226        | MT0124   | hypothetical protein MT0124     | NP_334533.1      | -                         |
| 12101 | A05           | 226        | MT1190   | hypothetical protein MT1190     | NP_335633.1      | 2                         |
| 12145 | A06           | 229        | MT0895   | hypothetical protein MT0895     | NP_335323.1      | -                         |
| 12024 | A07           | 229        | MT3879   | hypothetical protein MT3879     | NP_338430.1      | 2                         |
| 12123 | A08           | 229        | MT1520   | hypothetical protein MT1520     | NP_335971.1      | 2                         |
| 12137 | A09           | 229        | MT2365   | hypothetical protein MT2365     | NP_336838.1      | -                         |
| 12023 | A10           | 232        | MT3052.2 | 50S ribosomal protein L28       | NP_337566.1      | -                         |
| 12051 | A11           | 232        | MT2931   | hypothetical protein MT2931     | NP_337442.1      | -                         |
| 12064 | A12           | 232        | MT2473   | hypothetical protein MT2473     | NP_336955.1      | 2                         |
| 12178 | B01           |            | MT3631   | CLONE IS INVALID                |                  |                           |
| 12012 | B02           | 235        | MT3630   | hypothetical protein MT3630     | NP_338177.1      | 2                         |
| 12147 | B03           | 238        | MT3289   | hypothetical protein MT3289     | NP_337816.1      | -                         |
| 12107 | B04           | 238        | MT1571   | hypothetical protein MT1571     | NP_336024.1      | -                         |
| 12039 | B05           | 241        | MT0724.1 | hypothetical protein MT0724.1   | NP_335140.1      | -                         |
| 12099 | B06           | 244        | MT3033   | hypothetical protein MT3033     | NP_337545.1      | 2                         |
| 12009 | B07           | 244        | MT2565   | hypothetical protein MT2565     | NP_337055.1      | -                         |
| 12019 | B08           | 247        | MT2401.2 | hypothetical protein MT2401.2   | NP_336881.1      | -                         |
| 12190 | B09           | 247        | MT3767.2 | hypothetical protein MT3767.2   | NP_338319.1      | 2.704453441               |
| 12105 | B10           | 247        | MT2627.1 | hypothetical protein MT2627.1   | NP_337125.1      | -                         |
| 12175 | B11           | 247        | MT2455   | hypothetical protein MT2455     | NP_336936.1      | 2                         |
| 12103 | B12           | 250        | MT0761   | hypothetical protein MT0761     | NP_335181.1      | 2                         |
| 12111 | C01           | 250        | MT1055   | hypothetical protein MT1055     | NP_335493.1      | -                         |
| 12189 | C02           |            | MT0085.1 | CLONE IS INVALID                |                  |                           |
| 12083 | C03           | 250        | MT1086   | hypothetical protein MT1086     | NP_335526.1      | -                         |
| 12091 | C04           | 250        | MT3954   | hypothetical protein MT3954     | NP_338507.1      | -                         |
| 12097 | C05           | 250        | MT1547   | hypothetical protein MT1547     | NP_335999.1      | 2                         |
| 12109 | C06           | 250        | MT3718.1 | hypothetical protein MT3718.1   | NP_338264.1      | -                         |
| 12112 | C07           | 253        | MT3958   | hypothetical protein MT3958     | NP_338511.1      | 2                         |
| 12016 | C08           | 253        | MT2201   | hypothetical protein MT2201     | NP_336671.1      | 2                         |
| 12040 | C09           | 253        | MT0780   | hypothetical protein MT0780     | NP_335207.1      | 2                         |
| 12139 | C10           | 253        | MT2466   | hypothetical protein MT2466     | NP_336947.1      | -                         |
| 12034 | C11           | 253        | MT1742   | hypothetical protein MT1742     | NP_336197.1      | 2                         |
| 12049 | C12           | 256        | MT3615.4 | hypothetical protein MT3615.4   | NP_338161.1      | 2                         |
| 12159 | D01           | 256        | MT3080.1 | hypothetical protein MT3080.1   | NP_337595.1      | -                         |
| 12093 | D02           | 256        | MT3297   | hypothetical protein MT3297     | NP_337826.1      | -                         |
| 12160 | D03           | 256        | MT1924.1 | hypothetical protein MT1924.1   | NP_336382.1      | 1.984375                  |
| 12071 | D04           | 259        | MT0987   | hypothetical protein MT0987     | NP_335421.1      | 2                         |
| 12046 | D05           | 259        | MT4041.2 | hypothetical protein MT4041.2   | NP_338596.1      | 2.66023166                |
| 12020 | D06           | 262        | MT2606   | hypothetical protein MT2606     | NP_337102.1      | 2.645038168               |
| 12006 | D07           | 262        | MT3800   | CopG family DNA-binding protein | NP_338353.1      | 2.973282443               |
| 12157 | D08           | 265        | MT1232   | hypothetical protein MT1232     | NP_335675.1      | 2                         |
| 12214 | D09           | 265        | MT2418   | hypothetical protein MT2418     | NP_336897.1      | 2.633962264               |
| 12260 | D10           | 265        | MT3322   | hypothetical protein MT3322     | NP_337850.1      | 3.40754717                |
| 12226 | D11           | 268        | MT0694   | hypothetical protein MT0694     | NP_335106.1      | 2.402985075               |
| 12271 | D12           | 268        | MT3754   | hypothetical protein MT3754     | NP_338301.1      | -                         |
| 12284 | E01           | 268        | MT2038   | hypothetical protein MT2038     | NP_336499.1      | 2.973880597               |
| 12366 | E02           | 271        | MT1808   | hypothetical protein MT1808     | NP_336265.1      | 2.63099631                |
| 12216 | E03           | 271        | MT3204   | hypothetical protein MT3204     | NP_337730.1      | 1.992619926               |
| 12335 | E04           | 274        | MT0521   | hypothetical protein MT0521     | NP_334930.1      | 2                         |
| 12387 | E05           | 274        | MT1404   | hypothetical protein MT1404     | NP_335853.1      | 2                         |

## Master Clone List for NR-19274

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)                               | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|---|------------------|---------------------------|
| 12360 | E06           | 274        | MT2080.1 | hypothetical protein MT2080.1                         | NP_336545.1      | 2                         |
| 12287 | E07           | 274        | MT2297   | hypothetical protein MT2291                           | NP_336761.1      | -                         |
| 12373 | E08           | 277        | MT3560   | hypothetical protein MT3560                           | NP_338085.1      | 2                         |
| 12324 | E09           | 277        | MT0812   | phosphoribosylformylglycinamide synthase subunit PurS | NP_335240.1      | 2.783393502               |
| 12382 | E10           | 280        | MT1169   | ketoacyl-CoA thiolase-related protein                 | NP_335612.1      | 3.242857143               |
| 12242 | E11           | 280        | MT1777   | hypothetical protein MT1777                           | NP_336236.1      | 2                         |
| 12219 | E12           | 280        | MT3042   | hypothetical protein MT3042                           | NP_337554.1      | -                         |
| 12358 | F01           | 283        | MT3220.2 | hypothetical protein MT3220.2                         | NP_337746.1      | 2                         |
| 12234 | F02           | 283        | MT2589.1 | hypothetical protein MT2589.1                         | NP_337081.1      | 2                         |
| 12292 | F03           | 283        | MT2600.1 | hypothetical protein MT2600.1                         | NP_337094.1      | 3.438162544               |
| 12265 | F04           | 286        | MT1070.1 | hypothetical protein MT1070.1                         | NP_335508.1      | 2                         |
| 12255 | F05           | 286        | MT0407.1 | hypothetical protein MT0407.1                         | NP_334817.1      | 2                         |
| 12220 | F06           | 286        | MT2068   | hypothetical protein MT2068                           | NP_336532.1      | 1.968531469               |
| 12198 | F07           | 286        | MT2047   | CopG family DNA-binding protein                       | NP_336510.1      | 2.604895105               |
| 12329 | F08           | 289        | MT1025.2 | hypothetical protein MT1025.2                         | NP_335460.1      | -                         |
| 12343 | F09           | 289        | MT0662.1 | hypothetical protein MT0662.1                         | NP_335073.1      | -                         |
| 12238 | F10           | 289        | MT1490   | hypothetical protein MT1490                           | NP_335939.1      | 2.560553633               |
| 12294 | F11           | 292        | MT3292   | hypothetical protein MT3292                           | NP_337821.1      | 2.969178082               |
| 12272 | F12           | 295        | MT0036   | hypothetical protein MT0036                           | NP_334445.1      | 2.772881356               |
| 12369 | G01           | 295        | MT2554.1 | hypothetical protein MT2554.1                         | NP_337043.1      | 2                         |
| 12345 | G02           | 295        | MT0943   | hypothetical protein MT0943                           | NP_335376.1      | 2                         |
| 12322 | G03           | 295        | MT1676   | hypothetical protein MT1676                           | NP_336131.1      | 3.671186441               |
| 12330 | G04           | 295        | MT2710   | hypothetical protein MT2710                           | NP_337211.1      | 2.738983051               |
| 12312 | G05           | 295        | MT2045   | hypothetical protein MT2045                           | NP_336507.1      | 3.691525424               |
| 12266 | G06           | 298        | MT2035   | hypothetical protein MT2035                           | NP_336496.1      | 3.755033557               |
| 12305 | G07           | 301        | MT1537   | hypothetical protein MT1537                           | NP_335990.1      | -                         |
| 12319 | G08           |            | MT0910.2 | CLONE IS INVALID                                      | NP_335340.1      |                           |
| 12320 | G09           | 304        | MT3671.1 | hypothetical protein MT3671.1                         | NP_338215.1      | 1.789473684               |
| 12355 | G10           | 307        | MT1957.1 | hypothetical protein MT1957.1                         | NP_336415.1      | -                         |
| 12282 | G11           | 307        | MT2015.2 | hypothetical protein MT2015.2                         | NP_336475.1      | 3.553745928               |
| 12229 | G12           | 310        | MT2042.1 | hypothetical protein MT2042.1                         | NP_336504.1      | -                         |
| 12362 | H01           | 310        | MT2013   | hypothetical protein MT2013                           | NP_336471.1      | 4.670967742               |
| 12232 | H02           | 313        | MT3220.1 | hypothetical protein MT3220.1                         | NP_337745.1      | 3.623003195               |
| 12296 | H03           | 316        | MT2246   | hypothetical protein MT2246                           | NP_336718.1      | 3.253164557               |
| 12364 | H04           | 322        | MT0973   | hypothetical protein MT0973                           | NP_335407.1      | 3.388198758               |
| 12246 | H05           | 325        | MT2370.3 | hypothetical protein MT2370.3                         | NP_336849.1      | 3.64                      |
| 12381 | H06           | 325        | MT1602   | hypothetical protein MT1602                           | NP_336055.1      | 2                         |
| 12278 | H07           | 325        | MT2676   | hypothetical protein MT2676                           | NP_337178.1      | 3.664615385               |
| 12378 | H08           | 328        | MT0726.1 | hypothetical protein MT0726.1                         | NP_335143.1      | 2.844512195               |
| 12333 | H09           | 328        | MT2420   | hypothetical protein MT2420                           | NP_336899.1      | -                         |
| 12240 | H10           | 328        | MT3290.1 | hypothetical protein MT3290.1                         | NP_337818.1      | 2.853658537               |
| 12231 | H11           |            | MT3269   | CLONE IS INVALID                                      | NP_337794.1      |                           |
| 12350 | H12           | 331        | MT3304   | hypothetical protein MT3304                           | NP_337832.1      | 3.658610272               |

**Table 42: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 42 (ZMTMF), NR-19678**

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)       | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|-------------------------------|------------------|---------------------------|
| 12196 | A01           | 331        | MT1650.1 | hypothetical protein MT1650.1 | NP_336106.1      | 3.673716012               |
| 12224 | A02           | 334        | MT2165   | hypothetical protein MT2165   | NP_336633.1      | 3.538922156               |
| 12275 | A03           | 337        | MT2421   | hypothetical protein MT2421   | NP_336900.1      | 2                         |
| 12352 | A04           | 340        | MT3077   | hypothetical protein MT3077   | NP_337592.1      | 3.597058824               |
| 12205 | A05           | 340        | MT3174.2 | hypothetical protein MT3174.2 | NP_337698.1      | -                         |
| 12314 | A06           | 340        | MT1838.1 | hypothetical protein MT1838.1 | NP_336295.1      | 2.847058824               |

| Clone | Well Position | ORF Length | Locus ID | Description (Gene name)  | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|----------|--|------------------|---------------------------|
| 12209 | A07           | 343        | MT3318   | hypothetical protein MT3318  | NP_337846.1      | -                         |
| 12258 | A08           | 343        | MT1196   | pterin-4-alpha-carbinolamine dehydratase                                 | NP_335639.1      | 1.994169096               |
| 12276 | A09           | 346        | MT1071   | hypothetical protein MT1071  | NP_335509.1      | 2.817919075               |
| 12306 | A10           | 355        | MT3024   | hypothetical protein MT3024  | NP_337536.1      | 2.971830986               |
| 12248 | A11           | 358        | MT1118.2 | hypothetical protein MT1118.2  | NP_335561.1      | 3.379888268               |
| 12376 | A12           | 364        | MT2367.1 | hypothetical protein MT2367.1  | NP_336843.1      | 2.725274725               |
| 12310 | B01           | 370        | MT1713   | hypothetical protein MT1713  | NP_336167.1      | 3.594594595               |
| 12336 | B02           | 370        | MT3222   | hypothetical protein MT3222  | NP_337748.1      | 2.713513514               |
| 12299 | B03           | 370        | MT1181   | hypothetical protein MT1181  | NP_335625.1      | 2                         |
| 12340 | B04           | 370        | MT2367   | hypothetical protein MT2367  | NP_336842.1      | 3.208108108               |
| 12223 | B05           | 373        | MT2601.1 | hypothetical protein MT2601.1  | NP_337096.1      | -                         |
| 12290 | B06           | 373        | MT2045.1 | hypothetical protein MT2045.1  | NP_336508.1      | 2.970509383               |
| 12206 | B07           | 376        | MT1083.2 | hypothetical protein MT1083.2  | NP_335523.1      | 2.811170213               |
| 12375 | B08           | 382        | MT3413   | hypothetical protein MT3413  | NP_337942.1      | -                         |
| 12202 | B09           | 391        | MT1814.2 | hypothetical protein MT1814.2  |                  | 4.010230179               |
| 12237 | B10           | 394        | MT3767.1 | hypothetical protein MT3767.1  | NP_338318.1      | -                         |
| 12384 | B11           | 406        | MT2423.1 | PPE family protein   | NP_336902.1      | 4.007389163               |
| 12288 | B12           | 409        | MT0099.1 | hypothetical protein MT0099  | NP_334507.1      | 3.256723716               |
| 12302 | C01           | 412        | MT2625   | hypothetical protein MT2625  | NP_337122.1      | 3.985436893               |
| 12268 | C02           | 427        | MT3808.1 | hypothetical protein MT3808.1  | NP_338362.1      | 3.421545667               |
| 12252 | C03           | 427        | MT3117   | hypothetical protein MT3117  | NP_337633.1      | 4.206088993               |
| 12338 | C04           | 433        | MT0915.1 | hypothetical protein MT0915.1  | NP_335347.1      | 3.974595843               |
| 12317 | C05           | 439        | MT2586.1 | hypothetical protein MT2586.1  | NP_337077.1      | -                         |
| 12348 | C06           | 439        | MT2365.1 | hypothetical protein MT2365.1  | NP_336839.1      | 3.564920273               |
| 12200 | C07           | 445        | MT0937   | hypothetical protein MT0937  | NP_335370.1      | 4.483146067               |
| 12210 | C08           | 451        | MT3106.1 | PE family protein  | NP_337622.1      | 3.966740577               |
| 12347 | C09           | 457        | MT1560.1 | hypothetical protein MT1560.1  | NP_336013.1      | 2                         |
| 12431 | C10           | 469        | MT1945   | hypothetical protein MT1945  | NP_336402.1      | 2                         |
| 12410 | C11           | 490        | MT2015.1 | hypothetical protein MT2015.1  | NP_336474.1      | 3.93877551                |
| 12400 | C12           | 496        | MT1364   | 4-hydroxyphenylpyruvate dioxygenase C terminal domain-containing protein | NP_335813.1      | 4.304435484               |
| 12429 | D01           | 505        | MT1812   | hypothetical protein MT1812  | NP_336269.1      | 2                         |
| 12395 | D02           | 508        | MT0472.1 | hypothetical protein MT0472.1  | NP_334882.1      | 1.986220472               |
| 12422 | D03           | 517        | MT3437.1 | hypothetical protein MT3437.1  | NP_337967.1      | 3.442940039               |
| 12390 | D04           | 529        | MT3454   | hypothetical protein MT3454  | NP_337981.1      | 4.255198488               |
| 12436 | D05           | 532        | MT2277   | hypothetical protein MT2277  | NP_336748.1      | 3.851503759               |
| 12392 | D06           | 556        | MT3429   | hypothetical protein MT3429  | NP_337958.1      | 4.787769784               |
| 12407 | D07           | 568        | MT2924   | hypothetical protein MT2924  | NP_337435.1      | 2                         |
| 12418 | D08           | 589        | MT0856.1 | hypothetical protein MT0856.1  | NP_335285.1      | 4.750424448               |
| 12420 | D09           | 616        | MT0032   | hypothetical protein MT0032  | NP_334441.1      | 5.133116883               |
| 12434 | D10           | 626        | MT1483   | transcription regulator  |                  | 4.747603834               |
| 12412 | D11           | 631        | MT0085   | hypothetical protein MT0085  | NP_334495.1      | 5.141045959               |
| 12388 | D12           | 646        | MT1815   | IS3 family transposase   |                  | 5.020123839               |
| 12414 | E01           | 697        | MT2619   | putative lipoprotein   | NP_337116.1      | 4.994261119               |
| 12398 | E02           | 715        | MT2080   | hypothetical protein MT2080  | NP_336544.1      | 5.065734266               |
| 11880 | E03           | 982        | MT0573   | naphthoate synthase  | NP_334981.1      | 5.248472505               |
| 12074 | E04           | 982        | MT0573   | naphthoate synthase  | NP_334981.1      | 5.680244399               |
| 12212 | E05           | 982        | MT0573   | naphthoate synthase  | NP_334981.1      | 6.009164969               |
| 12396 | E06           | 982        | MT0573   | naphthoate synthase  | NP_334981.1      | 6.304480652               |
| 12404 | E07           | 1183       | MT1800   | glycosyl transferase   | NP_336259.1      | 6.723584108               |
| 12416 | E08           | 1183       | MT3428   | AfsR/DnrI/RedD family transcriptional regulator                          | NP_337957.1      | 6.844463229               |