

TABLE S1. Genes differentially expressed in aerobically grown  $\Delta qcrCAB::hyg$  mutant of *M. smegmatis*

ID <sup>a</sup>	Gene	TIGR annotation <sup>b</sup>	Function <sup>c</sup>	M <sup>d</sup>	P value	Class <sup>e</sup>
<b>Upregulated genes</b>						
ribA	<i>ribA2</i>	MSMEG3082	Probable riboflavin biosynthesis protein	-2.301	0.0020	7
ML2274		MSMEG3498	Probable conserved secreted protein	-1.914	0.0072	3
mihF	<i>mihF</i>	MSMEG3063	Putative integration host factor	-1.764	0.0003	2
glgC	<i>glgC</i>	MSMEG5067	glucose-1-phosphate adenylyl-transferase	-1.753	0.0072	7
ML1835		MSMEG6527	CHP	-1.556	0.0030	10
ML0510		MSMEG3035	CHP	-1.444	0.0004	10
ML0886		MSMEG4257	possible glycosyl transferase	-1.430	0.0024	7
ML1312		MSMEG4598	CHP	-1.229	0.0001	10
argD-g	<i>argD</i>	MSMEG2446	probable acetylornithine aminotransferase	-1.027	0.0033	7
gabD-q	<i>gabD</i>	MSMEG2554	probable aldehyde dehydrogenase (NAD-dependent)	-1.005	0.0052	7
Rv3134c	<i>uspL</i>	MSMEG5230	Universal stress protein	-0.990	0.0098	10
Rv1623c	<i>cydA</i>	MSMEG3243	Cytochrome <i>bd</i> oxidase subunit I	-0.931	0.0069	7
ML1926		MSMEG0828	putative tuberculin-related protein	-0.915	0.0058	3
Rv1592c		MSMEG3205	CHP	-0.878	0.0016	10
ML1783		MSMEG4344	possible transcriptional regulatory protein	-0.849	0.0080	9
PPE-b	<i>PPE</i>	MSMEG0063	PPE family domain	-0.807	0.0003	6
ML0663		MSMEG2085	CHP	-0.804	0.0016	10
argD-e	<i>argD</i>	MSMEG2971	probable acetylornithine aminotransferase	-0.767	0.0030	7
atpH	<i>atpH</i>	MSMEG4925	ATP synthase delta chain	-0.741	0.0024	7
ML0990		MSMEG2732	CHP	-0.701	0.0066	10
glpD-a	<i>glpD</i>	MSMEG6721	glycerol-3-phosphate dehydrogenase	-0.683	0.0017	7
menD	<i>menD</i>	MSMEG1225	bifunctional menaquinone biosynthesis protein	-0.677	0.0072	7
Rv3841	<i>bfrB</i>	MSMEG6385	bacterioferritin	-0.660	0.0062	7

bccA-c		MSMEG1807	biotin carboxy carrier protein & biotin carboxyl transferase	-0.641	0.0017	1
purM	<i>purM</i>	MSMEG5766	phosphoribosylformylglycinamide cyclo-ligase	-0.635	0.0082	7
fas	<i>fas</i>	MSMEG0552	fatty acid synthase	-0.633	0.0015	
lpqF	<i>lpqF</i>	MSMEG6050	probable conserved lipoprotein	-0.617	0.0062	3
ML0759	<i>fbiA</i>	MSMEG1829	probable F420 biosynthesis protein	-0.611	0.0015	7
gabD-y	<i>gabD</i>	MSMEG1497	succinate-semialdehyde dehydrogenase	-0.600	0.0075	7
glnA2-f	<i>glnA2</i>	MSMEG2596	probable glutamine synthetase	-0.593	0.0026	7
ML1094		MSMEG1104	short chain type dehydrogenase/ reductase	-0.590	0.0024	7
ML0596-a	<i>csd</i>	MSMEG4531	probable cysteine desulfurase	-0.576	0.0020	7
ML2203		MSMEG3807	CHP	-0.552	0.0020	10
ML2289		none	CHP	-0.537	0.0020	10
sdhC	<i>sdhC</i>	MSMeg1669	succinate dehydrogenase	-0.528	0.0082	7
lysX	<i>lysX</i>	MSMEG6531	lysyl-tRNA synthetase	-0.501	0.0070	2
phoT	<i>phoT</i>	MSMEG2124	phosphate transport ATP-binding protein	-0.496	0.0066	3
ML2053	<i>adhA</i>	MSMEG0251	probable alcohol dehydrogenase	-0.477	0.0041	7
uvrD2	<i>uvrD2</i>	MSMEG1956	ATP-dependent DNA helicase	-0.476	0.0051	2
gabD-e	<i>gabD</i>	MSMEG6662	aldehyde dehydrogenase family protein	-0.469	0.0062	7
folK	<i>folK</i>	MSMEG6064	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	-0.443	0.0071	7
miaA	<i>miaA</i>	MSMEG6675	probable tRNA delta(2)-isopentenylpyrophosphate transferase	-0.383	0.0100	7
<b>Downregulated genes</b>						
lytB2	<i>lytB</i>	MSMEG5208	probable LytB-related protein, LytB2	3.316	0.0002	3
xseA	<i>xseA</i>	MSMEG5210	exo-deoxyribonuclease VII, large subunit	2.737	0.0003	2
ML2088-a		MSMEG4807	putative cytochrome P450	2.039	0.0004	7
ctpC-a		MSMEG5384	cadmium-translocating P-type ATPase	1.789	0.0081	3

rpoT	<i>sigA</i>	MSMEG2759	RNA polymerase sigma factor, SigA	1.513	0.0000	2
rplE	<i>rplE</i>	MSMEG1464	ribosomal protein L5	1.198	0.0002	2
ML2661-e	<i>fadD7</i>	MSMEG3702	Fatty acid CoA ligase, FadD7	1.197	0.0051	1
fpg	<i>fpg</i>	MSMEG2417	formamidopyrimidine-DNA glycosylase	0.961	0.0078	7
ML1750		MSMEG2202	CHP	0.922	0.0098	10
uvrB	<i>uvrB</i>	MSMEG3820	excinuclease ABC, B subunit	0.843	0.0057	2
Rv1009	<i>rpfB</i>	MSMEG5419	probable resuscitation-promoting factor B, RpfB	0.835	0.0027	3
uspE	<i>uspB</i>	MSMEG4462	probable sugar ABC transporter	0.810	0.0024	3
ML0115		MSMEG6327	CHP	0.807	0.0051	10
ML2661-h	<i>fadD7</i>	MSMEG4041	Fatty acid CoA ligase, FadD7	0.805	0.0002	1
Rv2393		MSMEG4522	CHP	0.771	0.0041	10
ML2491-c		MSMEG4370	CHP	0.760	0.0033	10
ML0815		MSMEG1939	transcriptional regulator, TetR family domain	0.725	0.0002	9
rpsL	<i>rpsL</i>	MSMEG1393	ribosomal protein S12	0.724	0.0066	2
ML0691-b	<i>dacB</i>	MSMEG1659	probable D-alanyl-alanine carboxypeptidase	0.720	0.0005	3
ML0729		MSMEG1810	CHP	0.674	0.0039	10
ML0093	<i>glfT</i>	MSMEG5323	bifunctional UDP-galactofuranosyl transferase	0.668	0.0085	3
gatA-b	<i>gatA</i>	MSMEG1078	probable glutamyl-tRNA (GLN) amidotransferase	0.668	0.0024	2
atpD-c	<i>atpD</i>	MSMEG4939	probable ATP synthase Beta chain	0.660	0.0009	7
trpS	<i>trpS</i>	MSMEG1655	tryptophanyl-tRNA synthetase	0.655	0.0020	2
mce1A-a	<i>mce1A</i>	MSMEG6500	host cell invasion	0.650	0.0026	0
ML2549		MSMEG0428	CHP	0.628	0.0029	10
ML2620-b	<i>mmpL3</i>	MSMEG4733	possible conserved transmembrane transport protein	0.624	0.0024	3
pdc-a	<i>pdc</i>	MSMEG4455	probable pyruvate decarboxylase	0.590	0.0027	7
ML1115	<i>lprB</i>	MSMEG1390	possible lipoprotein	0.581	0.0031	3
ML0174	<i>mprA</i>	MSMEG5468	DNA-binding response regulator (persistence)	0.580	0.0016	9
umaA2-a	<i>umaA</i>	MSMEG1199	possible mycolic acid synthase	0.476	0.0041	1

ML1698		MSMEG5185	conserved membrane protein	0.464	0.0033	3
ML2140		MSMEG5666	transcriptional regulator, marR family	0.460	0.0070	9
ML2377	<i>mmpS4</i>	MSMEG0373	conserved membrane protein	0.455	0.0073	3
ML0243-b	<i>pks16</i>	MSMEG5415	putative polyketide synthase	0.440	0.0081	1
ung	<i>ung</i>	MSMEG3668	probable uracil-DNA glycosylase	0.422	0.0079	2

<sup>a</sup> Gene identifier as defined in the MIAME compliance file (<http://vbc.med.monash.edu.au/~powell/M.smegmatis>).

<sup>b</sup> TIGR annotation (<http://www.tigr.org/tigr-scripts/CMR2/CMRHomePage.spl>)

<sup>c</sup> Function as per Tuberculist and Leproma (<http://genolist.pasteur.fr>).

<sup>d</sup> Log<sub>2</sub> of the fold ratio

<sup>e</sup> Functional classification as per Tuberculist and Leproma. 1, Lipid metabolism; 2, Information pathways; 3, Cell wall & cell processes; 6, PE/PPE; 7, Intermediary metabolism & respiration; 9, Regulatory proteins; 10, Conserved hypotheticals.