**Supplemental Table S1. Bacterial strains used in this study.**

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| --- | --- | --- | --- | --- |
| **Name** | **Bacteria** | **Description** | **Use** | **Source** |
| Mtb Erdman | *M. tuberculosis* | Wild-type | RNA extraction | Lab strain |
| Mc2155 | *M. smegmatis* | Wild-type | RNA extraction; used to create *dciAMsm attB::*tet*dciAMtb* | Lab strain |
| *dciAMsm attB::*tet*dciAMtb* | Strain (*M. smegmatis)* | Endogenous dciAMsm (*MSMEG\_0004)* deleted; dciAMtb (Erdman\_0004) integrated at *attB* site by using pMSG430 (*kanR*) | Backbone to create other strains through allelic exchange; | This study |
| Tet-DciA | *M. smegmatis* | *dciAMsm attB::*tet*dciAMtb* transformed with pTetR (*hygR*) | Tet-On *dciAMtb* depletion strain | This study |
| rgm36 | *M. smegmatis* | Endogenous *dnaA* deleted; dnaA under the control of the amylase promoter [Greendyke et al. 2002] | Acetamide-On *dnaA* depletion strain | [1] |
| csm362 | *M. smegmatis* | Endogenous ftsZ deleted; ftsZ integrated at *attB* site by using pMSG430 (*kanR*); transformed with pTetR (*hygR*) | Tet-On *ftsZ* depletion strain | This study |
| *dciAMsm attB::*tet*dciAMtbZeo* | *M. smegmatis* | Endogenous dciAMsm (*MSMEG\_0004)* deleted; dciAMtb (Erdman\_0004) integrated at *attB* site by using pDB19 (*zeoR*) | Served as backbone to create HA-DciAMtb and W113A strains through gene-switching/marker exchange | This study |
| HA-DciAMtb | *M. smegmatis* | Generated through the process of gene-switching/marker-exchange by transforming *dciAMsm attB::*tet*dciAMtbzeo* with pMSG430 HA-DciAMtb | *In vivo* Immunoprecipitation experiments, as only allele of DciAMtb is HA-tagged. | This study |
| W113A | *M. smegmatis* | Generated through the process of gene-switching/marker-exchange by transforming *dciAMsm attB::*tet*dciAMtbzeo* with pMSG430 DciAMtbW113A | Only allele of DciA is point mutant DciAMtbW113A | This study |
| Wild-type Control (wt ctrl) | *M. smegmatis* | Generated through the process of gene-switching/marker-exchange by transforming *dciAMsm attB::*tet*dciAMtbzeo* with pMSG430 DciAMtb (genetically same as *dciAMsm attB::*tet*dciAMtb* but made through gene switching in parallel with the W113A strain) | Control for W113A | This study |
| HA-CarD | *M. smegmatis* | Endogenous *carDMsm* is deleted, C-terminally HA-tagged CarDMtb is expressed from the *attB* site as the only allele of *carD* | Used as positive control for ChIP | [2] |
| DH5 | *E. coli* |  | Used for cloning | Invitrogen |
| BL21 (DE3) | *E. coli* |  | Used to induce proteins through pGEX-6P and pET-SUMO | Novagen |

**Reference**

1. Greendyke R, Rajagopalan M, Parish T, Madiraju MVVS. Conditional expression of Mycobacterium smegmatis dnaA, an essential DNA replication gene. Microbiology. 2002;148: 3887–900. Available: http://www.ncbi.nlm.nih.gov/pubmed/12480893

2. Stallings CL, Stephanou NC, Chu L, Hochschild A, Nickels BE. CarD Is an Essential Regulator of rRNA Transcription Required for Mycobacterium tuberculosis Persistence. Cell. Elsevier Ltd; 2009;138: 146–159. doi:10.1016/j.cell.2009.04.041