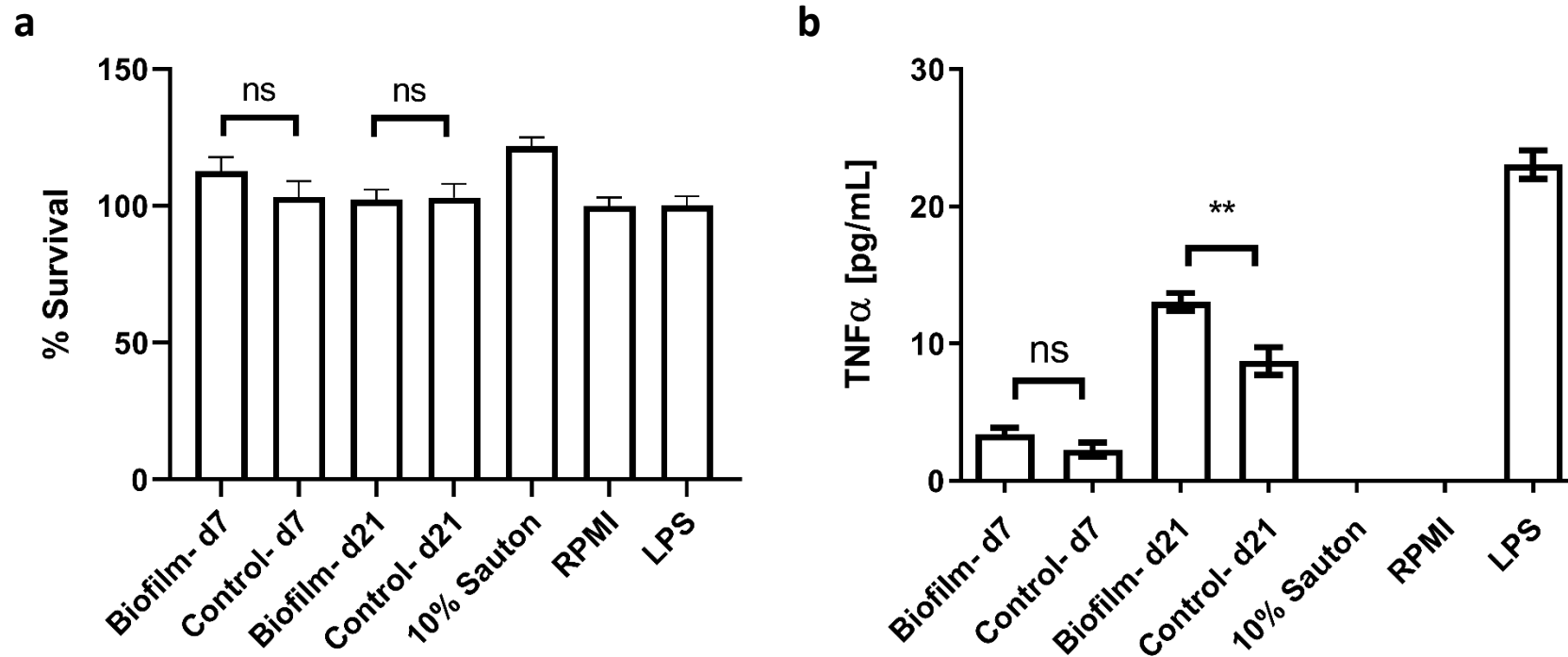


**Supplementary Figure 1: Preparation of the *M. bovis* BCG RCCS-biofilm.**

A glycerol stock (**A**) of *M. bovis* BCG was passaged in Middlebrook 7H9 ADC with 0.05% Tween 80 (**B**) for seven days. This was then passaged in Sauton media with 0.05% Tween 80 (**C**) for seven days, before diluting to  $\sim 1 \times 10^6$  CFU/mL (**D**) in Sauton media (no Tween 80), which was used to inoculate the RCCS vessels (**E**). The top two vessels were rotated to facilitate biofilm formation, while the lower two vessels remained static as non-rotating paired controls. Created with BioRender.



**Supplementary Figure 2: Biofilm supernatants are not cytotoxic and induce pro-inflammatory TNF $\alpha$  secretion.**

THP-1 macrophage-like cells were exposed to RCCS-biofilm and non-rotating control supernatants harvested at days 7 and 21. **(a)** Biofilm or control supernatants were not toxic to macrophages. **(b)** Day 21 biofilm supernatant significantly induced TNF $\alpha$  secretion compared to controls. Percentage survival calculated relative to untreated bacilli. Data points are from three biological replicates and statistical significance determined by t-test \*\* = p value  $\leq 0.01$ . Error bars are  $\pm$  standard error of the mean.

**Supplementary Table 1: Transcriptional response to *M. bovis* BCG corded biofilm growth.**

Differentially expressed genes were identified using a modified t-test with Benjamini-Hochberg multiple testing correction (adjusted p value <0.05) with fold change >2 comparing RCCS-biofilm to stationary phase bacilli. Table ordered by BCG identifier with updated *M. tb* H37Rv annotation from Mycobrowser.

| BCG ID    | BCG Name  | H37Rv ID | Rv Name (MB) | Regulation | FC (abs)  | p (Corr)    | Function (MB)   | Product (MB)  | Functional Category (MB)                | Target_ID |
|-----------|-----------|----------|--------------|------------|-----------|-------------|---|---|---|-----------|
| BCG_0133  | BCG_0133  | Rv0100   | Rv0100       | up         | 2.4253385 | 0.028632747 | Function unknown  | Conserved hypothetical protein  | conserved hypotheticals                 | Rv0100-R  |
| BCG_0507  | icl       | Rv0467   | icl1         | up         | 2.0022416 | 0.006544662 | Involved in glyoxylate bypass (at the first step), an alternative to the tricarboxylic acid cycle (in bacteria, plants, and fungi) [catalytic activity: isocitrate = succinate + glyoxylate]. Involved in the persistence in the host.  | Isocitrate lyase Icl (isocitrase) (isocitratase)                                | intermediary metabolism and respiration | Rv0467-R  |
| BCG_0559c | BCG_0559c | Rv0516c  | Rv0516c      | up         | 2.3294568 | 0.006817216 | May be involved in regulating sigma factor  | Possible anti-anti-sigma factor   | information pathways                    | Rv0516c-F |
| BCG_0731  | rpsL      | Rv0682   | rpsL         | up         | 2.1772966 | 0.002507199 | Protein S12 is involved in the translation initiation step.   | 30S ribosomal protein S12 RpsL  | information pathways                    | Rv0682-R  |
| BCG_1096c | esxJ      | Rv1038c  | esxJ         | up         | 2.6531754 | 0.04425926  | Function unknown  | ESAT-6 like protein EsxJ (ESAT-6 like protein 2)                                | cell wall and cell processes            | Rv1038c-F |
| BCG_1138c | greA      | Rv1080c  | greA         | up         | 3.11554   | 0.003307621 | Necessary for efficient RNA polymerase transcription elongation past template-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as GREA or GREB allows the resumption of elongation from the new 3'terminus. GREA releases sequences of 2 to 3 nucleotides | Probable transcription elongation factor GreA (transcript cleavage factor GreA) | information pathways                    | Rv1080c-F |
| BCG_1281  | sigE      | Rv1221   | sigE         | up         | 2.252617  | 0.044271644 | The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. Seems to be regulated by sigh (Rv3223c product). Seems to regulate the heat-shock response.  | Alternative RNA polymerase sigma factor SigE                                    | information pathways                    | Rv1221-R  |

|               |                 |                 |                     |                   |                 |                 |  |   |   |                  |
|---------------|-----------------|-----------------|---------------------|-------------------|-----------------|-----------------|--|---|---|------------------|
| BCG_1823      | PE19            | Rv1791          | PE19                | up                | 2.416305        | 0.013229125     | Function unknown   | PE family protein PE19  | PE/PPE                                  | Rv1791-R         |
| BCG_1824      | esxM            | Rv1792          | esxM                | up                | 2.7327416       | 0.034722216     | Function unknown   | ESAT-6 like protein EsxM  | cell wall and cell processes            | Rv1792-R         |
| BCG_2139c     | hisE            | Rv2122c         | hisE                | up                | 2.149715        | 0.005825038     | Involved in histidine biosynthesis.  | Phosphoribosyl-AMP pyrophosphatase HisE   | intermediary metabolism and respiration | Rv2122c-F        |
| BCG_2428      | rpsT            | Rv2412          | rpsT                | up                | 2.1110535       | 0.006734069     | Involved in translation mechanisms. Binds directly to 16S ribosomal RNA.   | 30S ribosomal protein S20 RpsT  | information pathways                    | Rv2412-R         |
| BCG_2471      | BCG_2471        | Rv2451          | Rv2451              | up                | 2.0198357       | 0.008232632     | Unknown  | Hypothetical proline and serine rich protein  | conserved hypotheticals                 | Rv2451-R         |
| BCG_2723      | sigB            | Rv2710          | sigB                | up                | 2.3562243       | 0.014988984     | The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. May control the regulons of stationary phase and general stress resistance. Seems to be regulated by sigh (Rv3223c product) and SIGE (Rv1221 product). Seems to regulate KATG Rv1908c and the heat-shock response.                    | RNA polymerase sigma factor SigB  | information pathways                    | Rv2710-R         |
| BCG_3527c     | infA            | Rv3462c         | infA                | up                | 2.2389758       | 0.00287755      | No specific function has so far been attributed to this initiation factor; however, it seems to stimulate more or less all the activities of the other two initiation factors, if-2 and if-3.  | Probable translation initiation factor if-1 InfA  | information pathways                    | Rv3462c-F        |
|               |                 |                 |                     |                   |                 |                 |  |   |   |                  |
| <b>BCG ID</b> | <b>BCG Name</b> | <b>H37Rv ID</b> | <b>Rv Name (MB)</b> | <b>Regulation</b> | <b>FC (abs)</b> | <b>p (Corr)</b> | <b>Function (MB)</b>   | <b>Product (MB)</b>   | <b>Functional Category (MB)</b>         | <b>Target_ID</b> |
| BCG_0061      | BCG_0061        | Rv0030          | Rv0030              | down              | 2.0172732       | 0.00339416      | Unknown  | Conserved hypothetical protein  | conserved hypotheticals                 | Rv0030-R         |
| BCG_0147      | BCG_0147        | Rv0114          | gmhB                | down              | 2.525326        | 0.002507199     | Involved in biosynthesis of nucleotide-activated glycerol-manno-heptose. Involved in two pathways, D-alpha-D pathway [catalytic activity: D-glycero-alpha-D-manno-heptose 1,7-biphosphate = D-glycero-alpha-D-manno-heptose 1-phosphate] and L-beta-D pathway [catalytic activity: D-glycero-beta-D-manno-heptose 1,7-biphosphate = D-glycero-beta-D-manno-heptose 1-phosphate]. | Possible D-alpha,beta-D-heptose-1,7-biphosphate phosphatase GmhB (D-glycero-D-manno-heptose 7-phosphate kinase) | cell wall and cell processes            | Rv0114-R         |

|           |           |         |         |      |           |             |  |   |   |           |
|-----------|-----------|---------|---------|------|-----------|-------------|--|---|---|-----------|
| BCG_0207  | mce1B     | Rv0170  | mce1B   | down | 2.4252424 | 0.00287755  | Unknown, but thought to be involved in host cell invasion.   | Mce-family protein Mce1B  | virulence, detoxification, adaptation   | Rv0170-R  |
| BCG_0233  | BCG_0233  | Rv0196  | Rv0196  | down | 2.5691757 | 0.002507199 | Possibly involved in transcriptional mechanism.  | Possible transcriptional regulatory protein   | regulatory proteins                     | Rv0196-R  |
| BCG_0267c | php       | Rv0230c | php     | down | 2.1670148 | 0.00287755  | Enzymatic activity unknown [catalytic activity: aryl dialkyl phosphate + H <sub>2</sub> O = dialkyl phosphate + an aryl alcohol].  | Probable phosphotriesterase Php (parathion hydrolase) (PTE) (aryldialkylphosphatase) (paraoxonase) (a-esterase) (aryltriphosphatase) (paraoxon hydrolase) | lipid metabolism                        | Rv0230c-F |
| BCG_0269  | BCG_0269  | Rv0232  | Rv0232  | down | 3.1657658 | 0.012182727 | Involved in transcriptional mechanism.   | Probable transcriptional regulatory protein (probably TetR/AcrR-family)   | regulatory proteins                     | Rv0232-R  |
| BCG_0270  | nrdB      | Rv0233  | nrdB    | down | 2.019661  | 0.003652177 | Involved in the DNA replication pathway (first reaction). Provides the precursors necessary for DNA synthesis [catalytic activity: 2'-deoxyribonucleoside diphosphate + oxidized thioredoxin + H <sub>2</sub> O = ribonucleoside diphosphate + reduced thioredoxin]. | Ribonucleoside-diphosphate reductase (beta chain) NrdB (ribonucleotide reductase small chain)   | information pathways                    | Rv0233-R  |
| BCG_0341  | BCG_0341  | Rv0301  | vapC2   | down | 2.2188537 | 0.00287755  | Unknown  | Possible toxin VapC2  | virulence, detoxification, adaptation   | Rv0301-R  |
| BCG_0342  | BCG_0342  | Rv0302  | Rv0302  | down | 2.3587484 | 0.006118542 | Involved in transcriptional mechanism.   | Probable transcriptional regulatory protein (probably TetR/AcrR-family)   | regulatory proteins                     | Rv0302-R  |
| BCG_0548c | serB1     | Rv0505c | serB1   | down | 2.2508147 | 0.00287755  | Removes a phosphate from phosphoserine [catalytic activity: phosphoserine + H <sub>2</sub> O = serine + phosphate].  | Possible phosphoserine phosphatase SerB1 (PSP) (O-phosphoserine phosphohydrolase) (pspase)  | intermediary metabolism and respiration | Rv0505c-F |
| BCG_0699  | BCG_0699  | Rv0650  | Rv0650  | down | 2.3578136 | 0.00287755  | Function unknown; probably involved in specific sugar metabolism or regulation.  | Possible sugar kinase   | intermediary metabolism and respiration | Rv0650-R  |
| BCG_0811c | BCG_0811c | Rv0759c | Rv0759c | down | 2.174622  | 0.005583438 | Function unknown   | Conserved hypothetical protein  | conserved hypotheticals                 | Rv0759c-F |
| BCG_0899  | lpqS      | Rv0847  | lpqS    | down | 2.625553  | 0.002507199 | Unknown  | Probable lipoprotein LpqS   | cell wall and cell processes            | Rv0847-R  |

|           |           |         |         |      |           |             |  |   |   |           |
|-----------|-----------|---------|---------|------|-----------|-------------|--|---|---|-----------|
| BCG_1040c | mScL      | Rv0985c | mScL    | down | 4.0564795 | 0.002507199 | Ion channel that opens in response to stretch forces in the membrane lipid bilayer. May participate in the regulation of osmotic pressure changes within the cell.   | Possible large-conductance ion mechanosensitive channel MscL  | cell wall and cell processes            | Rv0985c-F |
| BCG_1053  | BCG_1053  | Rv1190  | Rv1190  | down | 2.3303113 | 0.004252977 | Function unknown   | Conserved hypothetical protein  | conserved hypotheticals                 | Rv1190-R  |
| BCG_1068  | ispE      | Rv1011  | ispE    | down | 2.328591  | 0.002507199 | Thought to be involved in deoxyxylulose-5-phosphate pathway (DXP) of isoprenoid biosynthesis (at the fourth step). Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol [catalytic activity: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol]. | Probable 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase IspE (CMK) (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase)  | intermediary metabolism and respiration | Rv1011-R  |
| BCG_1103  | BCG_1103  | Rv1045  | Rv1045  | down | 2.0090392 | 0.004294436 | Unknown  | Hypothetical protein  | conserved hypotheticals                 | Rv1045-R  |
| BCG_1294  | BCG_1294  | Rv1234  | Rv1234  | down | 2.7355843 | 0.002507199 | Unknown  | Probable transmembrane protein  | cell wall and cell processes            | Rv1234-R  |
| BCG_1378c | alkA      | Rv1317c | alkA    | down | 2.5348155 | 0.002990481 | Involved in the adaptive response to alkylation damage in DNA caused by alkylating agents. Repairs the SP diastereomer of DNA methylphosphotriester lesions by a direct and irreversible transfer of the methyl group to one of its own cysteine residues. The methylated ALKA protein acts as a positive regulator of its own synthesis, as well as that of other proteins.     | Probable bifunctional regulatory protein and DNA repair enzyme AlkA (regulatory protein of adaptative response) (methylphosphotriester-DNA--protein-cysteine S-methyltransferase) | information pathways                    | Rv1317c-F |
| BCG_1428  | BCG_1428  | Rv1366  | Rv1366  | down | 2.8617003 | 0.002507199 | Unknown  | Hypothetical protein  | conserved hypotheticals                 | Rv1366-R  |
| BCG_1620c | BCG_1620c | Rv1567c | Rv1567c | down | 2.2951014 | 0.007566907 | Unknown  | Probable hypothetical membrane protein  | cell wall and cell processes            | Rv1567c-F |
| BCG_1780  | BCG_1780  | Rv1741  | vapC34  | down | 2.4141047 | 0.002507199 | Unknown  | Possible toxin VapC34. Contains PIN domain.   | virulence, detoxification, adaptation   | Rv1741-R  |
| BCG_1809c | BCG_1809c | Rv1776c | Rv1776c | down | 2.5397468 | 0.003397662 | Involved in transcriptional mechanism.   | Possible transcriptional regulatory protein   | regulatory proteins                     | Rv1776c-F |
| BCG_1847c | BCG_1847c | Rv1813c | Rv1813c | down | 5.443304  | 0.002507199 | Function unknown   | Conserved hypothetical protein  | conserved hypotheticals                 | Rv1813c-F |
| BCG_1849  | BCG_1849  | Rv1815  | Rv1815  | down | 2.1226277 | 0.00287755  | Function unknown   | Conserved protein   | conserved hypotheticals                 | Rv1815-R  |
| BCG_1897  | BCG_1897  | Rv1861  | Rv1861  | down | 2.5616987 | 0.003157753 | Function unknown   | Probable conserved transmembrane protein  | cell wall and cell processes            | Rv1861-R  |

|           |           |         |         |      |           |             |   |  |   |           |
|-----------|-----------|---------|---------|------|-----------|-------------|---|--|---|-----------|
| BCG_1937  | BCG_1937  | Rv1898  | Rv1898  | down | 2.4602568 | 0.005705643 | Function unknown  | Conserved hypothetical protein   | conserved hypotheticals                 | Rv1898-R  |
| BCG_1942  | BCG_1942  | Rv1903  | Rv1903  | down | 2.395231  | 0.00287755  | Unknown   | Probable conserved membrane protein  | cell wall and cell processes            | Rv1903-R  |
| BCG_1993c | BCG_1993c | Rv1954c | Rv1954c | down | 2.147341  | 0.00287755  | Unknown   | Hypothetical protein   | conserved hypotheticals                 | Rv1954c-F |
| BCG_2004  | BCG_2004  | Rv1988  | erm(37) | down | 2.1141493 | 0.00287755  | Thought to cause methylation of 23S rRNA  | Probable 23S rRNA methyltransferase Erm(37)  | intermediary metabolism and respiration | Rv1988-R  |
| BCG_2059c | BCG_2059c | Rv2040c | Rv2040c | down | 2.2476702 | 0.002507199 | Thought to be involved in active transport of sugar across the membrane (import). Responsible for the translocation of the substrate across the membrane.   | Probable sugar-transport integral membrane protein ABC transporter                               | cell wall and cell processes            | Rv2040c-F |
| BCG_2082  | BCG_2082  | Rv2063  | mazE7   | down | 2.1997433 | 0.004160331 | Function unknown  | Antitoxin MazE7  | virulence, detoxification, adaptation   | Rv2063-R  |
| BCG_2102  | BCG_2102  | Rv2083  | Rv2083  | down | 2.1493015 | 0.003274883 | Unknown   | Conserved hypothetical protein   | conserved hypotheticals                 | Rv2083-R  |
| BCG_2174c | murF      | Rv2157c | murF    | down | 2.0973208 | 0.00287755  | Involved in cell wall formation; peptidoglycan biosynthesis.  | Probable UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase MurF | cell wall and cell processes            | Rv2157c-F |
| BCG_2457c | nadE      | Rv2438c | nadE    | down | 2.0734065 | 0.003140178 | Involved in biosynthesis of NAD. Can use both glutamine or ammonia as a nitrogen source [catalytic activity: ATP + deamido-NAD(+) + L-glutamine + H(2)O = AMP + diphosphate + NAD(+) + L-glutamate].  | Glutamine-dependent NAD(+) synthetase NadE (NAD(+) synthase [glutamine-hydrolysing])             | intermediary metabolism and respiration | Rv2438c-F |
| BCG_2574c | BCG_2574c | Rv2551c | Rv2551c | down | 2.448835  | 0.002507199 | Function unknown  | Conserved hypothetical protein   | conserved hypotheticals                 | Rv2551c-F |
| BCG_2615c | ruvB      | Rv2592c | ruvB    | down | 2.141356  | 0.003397662 | forms a complex with RUVA. RUVB could possess weak ATPase activity, which will be stimulated by the RUVA protein in the presence of DNA. The RUVA-RUVB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. RUVAB is an helicase that mediates the holliday junction migration by localized denaturation and reannealing. | Probable holliday junction DNA helicase RuvB   | information pathways                    | Rv2592c-F |

|           |           |         |         |      |           |             |   |   |   |           |
|-----------|-----------|---------|---------|------|-----------|-------------|---|---|---|-----------|
| BCG_2666c | BCG_2666c | Rv2639c | Rv2639c | down | 2.1540549 | 0.003274883 | Unknown   | Probable conserved integral membrane protein  | cell wall and cell processes            | Rv2639c-F |
| BCG_2778c | BCG_2778c | Rv2762c | Rv2762c | down | 2.7919426 | 0.003397662 | Function unknown  | Conserved hypothetical protein  | conserved hypotheticals                 | Rv2762c-F |
| BCG_2780c | dfrA      | Rv2763c | dfrA    | down | 2.3156297 | 0.003307621 | Essential step for de novo glycine and purine synthesis, DNA precursor synthesis, and for the conversion of dUMP to dTMP [catalytic activity: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-dihydrofolate + NADPH].  | Dihydrofolate reductase DfrA (DHFR) (tetrahydrofolate dehydrogenase)  | intermediary metabolism and respiration | Rv2763c-F |
| BCG_2804c | ribF      | Rv2786c | ribF    | down | 2.0204735 | 0.00287755  | Involved in FAD biosynthesis [catalytic activity 1: ATP + riboflavin = ADP + FMN] [catalytic activity 2: ATP + FMN = diphosphate + FAD].  | Probable bifunctional FAD synthetase/riboflavin biosynthesis protein RibF: riboflavin kinase (flavokinase) + FMN adenyltransferase (FAD pyrophosphorylase) (FAD synthetase)(FAD diphosphorylase) (flavin adenine dinucleotide synthetase) | intermediary metabolism and respiration | Rv2786c-F |
| BCG_2928c | rimM      | Rv2907c | rimM    | down | 2.106887  | 0.00287755  | Essential for efficient processing of 16S rRNA. Probably part of the 30S subunit prior to or during the final step in the processing of 16S free 30S ribosomal subunits. It could be some accessory protein needed for efficient assembly of the 30S subunit. RIMM is needed in a step prior to RBFA during the maturation of 16S rRNA. Has affinity for free ribosomal 30S subunits but not for 70S ribosomes. | Probable 16S rRNA processing protein RimM   | information pathways                    | Rv2907c-F |
| BCG_2945c | BCG_2945c | Rv2923c | Rv2923c | down | 2.2120833 | 0.002507199 | Function unknown  | Conserved protein   | conserved hypotheticals                 | Rv2923c-F |
| BCG_3013c | gltS      | Rv2992c | gltS    | down | 2.1587343 | 0.002507199 | Involved in translation mechanisms [catalytic activity: ATP + L-glutamate + tRNA(GLU) = AMP + diphosphate + L-glutamyl-tRNA(GLU)].  | Glutamyl-tRNA synthetase GltS (glutamate--tRNA ligase) (glutamyl-tRNA synthase) (GLURS)   | information pathways                    | Rv2992c-F |
| BCG_3120  | BCG_3120  | Rv3095  | Rv3095  | down | 2.0427935 | 0.005279541 | Unknown. Could be involved in regulatory mechanism.   | Hypothetical transcriptional regulatory protein   | regulatory proteins                     | Rv3095-R  |



|           |           |         |         |      |           |             |   |  |   |           |
|-----------|-----------|---------|---------|------|-----------|-------------|---|--|---|-----------|
| BCG_3166  | BCG_3166  | Rv3143  | Rv3143  | down | 2.5728054 | 0.004182312 | Unknown, but could be involved in regulatory mechanism  | Probable response regulator  | regulatory proteins                     | Rv3143-R  |
| BCG_3189c | BCG_3189c | Rv3165c | Rv3165c | down | 2.0405302 | 0.02486292  | Unknown   | Unknown protein  | conserved hypotheticals                 | Rv3165c-F |
| BCG_3327c | lpqC_1    | Rv3298c | lpqC    | down | 2.152159  | 0.00287755  | Function unknown; lipolytic enzyme involved in cellular metabolism.   | Possible esterase lipoprotein LpqC   | cell wall and cell processes            | Rv3298c-F |
| BCG_3494c | BCG_3494c | Rv3424c | Rv3424c | down | 2.2704797 | 0.011512701 | Unknown   | Hypothetical protein   | conserved hypotheticals                 | Rv3424c-F |
| BCG_3567c | fdxD      | Rv3503c | fdxD    | down | 3.0570652 | 0.00287755  | Ferredoxins are iron-sulfur proteins that transfer electrons in a wide variety of metabolic reactions.                            | Probable ferredoxin FdxD   | intermediary metabolism and respiration | Rv3503c-F |
| BCG_3586  | BCG_3586  | Rv3522  | ltp4    | down | 2.2292593 | 0.00287755  | Function unknown; probably involved in lipid metabolism.  | Possible lipid transfer protein or keto acyl-CoA thiolase Ltp4   | lipid metabolism                        | Rv3522-R  |
| BCG_3611  | BCG_3611  | Rv3547  | ddn     | down | 2.1071537 | 0.00287755  | Function unknown. Converts bicyclic nitroimidazole drug candidate pa-824 to three metabolites, generating NO.                     | Deazaflavin-dependent nitroreductase Ddn   | intermediary metabolism and respiration | Rv3547-R  |
| BCG_3629  | aspB      | Rv3565  | aspB    | down | 2.0213947 | 0.004160331 | Thought to be involved in glutamate biosynthesis [catalytic activity: L-aspartate + 2-oxoglutarate = oxaloacetate + L-glutamate]. | Possible aspartate aminotransferase AspB (transaminase A) (ASPAT) (glutamic--oxaloacetic transaminase) (glutamic--aspartic transaminase) | intermediary metabolism and respiration | Rv3565-R  |
| BCG_3642  | BCG_3642  | Rv3577  | Rv3577  | down | 2.2855098 | 0.00401994  | Function unknown  | Conserved hypothetical protein   | conserved hypotheticals                 | Rv3577-R  |
| BCG_3698c | BCG_3698c | Rv3640c | Rv3640c | down | 2.20298   | 0.00339416  | Required for the transposition of an insertion sequence.  | Probable transposase   | insertion seqs and phages               | Rv3640c-F |
| BCG_3898  | BCG_3898  | Rv3835  | Rv3835  | down | 2.2190228 | 0.003378763 | Unknown   | Conserved membrane protein   | cell wall and cell processes            | Rv3835-R  |
| BCG_3903  | BCG_3903  | Rv3840  | Rv3840  | down | 2.985628  | 0.002507199 | Supposedly involved in transcriptional mechanism.   | Possible transcriptional regulatory protein  | regulatory proteins                     | Rv3840-R  |
| BCG_3961c | esxE      | Rv3904c | esxE    | down | 2.4624584 | 0.002507199 | Unknown   | Putative ESAT-6 like protein EsxE (hypothetical alanine rich protein) (ESAT-6 like protein 12)   | cell wall and cell processes            | Rv3904c-F |