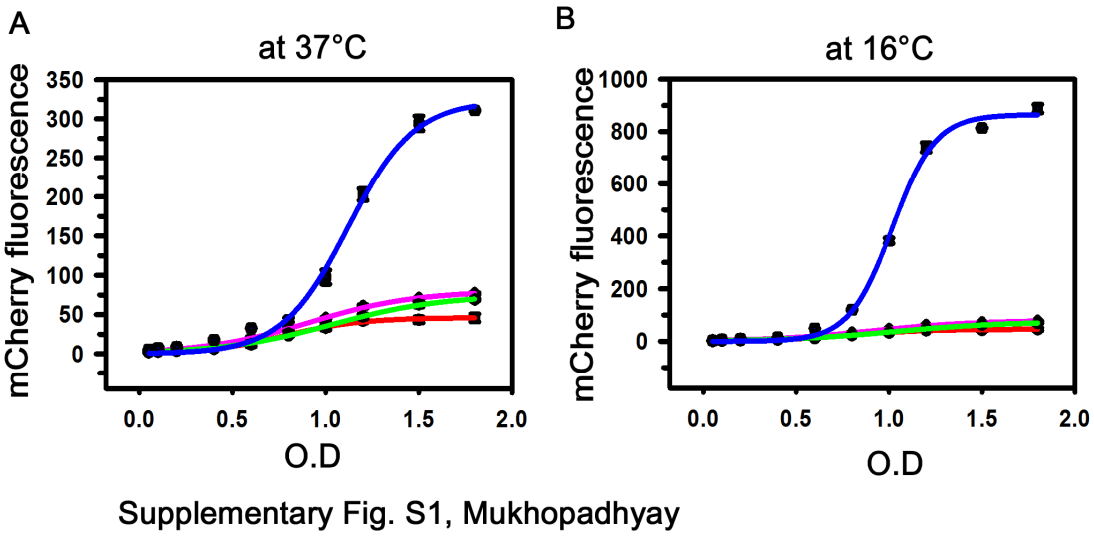
SUPPLEMENTARY DATA:

Supplementary Figures:

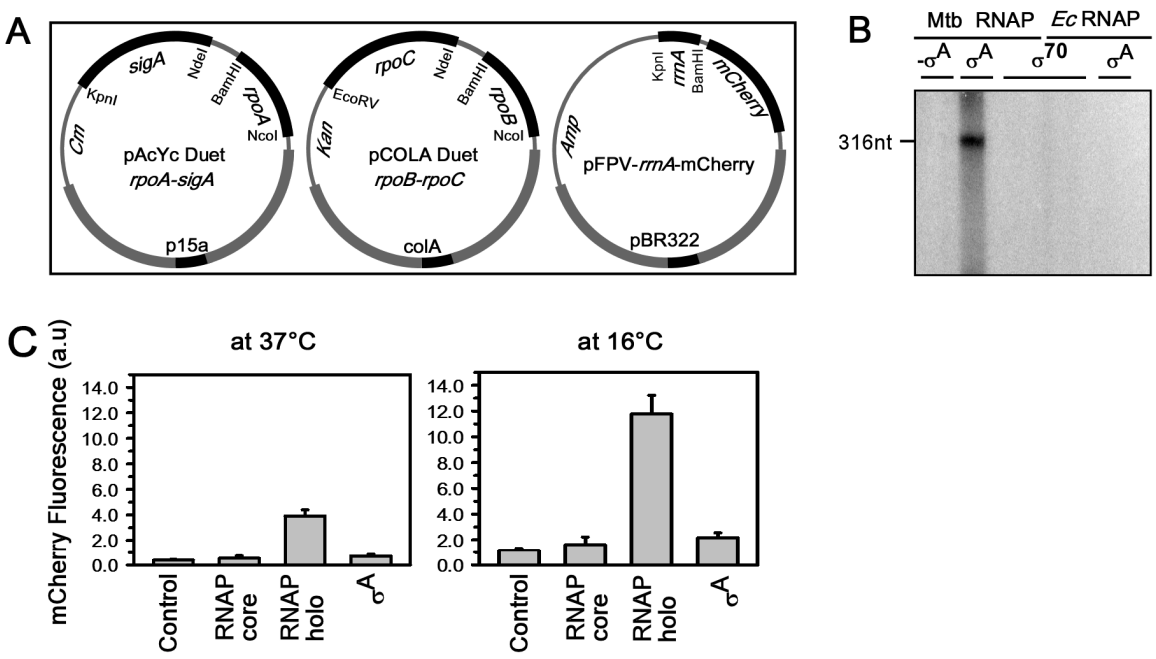


Supplementary Fig. S1, Mukhopadhyay

Supplementary Fig. S1: *In vivo* recombinant Mtb reporter assay: Dependence of mCherry expression as a function of *E. coli* growth:

A. Fluorescent intensity of mCherry was measured at regular intervals and plotted as a function of OD. Fluorescent intensity gets saturated at OD (595) = 1.5. Red Line: pFPVmCherry *sinP3*, Green Line: RNAP core + pFPVmCherry *sinP3*, Pink line: Mtb σ^A + pFPVmCherry *sinP3*, Blue line: RNAP-holo + pFPVmCherry *sinP3*. Assays were conducted at 37°C for 6 hours.
B. Same as (A), assays were conducted at 16°C for 16 hours.

The data represents the mean of three replicates and error bars represent standard deviations.



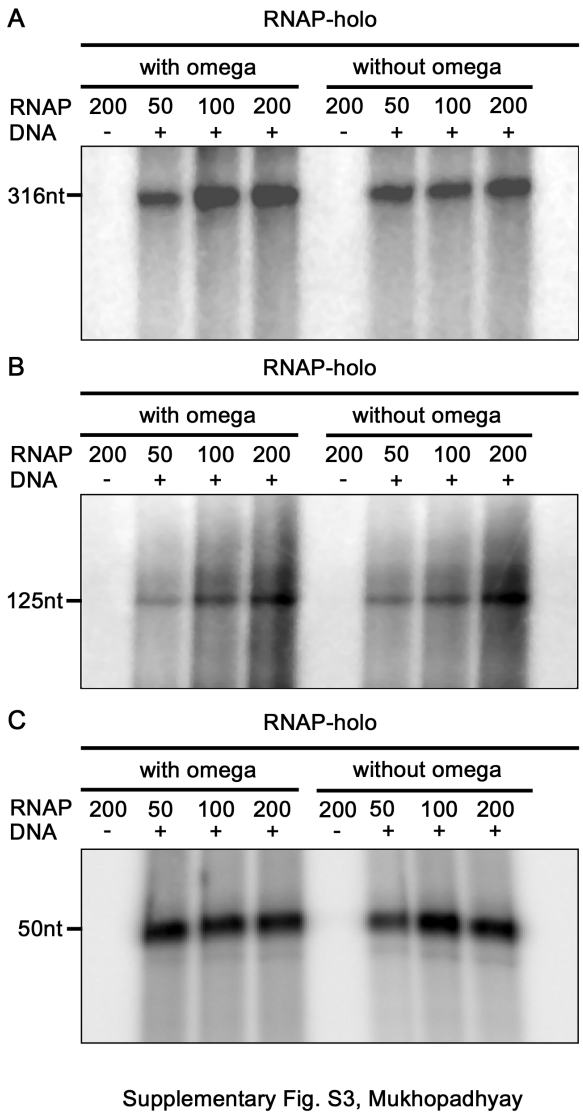
Supplementary Fig. S2, Mukhopadhyay

Supplementary Fig. S2: Recombinant *in vivo* Mtb reporter assay in *E. coli* using Mtb σ^A specific promoter *rrnA*:

A. Strategy: three plasmid expression system, dual plasmid (first two plasmids) for expression of Mtb RNAP holo and the third plasmid containing a σ^A dependent promoter element *rrnA* for expression of mCherry. All three plasmids were transformed in *E. coli* Bl21 (DE3) cells and then the cells were grown at 37^OC up to OD (at 595 nm) 0.4 and induced with 0.5 mM IPTG at different growth conditions.

B. *In vitro* transcription assay to assess the interactions between Mtb core and *E. coli* σ^{70} and *E. coli* RNAP core with Mtb σ^A. *rrnA* was used as a DNA fragment. Run-off transcripts of 316 nucleotides (nt) were produced. Lane 1: Mtb RNAP core, Lane 2: Mtb RNAP core + Mtb σ^A, Lane 3: Mtb RNAP core + *E. coli* σ^{70}, Lane 4: *E. coli* RNAP + *E. coli* σ^{70}, Lane 5*: E. coli* RNAP + Mtb σ^A.

C. Results for recombinant Mtb reporter assays: The bars represent mCherry fluorescence of *E. coli* cells containing pFPVmCherry-*rrnA* plasmid in presence of the following; 1. No Mtb RNAP; 2. Mtb RNAP core (pAcYc Duet *rpoA-rpoZ* + pCOLA Duet *rpoB-rpoC*); 3. Mtb RNAP holo (as in Fig. S2); 4. σ^A: (pAcYc Duet-*sigA*). The data represents the mean of three replicates and error bars represent standard deviations.
Left panel: cells were induced with 0.5 mM IPTG at 37^OC for 6 hrs.
Right panel: cells were induced with 0.5 mM IPTG at 16^OC for 16 hrs.
The data represents the mean of three replicates and error bars represent standard deviations.



Supplementary Fig. S3, Mukhopadhyay

Supplementary Fig. S3: Effect of ω subunit on *in vitro* transcriptional activity of Mtb RNAP:

Assays were performed with the purified Mtb RNAP holo (with and without ω subunit) samples.

A. Assays with RNAP-σ^A holo and *rrnA* promoter DNA fragment. Lane 1, 5: No DNA, Lane 2-4: RNAP holo with ω subunit; Lane 6-8: with RNAP holo without ω subunit. Run-off transcripts were 316 nt.

B. Same as (A) with Mtb CRP dependent promoter *WhiB1*. Mtb CRP was incubated with RNAP holo before open complex formation. Run-off transcripts were 125 nt.

C. Same as (A) with RNAP-*sigE* holo enzyme and *sigE* dependent promoter *SigBpr*. Run-off transcripts were 50 nt.

Supplementary Table S1: Oligonucleotides used in this study:

Name of the primer	Sequences
pFPV-mCherry *sinP3* fwd	GAATTCCAGCCAGAAGTCATACCGTA
pFPV-mCherry *sinP3* rv	GGATCCGTATTCGGTTTCATGTTTCT
pFPVmcherry *rrnA* fwd	TCTGGTACCTCGTGGAGAACCTGGTGAGTC
pFPVmcherry *rrnA* rv	TCTGGATCCTACGCCGCCAGCGTTCGT
pBlueScriptII *sigBpr* fwd	CGTCTGTTGGCCGGCG
pBlueScriptII *sigBpr* rv	CCCTTGTGGGTGCATCGG
pBSII- *WhiB1* fwd	GCTCTAGAGCAAGAAAGCGGATCTG
pBSII- *WhiB1* rv	GCAAGCTTGCCTTGTGGCGCCAATC
pET 28a-Mtb CRP fwd	CATCCGGAATTCGTGGACGAGATCCTGGCC
pET 28a-Mtb CRP rv	CATCATACTCGAGCACTATTACCTCGCTCGGCGGGC
pET 28a-*E. coli* CRP fwd	CGAAACATATGGTGCTTGGCAAACCGCA
pET 28a-*E. coli* CRP rv	GCGTTGGATCCAATTTAACGAGTGCCGT
pFPV mCherry-CRP fwd	CCCGCGAAATTAATACGACTCACTATAGGGG
pFPV mCherry-CRP rv	TTAAAGCTTTTACCTCGCTCGGCGG
pAcYc Duet *sigA* fwd	GGAATTCGTGGCAGCGACCAAAG
pAcYc Duet *sigA* rv	ATAAGAATGCGGCCGCTCAGTCCAGGTA
pAcYc Duet *sigE* fwd	CCAGGATCCGAATTCCATCATGGAACTCCTCGG
pAcYc Duet *sigE* rv	CCGAGGAGTTCCATGATGGAATTCGGATCCTGG

Supplementary Table S2: Cloning strategies:

Name of the plasmid	Restriction enzymes used and cloning strategies	Source of gene
pCOLA *rpoB-rpoC*		Banerjee *et al* (24)*
pAcYc Duet *rpoA-rpoZ*		Banerjee *et al* (24)*
pAcyC Duet *rpoA- sigA*		Banerjee *et al* (24)*
pCDF 1b *rpoZ*		Banerjee *et al* (24)*
pAcYc Duet *rpoA- sigE*	*rpoA:*NcoI & BamHI; *sigE*: EcoRV &XhoI	Genomic DNA
pFPVmcherry-*sinP3*	*sinP3*: EcoRI & BamHI	Synthetic DNA
pFPVmcherry-*rrnA*	*rrnA*: KpnI & BamHI	Verma *et al* (21)**
pFPV mcherry-*sigBpr*	*sigBpr*: KpnI & BamHI	Genomic DNA
pFPV-mcherry-*WhiB1*	*WhiB1*: KpnI & BamHI	Genomic DNA
pFPV-mcherry-*WhiB1*-CRP	*Rv3676*: EcoRV & Hind III	Genomic DNA
pET 28a-Mtb CRP	*Rv3676*: EcoRI & XhoI	Genomic DNA
pET 28a- *E. coli* CRP	*CRP*: NdeI & BamHI	Genomic DNA
pAcyC Duet- *sigA*	*sigA*: EcoRI & NotI;	Genomic DNA
pAcyC Duet- *sigE*	*sigE*: EcoRV &XhoI	Genomic DNA
pBluescript II Sk(+)-*WhiB1*	*WhiB1*:SmaI	Genomic DNA
pBluescript II Sk(+)-*rrnA*	*rrnA*: SmaI	Genomic DNA
pBluescript II Sk(+)-*sigBpr*	*SigBpr*:SmaI	Genomic DNA

Supplementary Reference:

*** Banerjee R, Rudra P, Prajapati RK, Sengupta S, Mukhopadhyay J.** 2014. Optimization of recombinant Mycobacterium tuberculosis RNA polymerase expression and purification. *Tuberculosis* (Edinb) **94:**397-404.

****Verma A, Sampla AK, Tyagi JS.** 1999. Mycobacterium tuberculosis rrn promoters: differential usage and growth rate-dependent control. Journal of bacteriology **181:**4326-4333.