

Table S3: Genes differentially expressed in MSMEG $\Delta$ smtB $\Delta$ zur

Orthologue genes (% similarity)								
RCN <sup>a</sup>	Annotation	MAP	Mtb	q-value	Fold change		Putative function <sup>d</sup>	
					$\Delta\Delta$	$\Delta$ smtB / $\Delta$ zur		
-	MSMEG_0217			< 0.0001	4.92		alcohol dehydrogenase	
-	MSMEG_0302			< 0.0001	4.06		peptidase, S9A/B/C families	
-	MSMEG_0424			< 0.0001	4.56		Hsp20/alpha crystallin family protein	
-	MSMEG_0755	MAP3865c (76.8)	Rv0359 (68.8)	< 0.0001	64.08	80.92	cobalt-zinc-cadmium resistance protein	
groEL	MSMEG_0880	MAP3936 (95.0)	Rv0440 (93.4)	< 0.0001	6.62	7.94	molecular chaperone GroEL	
-	MSMEG_1122	-	-	< 0.0001	6.14	4.69	hypothetical protein	
-	MSMEG_1123	MAP1730c (43.1)	-	< 0.0001	7.5	8.64	cobalamin synthesis protein	
-	MSMEG_1236			< 0.0001	4.09		Mpr protein	
-	MSMEG_1392			< 0.0001	6.79		alcohol dehydrogenase	
groES	MSMEG_1582	MAP4264 (96.0)	Rv3418c (99.0)	< 0.0001	4.66	5.23	co-chaperonin GroES	
groEL	MSMEG_1583	MAP4265 (82.5)	Rv3417c (81.1)	< 0.0001	4.18	6.02	molecular chaperone GroEL	
aspA	MSMEG_1677			< 0.0001	-4.01		aspartate ammonia-lyase	
mmsA	MSMEG_2449			< 0.0001	9.04		methylmalonate-semialdehyde dehydrogenase	
-	MSMEG_2450			< 0.0001	5.31		hypothetical protein	
-	MSMEG_3297			< 0.0001	-5.07		CadC family transcriptional regulator	
-	MSMEG_3300			< 0.0001	-7.0		oxidoreductase, Gfo/ldh/MocA family protein	
-	MSMEG_3301			< 0.0001	-4.36		hypothetical protein	
thpD	MSMEG_3898	-	-	< 0.0001	4.44	-4.94	ectoine hydroxylase	
ectC	MSMEG_3899	-	-	< 0.0001	4.55	-6.47	L-ectoine synthase	
-	MSMEG_3900	-	-	< 0.0001	(-3.86)	-5.74	diaminobutyrate-2-oxoglutarate aminotransferase	
-	MSMEG_3901	-	-	< 0.0001	(-2.82)	-4.05	L-2,4-diaminobutyric acid acetyltransferase	
-	MSMEG_3946			< 0.0001	4.16		transmembrane protein	
-	MSMEG_3948			< 0.0001	4.05		acyltransferase	
-	MSMEG_3959	-	-	< 0.0001	4.7	4.40	transcriptional regulator	
-	MSMEG_3960	-	Rv0067c (45.8)	< 0.0001	8.11	7.56	transcriptional regulator	
-	MSMEG_4207			< 0.0001	-43.0		universal stress protein family protein	
-	MSMEG_4208			< 0.0001	-45.33		integral membrane protein	
-	MSMEG_4209			< 0.0001	-91.0		integral membrane protein	
-	MSMEG_4210			< 0.0001	-57.75		hypothetical protein	
-	MSMEG_4486			< 0.0001	-13.5	94.76	ArsR family transcriptional regulator	
cysNC	MSMEG_4978			< 0.0001	-4.43		bifunctional sulfate adenyltransferase subunit 1/adenylsulfate kinase	
cysD	MSMEG_4979			< 0.0001	-4.29		sulfate adenyltransferase subunit 2	
-	MSMEG_5021	-	-	< 0.0001	-6.08	-10.57	alcohol dehydrogenase	
-	MSMEG_5022	-	-	< 0.0001	-5.91	-21.67	flavin-containing monooxygenase FMO	
-	MSMEG_5117	MAP2592c (71.6)	Rv1188 (68.3)	< 0.0001	5.9	4.32	proline dehydrogenase	
-	MSMEG_5241			< 0.0001	4.29		GAF family protein	
-	MSMEG_5244			< 0.0001	4.19		DevR family transcriptional regulator	
-	MSMEG_5576			< 0.0001	5.67		D-mannonate oxidoreductase	
-	MSMEG_5906			< 0.0001	4.18		acyl-CoA dehydrogenase	
-	MSMEG_5907			< 0.0001	4.50		acyl-CoA dehydrogenase	
-	MSMEG_5908			< 0.0001	6.33		acyl-CoA synthetase	
-	MSMEG_5909			< 0.0001	6.22		oxidoreductase	
-	MSMEG_5913			< 0.0001	4.77		dioxygenase	
-	MSMEG_5922			< 0.0001	7.45		lipid-transfer protein	
-	MSMEG_5923			< 0.0001	5.0		acetyl-CoA acetyltransferase	
-	MSMEG_5992			< 0.0001	5.66		hypothetical protein	
-	MSMEG_5993			< 0.0001	5.82		acyl-CoA dehydrogenase	
-	MSMEG_5994			< 0.0001	6.43		acyl-CoA dehydrogenase	
-	MSMEG_5995			< 0.0001	4.89		P450 heme-thiolate protein	
-	MSMEG_5997			< 0.0001	4.44		hypothetical protein	
-	MSMEG_5998			< 0.0001	4.21		hypothetical protein	
-	MSMEG_6037			< 0.0001	4.01		2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase	
-	MSMEG_6045	MAP3774c (70.1)	Rv2060 (43.7)	< 0.0001	24.42	24.62	heavy metal ABC transporter inner membrane protein	
-	MSMEG_6046	MAP3775c (61.2)	-	< 0.0001	19.9	20.65	ABC transporter ATP-binding protein	
-	MSMEG_6047	MAP3776c (56.4)	-	< 0.0001	25.5	26.24	cation ABC transporter periplasmic cation-binding protein	
-	MSMEG_6048	MAP3772c (72.6)	-	< 0.0001	10.000 2,903.0	3,288.5	cobalamin synthesis protein/P47K	
-	MSMEG_6049	-	-	< 0.0001	443.56	494.44	hypothetical protein	
-	MSMEG_6050	-	-	< 0.0001	849.0	917.25	solute-binding lipoprotein	
-	MSMEG_6051	-	-	< 0.0001	632.0	777.0	pseudo ABC transporter transmembrane protein	
-	MSMEG_6052	-	-	< 0.0001	23.42	18.17	ABC transporter ATP-binding protein	
bluB	MSMEG_6053			< 0.0001	19.9		cob(II)irinic acid a.c-diamide reductase	
-	MSMEG_6055	-	-	< 0.0001	25.5	498	hypothetical protein	
-	MSMEG_6057	-	-	< 0.0001	393	435	MspD protein	
-	MSMEG_6058	MAP3384 (77.7)	Rv3270 (77.2)	< 0.0001	9.59	9.21	cadmium transporting P-type ATPase	
-	MSMEG_6059	MAP3383 (69.1)	Rv3269 (71.6)	< 0.0001	11.73	13.42	hypothetical protein	
-	MSMEG_6062	-	Rv1473 (42.5)	< 0.0001	5.04	5.97	Fe uptake system permease	
-	MSMEG_6063	-	-	< 0.0001	8.69	8.73	Fe uptake system integral membrane protein	
-	MSMEG_6064	-	-	< 0.0001	21.76	27.42	lipoprotein	
rpsR	MSMEG_6065	MAP3767c (63.9)	Rv2055c (63.4)	10.000	3,080.0	5,107.67	30S ribosomal protein S18	
rpsN	MSMEG_6066	MAP3768c (75.2)	Rv2056c (72.3)	10.000	3,983.5	5,778.5	30S ribosomal protein S14	
rpmG	MSMEG_6067	MAP3769c (92.6)	Rv2057c (87.0)	10.000	5,015.0	5,856.67	50S ribosomal protein L33	
rpmB	MSMEG_6068	-	Rv2058c (82.1)	10.000	4,055.32	7.17	5,372.69	50S ribosomal protein L28
-	MSMEG_6069	MAP3770 (57.8)	Rv0106 (62.1)	10.000	4,340.0	3,492.0	CobW/P47K domain-containing protein	
rpmE2	MSMEG_6070	MAP3771 (79.3)	-	10.000	1,603.0	1,460.33	50S ribosomal protein L31	
-	MSMEG_6071	MAP0485c (66.9)	Rv3577 (68.3)	< 0.0001	33.42	27.95	metallo-beta-lactamase superfamily protein	
-	MSMEG_6072			< 0.0001	5.0		citrate transporter	
-	MSMEG_6237	-	-	< 0.0001	-4.62	-5.39	hypothetical protein	
-	MSMEG_6240	-	-	< 0.0001	-8.48	-4.64	hypothetical protein	
-	MSMEG_6241	MAP2246c (44.9)	Rv2426c (45.9)	< 0.0001	-8.66	-5.14	ATPase AAA	
-	MSMEG_6242	-	-	< 0.0001	-8.35	-6.40	alcohol dehydrogenase	
-	MSMEG_6272			< 0.0001	12.44		NAD-glutamate dehydrogenase	

<sup>a</sup>Reference Common Name.<sup>d</sup>Putative function based on NCBI blastx analysis or tdb.org database.