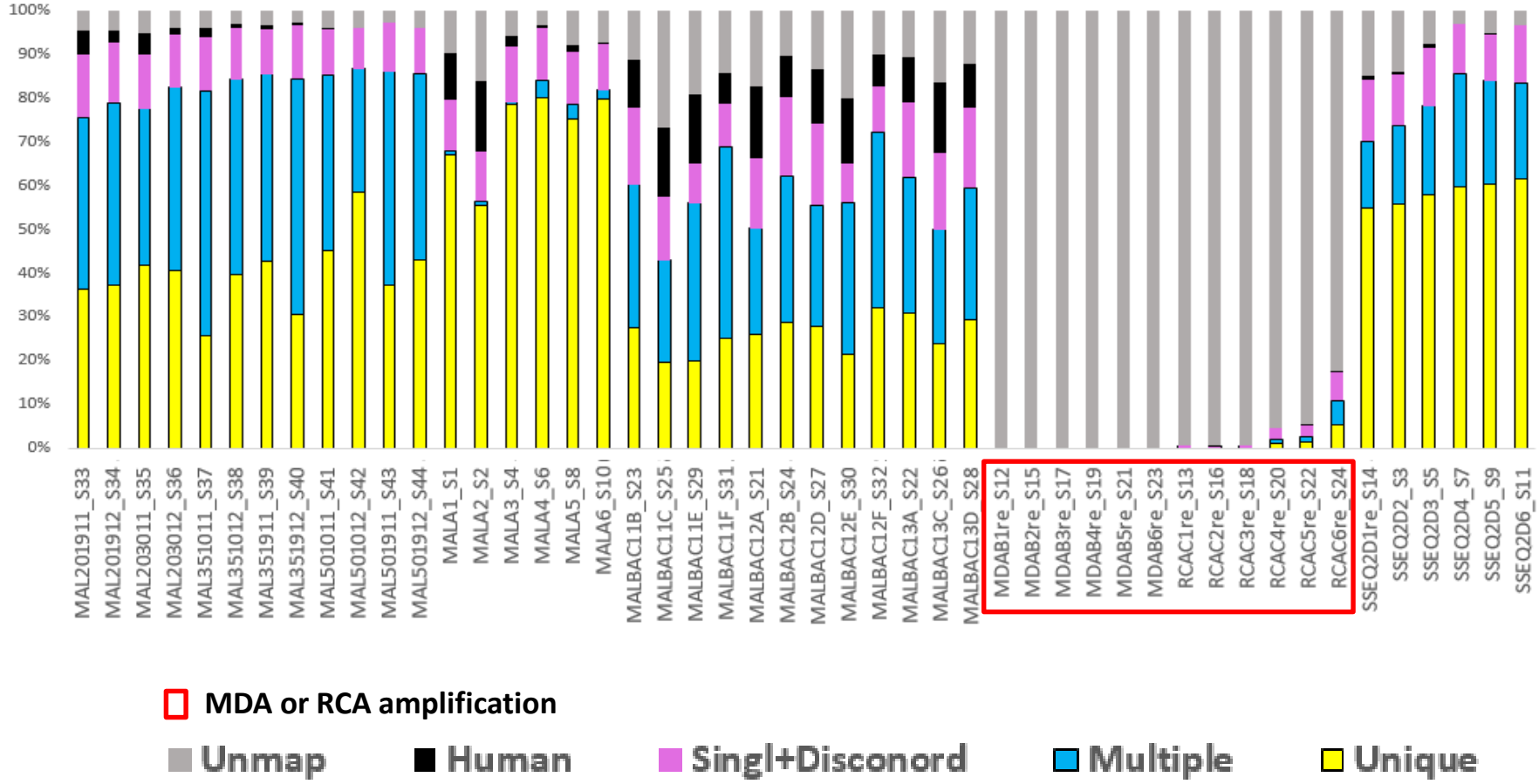
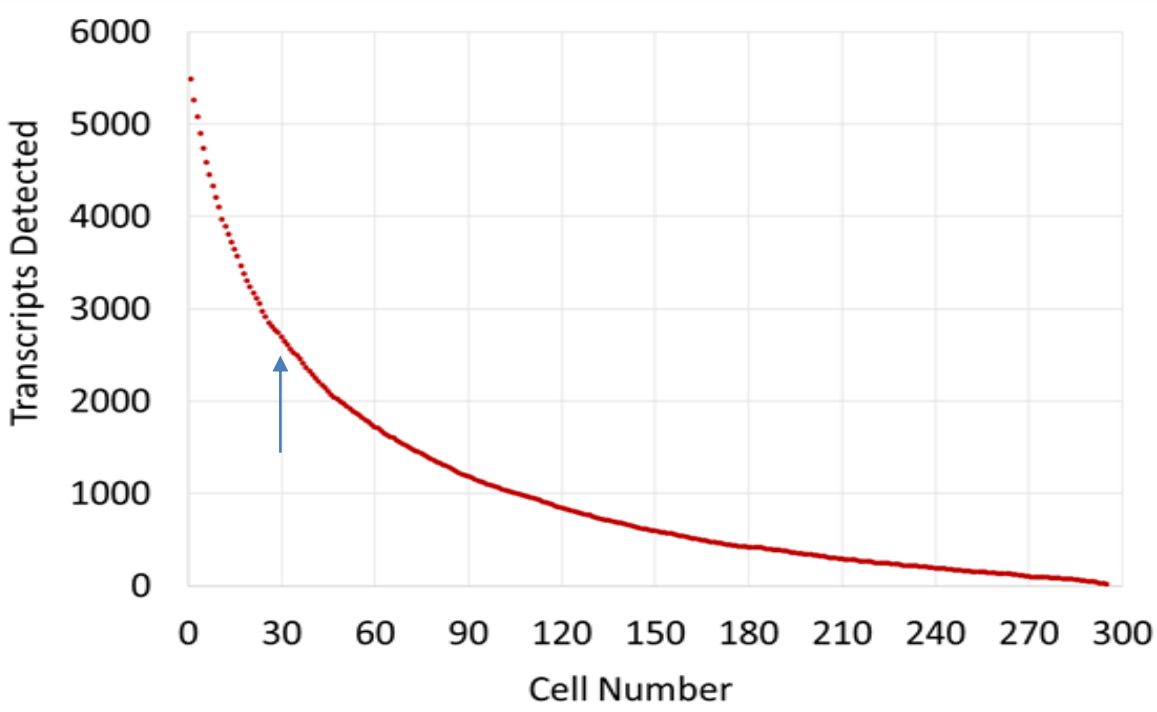
Supplementary Figures

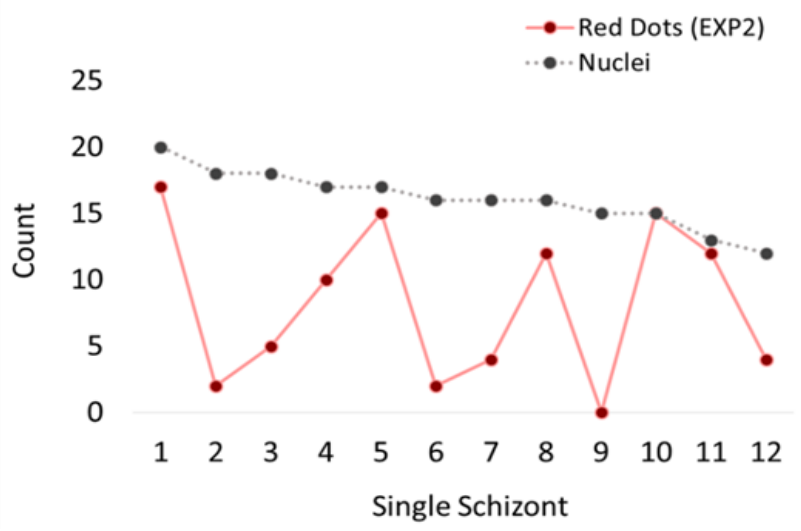
Supplementary Figure 1 (Related to Figure 1): **Sequencing Read Alignment Summary for Various Whole Transcriptome Amplification Methods Tested**. A bar graph representing the proportion of sequencing reads that were mapped to the *P. falciparum* genome either uniquely, at multiple loci, discordantly, singly, unmapped or mapped to the human genome after whole transcriptome amplification of 1-schizonts using either Multiple Displacement Amplification (MDA), Rolling Circle Amplification (RCA), Multiple Annealing and Looping Based Amplification (MALBAC) or SMARTseq2 method. All samples were sequenced on HiSeq2500 platform.

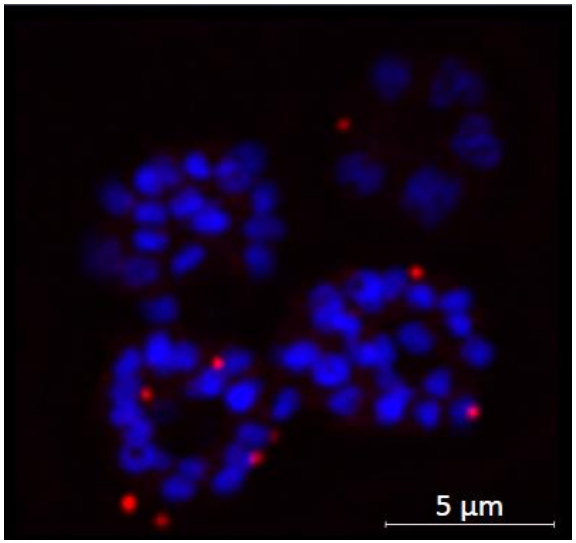


Supplementary Figure 2 (Related to Figure 1): **Cumulative Transcript Coverage in Schizont Population.** A dot plot depicting the cumulative number of transcripts detected in the 295 schizonts sequenced from non-isogenic *P. falciparum* 3D7MR4. Blue arrow represents the number of transcripts expressed in more than 10 % of cells.

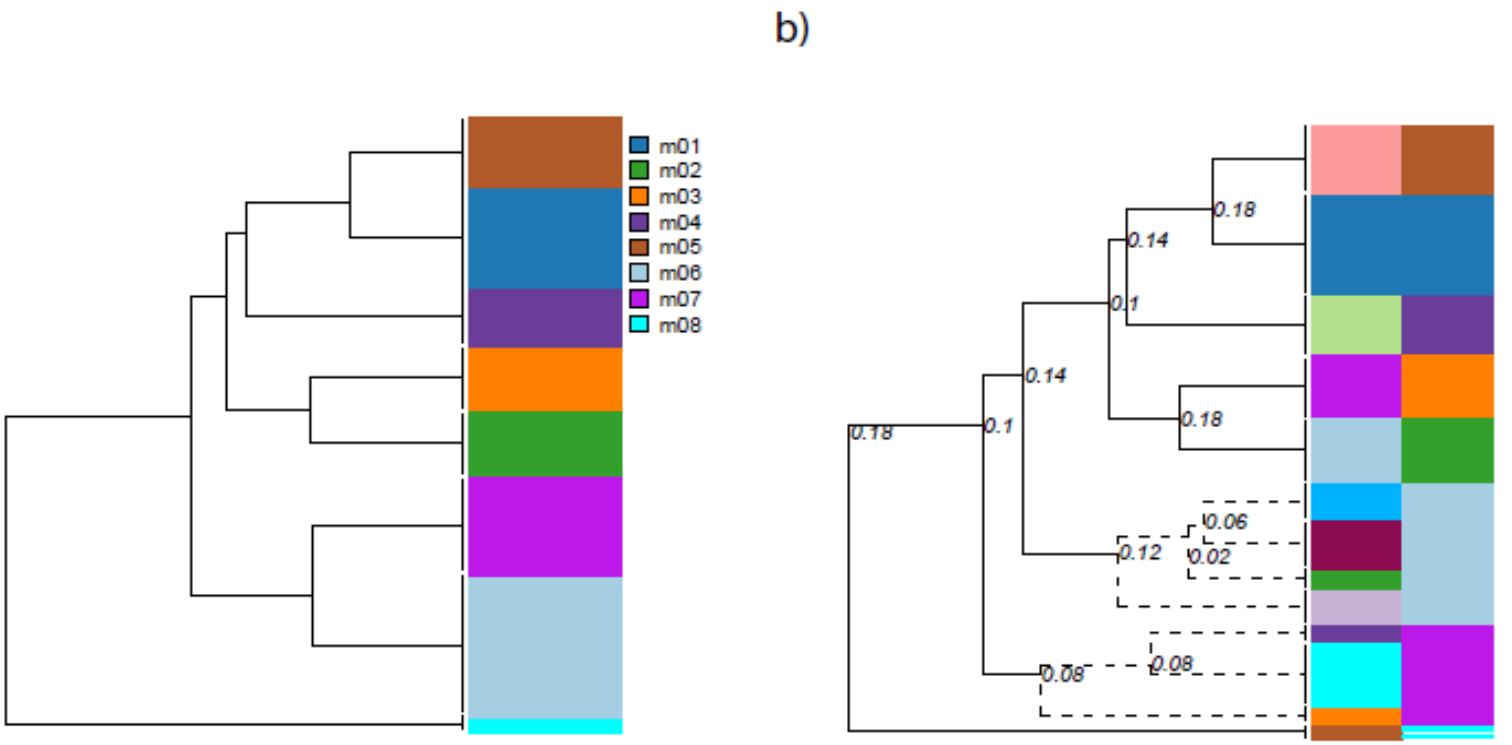


Supplementary Figure 3 (Related to Figure 4): Variable Expression of EXP2 Transcript Confirmed by RNA-FISH in 3D7MR4 Schizonts. A line graph showing the fluorescence intensity for EXP2 mRNA expression in individual 3D7MR4 schizonts imaged by confocal microscopy. Parasite nuclei was stained with DAPI. Scale bar = 5 µm. Mean intensity for EXP2 transcript was quantified in individual parasites using ZENlite software.





Supplementary Figure 4 (Related to 'Single Cell Clustering' in *Methods*): RSEC Based Clustering of Non-isogenic Schizonts. (a)The dendrogram represents the RSEC constructed 1-cell clusters (m01 to m08) with the merging criteria of <15% differential expression between clusters. (b) The dendrogram and blocks represent the merging steps for clusters constructed at lower threshold (blocks on the left column) compared to clusters constructed at higher threshold (blocks on the right column, same as clusters shown in **a**). The dotted lines indicate the merging steps from clusters in **b** to clusters in **a**. Here, the lower merging threshold was set as 5% differential expression between clusters with only cluster m06 and m07 showing further segregation at this lower threshold. This suggests the robustness of the clustering result at the merging threshold of 15%. The numbers along the dendogram indicate differentially expressed genes between the various parasite clusters.



Supplementary Figure 5 (Related to 'Single Cell Clustering' in *Methods*) : RSEC Based Clustering of Isogenic Schizonts. The dendrogram and blocks represents the merging process of clusters formed at threshold of 5% (blocks on the left) to 15% (blocks on the right) differential expression between parasite clusters.