Supp

Molecular basis for D

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RNA-Seq Dif

Overview of experimental set-up

	Biological Replicate 1	Biological Replicate 2	Biological Replicate 3	
U	1	4	7	BCG *darG* -sgRNA medium only,
ATC	2	5	8	BCG *darG* -sgRNA + 200 ng/ml A
MMC	3	6	9	BCG *darG* -sgRNA + 20 ng/ml mi

Abbreviations:

U	untreated
ATC	anhydrotetracycline to induce *darG* silencing
MMC	mitomycin C

Notes to experimental procedure (see material and methods for detailed information)

→ RNA was depleted of ribosomal RNA, fragmented and random primed for first and se
→ cDNA was end repaired, 5' phosphorylated and dA-tailed before adapter ligation, PCF

Notes to analysis procedure (see material and methods section for further information)

→ Reads were trimmed and aligned to the *M. bovis* BCG Pasteur 1173P2 genome (NC_
→ After extraction of gene hit counts, DESeq2 was used to compare gene expression bet
→ The Wald test was used to generate p-values and log2 fold changes, and adjusted p val
→ Genes with an adjusted p-value < 0.1 and absolute log2 fold change <-1, > 1 were call
→ DE genes padj <0.1, log2FC <-1, >1
→ Where adjusted p values were returned as 0, the value 1.83666353188857E-297 was a

Data accession

→ GSE number: GSE174526
→ Data page link: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE174

plementary Dataset 1

DarT ADP-ribosylation of a DNA base

ankevicius[1,3], Tim D. W. Claridge[4], Sharon L. Kendall[5], Shan Goh[5] and Graham R. Stewart[2,*],

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fferential Expression Analysis

incubation time: 48 h
.TC, incubation time: 48 h
tomycin C, incubation time: 24 h

cond strand cDNA synthesis.
R enrichment and sequencing on Illumina HiSeq (GENEWIZ).

_008769).
ween BCG *darG* -sgRNA uninduced and ATC-induced, and mitomycin C treated.
lues
ed as differentially expressed genes for each comparison.

ssigned (the lowest adjusted p value of the dataset) to allow -log10 transformation.

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