

IRF1 SCEPTRE vs Seurat With Score QC Individual

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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.

Table 1: Comparing target genes identified based on database and based directly on ChIP-seq data (at least one peak within 5kb).

Database \ ChIP-seq		
	FALSE	TRUE
FALSE	8392	94
TRUE	5134	885

Compare SCEPTRE and Seurat results with ChIP-seq scores

Let's first look at how the SCEPTRE and Seurat discoveries align with each other.

Table 2: Comparing SCEPTRE versus Seurat discoveries.

SCEPTRE \ Seurat		
	FALSE	TRUE
FALSE	11012	610
TRUE	420	1929

This table suggests that SCEPTRE and Seurat results have decent, but imperfect, agreement. Also note that the total numbers of discoveries made by the two methods are nearly the same. Next, let's look at how the SCEPTRE and Seurat discoveries align with the ChIP-seq target genes (as identified by either the hTFtarget database or directly from the ChIP-seq data).

Table 3: Comparing SCEPTRE to database.

<div>SCEPTRE</div> <div>Database</div>	FALSE	TRUE	Prop
FALSE	7126	967	0.119
TRUE	4496	1382	0.235
Prop	0.387	0.588	

Table 4: Comparing Seurat to database.

<div>Seurat</div> <div>Database</div>	FALSE	TRUE	Prop
FALSE	7052	1041	0.129
TRUE	4380	1498	0.255
Prop	0.383	0.59	

Table 5: Comparing SCEPTRE to ChIP-seq binary scores.

<div>SCEPTRE</div> <div>ChIP-seq</div>	FALSE	TRUE	Prop
FALSE	11065	1960	0.15
TRUE	557	389	0.411
Prop	0.048	0.166	

Table 6: Comparing Seurat to ChIP-seq binary scores.

<div>Seurat</div> <div>ChIP-seq</div>	FALSE	TRUE	Prop
FALSE	10884	2141	0.164
TRUE	548	398	0.421
Prop	0.048	0.157	

Table 7: Enrichment odds ratios, comparing to database and our ChIP-seq target assignments with pvalue quantile threshold equal to 0.75

<div>Method</div> <div>Ground truth</div>	SCEPTRE	Seurat
database	2.27	2.32
ChIP-seq	3.94	3.69