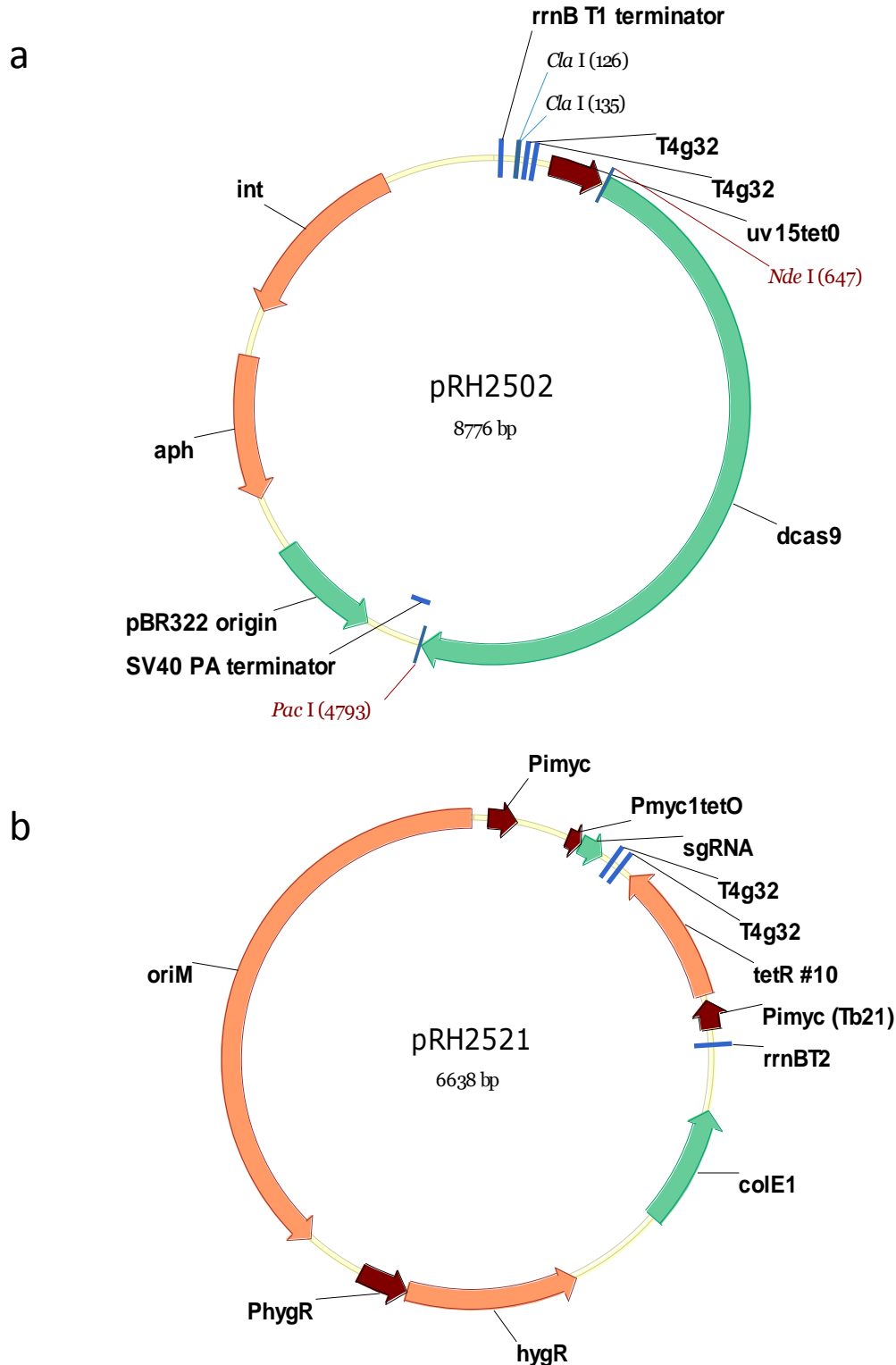


**Figure S1. Sequence of *dcas9* (*cas9* D10A and H840A) codon-optimized for *M. tuberculosis*.\***

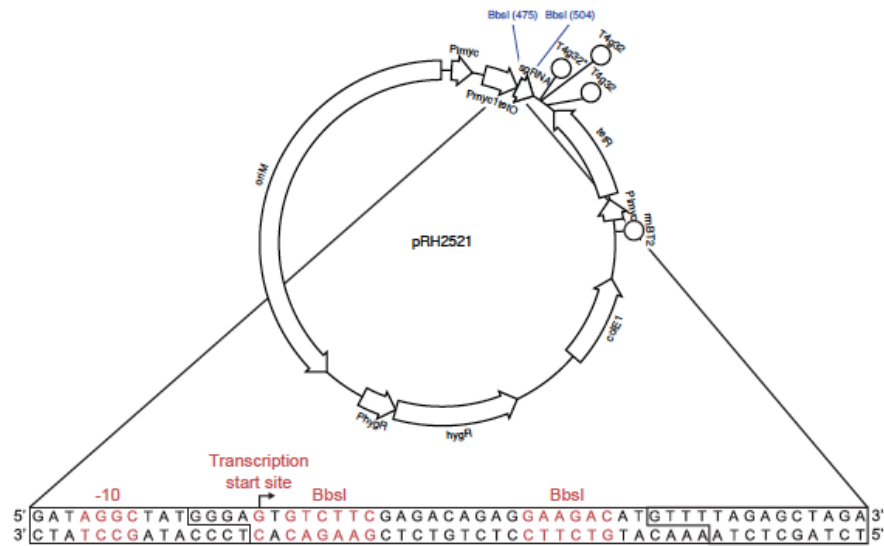
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\*Mutated codons 10 and 840 are shown in red and underlined.

**Figure S2. a) Integrating vector for expression *dcas9*; b) Replicating vector for sgRNA and *tetR* expression.** The integrating vector pRH2502 for induced expression of *dcas9* is derived from pTC-0X-1L (1), obtained from Addgene. The *PacI* site near the T4g32 sites was removed. *PacI* sites were introduced 15 bp after the *NdeI* site encompassing the start codon of *lacZl*, and 5' of the SV40 PA terminator. *lacZ* was removed and *dcas9* was inserted under the control of *uv15tetO* promoter at *NdeI* and *PacI* cloning sites. The replicative vector for sgRNA and TetR expression pRH2521 was derived from pTE-10M-0X (1) obtained from Addgene. The sequence *Pmyc1tetO* (2) followed by 2 *BbsI* sites and the sgRNA sequences were synthesized and cloned in pTE-10M-0X at a *Clal* site to produce pRH2521.



**Figure S3. Cloning strategy for construction of vectors to express sgRNAs to target genes of interest.** The example below incorporates sequences to target *M. smegmatis sigH*. The identical strategy is used to target genes in *M. tuberculosis* or *M. smegmatis*.



**1** Digest pRH2521 with BbsI and dephosphorylate



**2** Design oligos to generate sgRNA with 20 nt sequence complementary to the non-template strand of the target gene



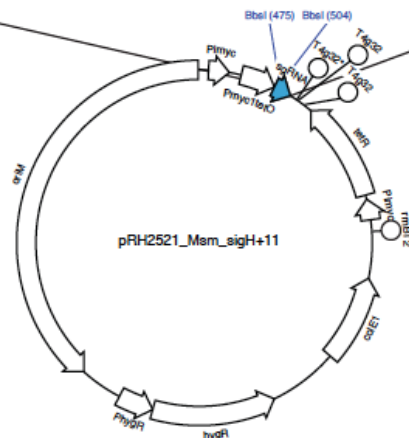
**3** Anneal oligos for Msm\_sigH+11 to create dsDNA inserts



**4** Phosphorylate dsDNA inserts



**5** Ligate phosphorylated dsDNA inserts into pRH2521



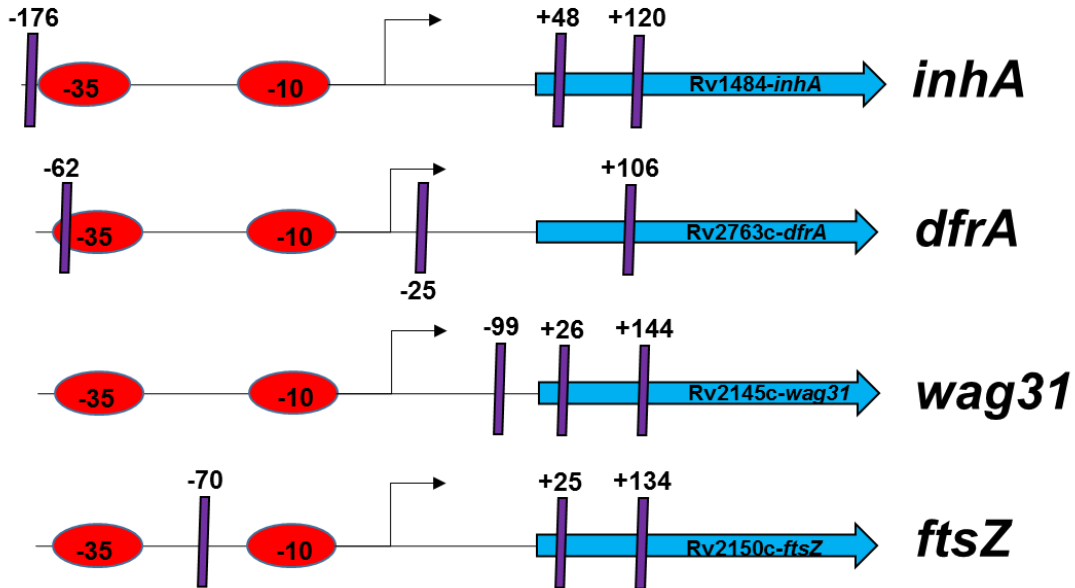
**6** Transform pRH2521-Msm\_sigH+11 into *M. smegmatis* that already contains pRH2502-dCas9

**Figure S4. a. Transcription start sites identified by 5' RACE. b. Locations targeted by sgRNAs in 4 essential genes of *M. tuberculosis*.** The locations in each gene targeted by CRISPRi are indicated by the vertical purple line. Numbering is the position of the first nt of the targeted sequence relative to the initiation codon.

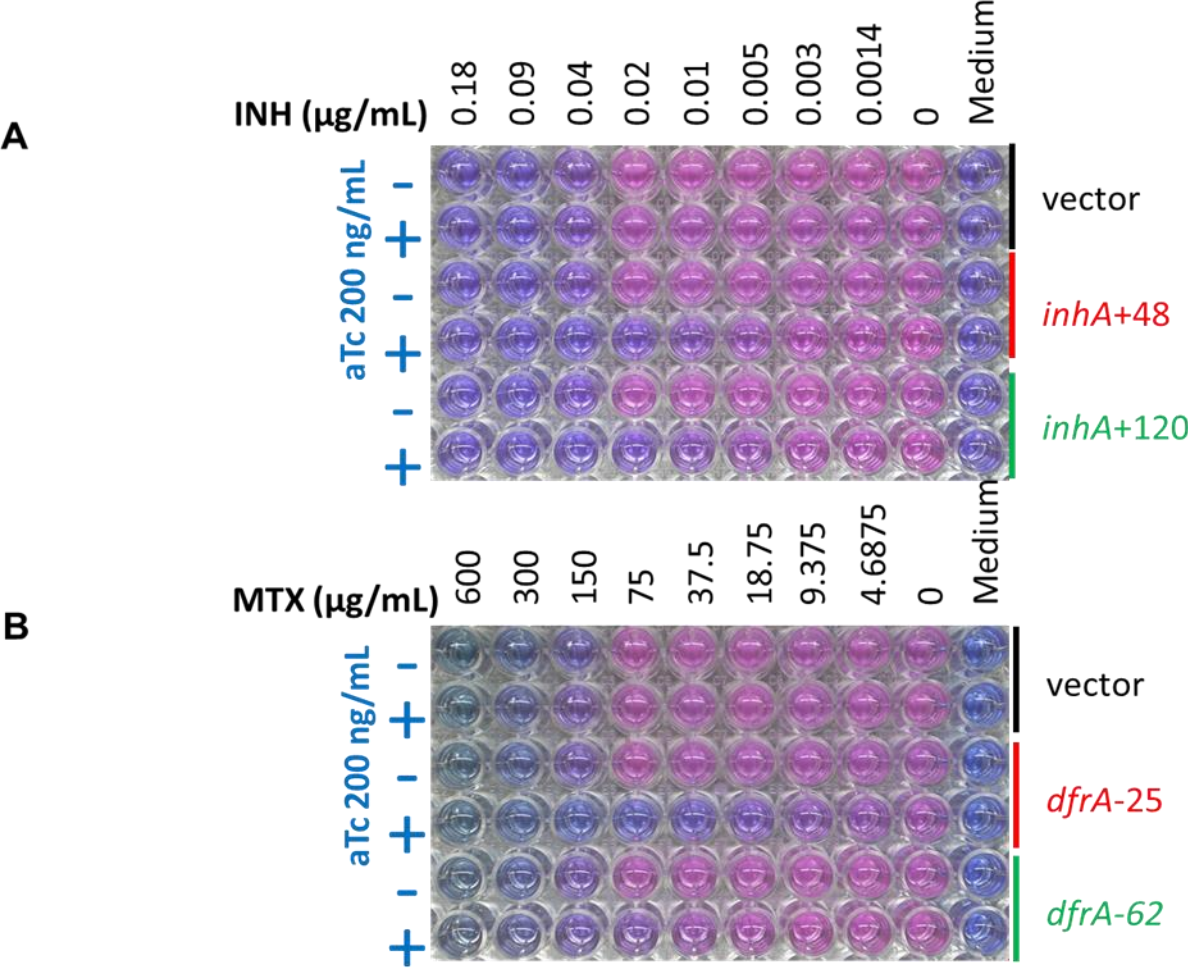
a

Rv1484- <i>inhA</i>	GATGAGCC <u>GGATTC</u> AGCAGGGGGCGCTGCAAT <u>TTTATC</u> CCAGCGAAG <u>C</u> GGGTCCG	-127/ATG	This study
Rv2763c- <i>dfrA</i>	CGCGGTATGAGGCGCGCCGACGACAATGAAGTCGGGCTCGGACAG <u>C</u> CTTCAAGC	-36/ATG	This study
Rv2145c- <i>wag31</i>	TGGCGCGCACGATTTCAAATCTAAGGATTGTGATTTATTTGGTCTT <u>A</u> GAGTTTGA	-147/ATG	This study
Rv2150c- <i>ftsZ</i>	ACTTGACATAACTCTAAGCCTATGGTTGAGGTTGAGAGTTTGCCAGCA <u>G</u> ACACA	-43/ATG	(3)

b



**Figure S5. Determination of minimum inhibitory concentration of (a) isoniazid (INH) and (b) methotrexate (MTX) in *M. tuberculosis* strains expressing *dcas9* and either gene-specific sgRNAs or the sgRNA vector control. The Microplate Alamar Blue Assay (MABA) was performed as described in the materials and methods section.**



**Figure S6. Effect of CRISPRi on off target genes that differ from the specific target sequence including the PAM by 2, 4 or 5nt.** Expression of all genes containing a sequence that diverged by 2 or 4 nt, regardless of the presence of an intact PAM, was measured. Of the genes containing a sequence that differed by 5 nt, expression was measured only for those that had an intact PAM sequence. **Panel a**, alignment of target gene sequences and the sequences for the off-target genes for which expression following *dcas9* and sgRNA induction was measured. Nucleotides that differ are shown in red. The PAM sequence is underlined. **Panels b-j**, expression of the off-target genes following induction of *dcas9* and the sgRNA indicated above each panel. No significant differences were observed at 24 or 48h for any of the 9 genes tested. **Table 1** below shows the number of mismatches for each off-target site compared the site targeted by the sgRNA indicated.

**a**

***sigH-222***                    5' - CCCG**C**TGGCGAACAC**CGGT**TGAT**T**-3'  
Rv3618-ATG-812nt- CCCG**T**TGGCGAACAC**CGT****GGA****A**G-341nt-TGA

***inhA+48***                    5' - CCG**A**CTCGTCGAT**C**CGTTTC**A**C-3'  
Rv0402c -GTG-1396nt- ACC**A**CTCGTCGAT**C**CGTTTC**A**G-1451nt-TAG

***inhA+120***                    5' - CCGG**C**TGCGGC**T**GAT**T****C**A**G**CGCA-3'  
Rv0352                            - ACGG**C**TGCGGC**C**GAT**G****C**GCGCA-594nt-ATG

***dfrA-25***                    5' - CCG**G**AAT**C****A**GGAGT**G****A**CGCGT**G**-3'  
Rv1778c -ATG-340nt- CAG**G**AAT**C****T****A**C**G**AGT**G****G**CGCGT**G**-81nt-TAG

***dfrA-25***                    5' - CCG**G**AAT**C**AAG**G****A**GT**G****A**CGCG**T****G**-3'  
Rv2885c-ATG-145nt - CCG**A****C**AT**C**AAG**G****C**GT**G****G**C**G****C**G-1206nt-TGA

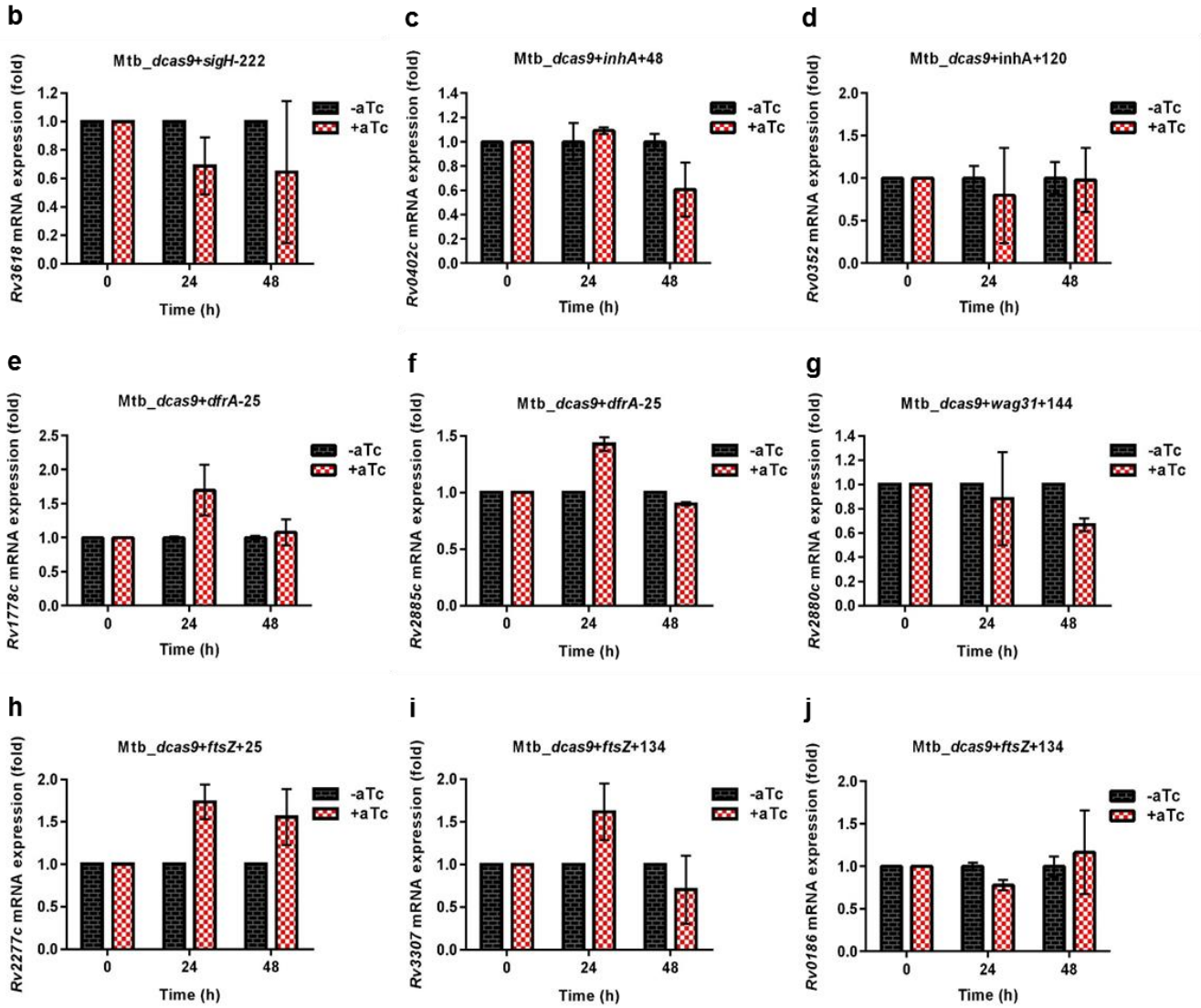
***Wag31+144***                    5' - CCG**A**T**C**T**G**CGTCAG**A**GG**A**T**C**A**C**-3'  
Rv2880c-ATG-157nt - CCG**A**T**C****C**GCGTCAG**A**T**G****A****C****C**G**A**C-642nt-TGA

***ftsZ+25***                    5' - CCG**T**CAT**C**AAGG**T****C**G**T**GGG**T****A**T**C**-3'  
Rv2277c-ATG-781nt - CCG**G**CAT**G**AAGG**T****C****A**TGGG**T****T**T**C**-96nt-TAA

***ftsZ+134***                    5' - CCAG**G****C**G**T**T**G**T**T**GAT**G**A**G**CGAT**G**-3'  
Rv3307-GTG-389nt - CCAG**C****C**G**T****G****C**T**G**A**T****C**A**G**CGAT**C**-389nt-TAA

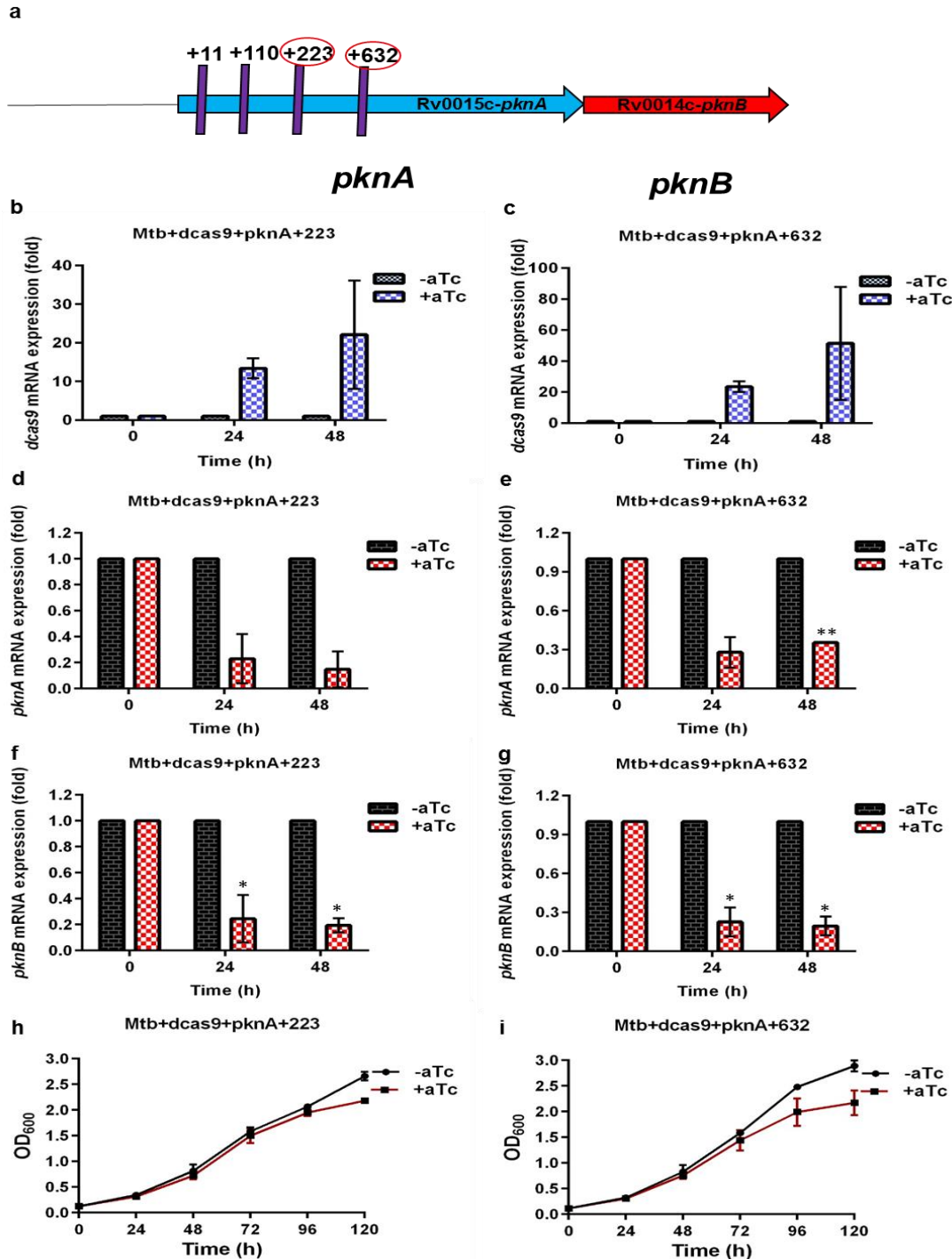
***ftsZ+134***                    5' - CC**A**GG**C****G**T**T**G**T**T**G**A**T**G**A**GCGAT**G**-3'  
Rv0186-ATG-134nt - CC**C**GG**C****C**T**T**G**T**T**G**A**T**G**A**GCGAT**G**-1913nt-TGA

Figure S6. (Continued)





**Figure S7. Polar effects on *pknB* (Rv0014c) of CRISPRi targeting *pknA* (Rv0015c)** a. Position of target sequences, shown by purple vertical lines. Numbering refers to the first nucleotide in the target sequence relative to annotated start of coding sequence. Circled sgRNAs are those for which expression data are shown. **b,c.** Expression of *dcas9* with and without induction of *dcas9* and the sgRNA indicated. **d,e.** Expression of *pknA* without induction of *dcas9* and the *pknA*-targeting sgRNA indicated. **f,g.** Expression of *pknB* without induction of *dcas9* and the *pknA*-targeting sgRNA indicated. **h,i.** Growth curves of culture with and without induction of *dcas9* and the sgRNA indicated.





**Supplementary Table 1: Potential off-target sequences for sgRNAs.**

S.N.	Gene	Position of sgRNA relative to translation start codon of target gene	Number of mismatches/gene with mismatch				
			1	2	3	4	5
1	<i>sigH</i>	-222	0	0	0	0	Rv2226, Rv3618
2		-11	0	0	0	0	0
3		+9	0	0	0	0	0
4	<i>pknB</i>	+8	0	0	0	0	Rv0691c
5		+51	0	0	0	0	Rv1904
6		+143	0	0	0	0	Rv2115c
7	<i>pknA</i>	+223	0	0	0	0	0
8		+632	0	0	0	0	Rv0753c
9	<i>inhA</i>	+48	0	0	0	Rv0402c	Rv0680c
10		+120	0	0	0	Rv0352	Rv0050,0130c,0676c
11	<i>dfrA</i>	-62	0	0	0	0	Rv3031
12		-25	0	0	0	Rv1778c	Rv2885c
13	<i>wag31</i>	+26	0	0	0	0	0
14		+144	0	0	0	Rv2880c	0
15	<i>ftsZ</i>	+25	0	0	0	Rv2277c	0
16		+134	0	Rv0186	0	0	Rv1050,Rv0934,Rv3307

Expression of off-target genes highlighted in red was measured in strains with and without induction of *dcas9* and the sgRNA that contains a similar sequence.

**Supplementary Table 2: List of oligonucleotides and primers used in this study.**

<b>oligonucleotides used for sgRNA</b>		
<b>sgRNA</b>	<b>Forward Primer</b>	<b>Reverse Primer</b>
Msm_sigH+11	GGGACCGGTTCGACGTCAGTCATCG	AAACCGATGACTGACGTCGACCGG
Msm_pknB+8	GGGAGTCGGAAAGGTGCTGAGGCG	AAACCGCCTCAGCACCTTTCCGAC
Mtb_pknB+8	GGGAGTCGGACAGGTGGGAAGGGG	AAACCCCTTCCCACCTGTCCGAC
Mtb_pknB+51	GGGACGGACATGCCCCAAATCCA	AAACTGGATTTGGGGGCATGTCCG
Mtb_pknB+143	GGGAAAGGTAAAAACTGGGATCGC	AAACGCGATCCCAGTTTTTTACCTT
Mtb_inhA+48	GGGAGTGAAACGCGATCGACGAGT	AAACACTCGTCGATCGCGTTTTAC
Mtb_inhA+120	GGGATGCGCTGAATCAGCCGACG	AAACGCTGCGGCTGATTCAGCGCA
Mtb_dfrA-62	GGGAGGCGCGCTCATACCGCGAC	AAACGTCGCGGTATGAGGCGCGCC
Mtb_dfrA-25	GGGACACGCGTCACTCCTTGATTC	AAACGAATCAAGGAGTGACGCGTG
Mtb_gyrA-110	GGGAGCGTCGACGTCCTCGCCCAT	AAACGATGGGCGAGGACGTGACG
Mtb_gyrA-25	GGGACCTCGTTTTGCAATCGAACGC	AAACGCGTTTCGATTGCAAACGAGG
Mtb_wag31+26	GGGACTTACTGAACGCCACATTGG	AAACCAATGTGGCGTTCAGTAAGC
Mtb_wag31+144	GGGAGTTGATCCTCTGACGCAGAT	AAACATCTGCGTCAGAGGATCAAC
Mtb_ftsZ+25	GGGAGATACCCACGACCTTGATGA	AAACTCATCAAGGTCGTGGGTATC
Mtb_ftsZ+134	GGGACATCGCTCATCAACAACGCC	AAACGGCGTTGTTGATGAGCGATG
Mtb_pknA+223	GGGATTTCGCCGTAGTCGTGCACGC	AAACGCGTGCACGACTACGGCGAA
Mtb_pknA+632	GGGATCCCAGTGAATAGACGTCGC	AAACGCGACGTCTATTCACTGGGA
<b>Gene</b>	<b>Primers used for qRT PCR</b>	
dcas9	AAGAAGTACAGCATCGGCCTGG	TTCTTGCGCCGCGTGTATCG
Msm_sigH	GAGACAGATGCCGAGCTCAC	AGGCCTTACCATCGTTTTCC
Msm_pknB	CATGGAGTACGTCGACGGTGTGAC	CTTGACATCGCGGTGGATGATG
Msm_sigA	TGCCGATCTGCTTGAGGTAGG	TTCGTGTGGGACGAGGAAGAG
Msm_5'sigA	GACCTTGAGGTGACCGACG	CTTCTTCTCGTCTCTGACTG
Msm_3'sigA	TCGACGAGATCGGCCAGG	TAGTCCAGGTAGTCGCGCAG
Mtb_pknB	ACATTGTCCACACCGAAGGG	GCTGATCATGATGTTTCGCCG
Mtb_inhA	ATCCACATCTCGGCGTATTC	ACGAACCTGTTGACCGACTC
Mtb_dfrA	AGATCACCATGGGGCACAC	GCCATAAAGTCAGCTTGGCG
Mtb_gyrA	TGACATCGAGCAGGAGATGC	AAGCCGGAATCGAACATTGC
Mtb_wag31	TAAGCCGCCTATCGGCAAAC	AGCTCGTTGATCCTCTGACG
Mtb_ftsZ	CAAGGACGAGATCGAAGAGC	GGAATCACGATGAGGGTGTGTC
Mtb_pknA	AAAGCCAGATGAACGGGGAG	TCGAGCATGTCCAGTGCG
Mtb_5'sigA	GAGGACCTCGACCTTGACG	GGCCGCCTCAGCTTCG
Mtb_3'sigA	ACCCACCGAAAAGGACAAGG	CTGTTTGAGGTAGGCGCGAA
Rv0402c	GTCCTCATCTGGCAGCACAT	GGCCCCGATTTCTTCTTGGA
Rv0352	AGACCGAGTTGGATTTCTGTG	TGCAAGTGGGACACACCTTT
Rv1778c	ATCCTCTTTGAAGCCGCCG	GCCACTCGTAGATTCTTGGT
Rv0186	GGATCCTGCGGTTCGATGTTT	TTTTGCAGCAGCAGGATTCC
Rv2880c	AATCGGTGCTGATGCGCTA	CCGTGATAGGTTGCGAGTC
Rv2277c	GTGAATGCCGAGTTGTGGGA	ACCGCATCGAGTCCGATTTT
Rv3307	GAGATCCGGATGTTGCAGA	GGATACGCCAGTACCTCAG
Rv3618	AGTCGTCTCGGGAATTCGT	CAGTAGCAACGTTCCGAAGC
Rv2885c	CAAAGACCAGGTGTGTGTCA	CAGCTCTGCCAGTTCCAATA
<b>Primers used for 5' RACE</b>		
Adapter	GCUGAUGGCGAUGAAUGAACACUGCGUUUGCUGGCUUUGAUGAAA	
Outer forward	GCTGATGGCGATGAATGAACACTG	
Inner forward	CGCGGATCCGAACACTGCGTTTTGCTGGCTTTGATG	
<b>Rv No.</b>	<b>GSP1 (Outer PCR Reverse)</b>	<b>GSP2 (Inner PCR Reverse)</b>
Rv1484	GATGATTCCGCTAACCCAGAAATCCG	GCCGCCGTCGACCGGGATGA
Rv2763c	ATGTGCGCCGGCCCATCACGA	TGTCGCTTGAGCCCAGATCAG
Rv2145c	CCGATAGGCGGCTTACTGAACGCC	ATAAGGACCAATTTCAAACCTAAG

## References

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