Papalexi Analysis SCEPTRE

2023-02-16

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.4.1     v purrr   1.0.1
## v tibble  3.1.8     v dplyr   1.1.0
## v tidyr   1.3.0     v stringr 1.5.0
## v readr   2.1.4     v forcats 1.0.0
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(httr)
library(rlist)
library(jsonlite)
```

```
##
## Attaching package: 'jsonlite'
##
## The following object is masked from 'package:purrr':
##
##     flatten
```

```
library(varhandle)
library(stringi)
library(kableExtra)
```

```
##
## Attaching package: 'kableExtra'
##
## The following object is masked from 'package:dplyr':
##
##     group_rows
```

Getting Results From SCEPTRE Analysis

```
#using absolute paths to download results since files exist on github
code_dir = .get_config_path("LOCAL_CODE_DIR")
data.dir = paste0(code_dir,"/sceptre2-manuscript/writeups/papalexi_analysis/")
gene_path = paste0(data.dir,
```

```
                    'sceptre_CUL3_and_PDL1_mrna_results_with_effect_size.rds')
protein_path = paste0(data.dir,'sceptre_protein_results_with_effect_size.rds')
seurat_path = paste0(data.dir,'papalexi_results_seurat.rds')
#Note that sceptre results have columns pvalue, grna, target
#get sceptre perturbation on PDL1 mrna results
gene_result = readRDS(gene_path)
gene_result$log_fold_change = signif(gene_result$log_fold_change, digits=2)
#get sceptre perturbation on protein results
protein_result = readRDS(protein_path)
protein_result$log_fold_change = signif(protein_result$log_fold_change,digits=2)
#get seurat DE results. Columns 1,2,and 6 correspond to pvalue, effect size
#and perturbation
seurat_result = readRDS(seurat_path)
#change seurat to numeric
seurat_result$p_val = as.numeric(seurat_result$p_val)
seurat_result$avg_log2FC = as.numeric(seurat_result$avg_log2FC)
#round
seurat_result$p_val = signif(seurat_result$p_val, digits=2)
seurat_result$avg_log2FC = signif(seurat_result$avg_log2FC, digits=2)
```

Adjusting Pvalues

```
#See which gene perturbations are associated with PDL1 protein expression

#get pvalues from sceptre
P_adj = protein_result$p_value
#unlist pvalues
P_adj = unlist(P_adj)
#some pvalues are negative so take absolute value
P_adj = abs(P_adj)
#make numeric
P_adj = as.numeric(P_adj)
#perform BH procedure
P_adj = p.adjust(P_adj,method = 'BH')

#replace results matrix pvalues with adjusted pvalues
protein_adjusted = data.frame(adj.Pval = P_adj,
                              log_fold_change = protein_result$log_fold_change,
                              response_id = protein_result$response_id,
                              grna_group = protein_result$grna_group)
```

Papalexi et al Comparison

Papalexi notes that there have been numerous studies showing that exposure to IFN-gamma induces PDL1 expression. Core components of the the IFN-gamma response include IRF1,JAK,STAT, and the IFN-gamma receptors themselves.We can think of these as positive controls that when knocked out, result in underexpression of PDL1.

PDL1 Protein Results

The authors state that they found 8 perturbations to be significantly associated with PDL1 protein expression. These 8 perturbations are BRD4,MYC,CUL3,IRF1,STAT1,IFNGR1,IFNGR2,and JAK2. The last 5 are positive controls identified in the paper.

```
#filter to just look at PDL1 pvalues
protein_PDL1 = protein_adjusted[which(protein_adjusted$response_id == 'PDL1'),]
#get significant perturbations
sig_genes = subset(protein_PDL1,adj.Pval < 0.05)$grna_group
#unfactor
sig_genes = unfactor(sig_genes)
A = 'Significant perturbations for the expression of PDL1 protein are:\n '
cat(paste0(A,paste(sig_genes,collapse = ',')))
```

```
## Significant perturbations for the expression of PDL1 protein are:
##  CUL3,CMTM6,CD274,BRD4,CD86,IFNGR1,IFNGR2,IRF1,JAK2,MYC,PDCD1LG2,STAT1
```

In addition to the 8 perturbations that papalexi et al found significant, SCEPTRE finds 4 more (CMTM6,CD86,PDCD1LG2,STAT3).

```
#get sceptre results on PDL1 protein
protein_PDL1_raw = subset(protein_result,response_id == "PDL1")
protein_PDL1_raw = subset(protein_PDL1_raw,select = c(grna_group,p_value,
                                                      log_fold_change))
#get seurat results on PDL1 protein. Columns 1,2, and 6 are pvalue,effect size
#and perturbation
seurat_PDL1_raw = subset(seurat_result,Target == "PDL1")
seurat_PDL1_raw = subset(seurat_PDL1_raw,select = c(p_val,avg_log2FC,PRTB))
#remove perturbations that aren't in both analyses
for(target in protein_PDL1_raw$grna_group){
  if (target %in% seurat_PDL1_raw$PRTB == F){
    seurat_PDL1_raw = rbind(seurat_PDL1_raw,c(NA,NA,target))
  }
}
protein_PDL1_raw = subset(protein_PDL1_raw,grna_group %in% seurat_PDL1_raw$PRTB)
#reorder rows of sceptre analysis
protein_PDL1_raw = protein_PDL1_raw[match(seurat_PDL1_raw$PRTB,
                                          protein_PDL1_raw$grna_group),]
protein_PDL1_raw$grna_group = unfactor(protein_PDL1_raw$grna_group)
#bind them
combined_results_PDL1 = data.frame(protein_PDL1_raw$p_value,
                                   protein_PDL1_raw$log_fold_change,
                                   seurat_PDL1_raw$p_val,
                                   seurat_PDL1_raw$avg_log2FC,
                                protein_PDL1_raw$grna_group)
colnames(combined_results_PDL1) = c("SCEPTRE Pvalues","SCEPTRE Log Change",
                                    "Seurat Pvalues",
                                    'Seurat Log Change',
                                    "Perturbation")
#reorder columns
combined_results_PDL1 = combined_results_PDL1 [,c(1,3,2,4,5)]
#order by pvalue
```

Table 1: SCEPTRE vs SEURAT PDL1 Protein Results

	SCEPTRE Pvalues	Seurat Pvalues	SCEPTRE Log Change	Seurat Log Change	Perturbation
1	0.0000800	5e-29	0.17000	0.22	BRD4
3	0.0000800	4.8e-303	-0.27000	-0.3	IFNGR1
4	0.0000800	3.1e-294	-0.31000	-0.31	IFNGR2
5	0.0000800	1.6e-70	-0.11000	-0.15	IRF1
6	0.0000800	1.3e-275	-0.34000	-0.31	JAK2
7	0.0000800	1.6e-08	0.15000	0.23	MYC
8	0.0000800	4e-124	-0.26000	-0.28	STAT1
12	0.0000800	NA	-0.18000	NA	CMTM6
13	0.0000800	NA	NaN	NA	CD274
16	0.0000800	NA	0.13000	NA	CD86
21	0.0000800	NA	0.05500	NA	PDCD1LG2
2	0.0014399	5.5e-11	0.07000	0.15	CUL3
23	0.0239044	NA	0.04100	NA	STAT3
22	0.1235060	NA	0.03600	NA	POU2F2
20	0.1314741	NA	0.01800	NA	NFKBIA
9	0.2430279	0.043	-0.00990	-0.017	STAT2
17	0.4302789	NA	0.01300	NA	ETV7
19	0.5298805	NA	0.01800	NA	MARCH8
18	0.5338645	NA	0.00093	NA	IRF7
15	0.5458167	NA	0.01200	NA	CAV1
24	0.8007968	NA	0.00930	NA	STAT5A
26	0.8207171	NA	0.00240	NA	UBE2L6
14	0.8247012	NA	0.00610	NA	ATF2
11	0.8964143	0.14	-0.03500	-0.072	SPI1
25	0.9402390	NA	0.00840	NA	TNFRSF14
10	0.9521912	0.66	-0.00650	-0.0065	SMAD4

```
combined_results_PDL1 = combined_results_PDL1[
  order(combined_results_PDL1$`SCEPTRE Pvalues`),]


results_table = kable(combined_results_PDL1,booktabs = TRUE, linesep = "",
                      caption = "SCEPTRE vs SEURAT PDL1 Protein Results")
kable_styling(results_table,position = "center", latex_options = "scale_down")
```

```
#View(combined_results_PDL1)
```

Other Protein Results

The authors state that "Importantly, perturbation of these eight genes did not result in appreciable shifts in CD86 or PD-L2 protein expression,suggesting that these regulatory effects are specific to PD-L1'. I will now check to see if this is true when using SCEPTRE.

CD86

```
#get sceptre results on CD86 protein
protein_CD86_raw = subset(protein_result,response_id == "CD86")
protein_CD86_raw = subset(protein_CD86_raw,select = c(grna_group,p_value,
                                                      log_fold_change))
#get seurat results on CD86 protein. Columns 1,2, and 6 are pvalue,effect size
#and perturbation
seurat_CD86_raw = subset(seurat_result,Target == "CD86")
seurat_CD86_raw = subset(seurat_CD86_raw,select = c(p_val,avg_log2FC,PRTB))
#remove perturbations that aren't in both analyses
for(target in protein_CD86_raw$grna_group){
  if (target %in% seurat_CD86_raw$PRTB == F){
    seurat_CD86_raw = rbind(seurat_CD86_raw,c(NA,NA,target))
  }
}
protein_CD86_raw = subset(protein_CD86_raw,grna_group %in% seurat_CD86_raw$PRTB)
#reorder rows of sceptre analysis
protein_CD86_raw = protein_CD86_raw[match(seurat_CD86_raw$PRTB,
                                          protein_CD86_raw$grna_group),]
protein_CD86_raw$grna_group = unfactor(protein_CD86_raw$grna_group)
#bind them
combined_results_CD86 = data.frame(protein_CD86_raw$p_value,
                                   protein_CD86_raw$log_fold_change,
                                   seurat_CD86_raw$p_val,
                                   seurat_CD86_raw$avg_log2FC,
                                protein_CD86_raw$grna_group)
colnames(combined_results_CD86) = c("SCEPTRE Pvalues","SCEPTRE Log Change",
                                    "Seurat Pvalues",
                                    'Seurat Log Change',
                                    "Perturbation")
#reorder columns
combined_results_CD86 = combined_results_CD86 [,c(1,3,2,4,5)]
#order by pvalue
combined_results_CD86 = combined_results_CD86[
  order(combined_results_CD86$`SCEPTRE Pvalues`),]


results_table = kable(combined_results_CD86,booktabs = TRUE, linesep = "",
                      caption = "SCEPTRE vs SEURAT CD86 Protein Results")
kable_styling(results_table,position = "center", latex_options = "scale_down")
```

```
#View(combined_results_CD86)
```

It seems as though these regulatory effects are not specific to PDL1. This is also true when using seurat. The positive controls for PDL1 (IRF1,IFNGR1,etc...) also seem to regulate expression of CD86.

PDL2

```
#get sceptre results on PDL2 protein
protein_PDL2_raw = subset(protein_result,response_id == "PDL2")
protein_PDL2_raw = subset(protein_PDL2_raw,select = c(grna_group,p_value,
```

Table 2: SCEPTRE vs SEURAT CD86 Protein Results

	SCEPTRE Pvalues	Seurat Pvalues	SCEPTRE Log Change	Seurat Log Change	Perturbation
1	0.0000800	2.5e-18	-0.3000	-0.16	BRD4
3	0.0000800	2.6e-53	0.2600	0.12	IFNGR1
4	0.0000800	1.3e-50	0.3000	0.12	IFNGR2
5	0.0000800	1.4e-26	0.1700	0.094	IRF1
6	0.0000800	1.6e-42	0.3200	0.12	JAK2
8	0.0000800	6.7e-29	0.2800	0.13	STAT1
12	0.0000800	NA	0.1500	NA	CMTM6
13	0.0000800	NA	NaN	NA	CD274
16	0.0000800	NA	-0.3900	NA	CD86
7	0.0002400	0.02	-0.2600	-0.1	MYC
22	0.0180786	NA	-0.0780	NA	POU2F2
23	0.0557769	NA	-0.0630	NA	STAT3
19	0.1912351	NA	-0.0360	NA	MARCH8
17	0.2669323	NA	-0.0270	NA	ETV7
21	0.3147410	NA	0.0450	NA	PDCD1LG2
9	0.4900398	0.072	0.0063	0.011	STAT2
26	0.5896414	NA	0.0270	NA	UBE2L6
15	0.6772908	NA	-0.0033	NA	CAV1
25	0.6932271	NA	0.0080	NA	TNFRSF14
11	0.7211155	0.28	0.0690	0.034	SPI1
14	0.7490040	NA	-0.0035	NA	ATF2
20	0.7928287	NA	0.0035	NA	NFKBIA
2	0.8047809	0.18	-0.0083	0.05	CUL3
24	0.8167331	NA	0.0110	NA	STAT5A
10	0.8486056	0.23	-0.0019	-0.014	SMAD4
18	0.9243028	NA	0.0057	NA	IRF7

```
                                                    log_fold_change))
#get seurat results on PDL2 protein. Columns 1,2, and 6 are pvalue,effect size
#and perturbation
seurat_PDL2_raw = subset(seurat_result,Target == "PDL2")
seurat_PDL2_raw = subset(seurat_PDL2_raw,select = c(p_val,avg_log2FC,PRTB))
#remove perturbations that aren't in both analyses
for(target in protein_PDL2_raw$grna_group){
  if (target %in% seurat_PDL2_raw$PRTB == F){
    seurat_PDL2_raw = rbind(seurat_PDL2_raw,c(NA,NA,target))
  }
}
protein_PDL2_raw = subset(protein_PDL2_raw,grna_group %in% seurat_PDL2_raw$PRTB)
#reorder rows of sceptre analysis
protein_PDL2_raw = protein_PDL2_raw[match(seurat_PDL2_raw$PRTB,
                                          protein_PDL2_raw$grna_group),]
protein_PDL2_raw$grna_group = unfactor(protein_PDL2_raw$grna_group)
#bind them
combined_results_PDL2 = data.frame(protein_PDL2_raw$p_value,
                                   protein_PDL2_raw$log_fold_change,
                                   seurat_PDL2_raw$p_val,
                                   seurat_PDL2_raw$avg_log2FC,
                                protein_PDL2_raw$grna_group)
colnames(combined_results_PDL2) = c("SCEPTRE Pvalues","SCEPTRE Log Change",
                                    "Seurat Pvalues",
                                    'Seurat Log Change',
                                    "Perturbation")
#reorder columns
combined_results_PDL2 = combined_results_PDL2 [,c(1,3,2,4,5)]
#order by pvalue
combined_results_PDL2 = combined_results_PDL2[
  order(combined_results_PDL2$`SCEPTRE Pvalues`),]


results_table = kable(combined_results_PDL2,booktabs = TRUE, linesep = "",
                      caption = "SCEPTRE vs SEURAT PDL2 Protein Results")
kable_styling(results_table,position = "center", latex_options = "scale_down")
```

```
#View(combined_results_PDL2)
```

For PDL2, the results are more or less in line with what paplexi reports. IRF1 seems to be the only gene that regulates PDL1 that also regulates PDL2.

mRNA Results

I will now analyze whether or not the perturbations affect PDL1 mRNA expression. I will compare results on the normalized and un-normalized assays when using seurat.

Table 3: SCEPTRE vs SEURAT PDL2 Protein Results

	SCEPTRE Pvalues	Seurat Pvalues	SCEPTRE Log Change	Seurat Log Change	Perturbation
1	0.0000800	0.013	-0.1100	-0.033	BRD4
2	0.0000800	4.8e-06	-0.1400	-0.064	CUL3
5	0.0000800	1.9e-23	-0.0960	-0.06	IRF1
12	0.0000800	NA	0.1400	NA	CMTM6
13	0.0000800	NA	NaN	NA	CD274
16	0.0000800	NA	0.0680	NA	CD86
21	0.0000800	NA	-0.3000	NA	PDCD1LG2
7	0.0013599	0.00042	-0.1500	-0.099	MYC
20	0.0018399	NA	-0.0530	NA	NFKBIA
9	0.0557769	0.55	0.0180	-0.0035	STAT2
26	0.0876494	NA	-0.0450	NA	UBE2L6
3	0.0956175	0.1	0.0240	-0.01	IFNGR1
15	0.1274900	NA	-0.0350	NA	CAV1
4	0.1633466	0.55	0.0290	-0.00065	IFNGR2
10	0.1673307	0.59	0.0250	-0.00088	SMAD4
18	0.1912351	NA	-0.0140	NA	IRF7
25	0.1912351	NA	-0.0260	NA	TNFRSF14
6	0.2509960	0.76	0.0190	-0.0037	JAK2
24	0.2669323	NA	-0.0350	NA	STAT5A
11	0.3944223	0.51	-0.0360	-0.024	SPI1
23	0.3984064	NA	-0.0220	NA	STAT3
19	0.4900398	NA	-0.0210	NA	MARCH8
22	0.5976096	NA	0.0018	NA	POU2F2
17	0.8804781	NA	-0.0140	NA	ETV7
8	0.8884462	0.00064	-0.0030	-0.029	STAT1
14	0.9203187	NA	-0.0085	NA	ATF2

Raw Data (Not Normalized)

```
#get sceptre results on PDL1 protein
gene_PDL1_raw = subset(gene_result,response_id == "CD274")
gene_PDL1_raw = subset(gene_PDL1_raw,select = c(grna_group,p_value,
                                                log_fold_change))
#get seurat results on PDL1 gene. Columns 1,2, and 6 are pvalue,effect size
#and perturbation
seurat_PDL1_raw = subset(seurat_result,Target == "PDL1_raw")
seurat_PDL1_raw = subset(seurat_PDL1_raw,select = c(p_val,avg_log2FC,PRTB))
#remove perturbations that aren't in both analyses
for(target in gene_PDL1_raw$grna_group){
  if (target %in% seurat_PDL1_raw$PRTB == F){
    seurat_PDL1_raw = rbind(seurat_PDL1_raw,c(NA,NA,target))
  }
}
gene_PDL1_raw = subset(gene_PDL1_raw,grna_group %in% seurat_PDL1_raw$PRTB)
#reorder rows of sceptre analysis
gene_PDL1_raw = gene_PDL1_raw[match(seurat_PDL1_raw$PRTB,
                                    gene_PDL1_raw$grna_group),]
gene_PDL1_raw$grna_group = unfactor(gene_PDL1_raw$grna_group)
#bind them
combined_results_PDL1 = data.frame(gene_PDL1_raw$p_value,
                                   gene_PDL1_raw$log_fold_change,
                                   seurat_PDL1_raw$p_val,
                                   seurat_PDL1_raw$avg_log2FC,
                                gene_PDL1_raw$grna_group)
colnames(combined_results_PDL1) = c("SCEPTRE Pvalues","SCEPTRE Log Change",
                                    "Seurat Pvalues",
                                    'Seurat Log Change',
                                    "Perturbation")
#reorder columns
combined_results_PDL1 = combined_results_PDL1 [,c(1,3,2,4,5)]
#order by pvalue
combined_results_PDL1 = combined_results_PDL1[
  order(combined_results_PDL1$`SCEPTRE Pvalues`),]


results_table = kable(combined_results_PDL1,booktabs = TRUE, linesep = "",
                      caption = "SCEPTRE vs SEURAT PDL1 mRNA Results (Raw Data)")
kable_styling(results_table,position = "center", latex_options = "scale_down")
```

```
#View(combined_results_PDL1)
```

We see that the positive controls indeed correspond to the strongest signals in the data. Interestingly, BRD4 perturbation does not affect gene expression of PDL1 while CUL3 does, consistent with the paper.

Normalized Data

Table 4: SCEPTRE vs SEURAT PDL1 mRNA Results (Raw Data)

	SCEPTRE Pvalues	Seurat Pvalues	SCEPTRE Log Change	Seurat Log Change	Perturbation
3	0.0000800	1.3e-79	-1.2000	-0.49	IFNGR1
4	0.0000800	3.9e-81	-1.3000	-0.52	IFNGR2
5	0.0000800	4.4e-07	-0.2800	-0.14	IRF1
6	0.0000800	6e-75	-1.3000	-0.53	JAK2
8	0.0000800	9.6e-34	-1.3000	-0.52	STAT1
13	0.0000800	NA	NaN	NA	CD274
2	0.0001600	1.4e-11	0.3700	0.7	CUL3
7	0.0001600	8.3e-10	0.6000	1.1	MYC
17	0.0438247	NA	0.1200	NA	ETV7
19	0.1235060	NA	0.0700	NA	MARCH8
23	0.1314741	NA	0.1100	NA	STAT3
21	0.1633466	NA	0.1100	NA	PDCD1LG2
20	0.2390438	NA	0.0590	NA	NFKBIA
11	0.2509960	0.9	0.2000	0.046	SPI1
25	0.3784861	NA	0.0390	NA	TNFRSF14
24	0.4143426	NA	0.0540	NA	STAT5A
22	0.4462151	NA	0.0700	NA	POU2F2
9	0.4940239	0.61	0.0410	0.028	STAT2
26	0.5059761	NA	0.0320	NA	UBE2L6
15	0.6454183	NA	0.0330	NA	CAV1
18	0.7370518	NA	-0.0140	NA	IRF7
10	0.7649402	0.16	0.0240	-0.08	SMAD4
14	0.8167331	NA	-0.0019	NA	ATF2
1	0.9123506	1.7e-05	-0.1100	0.39	BRD4
12	0.9482072	NA	0.0120	NA	CMTM6
16	0.9760956	NA	-0.0088	NA	CD86

```
#get sceptre results on PDL1 protein
gene_PDL1_norm = subset(gene_result,response_id == "CD274")
gene_PDL1_norm = subset(gene_PDL1_norm,select = c(grna_group,p_value,
                                                  log_fold_change))
#get seurat results on PDL1 gene. Columns 1,2, and 6 are pvalue,effect size
#and perturbation
seurat_PDL1_norm = subset(seurat_result,Target == "PDL1_norm")
seurat_PDL1_norm = subset(seurat_PDL1_norm,select = c(p_val,avg_log2FC,PRTB))
#remove perturbations that aren't in both analyses
for(target in gene_PDL1_norm$grna_group){
  if (target %in% seurat_PDL1_norm$PRTB == F){
    seurat_PDL1_norm = rbind(seurat_PDL1_norm,c(NA,NA,target))
  }
}
gene_PDL1_norm = subset(gene_PDL1_norm,grna_group %in% seurat_PDL1_norm$PRTB)
#reorder rows of sceptre analysis
gene_PDL1_norm = gene_PDL1_norm[match(seurat_PDL1_norm$PRTB,
                                      gene_PDL1_norm$grna_group),]
gene_PDL1_norm$grna_group = unfactor(gene_PDL1_norm$grna_group)
#bind them
combined_results_PDL1 = data.frame(gene_PDL1_norm$p_value,
                                   gene_PDL1_norm$log_fold_change,
                                   seurat_PDL1_norm$p_val,
                                   seurat_PDL1_norm$avg_log2FC,
                                gene_PDL1_norm$grna_group)
colnames(combined_results_PDL1) = c("SCEPTRE Pvalues","SCEPTRE Log Change",
                                    "Seurat Pvalues",
                                    'Seurat Log Change',
                                    "Perturbation")
#reorder columns
combined_results_PDL1 = combined_results_PDL1 [,c(1,3,2,4,5)]
#order by pvalue
combined_results_PDL1 = combined_results_PDL1[
  order(combined_results_PDL1$`SCEPTRE Pvalues`),]


results_table = kable(combined_results_PDL1,booktabs = TRUE, linesep = "",
            caption = "SCEPTRE vs SEURAT PDL1 mRNA Results (Normalized Data)")
kable_styling(results_table,position = "center", latex_options = "scale_down")
```

```
#View(combined_results_PDL1)
```

If we use the normalized data, we see that while the positive controls are still the strongest signal in the data, the direction of over/under expression is now flipped. From this I have two possible conclusions. Therefore I reasonably certain that they used the un-normalized data to perform all DE analyses. This is because if they used the normalized data, all their results would contradict the known controls. it is possible that their implementation of neighborhood adjustment is wrong in the sense that they are subtracting in the wrong direction (a-b instead of b-a). However, even if this is the case, the pvalues are much larger which casts doubt to if they would still be significant after pvalue adjustment.
If they did not use the normalized data, this begs the question as to if their results are driven by technical factors rather than true biological signal.

Table 5: SCEPTRE vs SEURAT PDL1 mRNA Results (Normalized Data)

	SCEPTRE Pvalues	Seurat Pvalues	SCEPTRE Log Change	Seurat Log Change	Perturbation
3	0.0000800	0.0021	-1.2000	0.14	IFNGR1
4	0.0000800	0.00012	-1.3000	0.16	IFNGR2
5	0.0000800	7e-26	-0.2800	0.2	IRF1
6	0.0000800	7.8e-05	-1.3000	0.16	JAK2
8	0.0000800	0.15	-1.3000	0.14	STAT1
13	0.0000800	NA	NaN	NA	CD274
2	0.0001600	0.96	0.3700	-0.065	CUL3
7	0.0001600	7e-05	0.6000	-0.58	MYC
17	0.0438247	NA	0.1200	NA	ETV7
19	0.1235060	NA	0.0700	NA	MARCH8
23	0.1314741	NA	0.1100	NA	STAT3
21	0.1633466	NA	0.1100	NA	PDCD1LG2
20	0.2390438	NA	0.0590	NA	NFKBIA
11	0.2509960	0.75	0.2000	-0.11	SPI1
25	0.3784861	NA	0.0390	NA	TNFRSF14
24	0.4143426	NA	0.0540	NA	STAT5A
22	0.4462151	NA	0.0700	NA	POU2F2
9	0.4940239	0.95	0.0410	-0.012	STAT2
26	0.5059761	NA	0.0320	NA	UBE2L6
15	0.6454183	NA	0.0330	NA	CAV1
18	0.7370518	NA	-0.0140	NA	IRF7
10	0.7649402	0.49	0.0240	-0.018	SMAD4
14	0.8167331	NA	-0.0019	NA	ATF2
1	0.9123506	0.12	-0.1100	-0.16	BRD4
12	0.9482072	NA	0.0120	NA	CMTM6
16	0.9760956	NA	-0.0088	NA	CD86