

Supplementary Table S1. Microarray analysis of *M.tb. ΔsigI* mutant with wild-type (*ΔsigI/WT*).

For each gene listed, the average signal (normalized by total signal intensity) from the *M.tb. ΔsigI* mutant transcripts was divided by the average signal from the wild-type transcripts, and this was determined at OD₆₀₀ of 1 (OD1) and OD₆₀₀ of 2 (OD2). A symbol in the “Q PCR” column indicates that transcription levels were validated by qRT-PCR. Q value represents the statistical significance of the expression ratio, determined with a false discovery rate of 1%.

| Rv No. | Description | Gene | OD1 | | OD2 | | Q PCR | (FDR 1%) Q value |
|---------|---|------------------|-----|-----|-----|-----|-------|---------------------|
| | | | Ave | SD | Ave | SD | | |
| Rv3121 | Probable cytochrome P450 141 CYP141 | <i>cyp141</i> | 0.0 | 0.6 | 0.6 | 0.1 | | 0 |
| Rv2351c | Probable membrane-associated phospholipase C 1 PlcA (MTP40 antigen) | <i>plcA</i> | 0.0 | 0.3 | 0.5 | 0.1 | | 0 |
| Rv1840c | PE-PGRS family protein | <i>PE_PGRS34</i> | 0.1 | 0.3 | 0.6 | 0.1 | | 0 |
| Rv1009 | Probable resuscitation-promoting factor RpfB | <i>rpfB</i> | 0.2 | 1.2 | 0.5 | 0.1 | | 0 |
| Rv0440 | Chaperonin GroEL | <i>groEL</i> | 0.2 | 0.0 | 0.2 | 0.0 | | 0 |
| Rv0350 | Molecular chaperone DnaK | <i>dnaK</i> | 0.2 | 0.0 | 0.3 | 0.0 | | 0 |
| Rv3417c | Chaperonin GroEL | <i>groEL</i> | 0.3 | 0.1 | 0.5 | 0.1 | | 0 |
| Rv2276 | Cytochrome P450 121 CYP121 | <i>cyp121</i> | 0.3 | 0.2 | 0.6 | 0.1 | | 0 |
| Rv2800 | Possible hydrolase | | 0.3 | 0.2 | 0.6 | 0.1 | | 0 |
| Rv1304 | ATP synthase subunit A | <i>atpB</i> | 0.3 | 0.0 | 0.6 | 0.0 | | 0 |
| Rv3074 | Hypothetical protein | | 0.3 | 0.1 | 0.5 | 0.1 | | 0 |
| Rv1307 | Probable ATP synthase delta chain AtpH | <i>atpH</i> | 0.3 | 0.0 | 0.5 | 0.0 | | 0 |
| Rv2193 | Probable cytochrome C oxidase (subunit III) CtaE | <i>ctaE</i> | 0.3 | 0.0 | 0.4 | 0.0 | X | 0 |
| Rv1310 | ATP synthase subunit B | <i>atpD</i> | 0.3 | 0.0 | 0.5 | 0.0 | | 0 |
| Rv3841 | Possible bacterioferritin BfrB | <i>bfrB</i> | 0.3 | 0.0 | 0.6 | 0.1 | | 0 |
| Rv1308 | ATP synthase subunit A | <i>atpA</i> | 0.3 | 0.0 | 0.4 | 0.0 | | 0 |
| Rv1309 | ATP synthase subunit C | <i>atpG</i> | 0.3 | 0.0 | 0.5 | 0.0 | | 0 |
| Rv1658 | Argininosuccinate synthase | <i>argG</i> | 0.3 | 0.1 | 0.5 | 0.1 | | 0 |
| Rv3418c | Co-chaperonin GroES | <i>groES</i> | 0.3 | 0.0 | 0.2 | 0.0 | | 0 |
| Rv0528 | Probable conserved transmembrane protein | | 0.3 | 0.1 | 0.6 | 0.0 | | 0 |
| Rv2845c | Prolyl-tRNA synthetase | <i>proS</i> | 0.4 | 0.1 | 0.5 | 0.1 | | 0 |
| Rv1253 | Probable cold-shock DeaD-box protein A homolog DeaD | <i>deaD</i> | 0.4 | 0.3 | 0.6 | 0.1 | X | 0 |
| Rv2463 | Probable esterase/lipase LipP | <i>lipP</i> | 0.4 | 0.2 | 0.6 | 0.0 | | 0 |
| Rv2992c | Glutamyl-tRNA synthetase | <i>gltX</i> | 0.4 | 0.1 | 0.6 | 0.0 | | 0 |
| Rv1305 | ATP synthase subunit C | <i>atpE</i> | 0.4 | 0.0 | 0.5 | 0.0 | | 0 |
| Rv1908c | Catalase-peroxidase-peroxynitritase T KatG | <i>katG</i> | 0.4 | 0.0 | 0.4 | 0.0 | X | 0 |
| Rv3446c | Hypothetical alanine and valine rich protein | | 0.4 | 0.7 | 0.6 | 0.1 | | 0 |
| Rv1765c | Hypothetical protein | | 0.4 | 0.4 | 0.1 | 1.9 | | 0 |
| Rv2184c | Hypothetical protein | | 0.4 | 0.3 | 0.6 | 0.1 | | 0 |
| Rv2357c | Glycyl-tRNA synthetase | <i>glyS</i> | 0.4 | 0.1 | 0.5 | 0.4 | | 0 |
| Rv0826 | Hypothetical protein | | 0.4 | 0.0 | 0.5 | 0.0 | X | 0 |
| Rv0352 | Probable chaperone protein DnaJ1 | <i>dnaJ1</i> | 0.4 | 0.1 | 0.5 | 0.2 | | 0 |

| Rv No. | Description | Gene | OD1 | | OD2 | | Q PCR | (FDR 1%) Q value |
|---------|---|---------------|-----|-----|-----|-----|----------|---------------------|
| | | | Ave | SD | Ave | SD | | |
| Rv3140 | Probable acyl-CoA dehydrogenase FadE23 | <i>fadE23</i> | 0.4 | 0.1 | 0.6 | 0.0 | | 0 |
| Rv1631 | Dephospho-CoA kinase/unknown domain fusion protein | <i>coaE</i> | 0.4 | 0.9 | 0.5 | 0.1 | | 0 |
| Rv0524 | Glutamate-1-semialdehyde aminotransferase | <i>hemL</i> | 0.4 | 0.1 | 0.5 | 0.1 | X | 0 |
| Rv0351 | Probable GrpE protein (Hsp70 co-factor) | <i>grpE</i> | 0.4 | 0.1 | 0.3 | 0.0 | | 0 |
| Rv2194 | Probable ubiquinol-cytochrome C reductase QcrC (cytochrome C subunit) | <i>qcrC</i> | 0.4 | 0.1 | 0.5 | 0.0 | | 0 |
| Rv1850 | Urease alpha subunit UreC (Urea amidohydrolase) | <i>ureC</i> | 0.4 | 0.0 | 0.6 | 0.1 | | 0 |
| Rv1303 | Hypothetical protein | | 0.4 | 0.0 | 0.6 | 0.0 | X | 0 |
| Rv1537 | DNA polymerase IV | <i>dinX</i> | 0.4 | 0.1 | 0.6 | 0.1 | | 0 |
| Rv2195 | Probable Rieske iron-sulfur protein QcrA | <i>qcrA</i> | 0.4 | 0.1 | 0.4 | 0.1 | | 0 |
| Rv1770 | Hypothetical protein | | 0.4 | 0.0 | 0.6 | 0.0 | | 0 |
| Rv1133c | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase | <i>metE</i> | 0.5 | 0.0 | 0.3 | 0.0 | | 0 |
| Rv0982 | Probable two component sensor kinase MprB | <i>mprB</i> | 0.5 | 0.1 | 0.6 | 0.1 | | 0 |
| Rv0368c | Hypothetical protein | | 0.5 | 0.6 | 0.6 | 0.2 | | 0 |
| Rv0093c | Probable conserved membrane protein | | 0.5 | 0.3 | 0.6 | 0.0 | | 0 |
| Rv3264c | D-alpha-D-mannose-1-phosphate guanylyltransferase | <i>manB</i> | 0.5 | 0.0 | 0.5 | 0.1 | | 0 |
| Rv2200c | Probable transmembrane cytochrome C oxidase (subunit II) CtaC | <i>ctaC</i> | 0.5 | 0.1 | 0.4 | 0.2 | X | 0 |
| Rv1596 | Nicotinate-nucleotide pyrophosphorylase | <i>nadC</i> | 0.5 | 0.0 | 0.3 | 0.0 | | 0 |
| Rv1387 | PPE family protein | <i>PPE20</i> | 0.5 | 0.1 | 0.5 | 0.1 | | 0 |
| Rv0280 | PPE family protein | <i>PPE3</i> | 0.5 | 0.1 | 0.4 | 0.0 | X | 0 |
| Rv1779c | Hypothetical integral membrane protein | | 0.5 | 0.2 | 0.6 | 0.1 | X | 0 |
| Rv3411c | Inositol-5-monophosphate dehydrogenase | <i>guaB2</i> | 0.5 | 0.1 | 0.5 | 0.0 | X | 0 |
| Rv0157 | Probable NAD(P) transhydrogenase (subunit beta) | <i>pntB</i> | 0.5 | 0.1 | 0.5 | 0.0 | | 0 |
| Rv2123 | PPE family protein | <i>PPE37</i> | 0.5 | 0.2 | 0.5 | 0.1 | X | 0 |

Supplementary Table S2. Primer Sequences.

| Primer Name | Primer Sequence (5' to 3') |
|--|--|
| <u>INV RT PCR (<i>katG</i>)</u> | |
| INV katG1 | GCCGACACGGAAACGATTTTC |
| INV katG2 | ACGCCATCCGGATAAACAGC |
| INV RT katG1 | CCCGTCGTGGGTCATATGAAA |
| INV RT katG2 | TCAACGTCGATGGTTCGCGAC |
| <u>Deletion of promoter region</u> | |
| INV katG1 | GCCGACACGGAAACGATTTTC |
| INV katG7 | GGAGTTGGTGTATCGGGCT AGTGTCGGATATCGAACAAAT |
| katG RT | TCAACGTCGATGGTTCGCGAC |
| primer6 | ATTACAGAAACCACCACCGG |
| primer5 | CGGGTTTTGGTGCAGTACCTT |
| <u>INV RT PCR: Rv1186 (Negative control)</u> | |
| Rv1186-1 | ATCCGCATGTTGTCCGATCC |
| Rv1186-2 | ACTTGGATTGGCCGAGCATG |
| Rv1186-3 | CTGCGCACCGAACTGGCCTC |
| Rv1186-4 | GGTGGCGTTGGTCAGGGTGC |
| <u>Run off <i>in vitro</i> transcription - <i>katG</i></u> | |
| INV katG1 F | GCCGACACGGAAACGATTTTC |
| INV KatG3 R | ACGGCCGGGTTTTGGTGCAG |
| <u>Knock out</u> | |
| sigIKO1 | ggcccatatgCATCGTCGAGCGCTCGCCGCTCACC |
| sigIKO2 | ggccactagtGTAGGCCCGATGCGCCCGCCAGGCC |
| sigIKO3 | ggcctaattaaGTGCAGCCTTCAACATTGGACCCGT |
| sigIKO4 | ggccctcagCCAATTTTCGGACGGGCAATAGCGAC |
| <u>Complementing</u> | |
| SigI comp 5 | gggcctctagaTGCTTGACGAAGATCGCCAC |
| sigI comp 6 | gggcctctagaAACACGTCACGCCAGACAAAG |
| pETsigI1 | ggccCATATGATGTCGCAACACGACCCGGT |
| pETsigI2 | ggccAAGCTTACCGCCGCCGAGTTCGGCCC |
| <u>pSCW-sigI (<i>sigI</i> overexpression in <i>M.tb.</i>)</u> | |
| pet1 | CGTAGAGGATCGAGATCTCGATCCCGCGA |
| pet2 | ggcctaattaaTCTCAGTGGTGGTGGTGGTG |
| <u>Southern blotting probe</u> | |
| STN-I-1 | CAAGAGGCATTTTCCCGCTTG |

| Primer Name | Primer Sequence (5' to 3') |
|--|-----------------------------------|
| STN-I-2 | TCGTGGCGATTTGCTGGTAG |
| <u>Real-time RT-PCR (<i>sigI</i> regulon)</u> | |
| Rv1908c-1(katG1) | CTGTTTATCCGGATGGCGTG |
| Rv1908c-2(katG2) | GAAAACAATCAGGTCCGCCC |
| Rv2123-1 | GACCCGACCAAATTGATCCTG |
| Rv2123-2 | GCGAACGGTCCGAAATAGATC |
| Rv3411-1 | CGCAACAAGATCGAGAAGCTG |
| Rv3411-2 | AGCGTCGACCAACATCATGG |
| Rv2280-1 | TTGACAACACTTCGATGGCCG |
| Rv2280-2 | TGAGCATTTCACCCACCGTC |
| Rv1303-1 | TGACGGTCGGGATGTTCTTG |
| rv1303-2 | TGGTGATAATCGCCAGTCGC |
| Rv0524-1 | TGGTTGGTACGGAATCGATCC |
| Rv0524-2 | AACGTGCCGGCCTGATACAC |
| Rv0826-1 | ACCTTCTTTGTCGGCACGTTG |
| Rv0826-2 | TTGTTCTCCAGCACGTTGCG |
| Rv1392-1 | AAGACGCTTGATCCCGACATC |
| Rv1392-2 | TGTCGACGATGATCTTGCGG |
| Rv1737-1 | TGGGGTCATGATCTCGCATC |
| Rv1737-2 | ATGATGCCAAGGACCAAGCC |
| Rv1253-1 | AGATGCTGACCATGGGTTTTCG |
| Rv1253-2 | GCGGTTTTTCGCCTTACAAGTG |
| Rv2193-1 | TGATCACATTCTGATGGGCC |
| Rv2193-2 | AGCAGGAAGATGAAGGCGATG |
| Rv2428-1 | GGCCGAAAGACTTCACGTTCTGTG |
| Rv2428-2 | GCGCGAATTCGCTGTCAATCG |