

Supplemental Figure 1

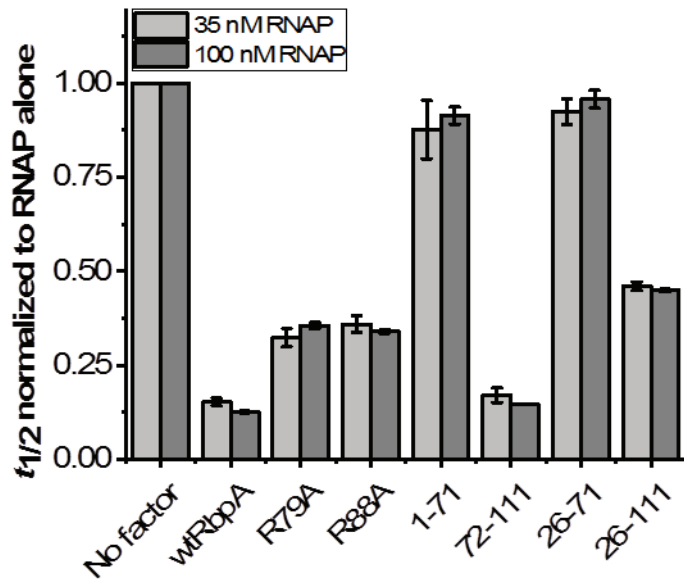


Fig S1. RbpA effects on kinetics at multiple RNAP concentrations. $t_{1/2}$ values, as calculated by the time required to reach half of the final fluorescence intensity, for each sample at 35 nM and 100 nM RNAP are reported, normalized to the $t_{1/2}$ at a given RNAP concentration. At least 3 replicates for each condition are reported, with statistical averages and errors calculated as in Fig 3B and C.

Supplemental Table 1 DEseq2 output for gene expression in *M. smegmatis* expressing RbpA_{Mtb}^{R79A}, RbpA_{Mtb}^{R88A} or RbpA_{Mtb}⁷²⁻¹¹¹ relative to *M. smegmatis* expressing RbpA_{Mtb}^{WT}. BaseMean = the average of the normalized counts of each sample, log2FoldChange = log₂ fold change of the mutant (RbpA_{Mtb}^{R79A}, RbpA_{Mtb}^{R88A} or RbpA_{Mtb}⁷²⁻¹¹¹) relative to wild-type (RbpA_{Mtb}^{WT}). lcfse = log fold change standard error, stat = Wald statistic, pvalue = unadjusted p-value, and padj = Benjamini-Hochberg adjusted p-value for multiple comparisons. Three replicates were included for each strain.

Supplemental Table 2 DEseq2 output for differentially expressed (log₂ fold change < -1.0 or log₂ fold change > 1.0 and padj ≤ 0.05) genes in *M. smegmatis* expressing RbpA_{Mtb}^{R79A}, RbpA_{Mtb}^{R88A} or RbpA_{Mtb}⁷²⁻¹¹¹ relative to *M. smegmatis* expressing RbpA_{Mtb}^{WT}. Columns are defined as in Supplemental Table 1 with the addition of the Mycobrowser product for the 30 genes with the greatest absolute value of log₂ fold change.

Supplementary
Table 3

Primer Name	Primer Sequence (5' - 3')
RbpA forward XbaI	GTCTAGAATGGCTGATCGTGTCTGAGGG
26-111 RbpA forward XbaI	GTCTAGAATGCCGCGCCAGATCGCGC
72-111 RbpA forward XbaI	GTCTAGAATGCCGAAGAAGGTTAAGCCGCC
RbpA forward BamHI	GGGATCCATGGCTGATCGTGTCTGAGGG
26-111 RbpA forward BamHI	GGGATCCATGCCGCGCCAGATCGCGC
72-111 RbpA forward BamHI	GGGATCCCCGAAGAAGGTTAAGCCGCC
RbpA reverse EcoRI	GGAATTCGGCATCGAGGGACGCCTTTC
1-71 RbpA reverse EcoRI	GGAATTCTCACTCGGGCAGGTGCGCCCTC
RbpA reverse HindIII	AAGCTTGGCATCGAGGGACGCCTTTC
1-71 RbpA reverse HindIII	GATAAGCTTCGAATTCTCACTCGGGC
R79A RbpA forward	GGTTAAGCCGCCCGCAGCAGTGGGA
R88A RbpA forward	CATGCTGCTGGAGGCCCGTTCCATCGAAG
R79A RbpA reverse	CCAGTGCCTCGCGGGCGGCTTAAC
R88A RbpA reverse	CTTCGATGGAACGGGCCTCCAGCAGCATG
RbpA 2XFLAG reverse EcoRI	GGAATTCCTCACTTATCGTCTCATCCTTGTAAATCCATCT TATCGTCTCATCCTTGTAAATCCATGCCGCGCCGACGTGAC
MSMEG_0281 RT forward	GGTGCATCAACACGCCAAAGG
MSMEG_0281 RT reverse	GCGAAGTACGTTGCCTCAGAC
MSMEG_1215 RT forward	AACCTGCGGTTCTGTGAACCTCCTC
MSMEG_1215 RT reverse	CGGCCGAGAAGATCTGTTTCGAC
MSMEG_1680 RT forward	ACGTCCTCCACCACGATCATTC
MSMEG_1680 RT reverse	CTGAACGGCTACACGACGAG
MSMEG_2259 RT forward	CACCGTCAGATCCCACATCAG
MSMEG_2259 RT reverse	GGCATCGCGAATCAGTTGCTC
MSMEG_2387 RT forward	GGAGGGCCGGATGACGATCTG
MSMEG_2387 RT reverse	GTGCGGACGACCCTTGAGGAAC
MSMEG_2528 RT forward	CGCGATCCTGATCTGGATGTC
MSMEG_2528 RT reverse	ACTGAGCGCGAGCACTTTC
MSMEG_2758 RT forward	TGCCGATCTGCTTGAGGTAGG
MSMEG_2758 RT reverse	CTTCGTGTGGGACGAGGAAGAG
MSMEG_3297 RT forward	GGTGCCTCACCAGGAAGAAGTTC
MSMEG_3297 RT reverse	ACCTCGATCTCGAGTGGCTCTTC
MSMEG_3499 RT forward	AGCTCTGGTGTATCGGCTGGAAC
MSMEG_3499 RT reverse	TGGTTGAACTGCGGCTGGTAG
MSMEG_3855 RT forward	GCACGATCCACGACGACCG
MSMEG_3855 RT reverse	GACATGACCGCGACCGACG
MSMEG_3966 RT forward	GTGACGGCGACACCTCTACC
MSMEG_3966 RT reverse	ATTGCCACCCGTGGGATCGATG
MSMEG_4222 RT forward	ACCGAGACCACGGGTGGAG
MSMEG_4222 RT reverse	GCCTGAAGGGCGTTCGAGTTCAT
MSMEG_4497 RT forward	GGGCCTCGTCCGAGGATGATGAAC
MSMEG_4497 RT reverse	ACGACATGATGGACACCGAAGTTC
MSMEG_5302 RT forward	GGTGTCTCCATCTTCGCGATGAGTC
MSMEG_5302 RT reverse	CGTGCTTCGTGTTTCGTGTTTCG
MSMEG_6466 RT forward	TGCTGCCGTAAGGATCGTG
MSMEG_6466 RT reverse	ACCGCGACCAAGTGAAGTAAAC
MSMEG_6947 RT forward	AGGAGGAGTTCCTCCACACCTTC
MSMEG_6947 RT reverse	GCTGGACATCGGTGATGAGGC

Supplemental Table 3 Sequences for primers used in this study.