

Supplementary Information

The proteome and transcriptome of the infectious metacyclic form of *Trypanosoma brucei* define quiescent cells primed for mammalian invasion

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Supplementary Figures

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Figure S6. Large fraction of the total protein mass in the cell is accounted for by a small number of proteins in both procyclics and metacyclics.

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Figure S8. Similarities between MF and BSF transcriptomes and proteomes. **(A)** Correlation of changes in mRNA abundance between metacyclics and procyclics (this study) and between bloodstream form and procyclics (Siegel *et al.*, 2010). **(B)** Correlation of changes in protein abundance between metacyclics and procyclics (this study) and between bloodstream form and procyclics (Butter *et al.*, 2013).

Figure S9. Assignment of the serine phosphorylation site in VSG653 from tandem mass spectrometry data.

Figure S10. Genome browser view of examples at the end of a transcription unit with several genes showing great differences in mRNA levels.

Supplementary Tables

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Table S2. SILAC All Data.

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Table S4. SILAC top 200.

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Table S7. SILAC 2-fold changes.

Table S8. DESeq2 GO Analysis.

Table S9. SILAC GO Analysis.

Table S10. DNASTAR All Data.

Table S11. DNASTAR DEG 2-fold changes.

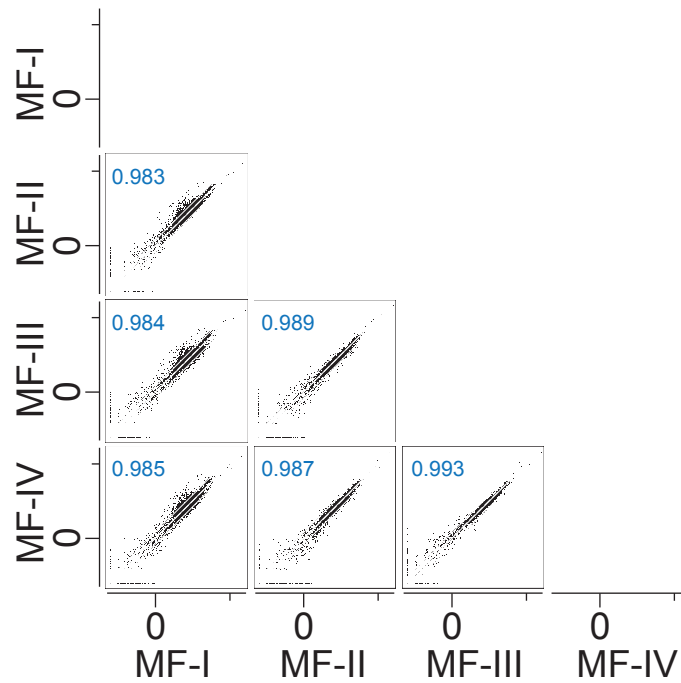
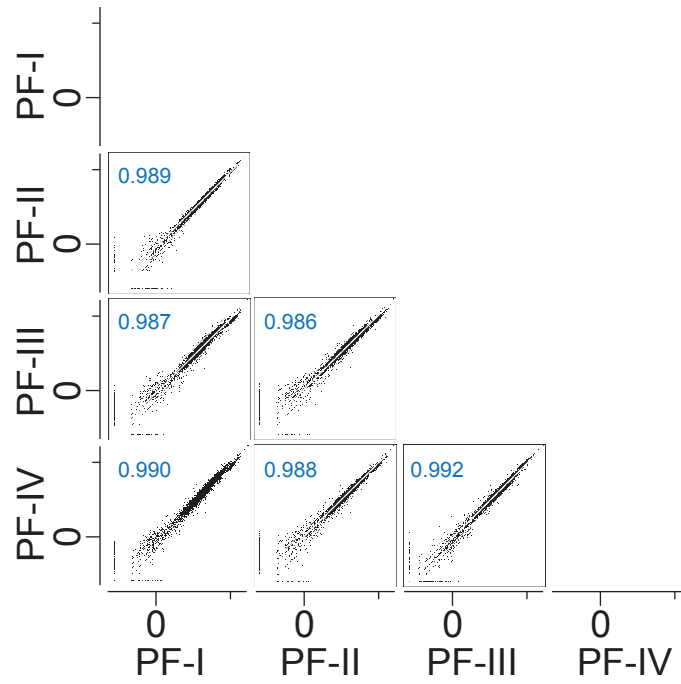


Figure S1

Biological replicates correlation for the RNA-Seq data. RPKM (\log_{10}) values for procyclics (top) and metacyclics (bottom).

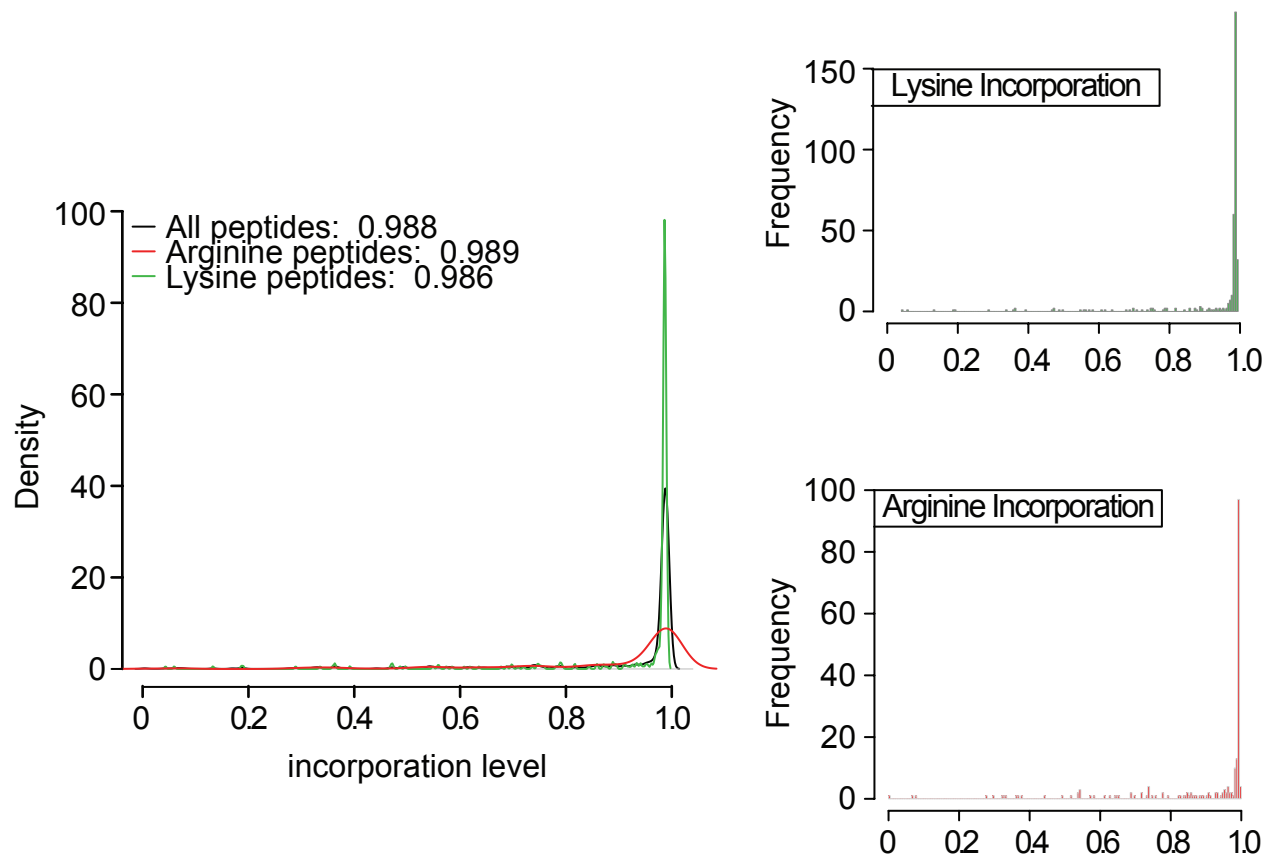


Figure S2

Incorporation efficiency for heavy lysine and arginine in the labeled procyclics.

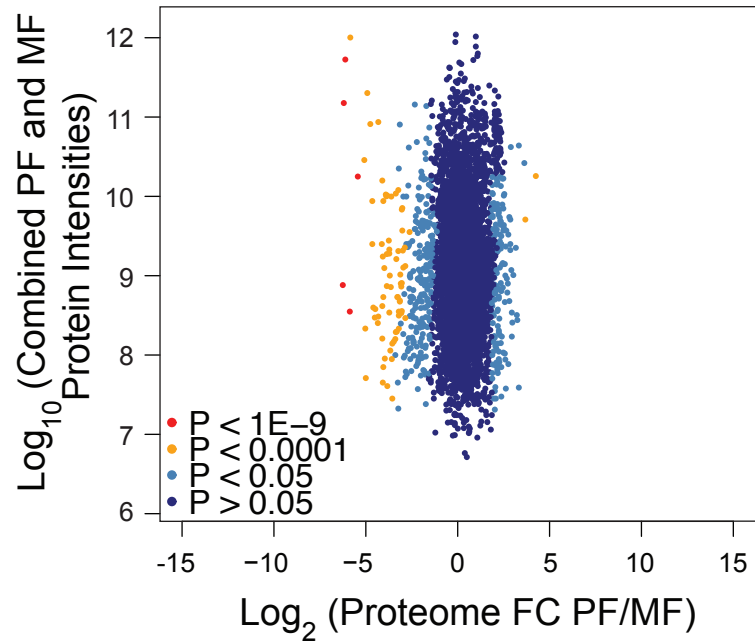


Figure S3

Changes in protein abundance between light metacyclics and heavy procyclic trypanosomes.

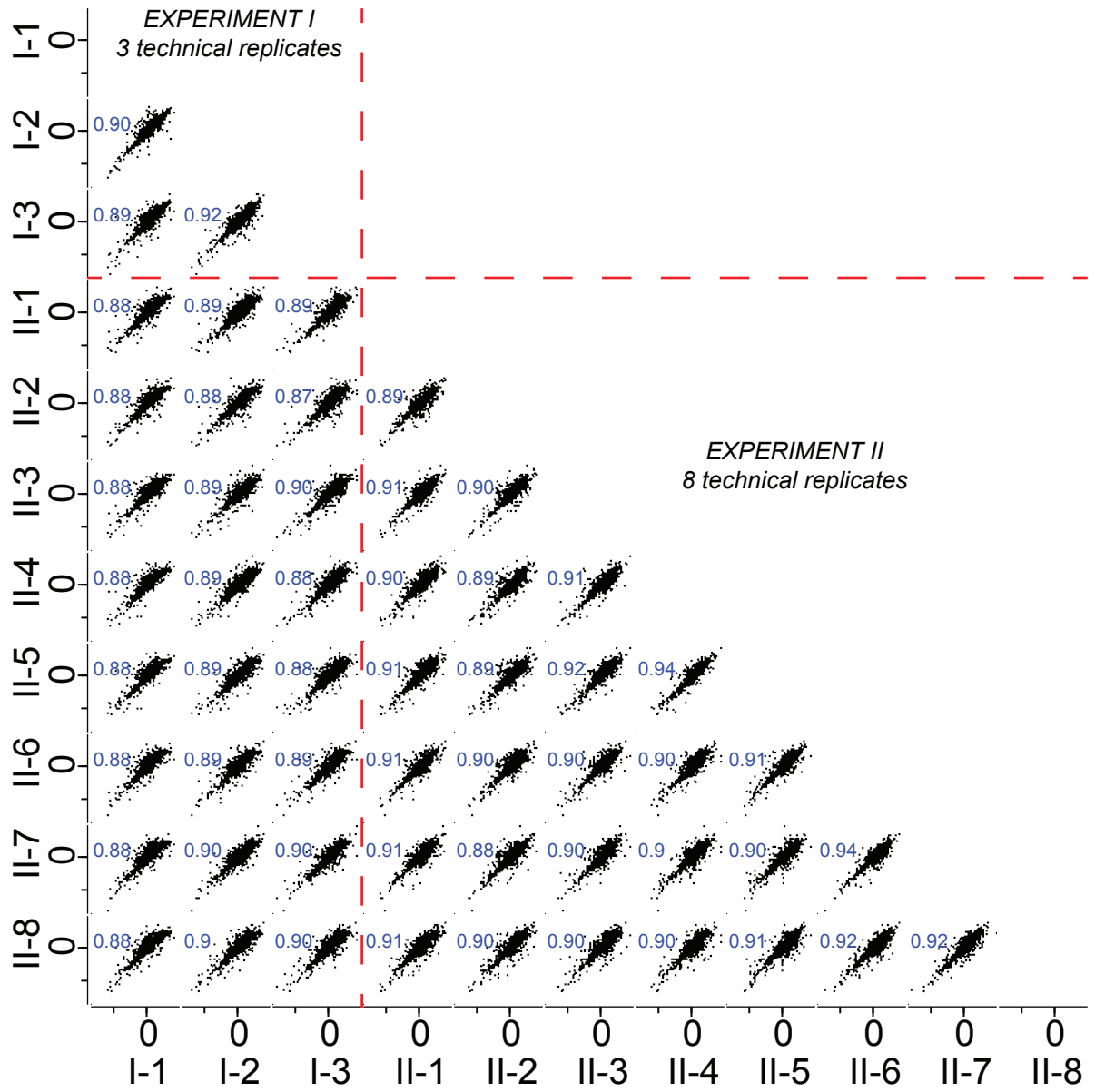


Figure S4

Biological and technical replicates correlation between proteomic data sets.

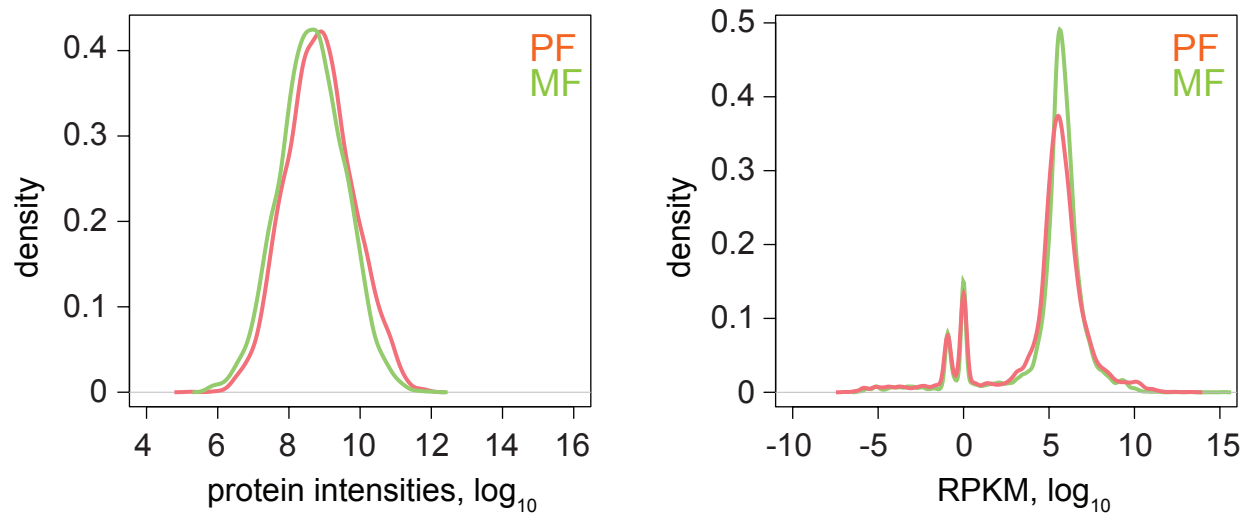


Figure S5

Abundance distribution of proteins (left) and transcripts (right) in procyclics and metacyclics.

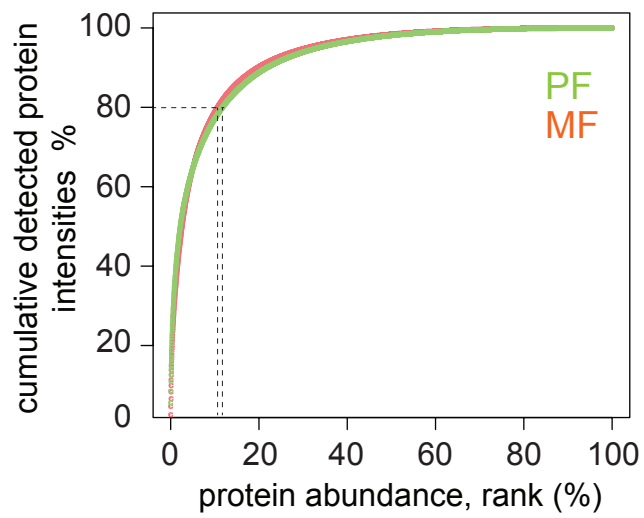


Figure S6

Large fraction of the total protein mass in the cell is accounted for by a small number of proteins in both procyclics and metacyclics.

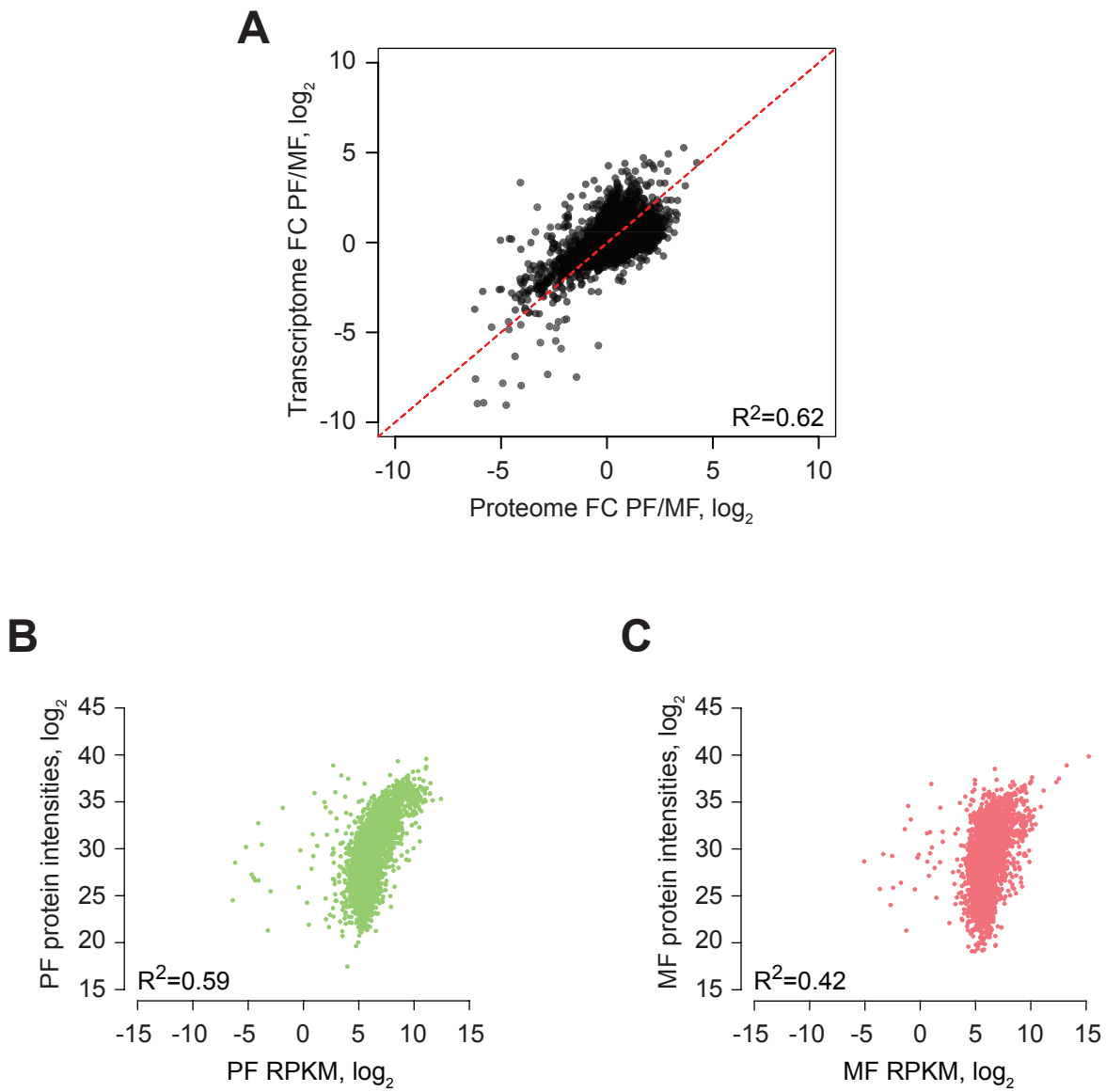


Figure S7

- (A) Comparison of differences in proteome and transcriptome changes between metacyclics and procyclics.
- (B) Correlation between protein and mRNA abundance in procyclics.
- (C) Correlation between protein and mRNA abundance in metacyclics.
- The RNA-Seq fold-change values used here were obtained by the DNASTAR analysis (see Experimental Procedures).

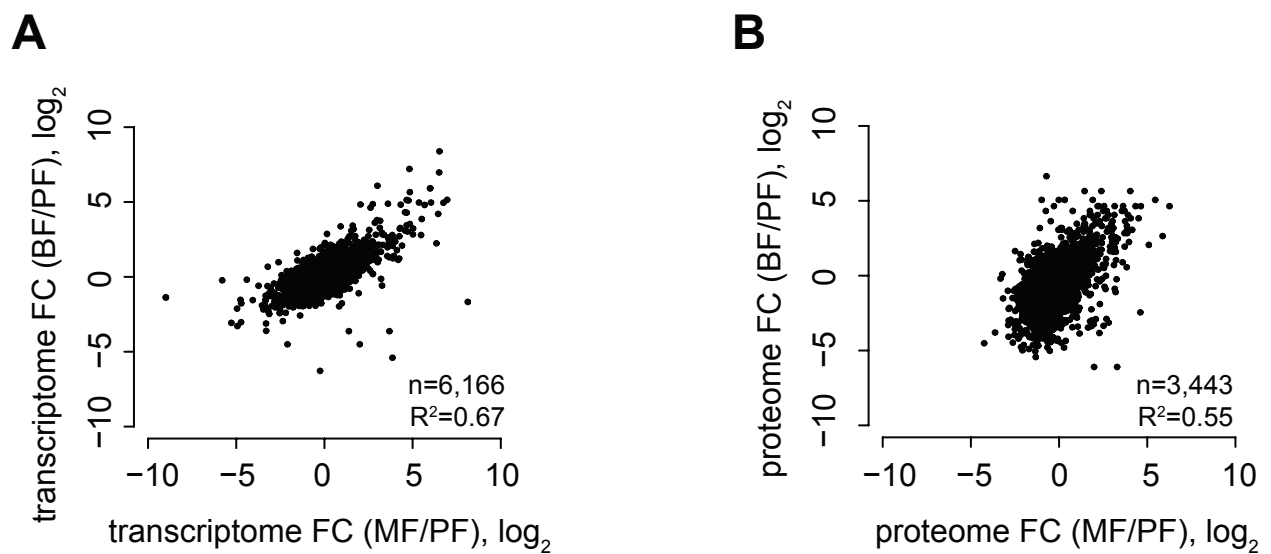


Figure S8

Similarities between MF and BF transcriptomes and proteomes. **(A)** Correlation of changes in mRNA abundance between metacyclics and procyclics (this study) and between bloodstream form and procyclics (Siegel et al., 2010). **(B)** Correlation of changes in protein abundance between metacyclics and procyclics (this study) and between bloodstream form and procyclics (Butter et al., 2013).

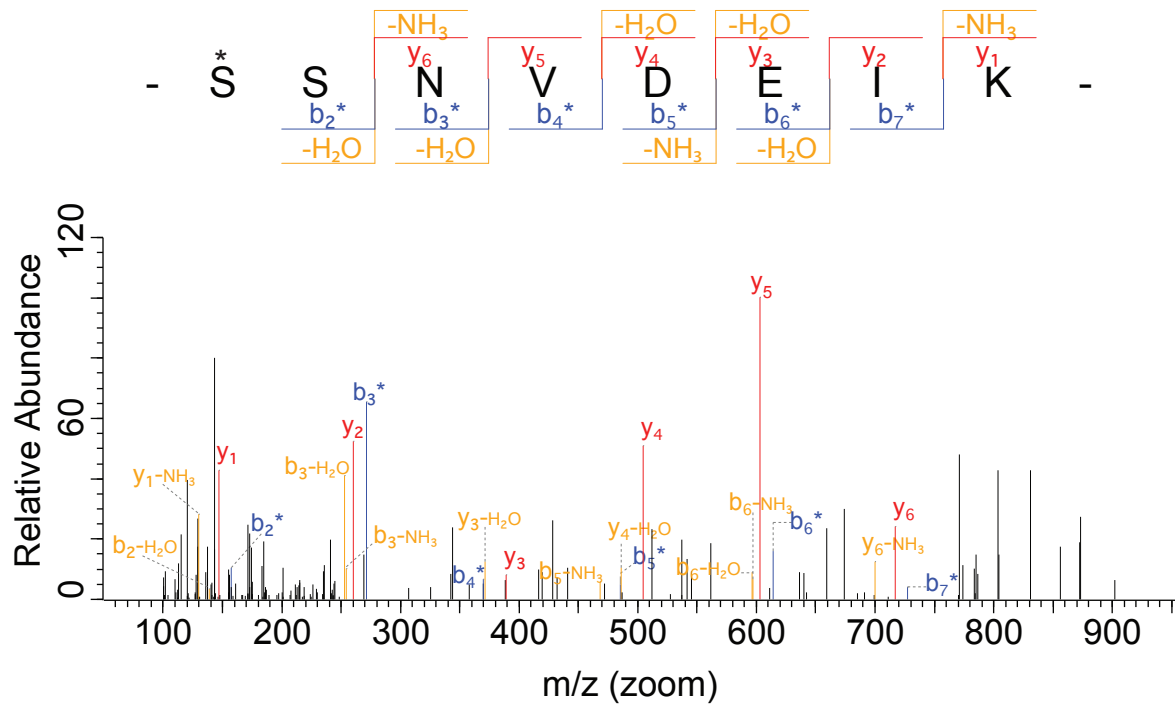


Figure S9

Assignment of the serine phosphorylation site in VSG653 from tandem mass spectrometry data.

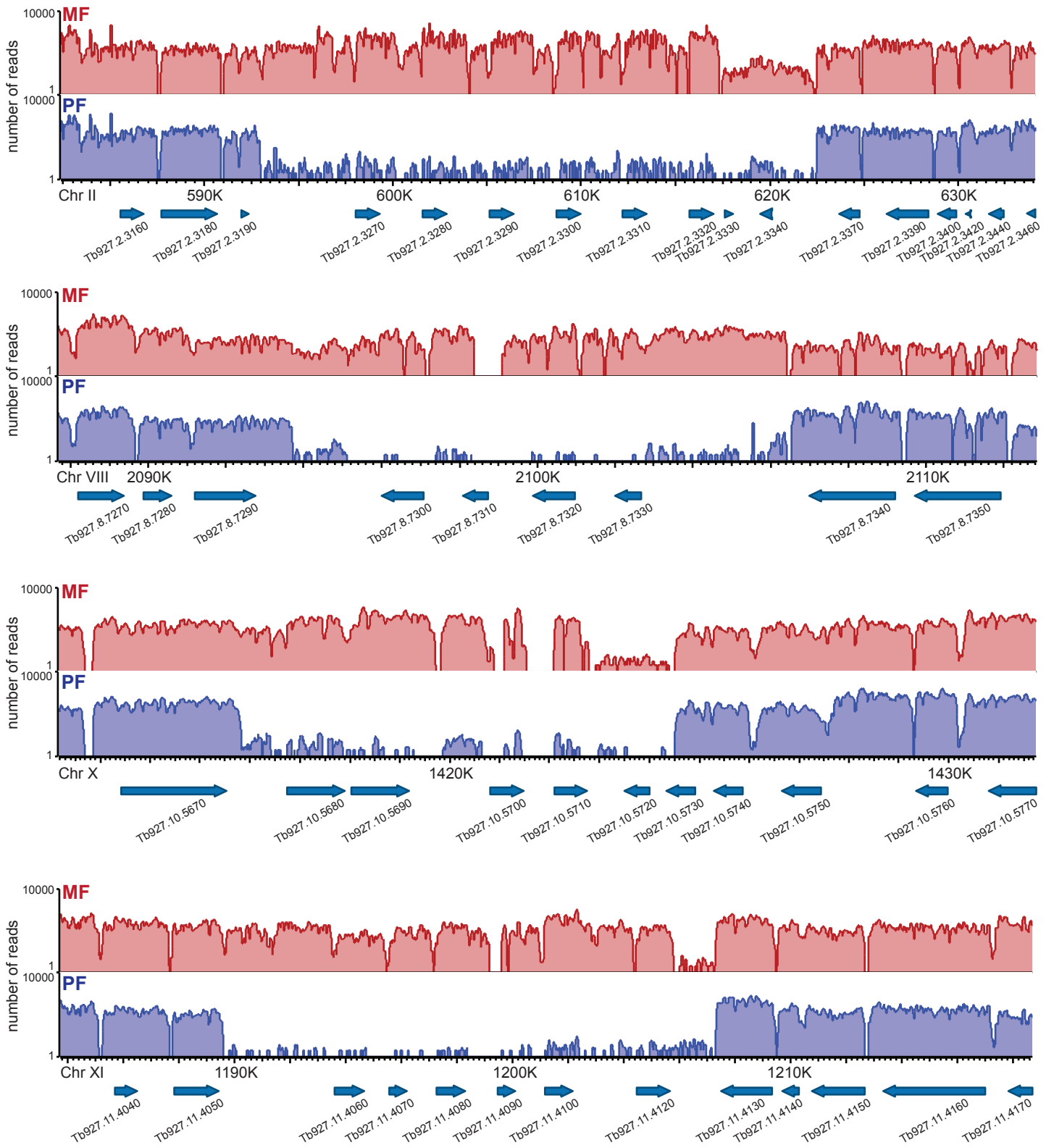


Figure S10

Genome browser view of examples at the end of a transcription unit with several genes showing great differences in mRNA levels.