

CORRECTION

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Correction to: Comparative transcriptomics reveals PrrABmediated control of metabolic, respiration, energy-generating, and dormancy pathways in *Mycobacterium smegmatis*

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Correction to: *BMC Genomics*

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Following the publication of the original article [1], the authors reported an error in Fig. 1 of the PDF version of their article. Due to a typesetting mistake, a previous version of the figure was placed in the PDF, which therefore did not match the correct Fig. 2 given in the HTML version.

The original article has been corrected.

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Reference

1. Maarsingh, et al. Comparative transcriptomics reveals PrrABmediated control of metabolic, respiration, energy-generating, and dormancy pathways in *Mycobacterium smegmatis*. *BMC Genomics*. 2019;20:942 <https://doi.org/10.1186/s12864-019-6105-3>.

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The incorrect figure was:

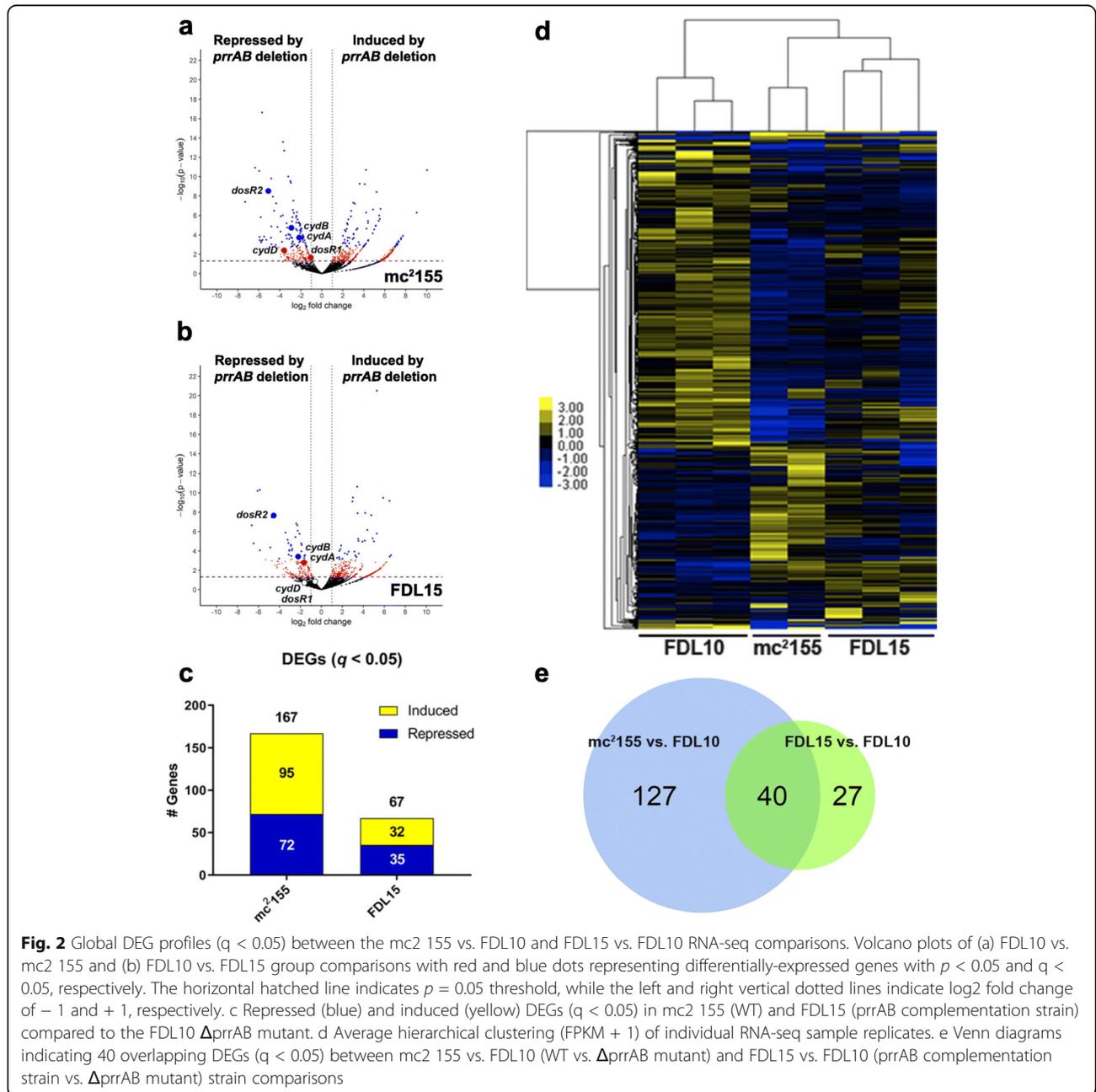


Fig. 2 Global DEG profiles ($q < 0.05$) between the mc2 155 vs. FDL10 and FDL15 vs. FDL10 RNA-seq comparisons. Volcano plots of (a) FDL10 vs. mc2 155 and (b) FDL10 vs. FDL15 group comparisons with red and blue dots representing differentially-expressed genes with $p < 0.05$ and $q < 0.05$, respectively. The horizontal hatched line indicates $p = 0.05$ threshold, while the left and right vertical dotted lines indicate log₂ fold change of - 1 and + 1, respectively. c Repressed (blue) and induced (yellow) DEGs ($q < 0.05$) in mc2 155 (WT) and FDL15 (*prrAB* complementation strain) compared to the FDL10 Δ *prrAB* mutant. d Average hierarchical clustering (FPKM + 1) of individual RNA-seq sample replicates. e Venn diagrams indicating 40 overlapping DEGs ($q < 0.05$) between mc2 155 vs. FDL10 (WT vs. Δ *prrAB* mutant) and FDL15 vs. FDL10 (*prrAB* complementation strain vs. Δ *prrAB* mutant) strain comparisons

The correct figure is:

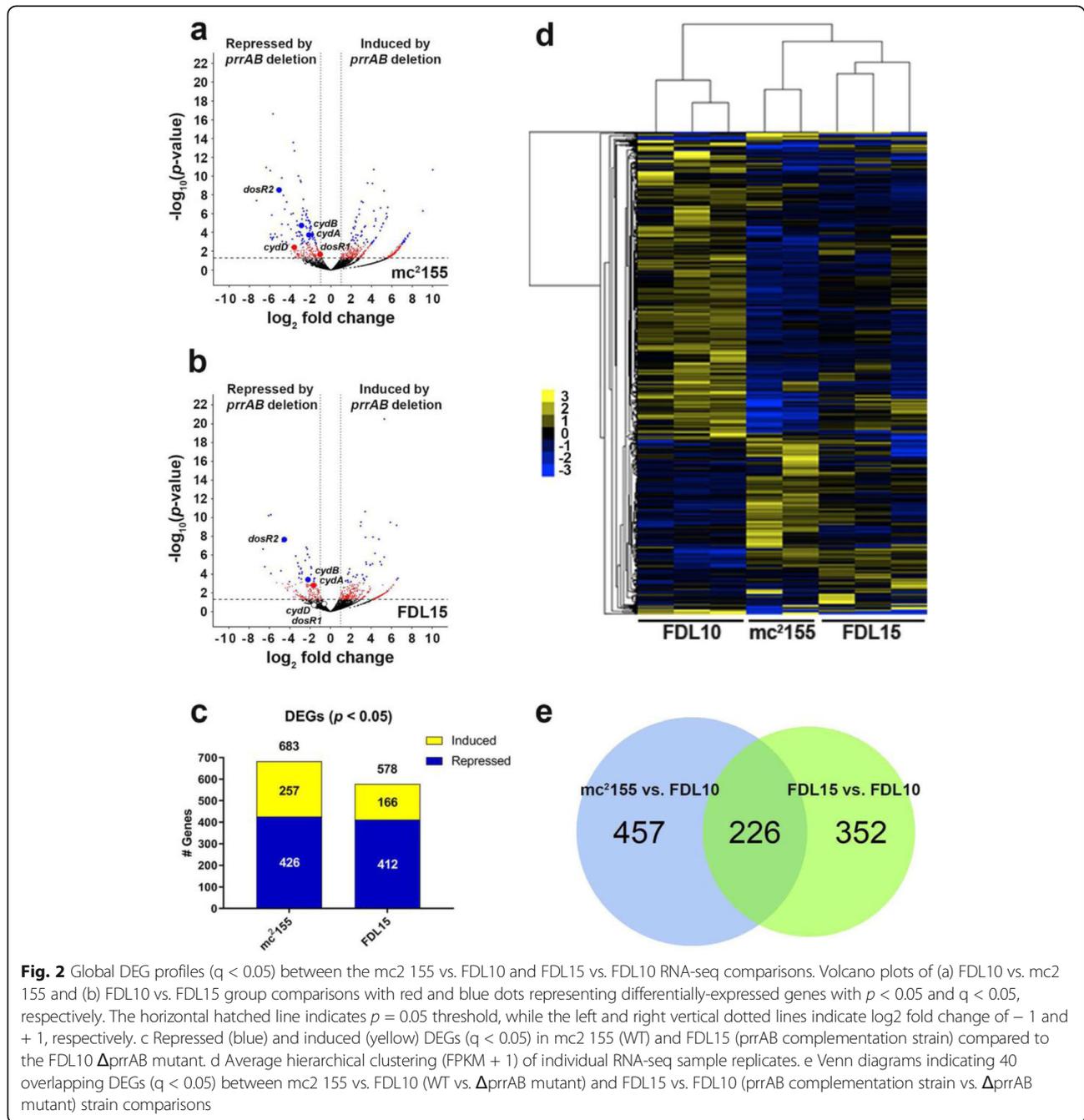


Fig. 2 Global DEG profiles ($q < 0.05$) between the mc²155 vs. FDL10 and FDL15 vs. FDL10 RNA-seq comparisons. Volcano plots of (a) FDL10 vs. mc²155 and (b) FDL10 vs. FDL15 group comparisons with red and blue dots representing differentially-expressed genes with $p < 0.05$ and $q < 0.05$, respectively. The horizontal hatched line indicates $p = 0.05$ threshold, while the left and right vertical dotted lines indicate \log_2 fold change of -1 and $+1$, respectively. c Repressed (blue) and induced (yellow) DEGs ($q < 0.05$) in mc²155 (WT) and FDL15 (*prrAB* complementation strain) compared to the FDL10 Δ *prrAB* mutant. d Average hierarchical clustering (FPKM + 1) of individual RNA-seq sample replicates. e Venn diagrams indicating 40 overlapping DEGs ($q < 0.05$) between mc²155 vs. FDL10 (WT vs. Δ *prrAB* mutant) and FDL15 vs. FDL10 (*prrAB* complementation strain vs. Δ *prrAB* mutant) strain comparisons