**Supplementary Figures**

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**S1 Fig.** Principal component analysis (PCA) plots for individual animal bAM gene expression data at **a** 2 hpi, **b** 6 hpi, **c** 24 hpi, and **d** 48 hpi. Red indicates *M. bovis*-infected animals and blue indicates non-infected control animals.

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**S2 Fig.** Gene ontology (GO) enrichment for functional modules identified from the differential co-expression correlation network generated from *M. bovis*-infected bAM gene expression at 24 hpi.

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**S3 Fig.** Gene ontology (GO) enrichment for functional modules identified from the differential co-expression correlation network generated from *M. bovis*-infected bAM gene expression at 48 hpi.