

TransPilot Tutorials

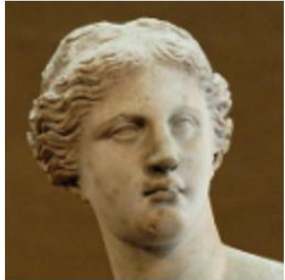
鉴定巨噬细胞M1极化中的关键转录因子

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1. Select TF-target set

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Select a genome using the select boxes on the right. By default, the first 15 genomes are listed. Type the scientific name of the organism in the search box to filter the results.



Homo sapiens is a species of primate in the family Hominidae (great apes).

Taxonomy ID: 9606

Common name: Human

Number of GSETs: not defined

Select a Genome

Homo sapiens PyTFBS ANN, GCF_000001405.40_GRCh38.p14 1 ▼

HOCOMOCO

Jaspar

2

Follow these steps to load the TF-target set. Note that multiple sets can be loaded into the system together. Don't forget to check the number of GSETs to verify whether the TF-target set was loaded successfully.

2. Upload DEG list

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We provide the RANKED DEG list in TAB-delimited text file format.

The RANKED DEG list file format is specified as one gene per line. The first column contains the official gene symbol, and the second column contains the RANK value, which can represent the extent of differential expression. Columns are separated by TAB characters.

The RANKED DEG list file can be generated by our gene list creation tool, [GENE_Spark](#), using your transcriptome profiling data.

8 CPU threads **1**

16 CPU threads

TransPilot Server Accumulated **993** Successful Runs.

Run TransPilot **4**

Demo (M1 Macrophage) **2**

```
# GENE RANK 3
A2M 121.189409307037
AANAT 38.99048167441
AATBC -24.1017165814092
ABCA1 467.048579669413
ABCA4 35.6944090492887
ABCB1 378.306269204409
ABCC3 129.868615037907
ABCC4 -38.8885919637865
ABCC5 -116.496960651783
ABCC6 141.228145052844
ABHD12B -31.0972156123706
ABHD14A -19.672676258547
ABHD17AP1 -6.62962082802056
ABHD17AP6 -25.6041291797303
ABL2 754.546318507998
```

Upload the DEG list by following these steps. In the tutorial, we uploaded the demo data in Step **2**. You can upload a custom DEG list in the edit box (marked as **3**). Once ready, click the “Run” button to start the TransPilot analysis.

3. Results

3. Result

CSV Excel PDF Copy Print Analyze ²

Search:

gene_set	count_n	cor_dir	tau	estimate	rank	pvalue	FDR
CEBPB_HUMAN.H11MO.0.A	478	+	0.3070	8.9134	0.0013	2.4744e-19	1.9771e-16
NFYA_HUMAN.H11MO.0.A	582	-	-0.2749	-8.8537	0.0025	4.2327e-19	1.9771e-16
KLF9_HUMAN.H11MO.0.C	686	+	0.2365	8.2603	0.0038	1.8367e-16	4.8916e-14
EPAS1_HUMAN.H11MO.0.B	440	+	0.2660	7.5074	0.0050	6.0361e-14	1.2057e-11
TF65_HUMAN.H11MO.0.A_RC ¹	860	+	0.1889	7.4194	0.0063	1.1768e-13	1.8805e-11
ETS2_HUMAN.H11MO.0.B_RC	652	+	0.2015	6.9022	0.0075	5.1217e-12	6.8203e-10
ZN467_HUMAN.H11MO.0.C_RC	346	+	0.2741	6.8071	0.0088	9.9607e-12	1.1369e-9
DUX4_							
JUNB_							
ELF2_HUMAN.H11MO.0.C_RC	488	-	-0.2233	-6.6675	0.0125	2.6024e-11	2.0793e-9

Select a result row in the table, and click the “Analysis” button to perform further analysis.

Showing 1 to 10 of 799 entries 1 row selected

Previous **1** 2 3 4 5 ... 80 Next

4. Correlation Graph

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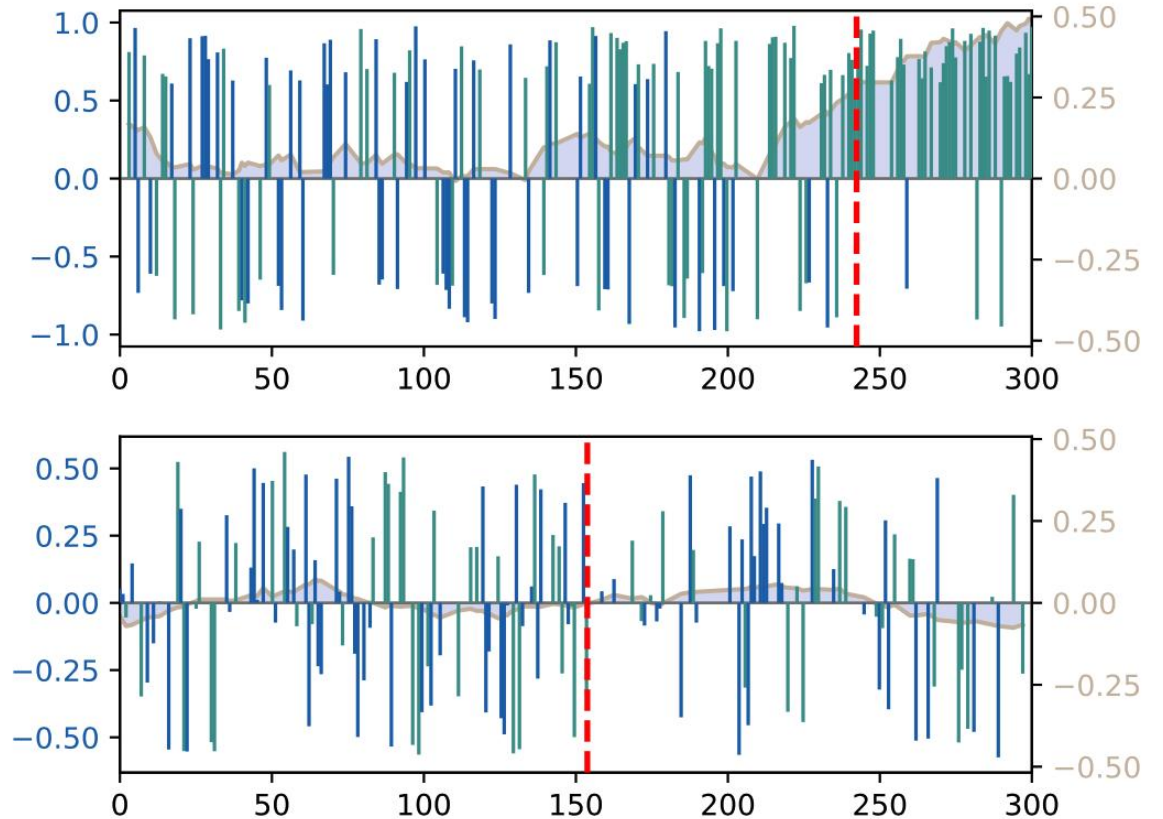
We provide correlation plots to illustrate the relationship between a TF-target set and a DEG list.

The upper plot illustrates genes that have transcription factor binding sites. The lower plot illustrates genes that do not have transcription factor binding sites. The X-axis represents the rank values of the extent of differential expression. Bar height is a quantitative metric representing the potential of binding with the transcription factor. Edge genes (bars) can be highlighted in green. The red vertical line represents the weighted average of the extent of differential expression values.

Graph

Target Genes ¹

Pathway ²



Push the “Target Genes” button to display the target genes for the key transcription factor. Then, push the “Pathway” button to identify the pathway in which the target genes are enriched.

5. Annotation

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CSV Excel PDF Copy Print Analyze ² Search:

pathway	es	nes	sidak	set_size	pval	fdp
REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.5970	6.3556	0.0000	73	2.0000e-10	1.1540e-7
REACTOME SIGNALING BY INTERLEUKINS	0.5449	5.2379	0.0001	45	1.6240e-7	0.0000451414
WP CYTOKINECYTOKINE RECEPTOR INTERACTION	0.6172	5.1559	0.0001	39	2.5240e-7	0.0000467741
KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION ¹	0.5855	4.8714	0.0006	39	0.00000110830	0.000154054
WP NETWORK MAP OF SARSCOV2 SIGNALING	0.6021	4.8026	0.0009	36	0.00000156620	0.000174164
REACTOME INTERFERON SIGNALING	0.7105	4.3980	0.0061	25	0.0000109274	0.00101261
REACTOME INTERFERON GAMMA	0.7010	4.0110	0.0110	10	0.00000000000	0.000011000
REACTOME INTERLEUKIN 10 SIGNALING	0.7371	4.0328	0.0302	17	0.0000551072	0.00340440
WP OVERVIEW OF PROINFLAMMATORY AND PROFIBROTIC MEDIATORS	0.6036	3.8441	0.0651	27	0.000120973	0.00648619

Select a result row in the table, and click the “Analysis” button to perform further analysis.

Showing 1 to 10 of 556 entries 1 row selected

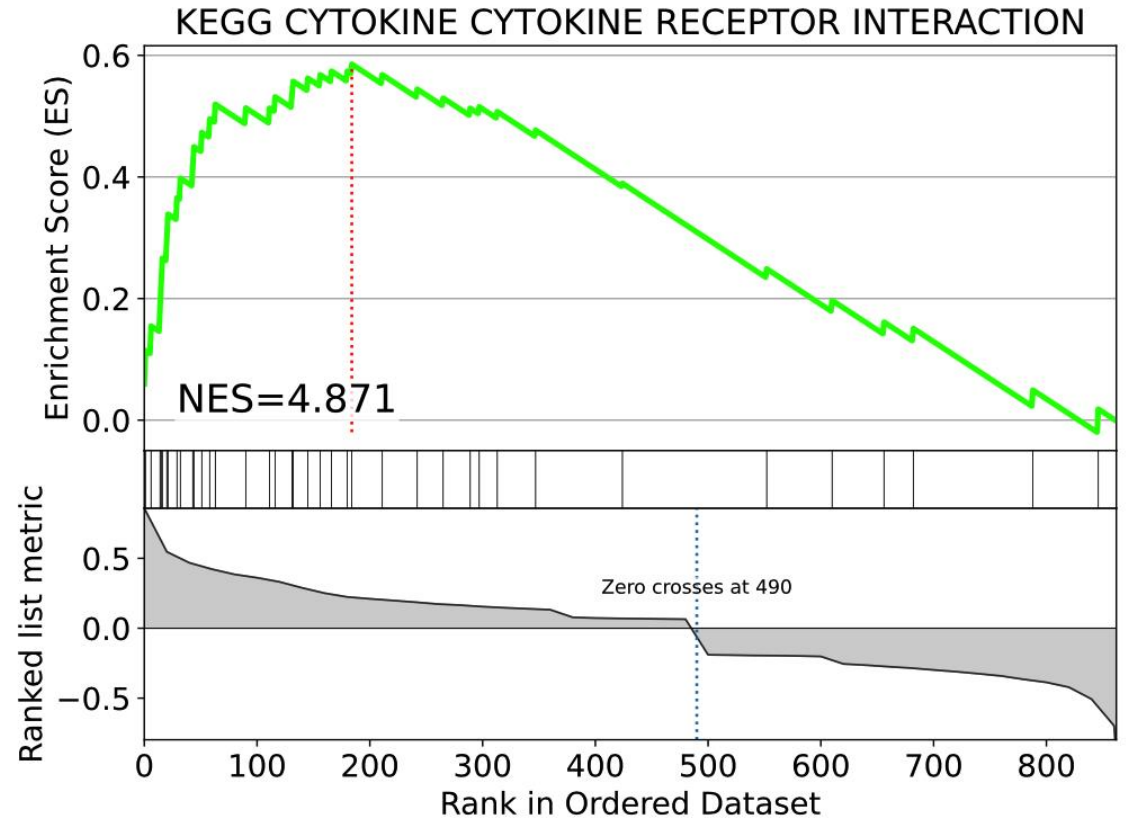
6. Plot Enrichment Graph

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We provide GSEA dot plots to illustrate the enrichment analysis of transcription factor target genes.

The top portion of the plot shows the running enrichment score (ES) for the gene set as the analysis walks down the ranked list of genes. The peak of the curve—the highest positive or negative point—represents the enrichment score (ES), which reflects how overrepresented the gene set is at the top or bottom of the ranked list. The middle portion indicates how the genes in the dataset are ranked (e.g., based on fold change or correlation with phenotype). The bottom portion shows where the genes from the gene set appear along the ranked list.

Graph Edge Genes ¹ Add to Network ²



Push the “Edge Genes” button to display the edge genes. Then, push the “Add to Network” button to add them to the transcription regulation network.

7. Build Network

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Target gene network regulated by key transcription factors.

The network can be exported to a file and imported into the Cytoscape software package for visualization.



```
{"TF65_HUMAN.H11MO.0.A_RC":{"KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION":  
["CSF1","CXCL1","IL15","IL1R1","CXCL2","PDGFRA","CXCL10","CXCL3","IL6","  
TNFRSF14","CCL5","CXCR5","CXCL9","IL15RA","CXCL6","CD40","IL1B","CXCL  
8","CXCL13","IL1R2","CCL8","TNFSF10","CSF2RB","CCL4"]}}
```

Push the “Draw” button to draw the transcription regulation network. Push the “Export” button to export the network to a file. Note that the network file can be directly imported into the Cytoscape desktop software for visualization.

Thank you and good luck..
Questions..?