

**A**

Browser Single cell chromatin accessibility data Trait or disease data

Metadata: Sample ID Metadata: Cell type

Tissue type	Sample ID	Tissue type	Health type Description	Cell count
Heart	sample_id_1	Skin	Basal cell carcinoma (BCC)	36721
Health type	sample_id_3	PBMC	Healthy blood development	32457
Disease	...	...	...	...

Type	Trait ID	Type	Trait Description
Category	trait_id_1	disease	Atopic dermatitis
Subcategory	trait_id_55	indicator	Monocyte
Source cohort	...	...	...

**B**

Sample overview

Sample ID: sample\_id\_3  
Tissue type: PBMC  
Cell type count: 26  
Cell count: 32457  
GSE ID: GSE139369  
PMID: 31792411, ...  
Genome: hg19  
...

Proportion of cell type

Legend:

- 01\_HSC
- 11\_CD14.Mono.1
- 02\_Early.Eryth
- 12\_CD14.Mono.2
- 03\_Late.Eryth
- 13\_Unk
- 04\_Early.Baso
- 14\_Unk
- 05\_CMP.LMP
- 15\_CLP.2
- 06\_CLP.1
- 16\_Pre.B
- 07\_GMP
- 17\_B
- 08\_GMP.Neut
- 18\_Plasma
- 09\_pDC
- 19\_CD8.N
- 21\_CD4.N2
- 24\_CD8.CM
- 22\_CD4.M
- 25\_NK
- 23\_CD8.EM
- 26\_Unk
- 10\_CD8.N
- 20\_CD4.N1

**C**

Fine-mapping result overview

Trait ID: trait\_id\_55  
Genome: hg19  
Trait Description: Monocyte  
ICD10: -  
Variant count: 3897  
Data source link: [View](#)

Chromosome count	Trait information
chr1	rs75963851 0.99998 ...
chr2	rs2292980 0.99983 ...
chr3	rs60984404 0.99973 ...
chr4	...
chr5	...
chr6	...
chr7	...
chr8	...
chr9	...
chr10	...
chr11	...
chr12	...
chr13	...
chr14	...
chr15	...
chr16	...
chr17	...
chr18	...
chr19	...
chr20	...
chr21	...
chr22	...
chr23	...
chr24	...
chr25	...
chr26	...
chr27	...
chr28	...
chr29	...
chr30	...
chr31	...
chr32	...
chr33	...
chr34	...
chr35	...
chr36	...
chr37	...
chr38	...
chr39	...
chr40	...

**D**

Traits/diseases enriched with sample\_id\_3

Method: SCAVENGE  
Search: Monocyte

Enriched traits	No enriched traits	
Trait ID: trait_id_55	Mono	Monocyte
Trait ID: trait_id_6692	MC_AT690	Monocyte count
...	...	...

**E**

Trait- or disease-relevant cell scores

Cell count: 40% Trait: Monocyte

Legend for cell types:

- 01\_HSC
- 02\_Early.Eryth
- 03\_Late.Eryth
- 04\_Early.Baso
- 05\_CMP.LMP
- 06\_CLP.1
- 07\_GMP
- 08\_GMP.Neut
- 09\_pDC
- 10\_CD8.N
- 11\_CD14.Mono.1
- 12\_CD14.Mono.2
- 13\_Unk
- 14\_Unk
- 15\_CLP.2
- 16\_Pre.B
- 17\_B
- 18\_Plasma
- 19\_CD8.N
- 20\_CD8.CM
- 21\_CD4.N2
- 22\_CD4.M
- 23\_CD8.EM
- 24\_CD8.CM
- 25\_NK
- 26\_Unk
- 10\_CD8.N
- 20\_CD8.CM
- 24\_CD8.CM
- 14\_Unk
- 02\_Early.Eryth
- 03\_Late.Eryth
- 04\_Early.Baso
- 05\_CMP.LMP
- 06\_CLP.1
- 07\_GMP
- 08\_GMP.Neut
- 09\_pDC
- 10\_CD8.N
- 11\_CD14.Mono.1
- 12\_CD14.Mono.2
- 13\_Unk
- 14\_Unk
- 15\_CLP.2
- 16\_Pre.B
- 17\_B
- 18\_Plasma
- 19\_CD8.N
- 20\_CD8.CM
- 21\_CD4.N2
- 22\_CD4.M
- 23\_CD8.EM
- 24\_CD8.CM
- 25\_NK
- 26\_Unk

**F**

Differential genes

Gene set: GO (Biological process)  
Visualization Display  
Cell type: 11\_CD14.Mono.1 P value: ≤ 0.05  
Odds ratio: 26  
-log(P value): 5

**G**

Gene hub regulatory network Strategy: Cicero

Cell type: 11\_CD14.Mono.1 Top count: All All: Core:  
Cell (Cicero): Co-score: >0.1  
Gene (Difference):  
P value: ≤ 0.05  
|Log2(Fold change)|: ≥ 0.5

**H**

TF hub regulatory network

Cell type: 11\_CD14.Mono.1 TF (Difference): All: Core: SnapATAC2  
TF (HOMER):  
P value: ≤ 0.05  
Q value: ≤ 0.05  
P value: ≤ 0.05  
Adjusted p value: ≤ 0.05  
|Log2(Fold change)|: ≥ 0.5  
Trait: TF (HOMER) Key TF: TF (Difference) Cell type: scATAC-seq

**I**

Search

Search by gene  
Search by category or source cohort  
Search by TF  
Search by tissue type or cell type  
Search by SNP

**J**

Analysis

Analyzing variant-to-function mapping  
Analyzing variant-to-function mapping with genes  
Analyzing variant-to-function mapping with TFs  
Comparative analysis between samples or traits

**K**

Download

Download trait/disease-relevant cell score (TRS) data  
Download fine-mapping result data  
Download other data