

TF SCEPTRE vs Seurat in monocytes, with same QC

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Introduction

This is a followup analysis of Gene's IRF1-analysis-v2 writeup, with two main differences: **The ChIP-seq data is from CD14+ monocytes rather than K562 and the Seurat QC is matched to that of SCEPTRE.** Here, we consider two ways of determining transcription factor target genes: those that are in the hTFtarget database and those that have at least one ChIP-seq peak within 5kb of their TSS. These two align reasonably well; see the table below.

```
## \begin{table}[!htbp]
## \caption{Enrichment odds ratios, comparing to database and our ChIP-seq target assignments.\label{ro
## \begin{center}
## \begin{tabular}{lrrrrr}
## \toprule
## \multicolumn{1}{l}{\diagbox{Ground truth}{Method}}&\multicolumn{1}{c}{SCEPTRE}&\multicolumn{1}{c}{Se
## \midrule
## STAT1&$1.202$&$1.183$&$0.000$&$0.000$\\tabularnewline
## STAT2&$4.031$&$4.039$&$0.000$&$0.000$\\tabularnewline
## BRD4&$0.866$&$1.172$&$0.180$&$0.076$\\tabularnewline
## MYC&$1.090$&$0.991$&$0.708$&$0.937$\\tabularnewline
## SMAD4&$1.257$&$1.227$&$0.000$&$0.001$\\tabularnewline
## IRF1&$1.142$&$1.056$&$0.008$&$0.272$\\tabularnewline
## \bottomrule
## \end{tabular}\end{center}
## \end{table}
```