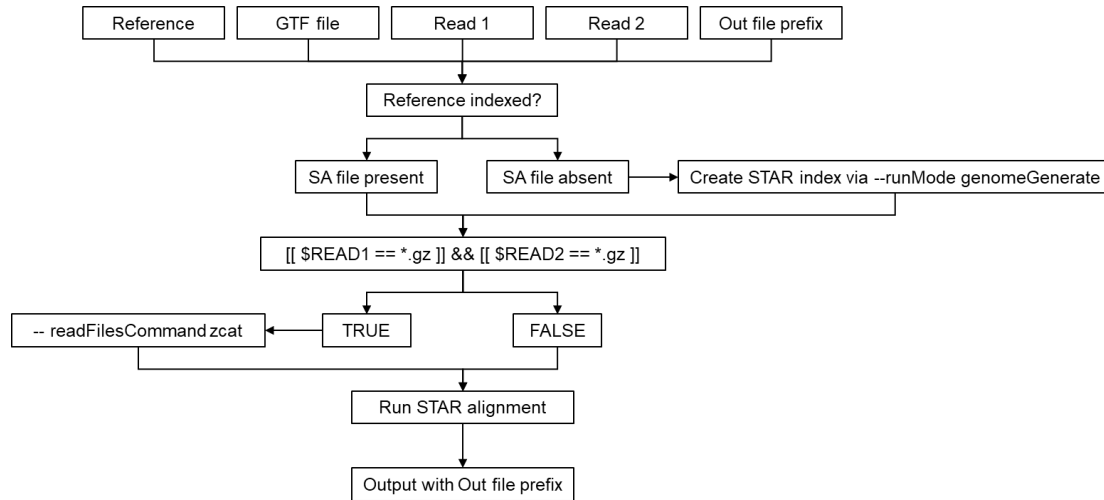
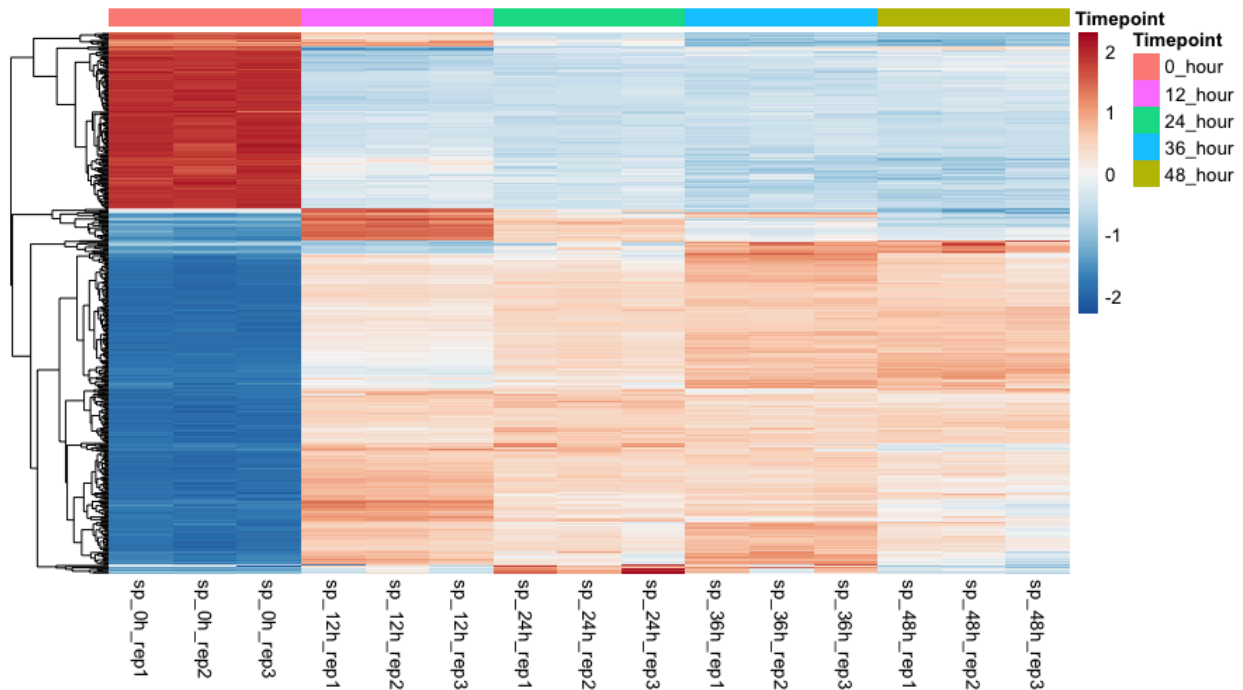


SUPPLEMENTAL FIGURES



Supplemental Figure 1: Bash script flowchart showing the five inputs on the top row, all of the checks that the script performs, with the output on the bottom row. The two checks it performs are whether an indexed reference file is present and FASTQ files are zipped or not.



Supplemental Figure 2: Top 500 most variable genes across timepoints. Counts from the DESeq object were regularized log transformations. Red boxes correspond to high log transformed normalized counts while blue to low log transformed normalized counts. The x axis lists the sample IDs which are also grouped by color. Gene IDs on the y axis were converted to gene names when possible and then clustered based on variability across samples.