

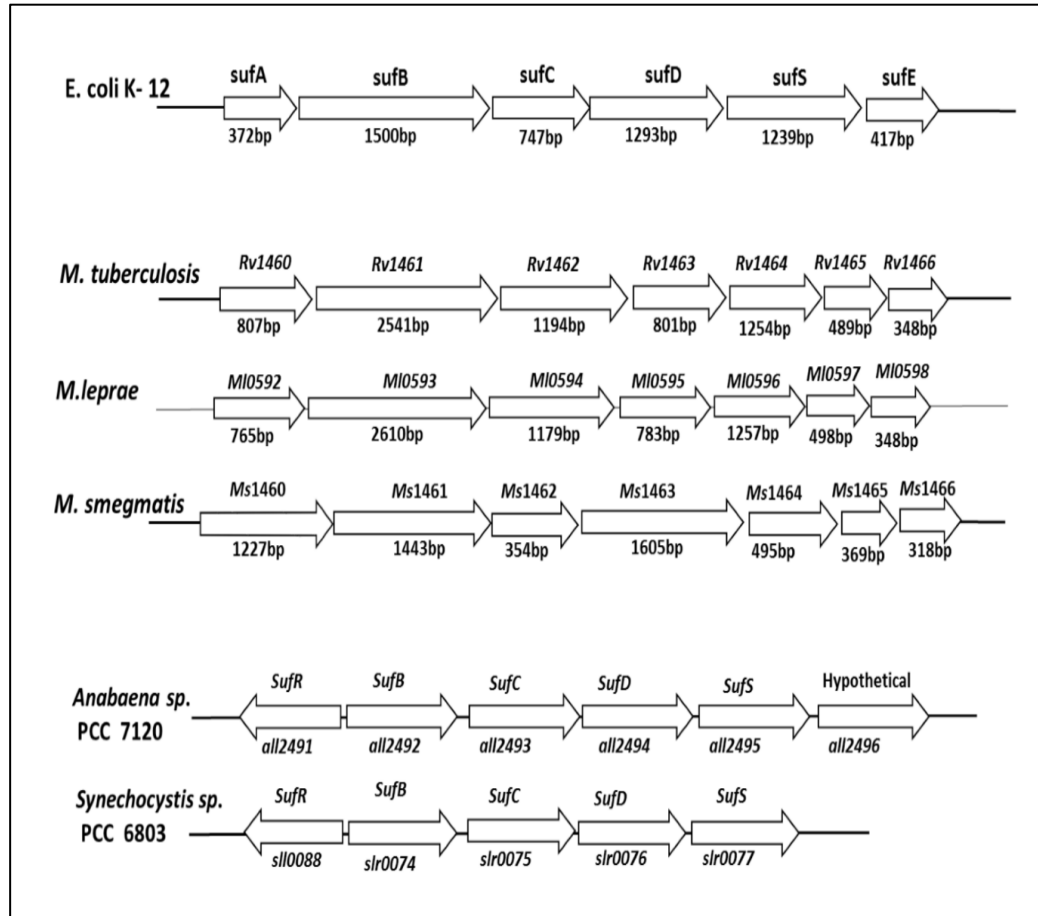
**Title: Iron homeostasis in *Mycobacterium tuberculosis* is essential for persistence**

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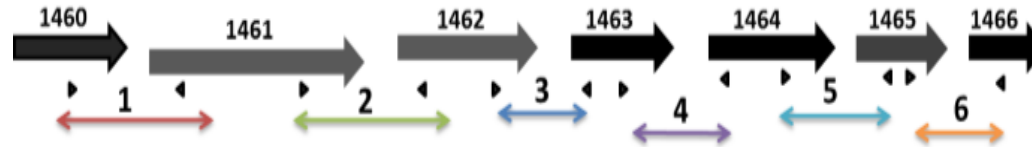
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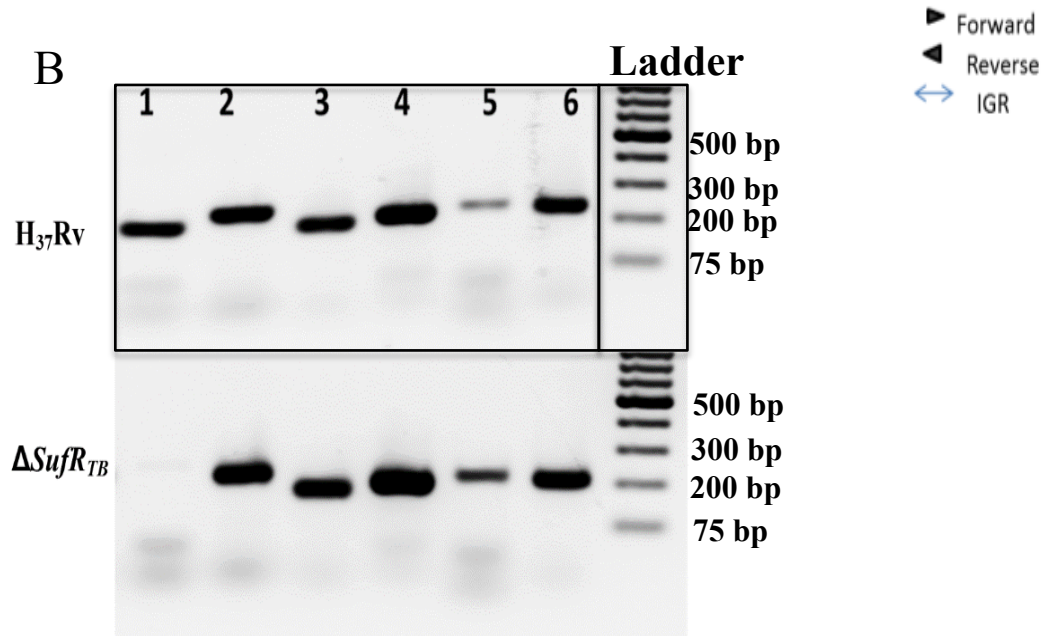


**Supplementary Figure: 1**

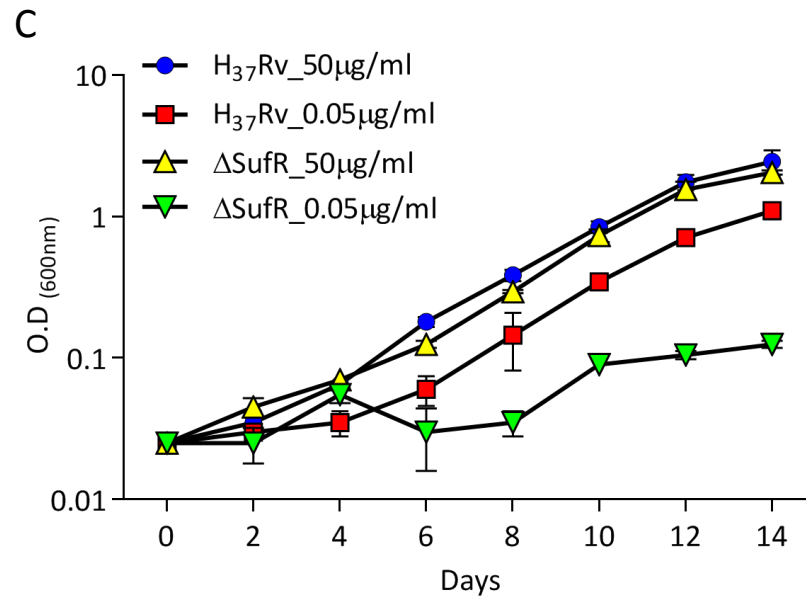
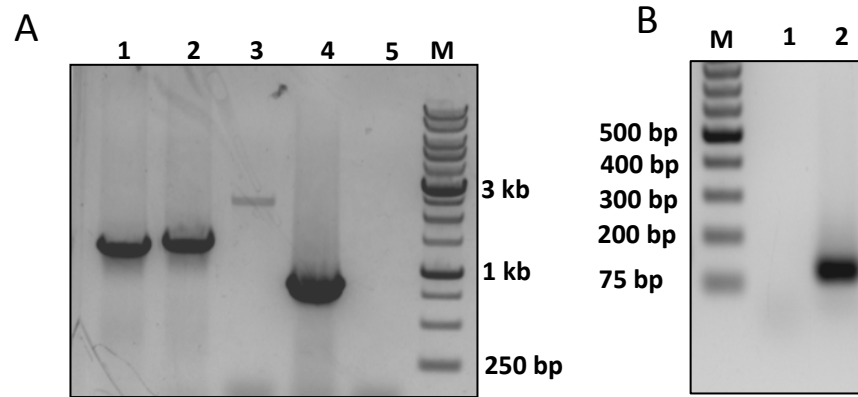
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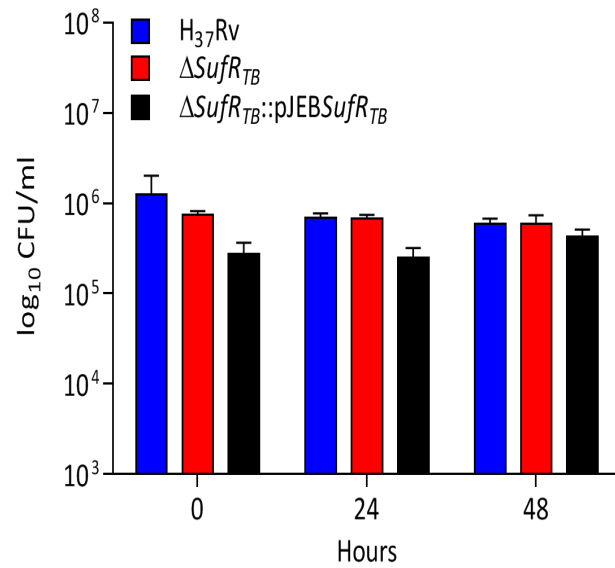
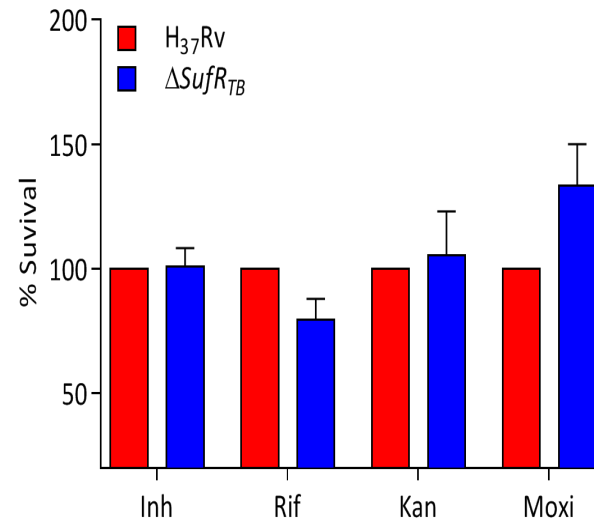
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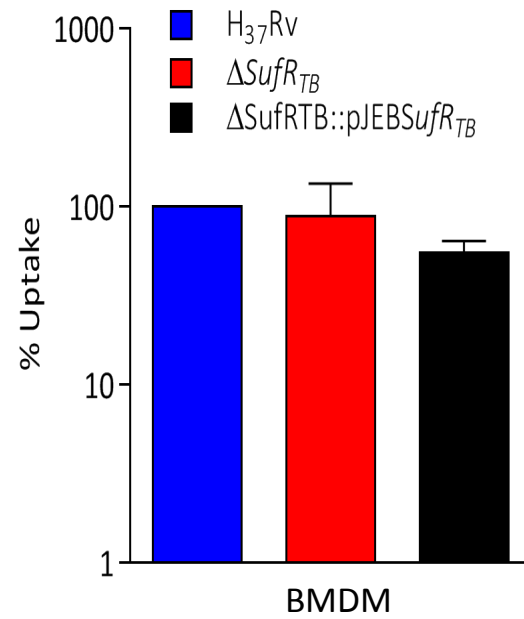
**Supplementary Figure: 2**



**Supplementary Figure: 3**

**A****B****Supplementary Figure: 4**

A



**Supplementary Figure: 5**

## Supplementary figure Legends

**Supplementary Figure 1: Map depicting comparative gene organization of the ISC locus in different bacteria.** The gene organization of the ISC locus from three mycobacterial species were compared with the available sequence of *Synechocystis* sp. Strain PCC 6803, *Anabaena* sp. Strain PCC 7120 and the *E. coli* genome sequence. The arrows indicate the direction of the transcription.

**Supplementary Figure 2: Transcript analysis of Suf operon in Mtb** **A.** Schematic representation of ISC operon in Mtb, arrowheads show the primers used for the transcript analysis. **B.** PCR amplification of intergenic regions using cDNA from wild type and  $\Delta$  *sufR*<sub>TB</sub> strains as a template.

**Supplementary Figure 3: Mutant confirmation:** **A.** *sufR*<sub>TB</sub> gene deletion mutant ( $\Delta$ *sufR*<sub>TB</sub>) confirmation by PCR. Lane 1 & 2: Amplification of the *sufR* flanking region confirms gene specific insertion of the hygromycin cassette, Lane 3: 2.0 kb amplicon using *sufR*<sub>TB</sub> gene specific primers further confirms the insertional deletion of the *sufR*<sub>TB</sub> gene, lane 4: Depicts amplification of *sufR*<sub>TB</sub> gene (807bp) using H37Rv genomic DNA as a positive control, lane 5: No template control. **B.** The absence of *sufR* transcript in  $\Delta$  *sufR*<sub>TB</sub> strains is further confirmed by semi-quantitative PCR using  $\Delta$  *sufR*<sub>TB</sub> cDNA as a template (Lane 1) and wild type H37Rv (Lane 2) strains. **C.** Growth kinetics of unmarked *sufR*<sub>TB</sub> gene in minimal media at different iron concentrations.

**Supplementary Figure 4: SDS and Drugs susceptibility assay:** **A.** Survival of wild type, mutant and complemented strain in 7H9 enriched media containing 0.1% SDS. Growth differences were estimated by CFU plating at 24 and 48 hours post treatment. **B.** Survival of wild type, mutant and complemented strain in 7H9 enriched media containing 1X MIC of different anti TB drugs. Difference was estimated by CFU plating at 72 Hours.

**Supplementary Figure 5: Drugs susceptibility:** **A.** Survival of wild type, mutant and complemented strain in 7H9 enriched media with MIC of different anti TB drugs. Difference was estimated by CFU plating at 72 Hours.

**Supplementary Figure 6: BMDM uptake assay:** **A.** Relative uptake of H37Rv,  $\Delta$  *sufR<sub>TB</sub>* and  $\Delta$  *sufR<sub>TB</sub>*:pJEB *sufR<sub>TB</sub>*) in bone marrow derived macrophages, 4 hours post infection.



**Table: S1**  
**Mutant confirmation primers**

<b>Primer</b>	<b>Sequence</b>
1460_F1	ATGATATCATTCCGGACGGGGTTTGACTG
1460_R1	ATGCGGCCGCTGATCGGTCTACCAGGGATGC
1460_F2	ATCTCGAGGGAGCGTCCCGATGACAC
1460_R2	ATGGGCCCTTCAGCCTTCCACCCATTGCG
Rv1460-conf1	CAGCGTGATCAGGATGGAACC
Rv1460-conf2	GGTAGATCAGGAAGTCACCCTC

**Table: S2**  
**Quantitative analysis primers**

<b>Primers</b>	<b>Sequence</b>
1460-RT-F	ATCGCAACGGCGCTCAGCAAAG
1460-RT-R	CTGCTGCTCGGTTTCGCACAAT
1461-RT-F	CGTTCCAGTTGCAGTCCATCC
1461-RT-R	CACCTGGTAGATGTCCTTGCGAAC
1462-RT-F	CGACAACACCGTTCACCTCAGC
1462-RT-R	CGTCGTCGGCGAAATACAGC
1463-RT-F	CTGGGTCAAAGAGGTCAAGGC
1463-RT-R	GCGATCTTGGGCTTGAGCAG
1464-RT-F	GGCCCCGGCGACGTGATCGT
1464-RT-R	GTCCAGATACAGCGAGTCCAG
1465-RT-F	CACTACAAGCATCCGCAGCATC
1465-RT-R	ACAGCCTTGTCCGTCATAGGAAAC
1466-RT-F	GTGCAAGACGGTGACGAAGG
1466-RT-R	CCCAGTTGATGCGGATGTCGTC
1460/61-RT-F	CATCGTCAACGGAGACTGCG
1460/61-RT-R	ATCGCCTCTTCCTGGGTCAG
1461/62-RT-F	CTGTTCTACCTGATGAGCCGC
1461/62-RT-R	TCGCCCTTGTTGTGTGCGATC
1462/63-RT-F	CGCGGCTTCTTCGGTGAG
1462/63-RT-R	TCCGCGGGGTTCTCCAC
1463/64-RT-F	CGAACTCGACCAGAACGGC
1463/64-RT-R	CCGGAGTCCAAATACGCCAAC
1464/65-RT-F	GCGTCGTTGCGGGTGTAC
1464/65-RT-R	GCCGCAGATCGGGTTCAC
1465/66-RT-F	GTGAAATGCGCGCTGCTC
1465/66-RT-R	CGTCCAAGCCGTAGACCAG
SigA-RT-F	GAGGACCACGAAGCCTCGAAG
SigA-RT-R	GTTTGAGGTAGGCGCGAACC

**Table: S3**  
**Strains and Plasmids**

Strains/Plasmids	Description	Source
XL-1 Blue (E. coli)	recA1 endA1 gyrA96 thi-1hsdR17 supE44 relA1 lac [F' proAB lacIq ZM15 Tn (Tetr)]	Stratagene, USA
H <sub>37</sub> Rv	Laboratory strain of M.tb	A generous gift from Christopher M. Sassetti.
$\Delta$ sufR <sub>TB</sub> Rv1460 mutant	Mutant strain of H <sub>37</sub> Rv	This study
$\Delta$ sufR <sub>TB</sub> (Unmarked strain)	Unmarked mutant strain of H <sub>37</sub> Rv	This study
$\Delta$ sufR <sub>TB</sub> :pJEB $\Delta$ sufR <sub>TB</sub> Rv1460 complemented	Rv1460: kan complemented with Rv1460 at attB site.	This study
pJM1	Suicidal vector Hyg <sup>R</sup>	A generous gift from Christopher M. Sassetti.
pJEB-402	Shuttle vector kan <sup>K</sup>	A generous gift from Christopher M. Sassetti.

**Table: S4**  
**Standard operating conditions of the ICP-MS used for the analysis**

<b>PARAMETER</b>	<b>ICPMS (Thermo Scientific X-Series 2)</b>
RF Power	4.2 Kw
Carrier Gas Flow Rate	20 ml/min
Collision Cell Gas	He (93%) + H (7%)
Collision Cell Gas Flow Rate	2-10 ml /min
Nebulizer Pump Rate	0.5 rps (30 RPM)
Uptake Time	30 s
Wash Time	60- 70 s
Standard Used (NIST 2711a)	2.82±0.04 (in %)