Supplemental Figure 1

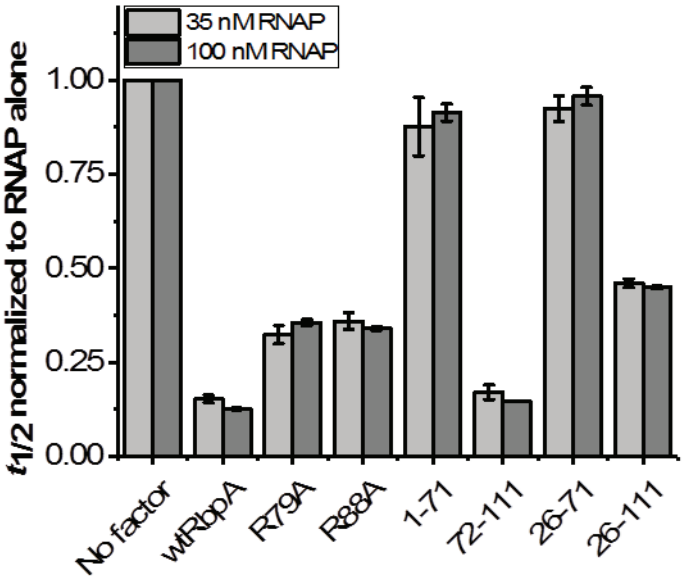

Fig S1. RbpA effects on kinetics at multiple RNAP concentrations. $t_{1/2}$ values, as calculated by the time required to reach half of the final fluorescence intensity, for each sample at 35 nM and 100 nM RNAP are reported, normalized to the $t_{1/2}$ at a given RNAP concentration. At least 3 replicates 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 $RbpA_{Mtb}^{72\text{-}111}$ relative to *M. smegmatis* expressing $RbpA_{Mtb}^{WT}$. BaseMean = the average of the normalized counts of each sample, log2FoldChange = $\log_2$ fold change of the mutant ($RbpA_{Mtb}^{R79A}$, $RbpA_{Mtb}^{R88A}$ or $RbpA_{Mtb}^{72\text{-}111}$) 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 ($\log_2$ fold change < -1.0 or $\log_2$ fold change > 1.0 and padj ≤ 0.05) genes in *M. smegmatis* expressing $RbpA_{Mtb}^{R79A}$, $RbpA_{Mtb}^{R88A}$ or $RbpA_{Mtb}^{72\text{-}111}$ 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	GTCTAGAATGGCTGATCGTGTCCTGAGGG
26-111 RbpA forward XbaI	GTCTAGAATGCCGCGCCAGATCGCGC
72-111 RbpA forward XbaI	GTCTAGAATGCCGAAGAAGGTTAAGCCGCCC
RbpA forward BamHI	GGGATCCATGGCTGATCGTGTCCTGAGGG
26-111 RbpA forward BamHI	GGGATCCATGCCGCGCCAGATCGCGC
72-111 RbpA forward BamHI	GGGATCCCCGAAGAAGGTTAAGCCGCCCC
RbpA reverse EcoRI	GGAATTCGGCATCGAGGGACGCCTTTC
1-71 RbpA reverse EcoRI	GGAATTCTCACTCGGGCAGGTCGCCCTC
RbpA reverse HindIII	AAGCTTGGCATCGAGGGACGCCTTTC
1-71 RbpA reverse HindIII	GATAAGCTTCGAATTCTCACTCGGGC
R79A RbpA forward	GGTTAAGCCGCCCGCGACGCACTGGGA
R88A RbpA forward	CATGCTGCTGGAGGCCCGTTCCATCGAAG
R79A RbpA reverse	CCAGTGCGTCGCGGGCGGCTTAAC
R88A RbpA reverse	CTTCGATGGAACGGGCCTCCAGCAGCATG
RbpA 2XFLAG reverse EcoRI	GGAATTCTCACTTATCGTCGTCATCCTTGTAATCCATCT TATCGTCGTCATCCTTGTAATCCATGCCGCGCCGACGTGAC
MSMEG_0281 RT forward	GGTGCGATCAACACGCCAAAGG
MSMEG_0281 RT reverse	GCGAAGTACGTTGCCTCAGAC
MSMEG_1215 RT forward	AACCTGCGGTTCGTGAACTTCCTC
MSMEG_1215 RT reverse	CGGCCGAGAAGATCTGTTCGAC
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	GGTGCGTCACCAAGGAAGAACTC
MSMEG_3297 RT reverse	ACCTCGATCTCGAGTGGCTCTTC
MSMEG_3499 RT forward	AGCTCTGGTGATCGGCTGGAAC
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	GCCTGAAGGGCGTCGAGTTCAT
MSMEG_4497 RT forward	GGGCCTCGTCGAGGATGATGAAC
MSMEG_4497 RT reverse	ACGACATGATGGACACCGAACTC
MSMEG_5302 RT forward	GGTGCTCCATCTTCGCGATGAGTC
MSMEG_5302 RT reverse	CGTGCTTCGTGTTCGTGTTCG
MSMEG_6466 RT forward	TGCTGCCGTACTGGATCGTG
MSMEG_6466 RT reverse	ACCGCGACCAGTGAGTAACC
MSMEG_6947 RT forward	AGGAGGAGTTCTTCCACACCTTC
MSMEG_6947 RT reverse	GCTGGACATCGGTGATGAGGC

Supplemental Table 3 Sequences for primers used in this study.