

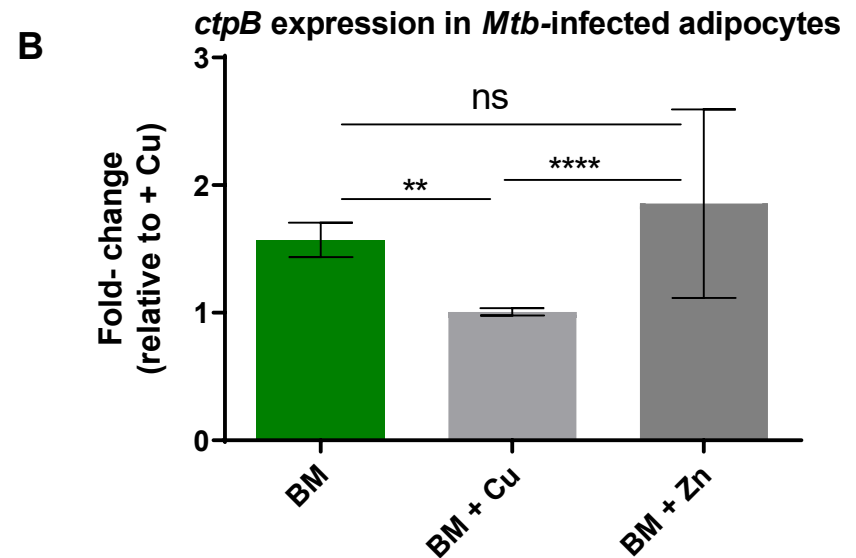
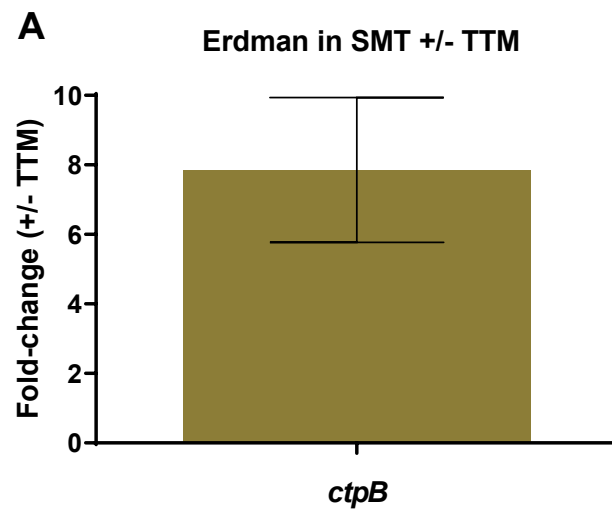


Figure S1. Transcription of *ctpB* in *M. tuberculosis* Erdman increases in response to copper limitation. Gene expression of *ctpB* was examined by quantitative RT-PCR after culture of strain Erdman in A) STM +/- 20 μ M TTM or B) after infection of 3T3-L1 adipocytes cultured DMEM-FBS (basal medium, BM) or BM supplemented with 0.1 mM CuCl_2 or ZnCl_2 . Gene expression was normalized to *sigA*.

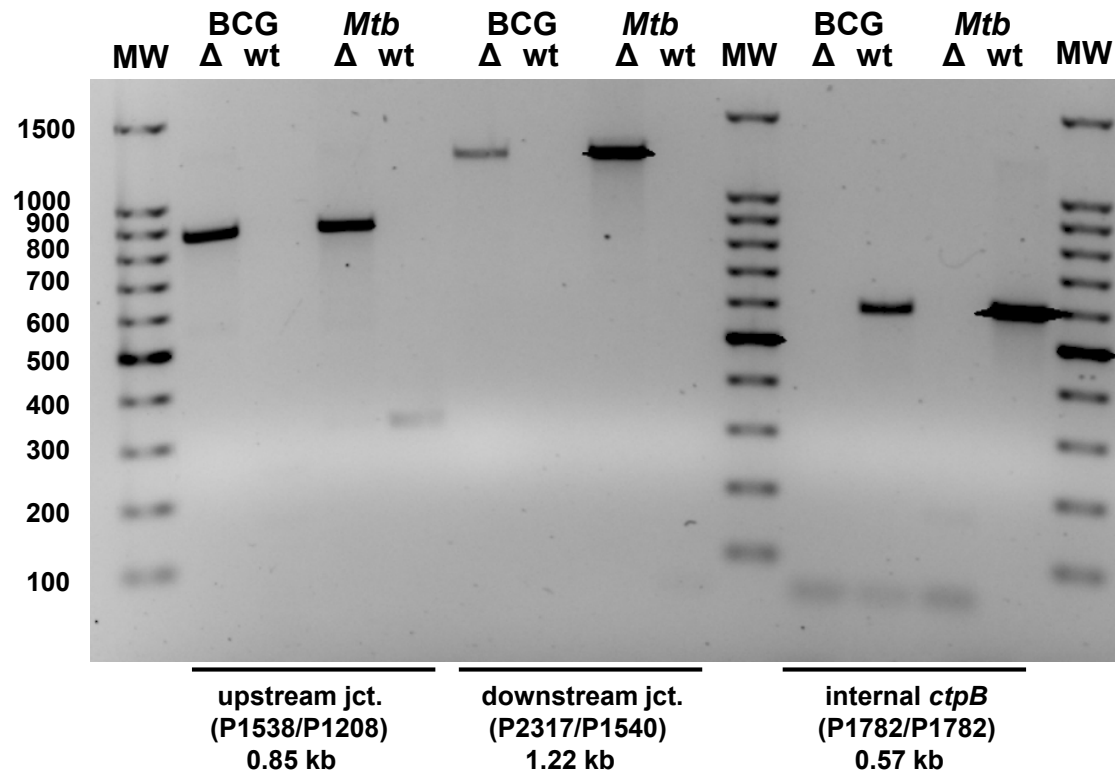
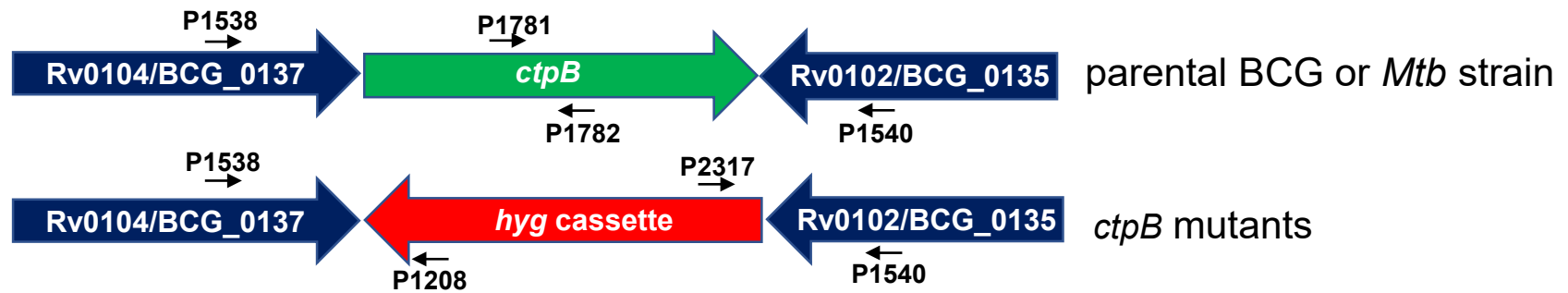


Figure S2. Confirmation of *ctpB* deletion mutants. (Top) Drawing of conserved (99% identical) *ctpB* genomic *M. bovis* BCG and *M. tuberculosis* (*Mtb*) before and after replacement of *ctpB* with a hygromycin-resistance (*hyg*) cassette. Primers used for PCR are indicated (small arrows). (Bottom) Resolution of PCR products on a 1.4% agarose gel. Expected band sizes for the inserted *hyg* cassette in a *ctpB* mutant (Δ) is indicated, as is the expected size of an internal *ctpB* product in the parent strains. Size standards are Promega 100-bp ladder (MW).

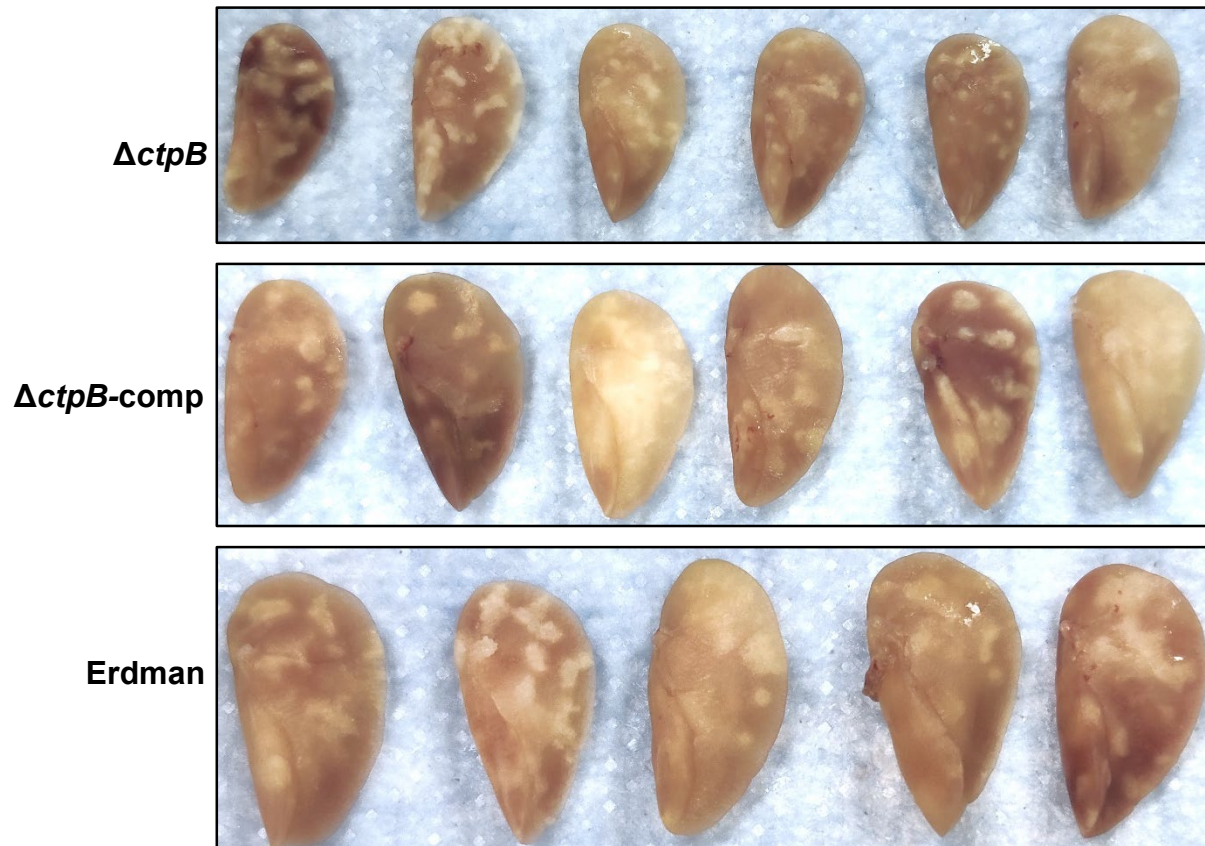


Figure S3. Gross pathology of lungs at time of death is similar for DBA/2 mice infected with $\Delta ctpB$, $\Delta ctpB\text{-comp}$, or *M. tuberculosis* Erdman. After euthanization of infected DBA/2 mice when moribund (Figure 5), the lungs, liver, and spleen were removed. Gross pathology of one lung lobe from each animal is shown. Granulomas are evident by the white foci.

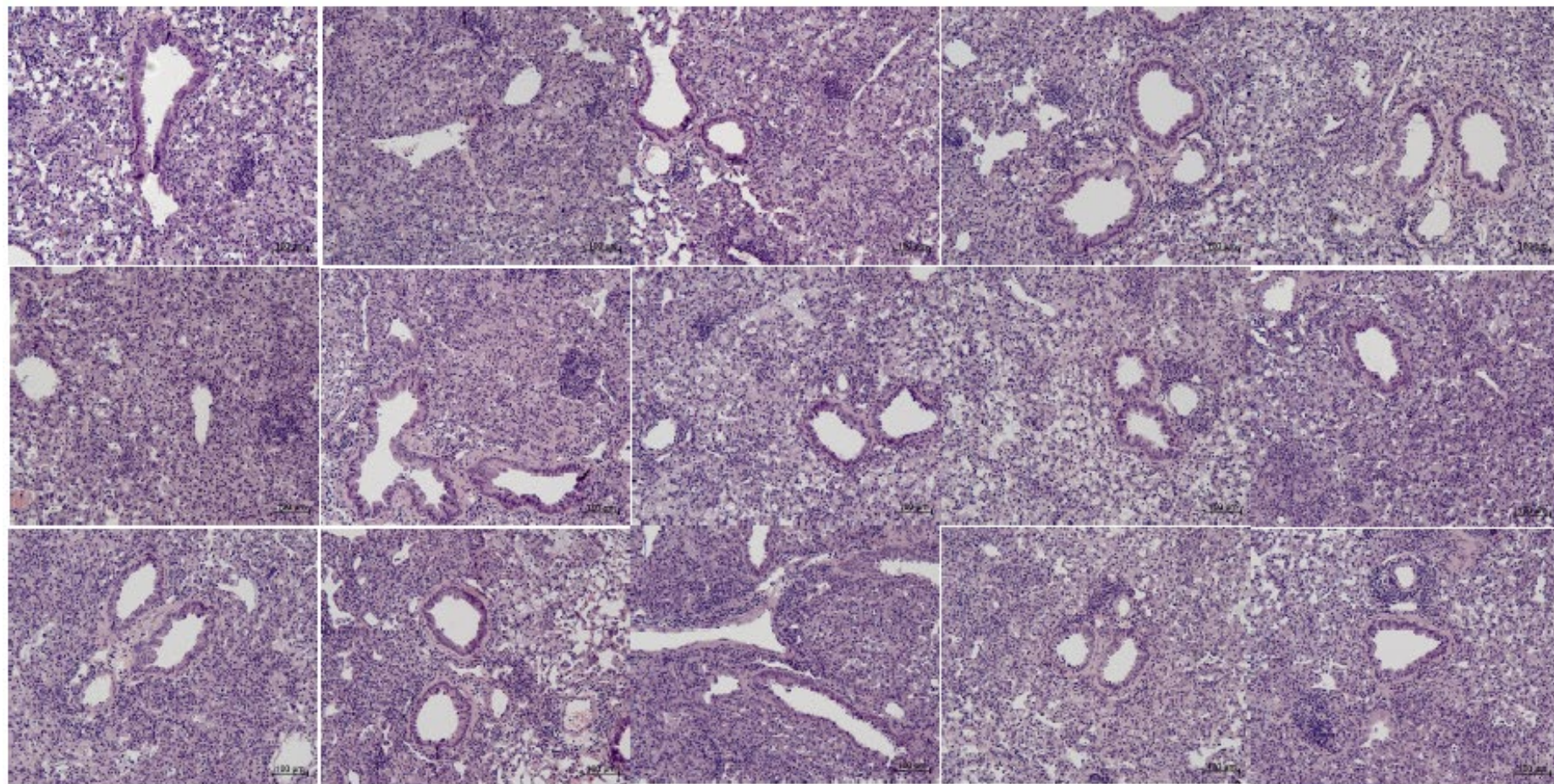


Figure S4. No difference in histopathology of lungs harvested from moribund DBA/2 mice following infection with $\Delta ctpB$, $\Delta ctpB$ -comp, or *M. tuberculosis* Erdman. A) Microscopic visualization of hematoxylin & eosin-stained lung sections from DBA/2 survival study mice infected with strain $\Delta ctpB$ (top row), $\Delta ctpB$ -comp (middle row), or *M. tuberculosis* Erdman (bottom row) harvested when animals were moribund.

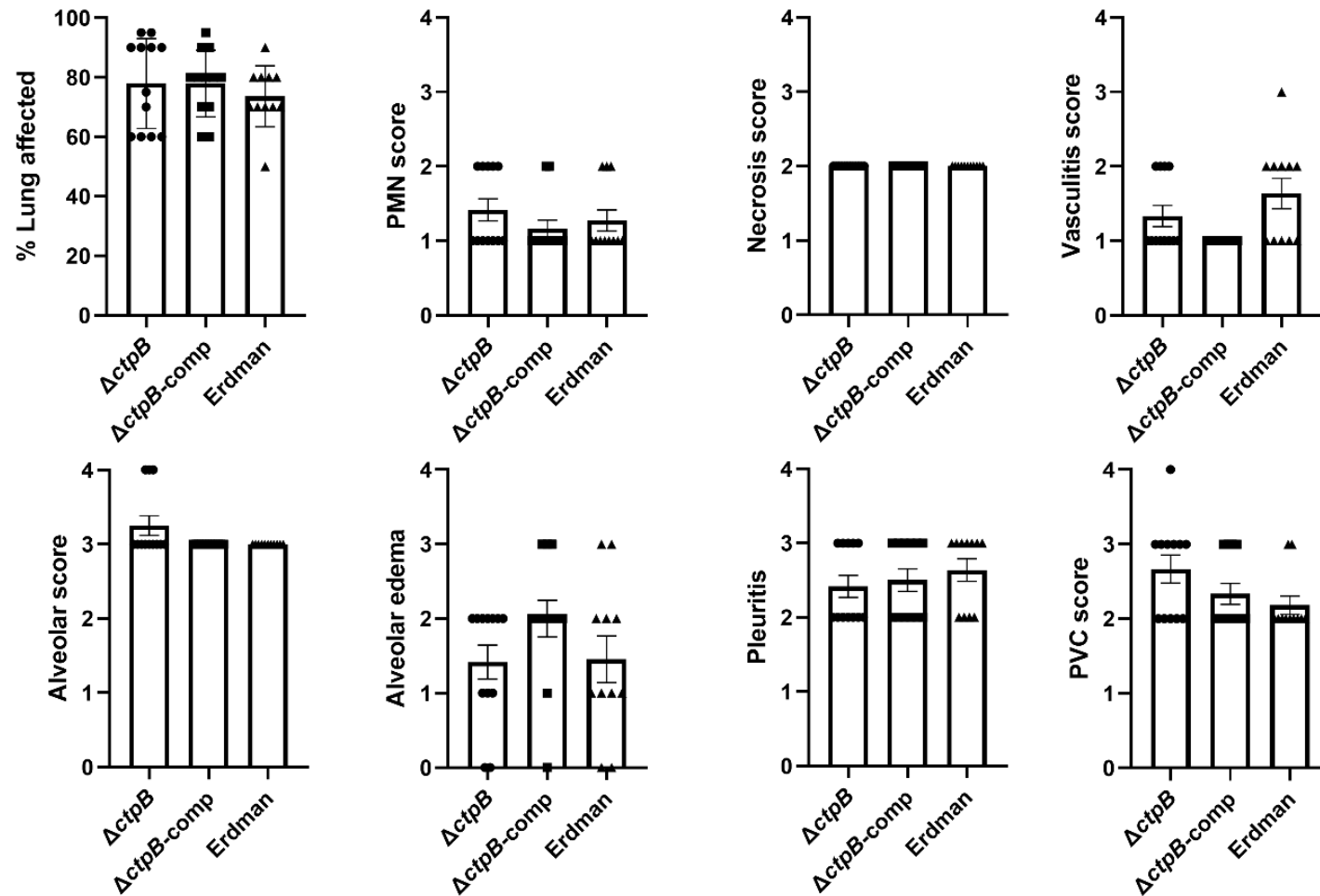


Figure S4 (continued) B) Semi-quantitative histopathological assessments of lung tissues were examined as detailed in the Methods section by a board-certified pathologist. No significant differences in pathology measures at the time of death were observed regardless of the infecting strains.

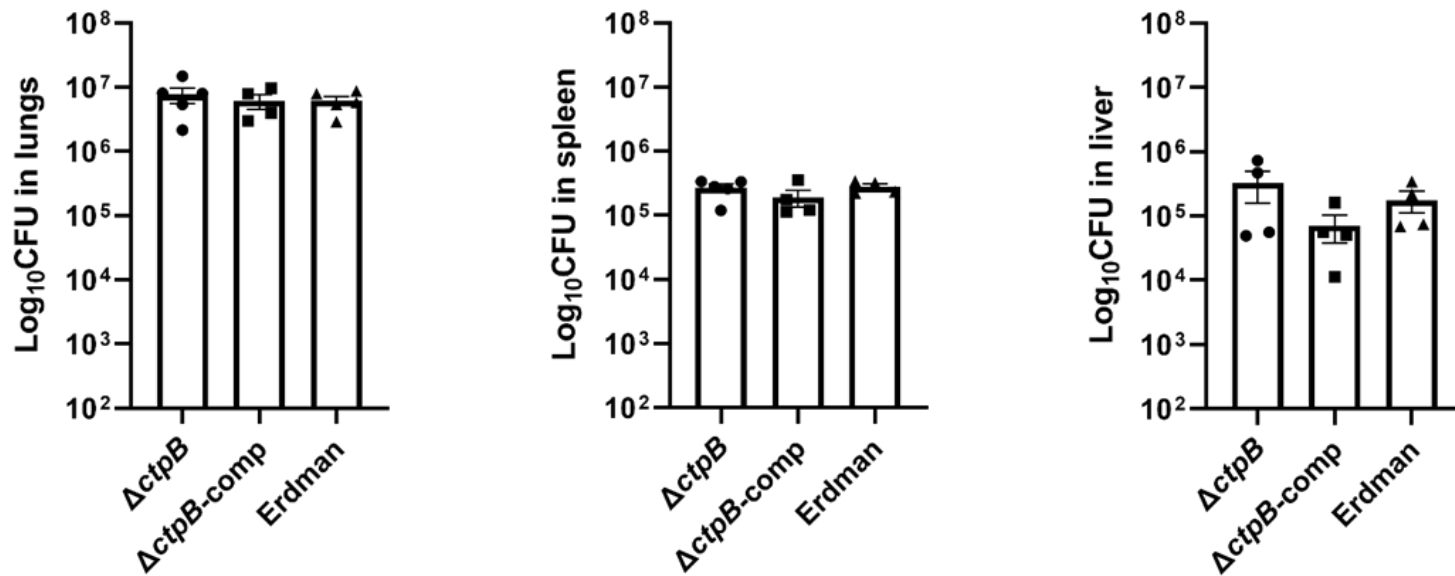


Figure S5. No significant differences in *M. tuberculosis* colony-forming units in the lungs, liver, or spleen at time of death of DBA/2 mice infected with $\Delta ctpB$, $\Delta ctpB$ -comp, or *M. tuberculosis* Erdman. Mycobacterial burdens in DBA/2 mice infected with $\Delta ctpB$ (circles), $\Delta ctpB$ -comp (squares), or *M. tuberculosis* Erdman (triangles) were quantified by homogenization and plating lung, liver, and spleen tissues harvested at necropsy of the animal euthanized upon becoming moribund. After counting colonies, no significant differences in mycobacterial counts were observed between infecting strains in the lungs, liver, or spleen.

Figure S6. Alignment of mycobacterial CtpB homologs. Mycobacterial CtpB alignment output generated in Phylogeny was pasted into the Sequence Manipulation Suite (https://www.bioinformatics.org/sms2/color_align_prop.html) set to highlight similar residues present in 70% of the homologs with the same color. The same mycobacterial CtpB homologs used in the phylogram shown on Figure 7 were used. Species/strain names in order of appearance: *M. leprae*, *M. canettii*, *M. tuberculosis* H37Rv, *M. tuberculosis* CDC1551, *M. bovis*, *M. microti*, *M. tuberculosis* Erdman, *M. africanum*, *M. ulcerans*, *M. tuberculosis* F11, *M. tuberculosis* H37Rv.

Color Align Code:

G, A, V, L, I
F, Y, W
C, M
S, T
K, R, H
D, E
N, Q
P

CtpB-Mlepra	-MTASLVE	D	TNNNH-E	SVRR	IQLDVAGML	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVD-VAV	DEL	RQVIE	EQAGY	77															
CtpB-Mcanet	-MAAPVVG	DADL---	QSVRR	IRLD	VSGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-H37Rv	-MAAPVVG	DADL---	QSVRR	IRLD	VLGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-CDC1551	-MAAPVVG	DADL---	QSVRR	IRLD	VSGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-Mbovis	-MAAPVVG	DADL---	QSVRR	IRLD	VSGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-Mmicro	-MAAPVVG	DADL---	QSVRR	IRLD	VSGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-Erdman	-MAAPVVG	DADL---	QSVRR	IRLD	VSGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-Mafrica	-MAAPVVG	DADL---	QSVRR	IRLD	VSGMS	CAACAS	RVETKLN	KIPGVR	ASVNF	ATRVAT	I	DAVG-MAA	DEL	CGVVE	KAGY	75															
CtpB-Mmarin	-MAAPITG	DLDL---	GSARR	IQLD	VSGMS	CAACAS	RVETKLN	KVPGVR	ASVNF	ATRVAT	I	DAVD-VAAD	Q	ICELVE	KAGY	75															
CtpB-Mulcer	-MAAPITG	DLDL---	GSARR	IQLD	VSGMS	CAACAS	RVETKLN	KVPGVR	ASVNF	ATRVAT	I	DAVD-VAAD	Q	ICELVE	KAGY	75															
CtpA-Mlepra	-MRAP	NGWNNL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	49															
CtpA-Mulcer	MSTTIVTT	DKHLERD	Q	QVQ	R	FQLGIT	TGMS	C	FACAR	KVQ	STLN	KVPGVR	ASVNF	G	TRTAIVE	EAGED	VDA	AALCE	VIQAGY	80											
CtpA-MtbF11	-MTTAVTG	EH	H----	ASVQ	R	IQLR	I	SGMS	C	SAC	AHRV	ESTLN	K	LP	G	RAAVN	F	G	TRVAT	IDT	SEAVD	A	AALC	QAVRR	BAGY	75					
CtpA-H37Rv	-MTTAVTG	EH	H----	ASVQ	R	IQLR	I	SGMS	C	SAC	AHRV	ESTLN	K	LP	G	RAAVN	F	G	TRVAT	IDT	SEAVD	A	AALC	QAVRR	BAGY	75					
CtpB-Mlepra	RATAHA	ESAVE	E	I---	DPD	ADYARN	LLRRL	LIVA	ALL	FVPLAD	L	STMF	AI	VP	TNR	FPGW	G	YLL	TALA	API	V	TWAA	P	FH	RV	154					
CtpB-Mcanet	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-H37Rv	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-CDC1551	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-Mbovis	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-Mmicro	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-Erdman	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-Mafrica	HAAPHT	ETTVL	DKRTK	DPD	GAH	ARRLL	RRL	LLVA	AVL	FVPLAD	L	STL	F	AI	VP	SAR	VP	GW	G	YIL	TALA	APV	V	TWAA	P	FH	SV	155			
CtpB-Mmarin	QAVPHA	ESA	ADDR---	DPDA	E	HARTL	LRRL	LLVA	AVL	FVPLAD	L	STMF	AI	VP	STR	FPGW	G	YLL	TALA	API	V	TWAA	P	FH	SV	152					
CtpB-Mulcer	QAVPHA	ESA	ADDR---	DPDA	E	HARTL	LRRL	LLVA	AVL	FVPLAD	L	STMF	AI	VP	STR	FPGW	G	YLL	TALA	API	V	TWAA	P	FH	SV	152					
CtpA-Mlepra	---	LCTD	GGEAL	QR	RQAD	ADN	ARYLL	IRL	AVAA	AL	FVPLAHL	S	VMF	AVLP	STH	FPGW	E	WML	TALA	I	P	V	TWAA	P	FH	RV	125				
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CtpA-H37Rv	QADLC	T	DDGR	SAS---	DPDA	D	HAR	QLLIR	L	AVAA	AL	FV	PVADL	S	VMF	G	VVP	AT	R	F	TGW	Q	WVL	SAL	ALP	V	TWAA	P	FH	RV	152

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CtpB-H37Rv	ALRNARHRTTSMETLISVGIVAATAWSLSSVFGDQPPREGSGIWRAILNSDSIYLEVAAGVTVFVLAGRIFYFEAPAKSKAG	235
CtpB-CDC1551	ALRNARHRTTSMETLISVGIVAATAWSLSSVFGDQPPREGSGIWRAILNSDSIYLEVAAGVTVFVLAGRIFYFEAPAKSKAG	235
CtpB-Mbovis	ALRNARHRTTSMETLISVGIVAATAWSLSSVFGDQPPREGSGIWRAILNSDSIYLEVAAGVTVFVLAGRIFYFEAPAKSKAG	235
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CtpB-Mbovis	SALRALAELGAKNVAVLLPDGAELVIPASELKKRQRFVTRPGETIAADGVVVDGSAIDMSAMTGEAKPVRAYPAASVVG	315
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CtpB-Mbovis	GTIVMDGRLVIEATAVGADTQFAAMVRLVEQAQTQKARAQRLADHIAGVFVPVVEVIAGLAGAAWLVSGAGADRAFSVTL	395
CtpB-Mmicro	GTIVMDGRLVIEATAVGADTQFAAMVRLVEQAQTQKARAQRLADHIAGVFVPVVEVIAGLAGAAWLVSGAGADRAFSVTL	395
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CtpB-Mlepra	GVLVIA	CP	CTLGLATPTAMMVAS	SGRGAQLGFIKGYRALETINAI	DTVVFDKGTGLTLGQLSVSTVTSTGG----	WCSGE	470	
CtpB-Mcanet	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYRALETIRSI	DTVVFDKGTGLTVGQLAVSTVTMAGSGT	SERDREE	475	
CtpB-H37Rv	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYRALETIRSI	DTVVFDKGTGLTVGQLAVSTVTMAGSGT	SERDREE	475	
CtpB-CDC1551	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYRALETIRSI	DTVVFDKGTGLTVGQLAVSTVTMAGSGT	SERDREE	475	
CtpB-Mbovis	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYRALETIRSI	DTVVFDKGTGLTVGQLAVSTVTMAGSGT	SERDREE	475	
CtpB-Mmicro	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYRALETIRSI	DTVVFDKGTGLTVGQLAVSTVTMAGSGT	SERDREE	475	
CtpB-Erdman	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYRALETIRSI	DTVVFDKGTGLTVGQLAVSTVTMAGSGT	SERDREE	475	
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CtpB-Mmarin	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYQALETIHGI	DAVVFDKGTGLTVGKLTVNTVTTTGG----	RVREE	468	
CtpB-Mulcer	GVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGFIKGYQALETIHGI	DAVVFEKGTGLTVGKLTVNTVTTTGG----	RVREE	468	
CtpA-Mlepra	AVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGILLKGHSF	EATRAVDTVVFDKGTGLTTGQLKVS	SAVTAAPG----	WQANE	441
CtpA-Mulcer	AVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGIFLKGYSLEATRSVD	TVVFDKGTGLTSGQLKVS	SAVVAAPG----	WDADE	473
CtpA-MtbF11	AVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGIFLKGYSLEATRAVD	TVVFDKGTGLTTGRLQVS	SAVTAAPG----	WDAQ	468
CtpA-H37Rv	AVLVIA	CP	CALGLATPTAMMVAS	SGRGAQLGIFLKGYSLEATRAVD	TVVFDKGTGLTTGRLQVS	SAVTAAPG----	WDAQ	468

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CtpB-H37Rv	VLGLAAAVE	ESASEHAMAAAIVAA	SPDPGPVNGFVAVAG	CGVSGEVGGHHVEVGKPSWITR	TTTCHDAALV	SARLDGHS	SRG	555
CtpB-CDC1551	VLGLAAAVE	ESASEHAMAAAIVAA	SPDPGPVNGFVAVAG	CGVSGEVGGHHVEVGKPSWITR	TTTCHDAALV	SARLDGHS	SRG	555
CtpB-Mbovis	VLGLAAAVE	ESASEHAMAAAIVAA	SPDPGPVNGFVAVAG	CGVSGEVGGHHVEVGKPSWITR	TTTCHDAALV	SARLDGHS	SRG	555
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CtpB-Erdman	VLGLAAAVE	ESASEHAMAAAIVAA	SPDPGPVNGFVAVAG	CGVSGEVGGHHVEVGKPSWITR	TTTCHDAALV	SARLDGHS	SRG	555
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CtpB-Mulcer	VLALASAVEAASEH	AVATAIVAASPHAPVTD	FVAVAGCGVSRIVDGHRIE	VGKPSWITRNTAA-	DEVLD	TAAQGH	SRG	547
CtpA-Mlepra	VLQMAATVE	ESASEHAVALAIAAST	THREPVANFRAPVGHVSGTVAER	AVRVGKPSWI--ASR	CNSTTLVTA	RNAH	SLG	519
CtpA-Mulcer	VLAIAATVEAASEH	SVALAIAAAT	TQHDTVTEFRAIPGRGVSGTVSGR	SVRVGKPSWIG-SSSS-	DTALRAAL	RNAH	SLG	551
CtpA-MtbF11	VLAIAATVEAASEH	SVALAIAAAT	TRRDAVTD	FRAIPGRGVSGTVSGRAVRVGKPSWIG-SSSC-	HPNMSAAR	RHAH	SLG	546
CtpA-H37Rv	VLAIAATVEAASEH	SVALAIAAAT	TRRDAVTD	FRAIPGRGVSGTVSGRAVRVGKPSWIG-SSSC-	HPNMRAAR	RHAH	SLG	546

CtpB-Mlepra	ETVVEFVSVDGV	ACGAVAIADTVKDS	AADAISALCS	RGLHTILLTGDN	QAAARAVAAQ	VGIDTVIAD	MPLPEAKVD	VVIQRLR	629	
CtpB-Mcanet	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-H37Rv	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-CDC1551	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-Mbovis	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-Mmicro	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-Erdman	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-Mafrica	ETVVEFVSVDGV	VRAALTIADTLKDS	AAAAVAALRSR	GLRTILLTGDN	RAAADAVAAQ	VGIDSAVAD	MPLPEGKVD	VVIQRLR	635	
CtpB-Mmarin	ETIVEFVSVDGEV	CAAVTISDTVKDS	AADAIAALRSR	GLRTILLTGDN	QAAADSVAT	QLGIDTAIAD	VDLPDGKVN	VVIQRLR	627	
CtpB-Mulcer	ETIVEFVSVDGEV	CAAVTISDTVKDS	AADAIAALRSR	GLRTILLTGDN	QAAADSVAT	QLGIDTAIAD	VDLPDGKVN	VVIQRLR	627	
CtpA-Mlepra	ETAVEVEIDGEC	GVIAVADAVKDS	AADAVALH	DRGFR	TALLTGDN	PASAAAVAS	RIGIDEVIAD	DILPEKVD	VVIEQLR	599
CtpA-Mulcer	ETAVEVEIDGEC	GVIAVADAVKDS	AADAVALR	ERGLR	TMLLTGDN	PASAAAVAD	RVGIDEVIANIL	PEGKVD	VVIEQLR	631
CtpA-MtbF11	ETAVEVEVDGEC	GVIAVADAVKDS	ARDAVALAD	RGLR	TMLLTGDN	PESAAAVAT	RVGIDEVIAD	DILPEGKVD	VVIEQLR	626
CtpA-H37Rv	ETAVEVEVDGEC	GVIAVADAVKDS	ARDAVALAD	RGLR	TMLLTGDN	PESAAAVAT	RVGIDEVIAD	DILPEGKVD	VVIEQLR	626

CtpB-Mlepra	DQGH TVAMVGDGINDGPALACADLGLAMGRGTDVAIGAADLILVRDSLGVVPVALDLARATMRTIRINMIWAFGYNVAAI	709
CtpB-Mcanet	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-H37Rv	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-CDC1551	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-Mbovis	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-Mmicro	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-Erdman	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-Mafrica	EEGH TVAMVGDGINDGPALVGADLGLAIGRGTDVALGAADIILVRDDLNTVPQALDLARATMRTIRMNMIWAFGYNVAAI	715
CtpB-Mmarin	DQGH TVAMVGDGINDGPALVSADLGLAIGRGTDVAIGAADIILVRDDLHIVGQALDLARATLRTIRTNMIWAFGYNVAAI	707
CtpB-Mulcer	DQGH TVAMVGDGINDGPALVSADLGLAIGRGTDVAIGAADIILVRDDLHIVGQALDLARATMRTIRTNMIWAFGYNVAAI	707
CtpA-Mlepra	DRGH VVAMVGDGINDGPALARADLGMAIGRGTDVAIGAADIILVRDNLDVVPITLGLAAATMRTIKFNMVWAFGYNIAAI	679
CtpA-Mulcer	DRGH VVAMVGDGINDGPALARADLGMAIGRGTDVAIGAADIILVRDNLDVVPPLALGLAAATMRTVKLNLAWAFGYNIAAI	711
CtpA-MtbF11	DRGH VVAMVGDGINDGPALARADLGMAIGRGTDVAIGAADIILVRDHLDVVPPLALDLARATMRTVKLNLMVWAFGYNIAAI	706
CtpA-H37Rv	DRGH VVAMVGDGINDGPALARADLGMAIGRGTDVAIGAADIILVRDHLDVVPPLALDLARATMRTVKLNLMVWAFGYNIAAI	706

CtpB-Mlepra	PIASSGLLNPLIAGAAMAFSSFFVVSNSLRLSNFG-----	744
CtpB-Mcanet	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-H37Rv	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-CDC1551	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-Mbovis	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-Mmicro	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-Erdman	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-Mafrica	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	750
CtpB-Mmarin	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	742
CtpB-Mulcer	PIAAAGLLNPLIAGAAMAFSSFFVVSNSLRRLRNFG-----	742
CtpA-Mlepra	PIAAAGLLNPLVAGAAMAFSSFFVVSNSLRRLRNFG-AILSCGTSRHRTVKRWRCPPPTRLRSTACSPVDASPLRPVAHRT	758
CtpA-Mulcer	PIAAAGVLNPLVAGAAMAFSSFFVVSNSLQLRNFGAATSQTTT-----S	755
CtpA-MtbF11	PVAAAGLLNPLVAGAAMAFSSFFVVSNSLRRLRKFGRYPLGCGT-----VGGP	753
CtpA-H37Rv	PVAAAGLLNPLVAGAAMAFSSFFVVSNSLRRLRKFGRYPLGCGT-----VGGP	753

CtpB-Mlepra	--LSQTS-----	750
CtpB-Mcanet	-----AQ-----	752
CtpB-H37Rv	-----AQ-----	752
CtpB-CDC1551	-----AQ-----	752
CtpB-Mbovis	-----AQ-----	752
CtpB-Mmicro	-----AQ-----	752
CtpB-Erdman	-----AQ-----	752
CtpB-Mafrica	-----AQ-----	752
CtpB-Mmarin	---PPTARIVASNGEIDD	757
CtpB-Mulcer	---PPTARIVASNGEIDD	757
CtpA-Mlepra	GVKPPTHR-----	766
CtpA-Mulcer	TTEPGATE-----	763
CtpA-MtbF11	QMTAPSSA-----	761
CtpA-H37Rv	QMTAPSSA-----	761

Table S1. Plasmids		
Plasmid	Relevant features	Source/Reference
pGH542	<i>oriM</i> , <i>oriE</i> , Tet ^R , Tn1000 $\gamma\delta$ -resolvase gene <i>tnpR</i> under control of mycobacterial Hsp60 promoter	DOI:10.1007/978-1-59745-232-8_15
pJV53	Kan ^R , <i>oriE</i> , <i>oriM</i> , mycobacteriophage Che9c gp60/gp61 controlled from an acetamide-inducible promoter	DOI:10.1007/978-1-59745-232-8_15
pMV306	<i>oriE</i> , <i>aph</i> , mycobacteriophage L5 <i>att/int</i>	DOI:10.1128/iai.63.3.799-803.1995
pOSN5	pMV306 containing <i>M. tuberculosis ctpB</i> with upstream regulatory sequences	This study
pOSN19	pOSN20 after removal of <i>sigC</i>	This study
pOSN20	pSR173 with <i>lacZ</i> promoter cloned upstream of P _{tb21} to enhance expression <i>tetR(B)</i>	This study
pOSN21	pYUB854 with ~1-kb regions upstream and downstream of <i>M. tuberculosis ctpB</i> gene flanking the Hyg ^R cassette	This study
pOSN26	pOSN20 with <i>M. tuberculosis ctpB</i> downstream of the P _{myctetO} promoter	This study
pOSN30	pOSN20 encoding <i>M. tuberculosis ctpV</i> downstream of the P _{myctetO} promoter	This study
pOSN37	pOSN20 encoding c-myc tag fusion to <i>M. tuberculosis ctpB</i> downstream of the P _{myctetO} promoter	This study
pOSN38	pOSN20 encoding c-myc tag fusion to <i>M. tuberculosis ctpV</i> downstream of the P _{myctetO} promoter	This study
pOSN40	pOSN5 with the kanamycin-resistance gene replaced with a gentamycin-resistance gene	This study
pSR173	<i>oriE</i> , <i>oriM</i> , <i>tetR(B)</i> , <i>hygR</i> , P _{myctetO-sigC}	DOI:10.1128/JB.01371-06
pYUB854	<i>cos</i> , <i>oriE</i> , <i>hyg</i> flanked by $\gamma\delta$ -resolvase sites	DOI:10.1016/s0076-6879(02)58081-2

Table S2. Bacterial strains		
Strain ID	Relevant features	Reference/source
TAM1	<i>E. coli</i> : <i>mcrA</i> , $\Delta(mrr-hsdRMS-mcrBC)$, $\Phi80lacZ\Delta M15$, $\Delta lacX74$, <i>recA1</i> , <i>ara</i> Δ 139, (<i>ara-leu</i>)7697, <i>galU</i> , <i>galK</i> , <i>rpsL</i> , <i>endA1</i> , <i>nupG</i>	Active Motif, Inc.
GA1505	TAM1/pOSN5	This study
GA1530	TAM1/pOSN21	This study
GA1568	TAM1/pOSN40	This study
GA1528	TAM1/pOSN19	This study
GA1509	TAM1/pOSN20	This study
GA1565	TAM1/pOSN37	This study
GA1566	TAM1/pOSN38	This study
mc ² 155	<i>M. smegmatis</i> wildtype strain	DOI:10.1111/j.1365-2958.1990.tb02040.x
BCG	<i>M. bovis</i> bacille Calmette-Guérin Pasteur	Sakamoto laboratory
BD3	mc ² 155/pOSN19	This study
BD4	mc ² 155/pOSN20	This study
BD5	mc ² 155/pOSN26	This study
BD6	mc ² 155/pOSN29	This study
BD7	mc ² 155/pOSN30	This study
BD9	mc ² 155/pOSN37	This study
BD10	mc ² 155/pOSN38	This study
BD43	BCG Δ <i>ctpB::hyg</i>	This study
BD63	mc ² 6206/pOSN19	This study
BD65	mc ² 6206/pOSN37	This study
BD66	mc ² 6206/pOSN38	This study
Erdman	<i>M. tuberculosis</i> strain Erdman	TB Branch, CDC
TB716	<i>M. tuberculosis</i> Δ <i>ctpB::hyg</i>	This study
TB717	<i>M. tuberculosis</i> Δ <i>ctpB::hyg</i> /pOSN40	This study
<i>M.tb</i> Δ <i>sigC</i>	<i>M. tuberculosis</i> Δ <i>sigC</i>	DOI:10.3390/ijms22042118
TB722	<i>M. tuberculosis</i> Δ <i>sigC</i> /pOSN19	This study
TB723	<i>M. tuberculosis</i> Δ <i>sigC</i> /pOSN20	This study
TB724	<i>M. tuberculosis</i> Δ <i>sigC</i> /pOSN36	This study
TB725	<i>M. tuberculosis</i> Δ <i>sigC</i> /pOSN37	This study
TB726	<i>M. tuberculosis</i> Δ <i>sigC</i> /pOSN38	This study

Table S3. Primers	
Primer	Sequence 5' to 3'
P1196	AGTGAGCTCTACGCCATCCC
P1575	GTGAAGCTTGTCAAGG TTGCGGTTCGC GAC
P1576	GTGAAGCTTGCGGTCCATCGACGGAAAATTGC
P1629	CAA CAG CGA CTC GAT CTA CCT CG
P1630	G GAC CGT CGT TGA TGC CGT C
P1631	GGT TAT CAA GTG AGA AAT CAC CAT GAG TGA CG
P1703	CACGTG CAC CCC AGG CTT TAC ACT TTA TGC TTC CGG CTC GTA TGT TGT GTG GA GTTAAC
P1704	GTTAAC TC CAC ACA ACA TAC GAG CCG GAA GCA TAA AGT GTA AAG CCT GGG GTG CACGTG
P1705	CACGTG CTT TAC ACT TTA TGC TTC CGG CTC GTA TGT TGT GTG GAA TTG TGA GCG GAT AAC AAT TTC GTTAAC
P1706	GTTAAC GAA ATT GTT ATC CGC TCA CAA TTC CAC ACA ACA TAC GAG CCG GAA GCA TAA AGT GTA AAG CACGTG
P1896	AA GGA AGC CAC GCT GCT TGT CGA CG
P1897	TCT CCG ACT TGG ACC TGA TCG ACC
P2040	A CTC TGG GCT GG GTG GAG CAG AAG CTG ATC TCG GAA GAG GAC CTG GCG GCT CCA GTT GTG GGA GAT GCC
P2041	CCAATGCATCTA TTG AGC GCC AAA ATT GCG TAG CCG CAA GC
P2042	CACTACTTAAGCTCGCGATCGGACGAAGA
P2043	GCTCTAGACACGGCCCTCCTCGGATC
P2044	TTAGCCATGGGCTCAATAGCATGCCCAGC
P2045	TAGAAGATCTTGATCGCCTGGCTGACTGG
P2250	GTGTGCTAGCCCCGG GAA TTA ATT CTG CTC GCG CAG
P2251	GGACTAGT GGC CGC GGC GTT GTG AC
P2057	GAGGTTAATTAAGGTGA CGA CGG CCG TGA CCG
P2058	TGACATGCAT TC ACG CGG ACG ACG GCG C
P2059	GAGGTTAATTAAG GTG GCG GCT CCA GTT GTG GG
P2060	GAGGTTAATTAAGGT GCG CGT GTG CGT CAC CGG
P2061	TGACATGCATT CAT GCG GTT CGG CCG TCG C