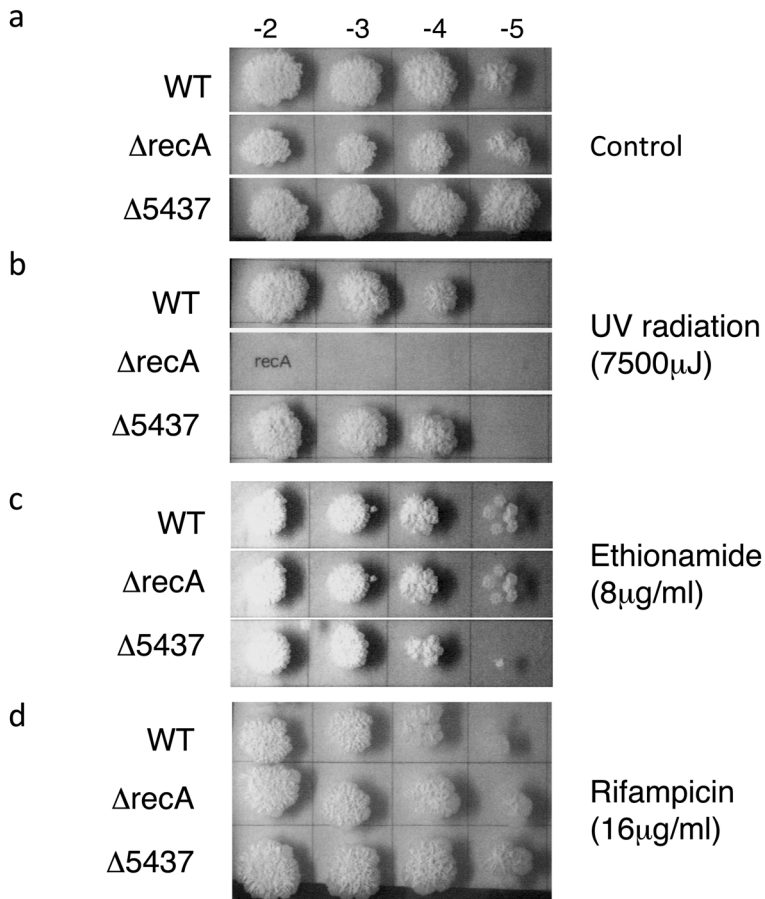


SUPPLEMENTARY MATERIAL

Figure S1. Δ MSMEG_5437 is indistinguishable from wild type in its sensitivity to ultraviolet radiation, rifampicin and ethionamide. (a) One milliliter of culture of wild type and *mc²155: Δ 6129* at an A_{600} of 0.3 was spread as a thin layer on a petri dish and exposed to varying intensities of UV radiation (2500, 5000, 7500 and 10,000 μ J) Ten fold serial dilutions of wild type and *mc²155: Δ 6129* were spotted on Middlebrook 7H10 containing a 2-fold dilution series of antibiotics. The most prominent differences the two strains are seen in (c) 8 μ g/ml of ethionamide and (d) 16 μ g/ml of rifampicin.

Table S1: Identification of genes required for survival in the presence of MMC using Transposon Site Hybridization (TraSH). 28 genes corresponding to a variety of different pathways or processes that are at least five-fold underrepresented when *M. smegmatis* is exposed to MMC. Corresponding homologues in *M. tuberculosis* are also shown. Genes are grouped and colored according to their functional categories.

Table S2. RNA seq profile of wild type and *M. smegmatis mc²155: Δ 6129*. The number of reads corresponding to each ORF was calculated, and the data were normalized to a million reads as well as to the size of each ORF, and expressed as Reads per Kilobase per million mapped reads. The ratio of RPKM values of Δ 6129 to the wild type strain was calculated and ORFs showing a 2.5 fold change in expression are listed. Genes that fall into discernable functional categories are grouped and shaded using different colors.



M.smegmatis gene	Fold under-representation $n \pm sd$	Homologue in M.tb	Proposed function
MSMEG_3018	9.6 ± 1.9	Rv2569c	Transglutaminase domain protein/ peptidase activity
MSMEG_3637	13.4 ± 1.4	Rv1842c	CBS domain protein- bind to the adenosyl portion of molecules such as ATP, AMP and SAM& constitute channel proteins and transporters
MSMEG_5266	9.4 ± 1.6	Rv0176	RDD family protein involved in transport of an as yet unknown set of ligands
MSMEG_0658	17.64	-	polyamine ABC-transporter
MSMEG_2172	6.8 ± 1.1	-	Dicarboxylate-carrier protein possibly in organic acid transport
MSMEG_3146	32 ± 2.1	Rv1478	Invasin/ Pathogenesis- cell wall associated hydrolysis
MSMEG_0385	8.4 ± 2.5	Rv1524	Hypothetical glycosyl transferase-/ Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
MSMEG_5981	19.36	-	Putative glycosyl transferase, / Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
MSMEG_4643	8.4 ± 1.5	Rv2389c	Resuscitation-promoting factor/ cell wall remodeling
MSMEG_5437	23.1 ± 1.1	Rv1746	Probable serine /threonine-protein kinase PknB/ Kinase / regulation
MSMEG_6921	7.6 ± 1.5	Rv0038	Conserved hypothetical protein/ domain present in transcriptional regulator
MSMEG_2538	10.8 ± 3.9	Rv2887	MarR-family protein transcriptional regulator/ regulation/ transcription factor
MSMEG_4629	27.8	Rv2447c	FolC bifunctional protein; folic acid biosynthesis
MSMEG_1820	15.6 ± 3.4	Rv3275c	Phosphoribosylaminoimidazole carboxylase, / purine biosynthesis from ribose-5-phosphate
MSMEG_2671	8.8 ± 1.5	Rv2763c	Dihydrofolate reductase/ tetrahydrofolate biosynthetic process
MSMEG_4270	5.1 ± 1.4	Rv2202c	Adenosine kinase
MSMEG_2337	7.5 ± 1.9	-	Isopentenyl-diphosphate delta-isomerase - isoprenoid biosynthetic process
MSMEG_6013	20.1 ± 2.9	Rv3561	Probable fatty-acid-coa ligase -Fatty acid and phospholipid metabolism
MSMEG_3015	8 ± 1.8	Rv1517	Conserved hypothetical protein/ conservation to integral membr prots
MSMEG_5585	10.5	-	Hypothetical protein/ sililarity to AraC like DNA-binding protein
MSMEG_3639	10.6 ± 1.4	-	Conserved hypothetical protein
MSMEG_0354	22.1 ± 1.8	Rv1974	Conserved hypothetical protein
MSMEG_1163	8 ± 1.6	-	Hypothetical protein
MSMEG_2897	10.6 ± 2.7	-	Conserved hypothetical protein
MSMEG_4192	18.34 ± 2.2	Rv2134c	Conserved hypothetical protein/ Unknown
MSMEG_3426	40.1 ± 1.4	-	Short chain dehydrogenase/ NAD or NADH binding/ nucleotide-sugar metabolic process
MSMEG_5812	33.6	Rv2750	Carveol dehydrogenase - Electron transport
MSMEG_5350	11.1 ± 1.7	Rv3539	PPE family protein, putative