Intricate Genetic Programs Controlling Dormancy in *Mycobacterium tuberculosis*

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In the originally published version of this manuscript, the supplemental files were inadvertently duplicated and the Data S1 file was not uploaded. The correct files, which are detailed below, have now been included with the article online.

The production team apologizes for the error.

Data S1. Each cluster represents a distinct transcriptional state and was classified with sets of non-overlapping differentially expressed genes (see STAR Methods): Normoxia (81 Genes), Depletion (446 Genes), Early Hypoxia (328 Genes), Mid Hypoxia (320 Genes), Late Hypoxia (978 Genes), and Resuscitation (429 Genes), related to Figures 2 and S1

Data S2. Zip folder with files to recreate DREM output, related to Figure 3A and STAR Methods section "DREM Analysis"

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