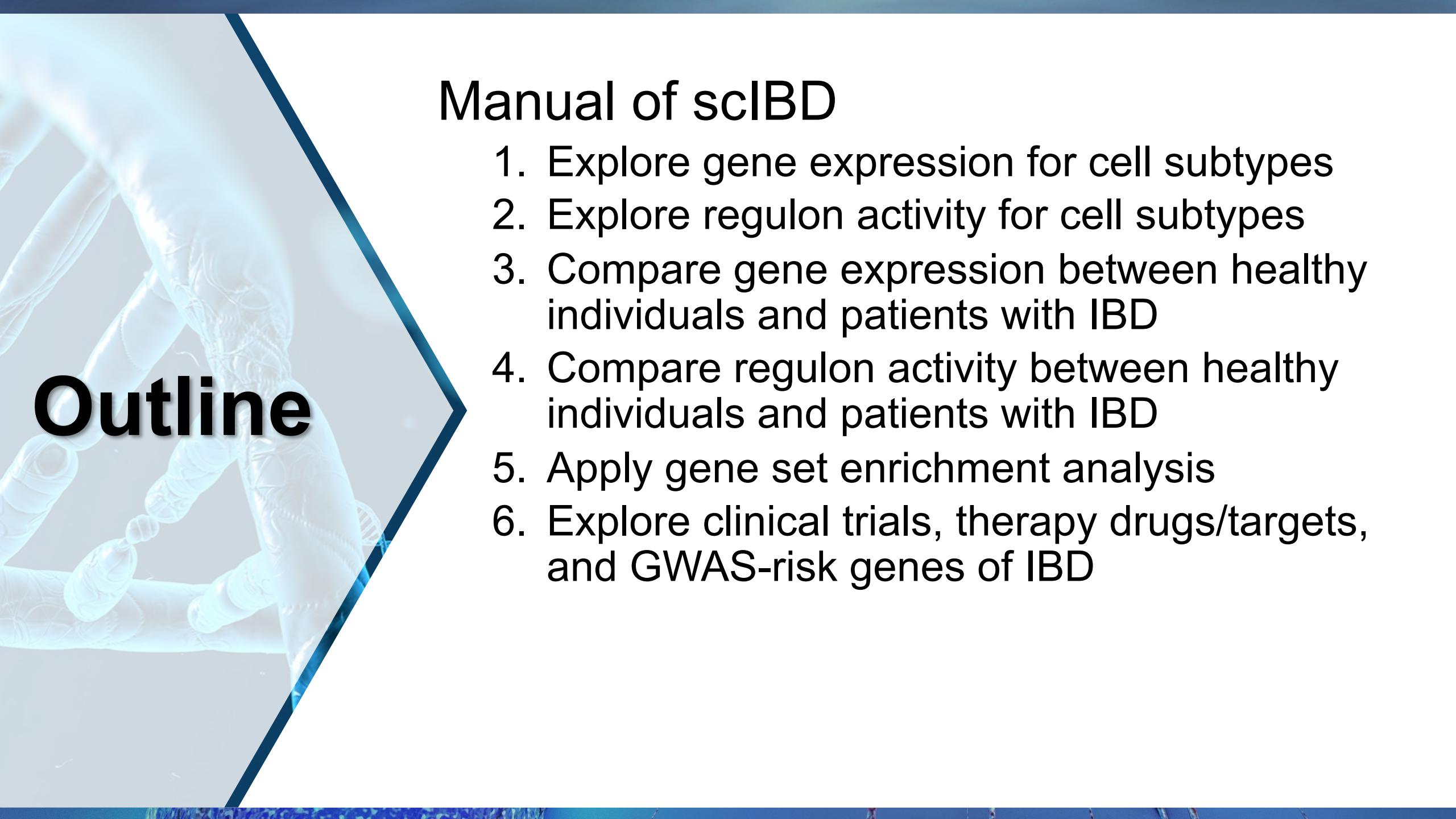


# sclBD manual

Peilu Lin & Hu Nie

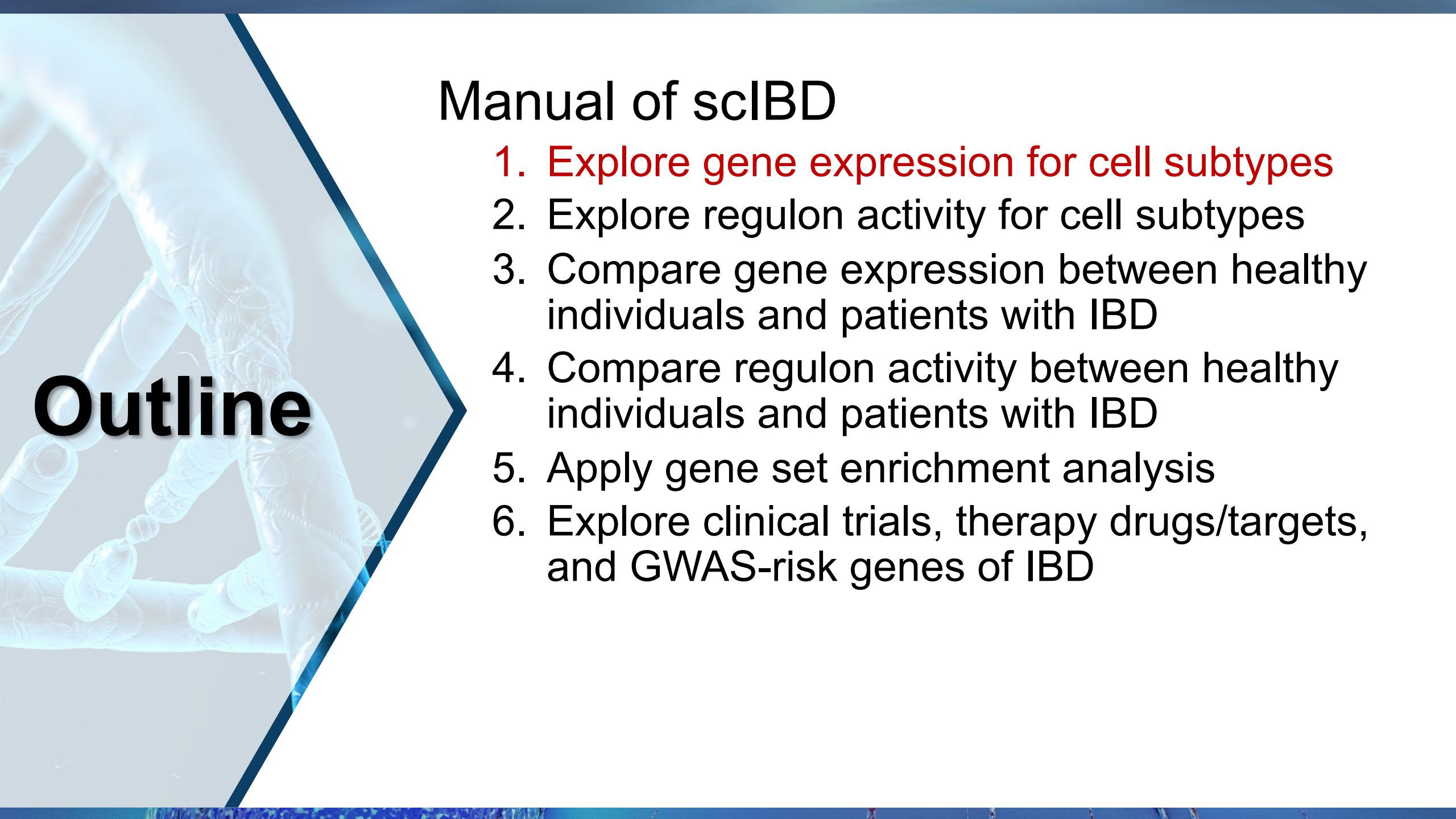
August 13, 2022



# Outline

## Manual of scIBD

1. Explore gene expression for cell subtypes
2. Explore regulon activity for cell subtypes
3. Compare gene expression between healthy individuals and patients with IBD
4. Compare regulon activity between healthy individuals and patients with IBD
5. Apply gene set enrichment analysis
6. Explore clinical trials, therapy drugs/targets, and GWAS-risk genes of IBD



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# Explore gene expression for cell subtypes

sciBD Home Exploration Documents References Downloads Help

Gene Expression Profile  
Regulon Activity Profile  
Gene Expression Comparison  
Regulon Activity Comparison  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

Options

Major cluster: Myeloid

Select genes: CPA3, TPSAB1

Embedding used: UMAP

Color profile: Reds

Dot size: 0.1

GO

Change the dimensional reduction method  
Change the color profile  
Drag to change the dot size

1. Choose a major cluster to study  
2. Choose one or more genes

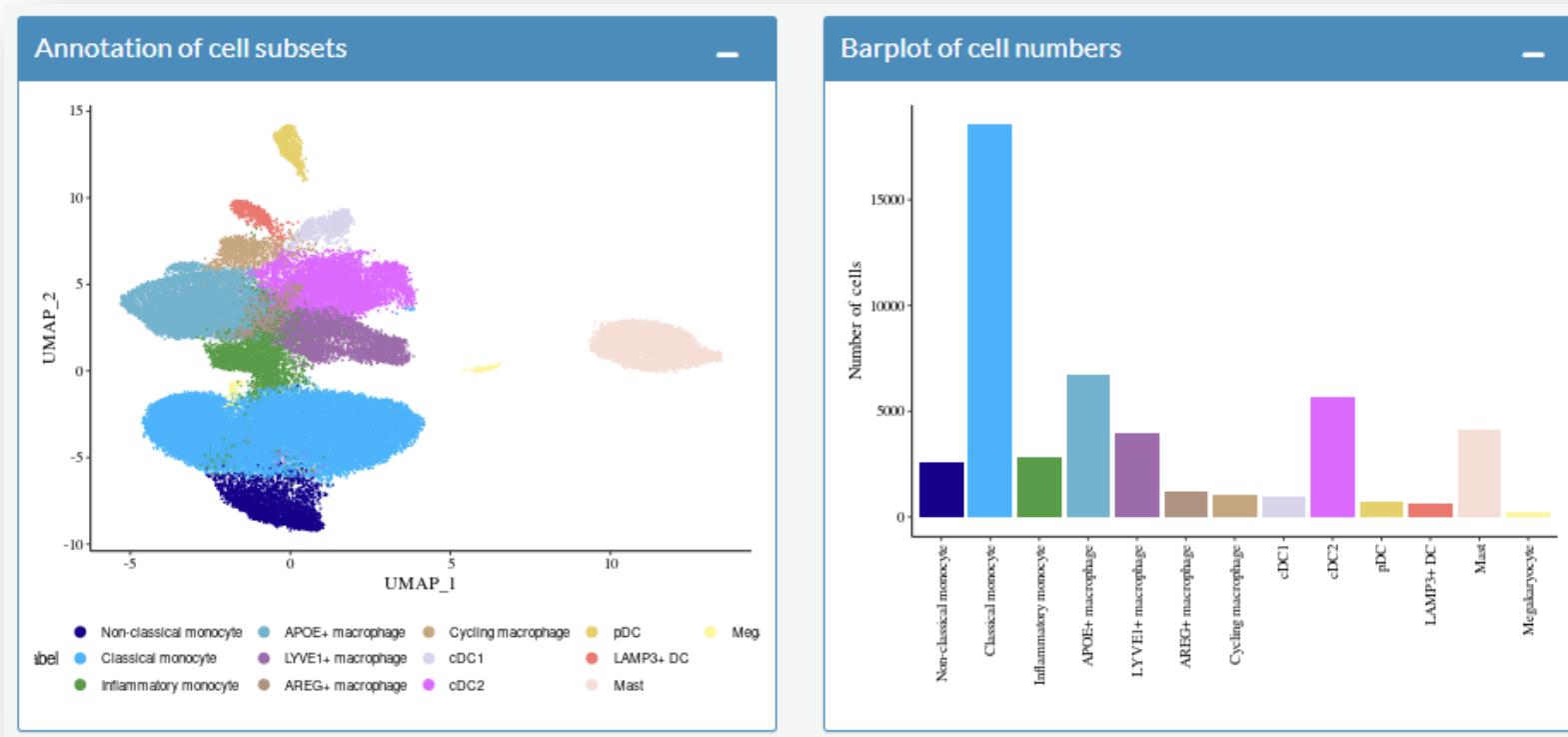
Dot plot of gene expression

Annotation of cell subsets

Barplot of cell numbers

# Cell subsets in myeloid compartment

After selecting Myeloid as major cluster, annotations of cell subsets (left) and number of cells (right) in myeloid compartment will be shown.

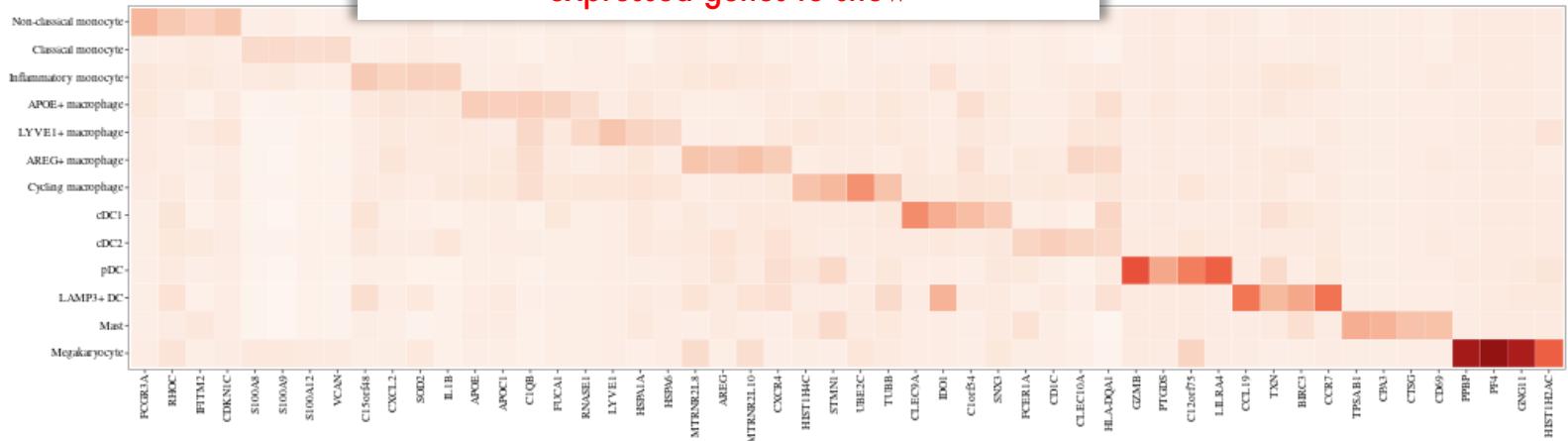


## Heatmap plot of marker genes

Number of top marker genes:

4

Assign the number of top differentially expressed genes to show



## Marker genes of each minor cluster

Show 10 entries

Differentially expressed gene signatures of each minor cluster are shown

Search:

gene	cluster	pct.1	pct.2
All	All	All	All
FCGR3A	Non-classical monocyte	0	0
RHOC	Non-classical monocyte	0	0
IFITM2	Non-classical monocyte	0	0
CDKN1C	Non-classical monocyte	0	0
LST1	Non-classical monocyte	0	0
TCF7L2	Non-classical monocyte	0	0
MTSS1	Non-classical monocyte	0	0
IFITM3	Non-classical monocyte	0	0
SERPINA1	Non-classical monocyte	0	0
LY6E	Non-classical monocyte	0	0

# Explore differential expressed genes in myeloid compartment

After choosing **Mast** cell and ranking the list according to **avg\_log2FC**, differential expressed genes are listed. You can explore and compare their expression profiles in “gene expression profile” and “gene expression comparison”.

Marker genes of each minor cluster							
		Show 10 entries	cluster	p_val_adj	p_val	avg_log2FC	pct.1
gene	cluster	All	All	All	All	All	pct.2
TPSAB1	Mast	0	0	8.51098583892784	0.973	0.005	
CPA3	Mast	0	0	5.66481572165582	0.878	0.002	
CTSG	Mast	0	0	4.88303096596334	0.542	0.002	
CD69	Mast	0	0	4.86775796436058	0.716	0.084	
HPGDS	Mast	0	0	4.26870211884618	0.764	0.026	
GATA2	Mast	0	0	3.8625573317653	0.618	0.002	
HPGD	Mast	0	0	3.85574072043881	0.572	0.009	
VWA5A	Mast	0	0	3.85398974788839	0.681	0.012	
CLU	Mast	0	0	3.64315077986136	0.624	0.025	
CD9	Mast	0	0	3.46607729759525	0.725	0.099	
Showing 1 to 10 of 248 entries (filtered from 5,351 total entries)				Previous	1	2	3
				4	5	...	25
							Next

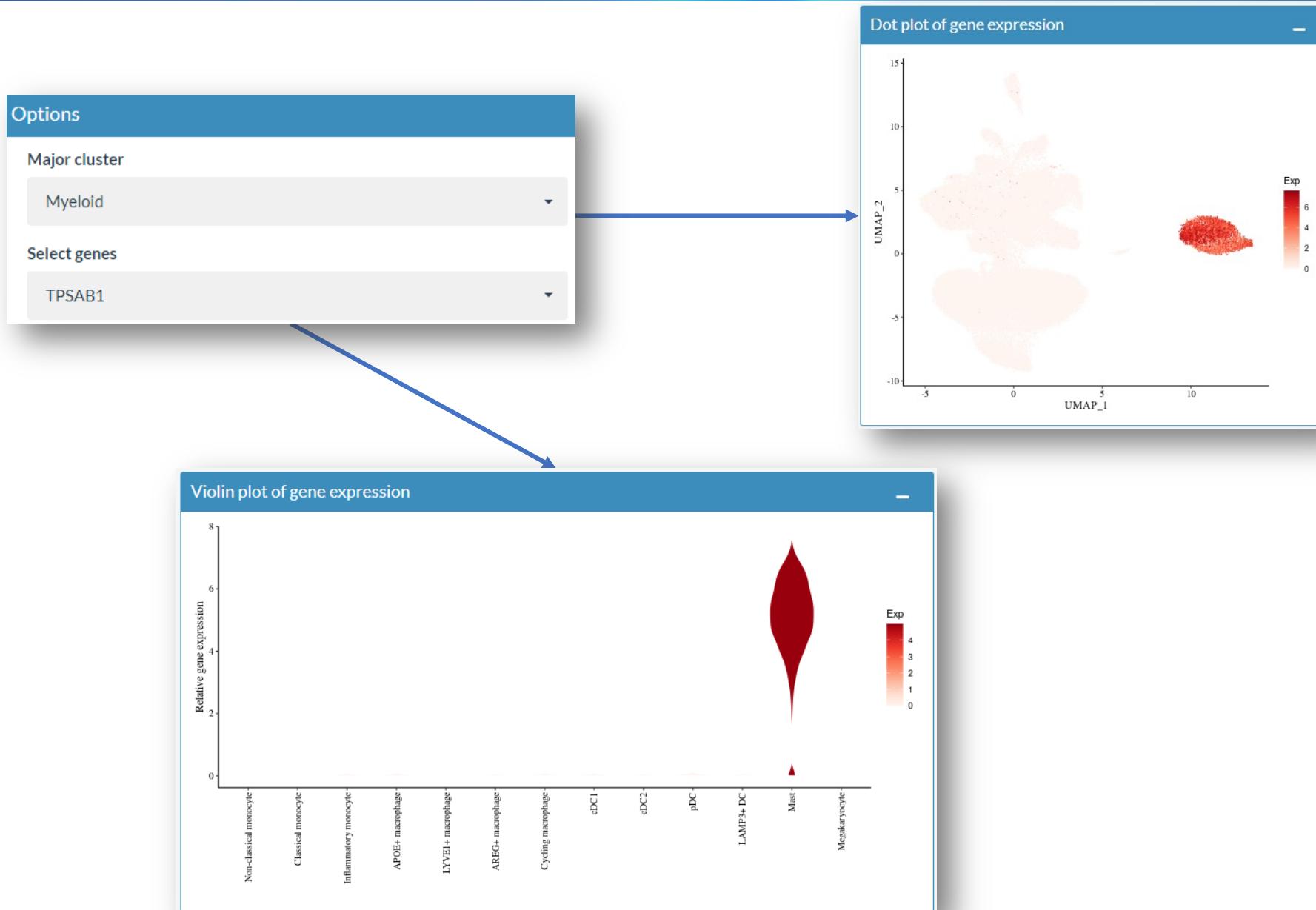
cluster: cell subtypes in myeloid compartment

p\_val: p value calculated by wilcoxon test

p\_val\_adj: adjusted p value, based on based on bonferroni correction using all genes in the dataset.

avg\_log2FC: average log 2 fold change

# Select one gene of interest



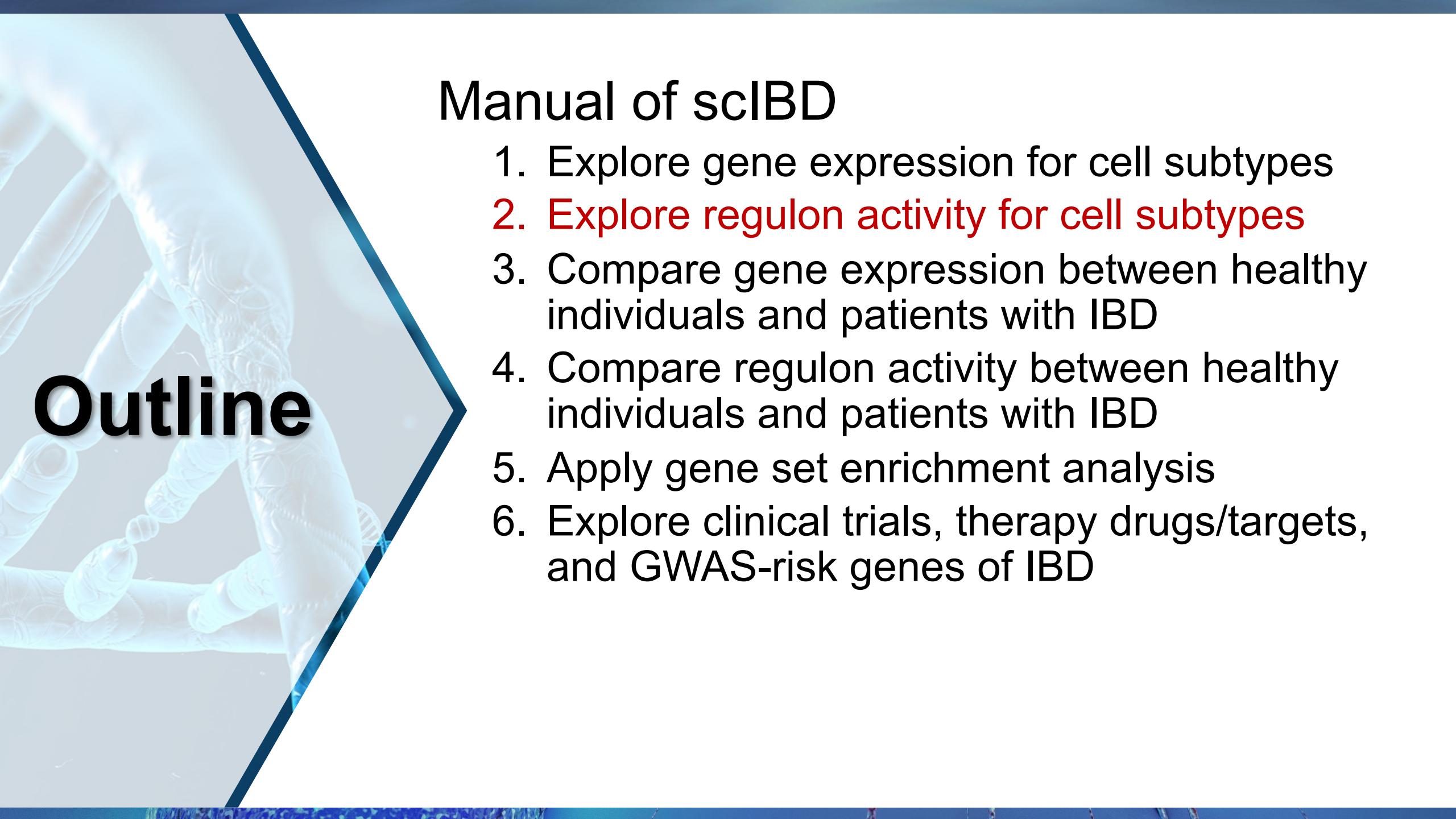
# Explore differential expressed genes in myeloid compartment

Similarly, after choosing **LAMP3+ DC** and ranking the list according to **avg\_log2FC**, differential expressed genes are listed. You can explore and compare their expression profiles in “gene expression profile” and “gene expression comparison”.

Marker genes of each minor cluster													
Show	10	entries	Search:										
gene	cluster	p_val_adj	p_val	avg_log2FC	pct.1	pct.2							
All	LAMP3+ DC	All	All	All	All	All							
CCL19	LAMP3+ DC	0	0	4.94871501941306	0.687	0.013							
TXN	LAMP3+ DC	0	0	4.38437760248867	0.972	0.469							
BIRC3	LAMP3+ DC	0	0	4.30084604779606	0.92	0.166							
CCR7	LAMP3+ DC	0	0	4.03708017330076	0.806	0.016							
CCL22	LAMP3+ DC	0	0	4.03289766003364	0.485	0.004							
MARCKSL1	LAMP3+ DC	0	0	3.89773932129738	0.908	0.203							
FSCN1	LAMP3+ DC	0	0	3.87983264455751	0.805	0.061							
LAMP3	LAMP3+ DC	0	0	3.49412604166946	0.817	0.021							
CCL17	LAMP3+ DC	1.62348874071211e-258	1.02752451943804e-262	3.39859367336127	0.255	0.003							
IDO1	LAMP3+ DC	0	0	3.06116580349576	0.659	0.049							
Showing 1 to 10 of 383 entries (filtered from 5,351 total entries)					Previous	1	2	3	4	5	...	39	Next

# Select multiple genes of interest





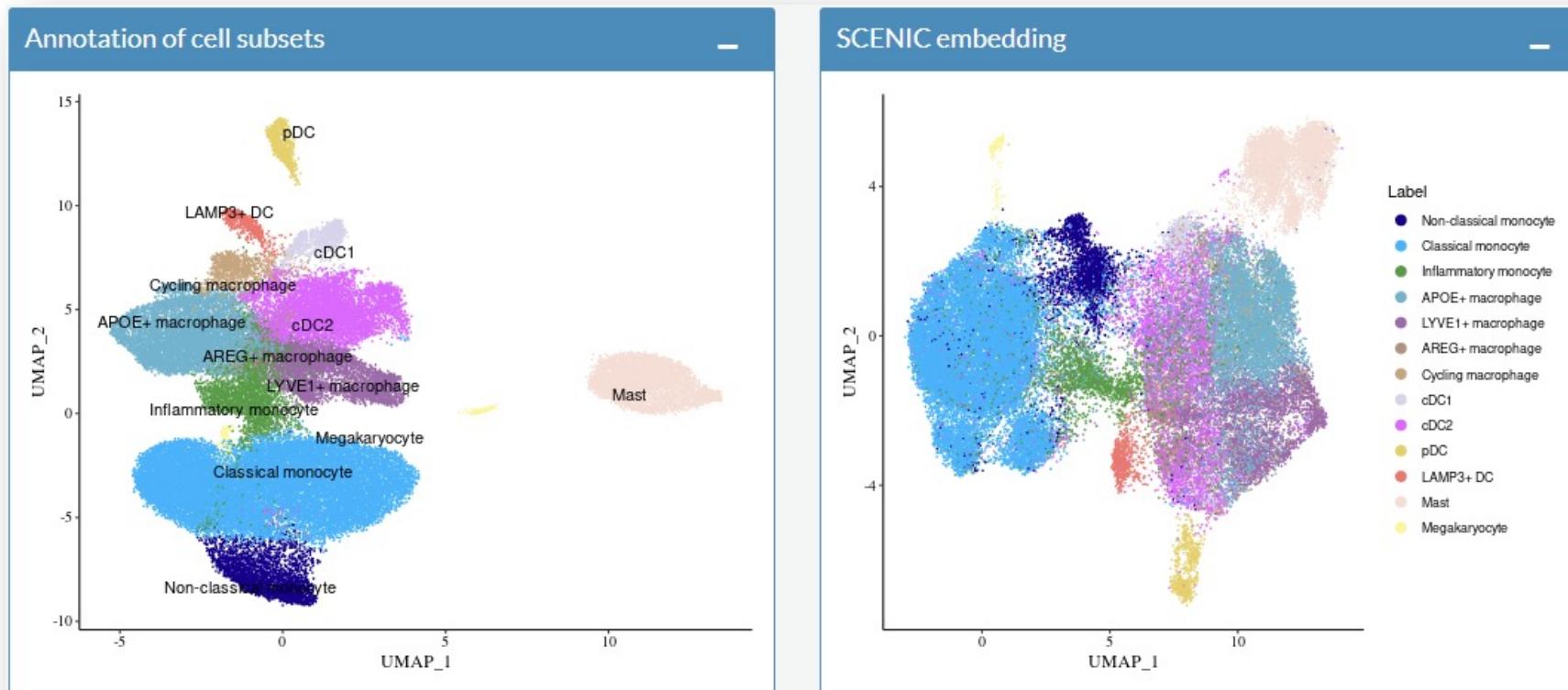
# Outline

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# Cell subsets in myeloid compartment

After selecting **Myeloid** as major cluster, UMAP embedding (left) and SCENIC embedding (right) with annotations of cell subsets in myeloid compartment will be shown.



# Explore regulons in myeloid compartment

- After ranking the list according to regulon specificity scores of pDC, regulon with highest specificity in pDC are listed.
- The values in the table represents the average regulon specificity scores of the regulons in the corresponding cell type.

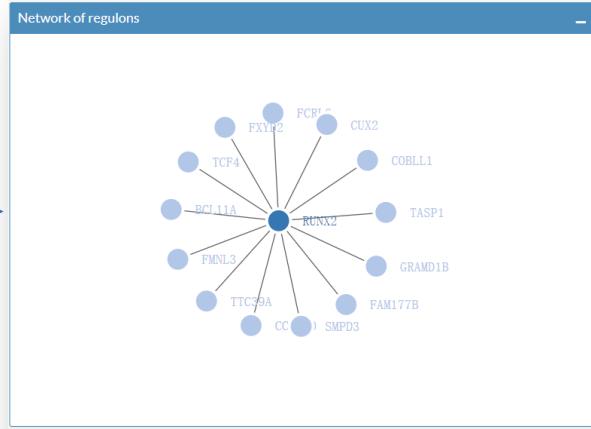
Regulon specificity scores (RSS) in each cell type													-					
	Show 10 entries												Search:					
	APOE+ macrophage	AREG+ macrophage	LYVE1+ macrophage	Cycling macrophage	Classical monocyte	Non-classical monocyte	Inflammatory monocyte	cDC1	cDC2	pDC	LAMP3+ DC	Mast	Megakaryocyte					
RUNX2	0.08	0.02	0.09	0.01	0.08	0.02	0.03	0.01	0.08	0.27	0.03	0.04	0.00					
ZNF646	0.09	0.03	0.07	0.01	0.19	0.08	0.07	0.01	0.05	0.10	0.01	0.05	0.01					
ZNF569	0.02	0.01	0.02	0.00	0.13	0.03	0.06	0.00	0.01	0.09	0.01	0.04	0.00					
ZNF335	0.01	0.01	0.02	0.00	0.03	0.01	0.01	0.00	0.01	0.08	0.00	0.02	0.00					
ZFP64	0.08	0.02	0.12	0.03	0.11	0.04	0.03	0.05	0.06	0.07	0.01	0.07	0.02					
SOX4	0.09	0.02	0.08	0.02	0.17	0.04	0.05	0.03	0.08	0.06	0.02	0.20	0.01					
ETV2	0.14	0.03	0.09	0.03	0.35	0.07	0.07	0.03	0.12	0.06	0.03	0.14	0.02					
BCL11A	0.14	0.04	0.11	0.03	0.36	0.08	0.09	0.03	0.15	0.05	0.03	0.10	0.01					
IRF4	0.14	0.05	0.11	0.03	0.33	0.07	0.09	0.03	0.16	0.05	0.04	0.12	0.01					
SOX7	0.07	0.02	0.04	0.02	0.13	0.03	0.05	0.06	0.08	0.05	0.02	0.09	0.01					
Showing 1 to 10 of 355 entries										Previous	1	2	3	4	5	...	36	Next

# Select one regulon of interest

**Options**

**Major cluster**  
Myeloid

**Transcript factor**  
RUNX2



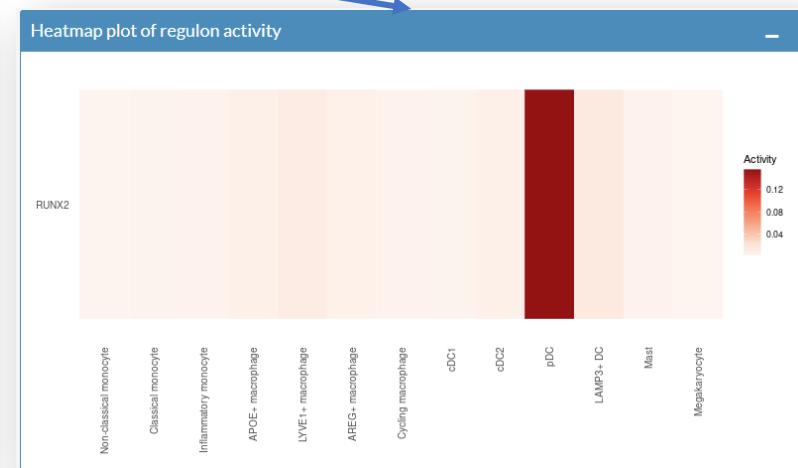
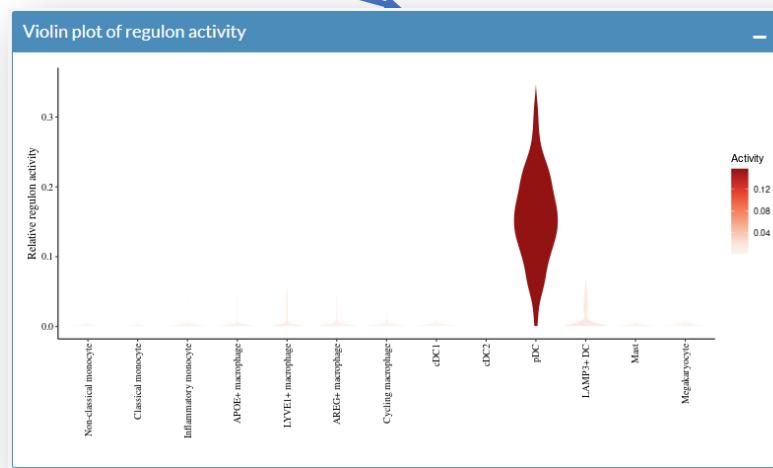
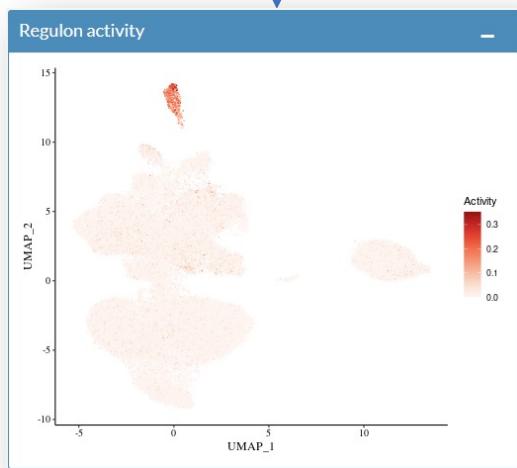
Network of regulons

Show 10 entries

TF	target	correlation	p-value	expression	
All	All	All	All	All	
7	RUNX2	RUNX2	1	0e+00	1.2784
12	RUNX2	SMPD3	0.385	1.299e-09	1.6395
10	RUNX2	FMNL3	0.779	1.594e-59	1.06
13	RUNX2	TCF4	0.7414	2.251e-135	1.6541
9	RUNX2	GRAMD1B	0.723	2.45e-32	1.2459
1	RUNX2	TTC39A	0.5055	2.472e-04	1.19
5	RUNX2	COBLL1	0.4592	2.682e-09	1.3035
4	RUNX2	BCL11A	0.7126	3.01e-84	1.4276
11	RUNX2	CUX2	0.355	3.71e-03	1.2617
8	RUNX2	FXYD2	0.5568	3.961e-05	1.047

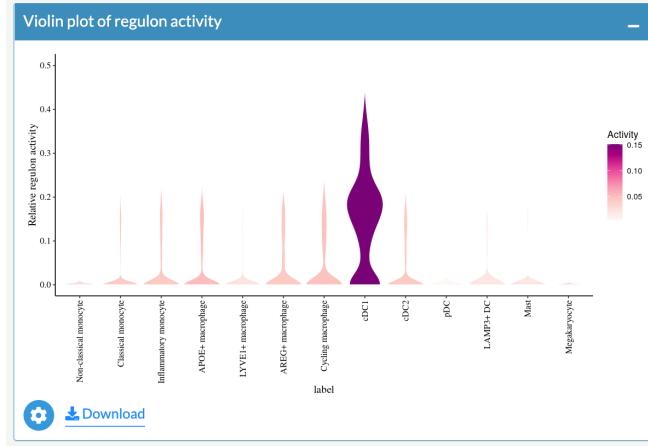
Showing 1 to 10 of 14 entries

Previous 1 2 Next

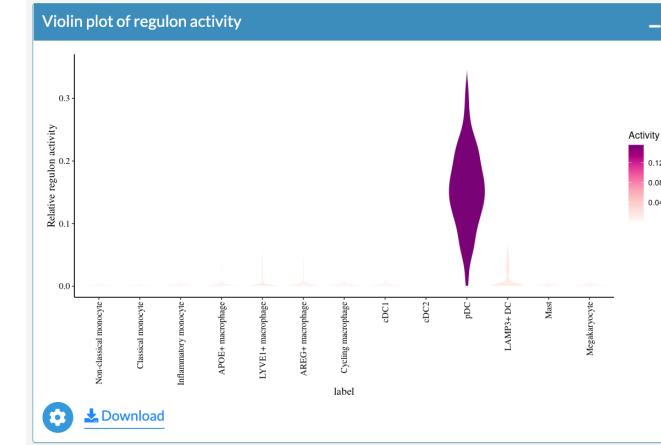


# Activities of regulons showed in our manuscript

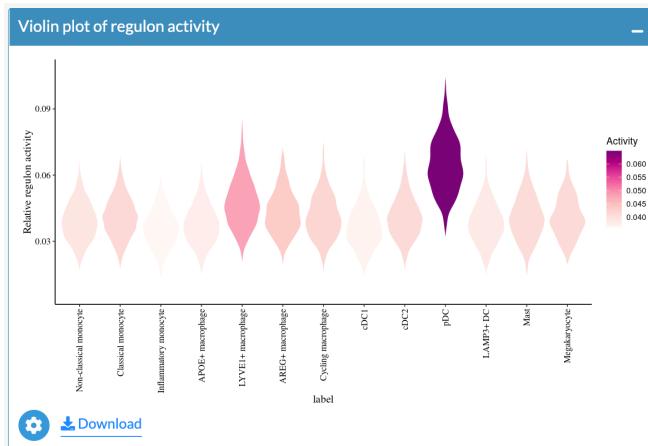
## BATF3 in myeloid compartment



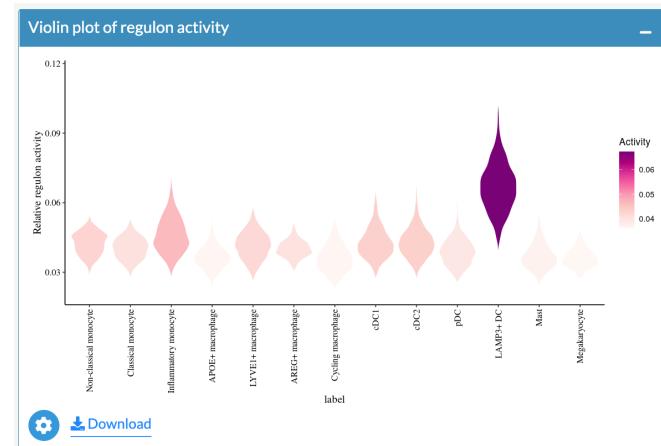
## RUNX2 in myeloid compartment



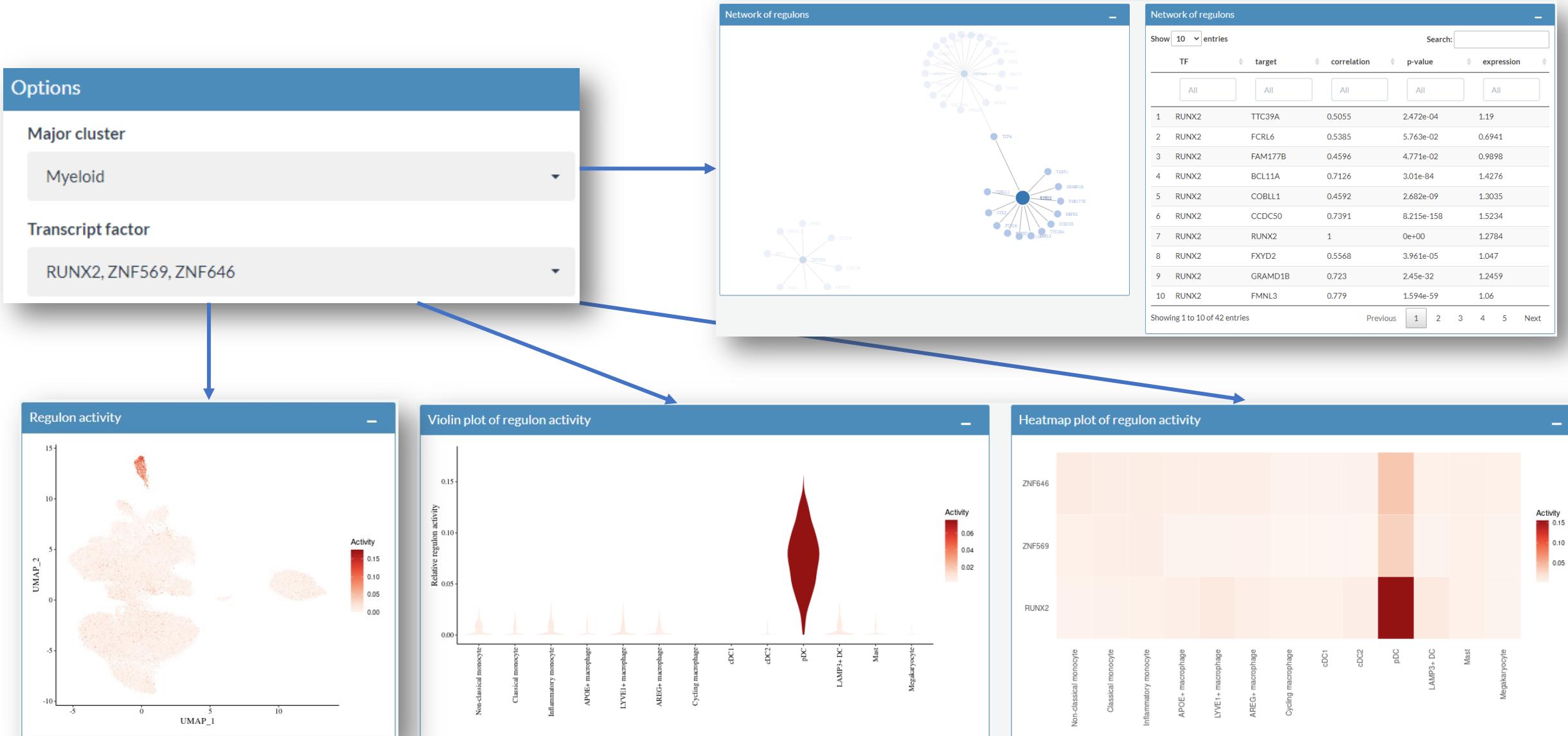
## TCF4 in myeloid compartment



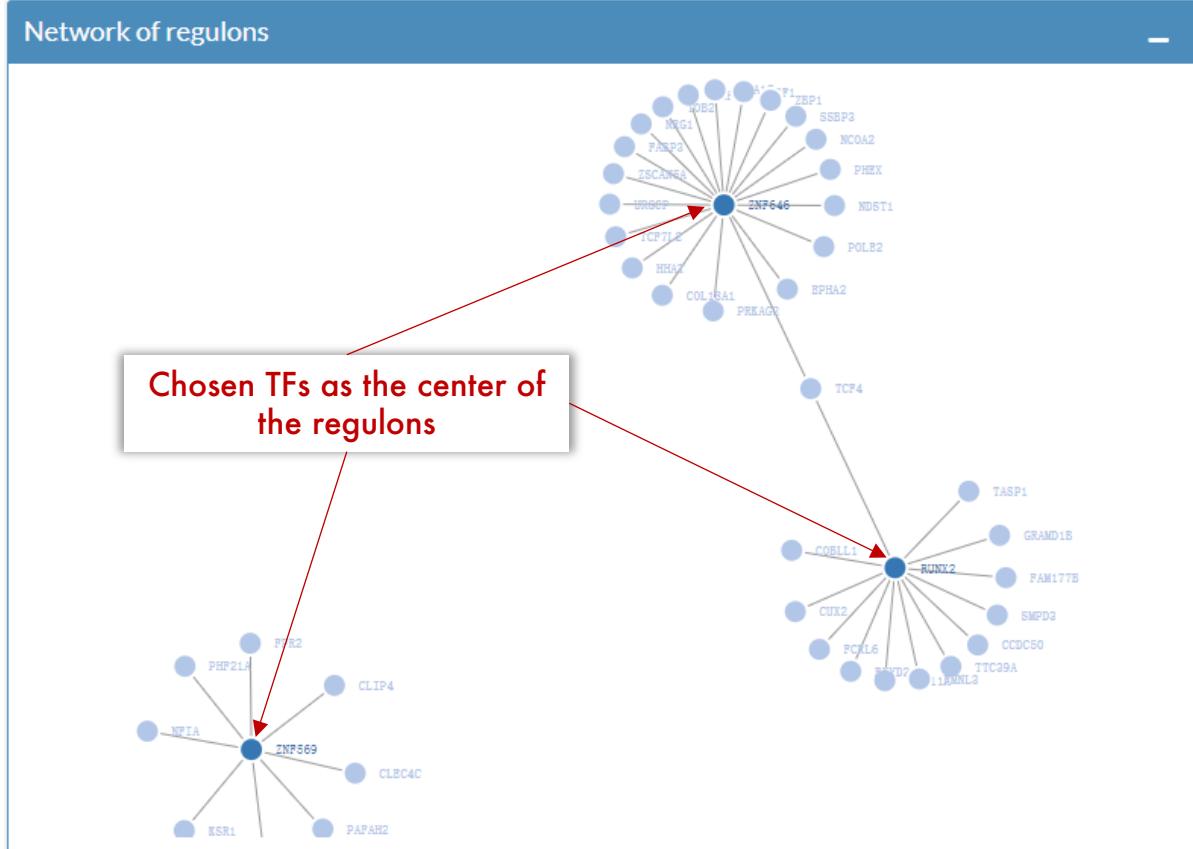
## RELB in myeloid compartment



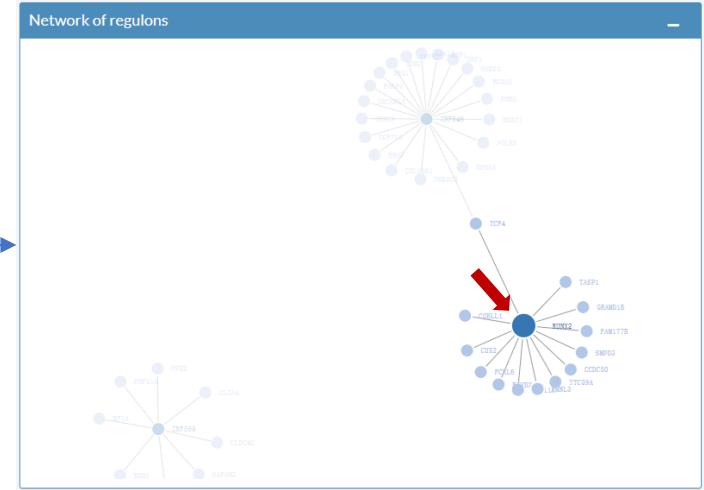
# Select multiple regulons of interest

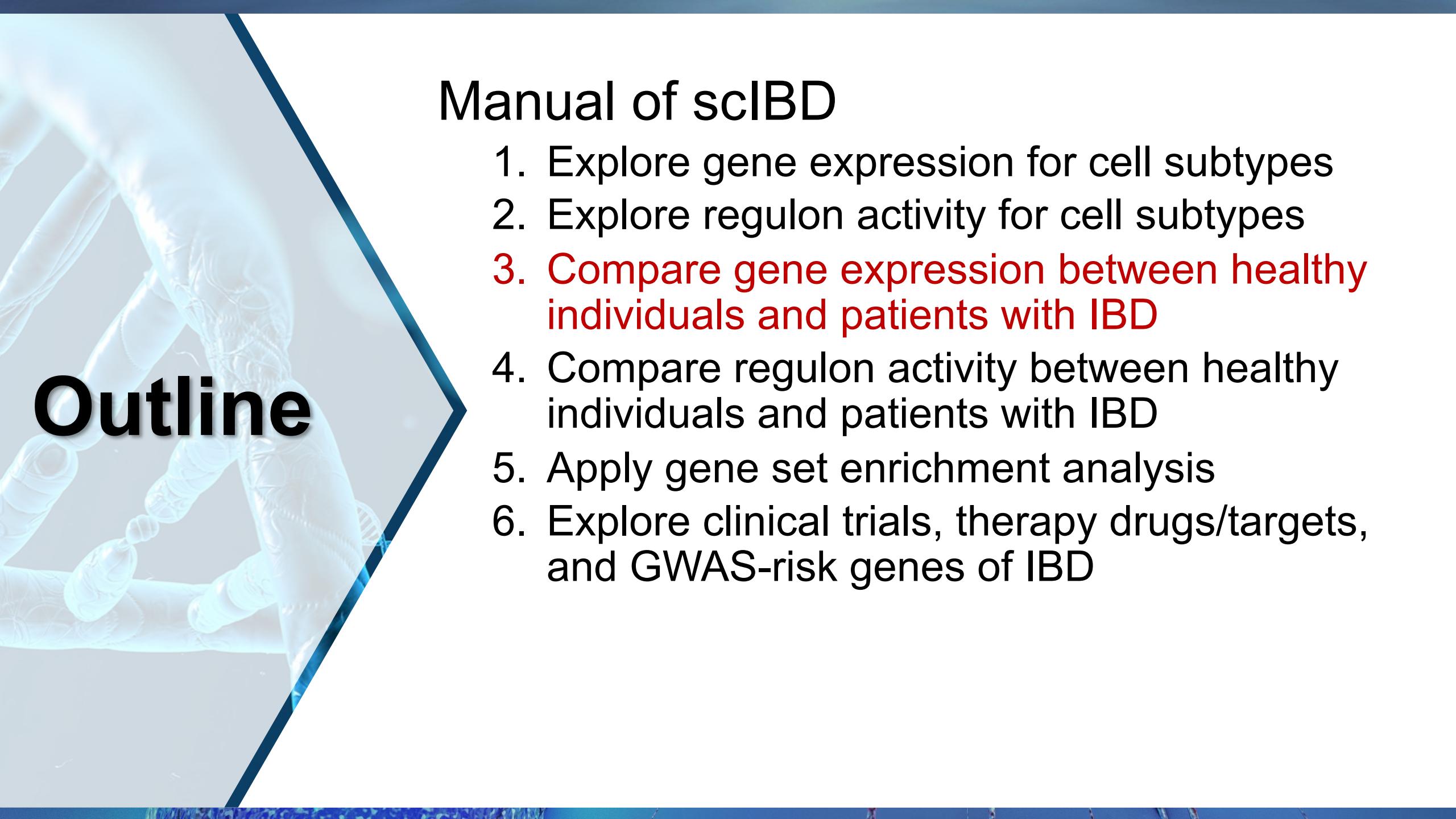


# Network of regulons



Place your mouse pointer on the center to highlight the regulon





# Outline

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# The control panel for “Gene Expression Comparison” part

## Control panel

Select dataset

Select genes	Major cluster	Tissue	Development stage	Study	Color profile
S1PR5	ILC	smallInt, largeInt, blood, lym	adult	AlisonSimmons_2018Cell_uc	Reds
Embedding used	Minor cluster	Location	Disease state	Sample	Dot size
UMAP	Non-classical monocyte, Clas	colon	CD_PBMC, CD_inflamed, CD	GSM3140593, GSM314059	<input type="range" value="0.1"/> 0 0.2 0.4 0.6 0.8 1 1.2 1.4 1.6 1.8 2

**GO**

	Select All	Deselect All
CD_PBMC	✓	
CD_inflamed	✓	
CD_inflamed/CD_non_inflamed	✓	
CD_non_inflamed	✓	
Colitis_inflamed	✓	
Healthy	✓	
Healthy_PBMC	✓	
UC_PBMC	✓	
UC_inflamed	✓	
UC_non_inflamed	✓	

- smallInt: small intestine  
largeInt: large intestine
- CD\_PBMC: PBMC of CD patients  
CD\_inflamed: Inflamed tissue of CD patients  
CD\_inflamed/ CD\_non\_inflamed: Intestinal tissue of CD patients  
CD\_non\_inflamed: Non-inflamed tissue of CD patients  
Colitis\_inflamed: Inflamed tissue of patients with colitis (not IBD)  
Healthy: Intestinal tissue of healthy individuals  
Healthy\_PBMC: PBMC of healthy individuals  
UC\_PBMC: PBMC of UC patients  
UC\_inflamed: Inflamed tissue of UC patients  
colitisUC\_non\_inflamed: Non-inflamed tissue of UC patients

# Explore the gene expression of HLA-II molecules in all major clusters



# Explore the gene expression of HLA-II molecules in epithelial cells

Gene Expression Profile  
Regulon Activity Profile  
**Gene Expression Comparison**  
Regulon Activity Comparison  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

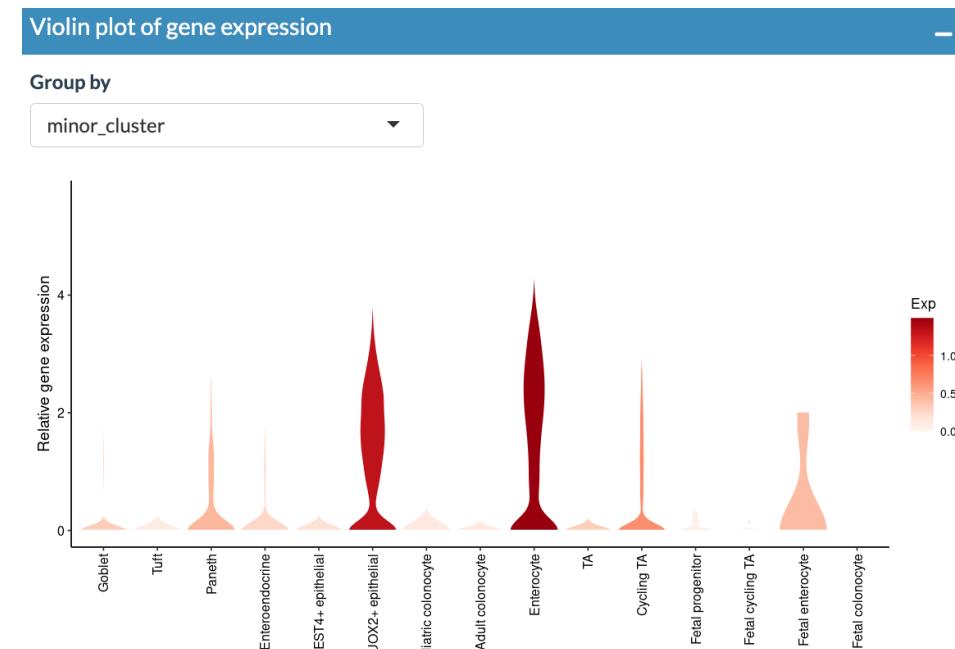
→

Select dataset

Select genes: HLA-DRA, HLA-DRB1  
Major cluster: Epithelial  
Tissue: smallInt, largeInt, blood, ly  
Development stage: adult  
Study: AlisonSimmons\_2018Cell  
Color profile: Reds

Embedding used: UMAP  
Minor cluster: Non-classical monocyte, C  
Location: duodenum, ileum, jejunum  
Disease state: CD\_PBMC, CD\_inflamed, l  
Sample: GSM3140593, GSM3140  
Dot size: 0 0.1 1

GO



# Compare gene expression of MHC-II molecules between health and UC in DUOX2+ epithelial cells

Gene Expression Profile  
Regulon Activity Profile  
**Gene Expression Comparison**  
Regulon Activity Comparison  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

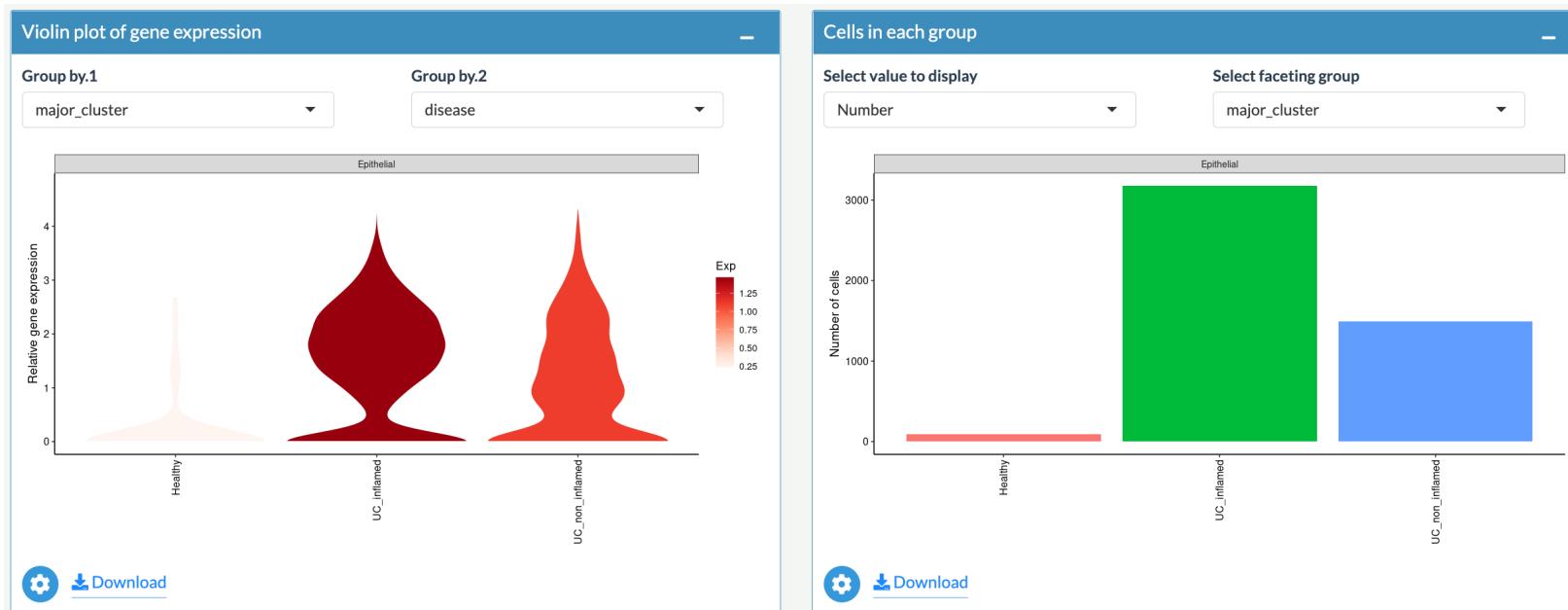


Select dataset

Select genes	Major cluster	Tissue	Development stage	Study	Color profile
HLA-DRA, HLA-DRB1	Epithelial	smallInt, largeInt, blood, ly	adult	AlisonSimmons_2018Cell.	Reds
Embedding used	Minor cluster	Location	Disease state	Sample	Dot size
UMAP	DUOX2+ epithelial	duodenum, ileum, jejunum	Healthy, UC_inflamed, UC	GSM3140593, GSM3140	<input type="range" value="0.1"/>

**GO**

**Selected groups:**  
Healthy, UC\_inflamed and UC\_non\_inflamed



# Compare gene expression of MHC-II molecules between health and CD in enterocytes

Gene Expression Profile  
Regulon Activity Profile  
**Gene Expression Comparison**  
Regulon Activity Comparison  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration



Select dataset

Select genes	Major cluster	Tissue	Development stage	Study	Color profile
HLA-DRA, HLA-DRB1	Epithelial	smallInt, largeInt, blood, ly	adult	AlisonSimmons_2018Cell	Reds

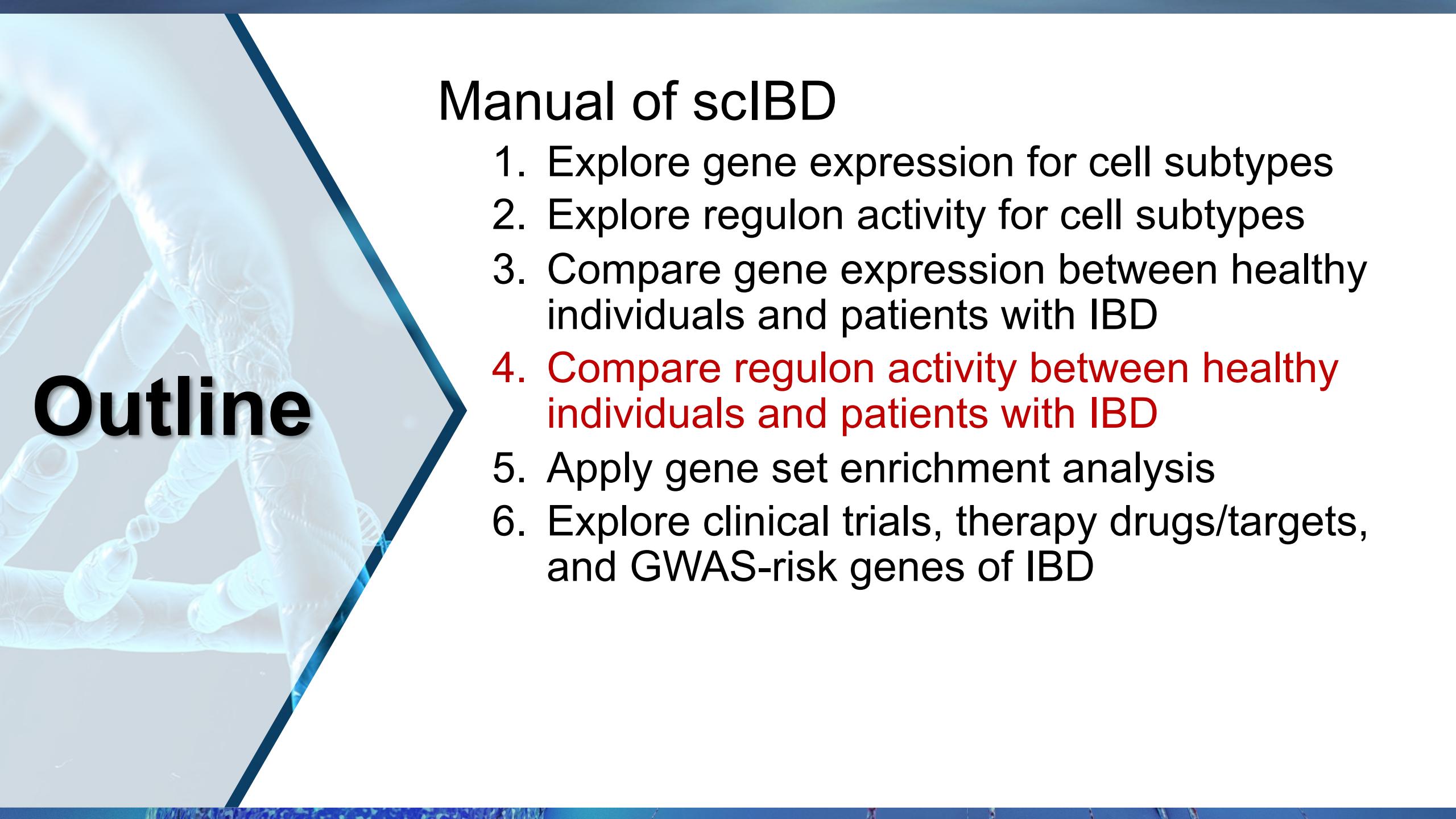
  

Embedding used	Minor cluster	Location	Disease state	Sample	Dot size
UMAP	Enterocyte	duodenum, ileum, jejunum	CD_inflamed, CD_non_infl	GSM3140593, GSM3140	0 to 1

**GO**

Selected groups:  
Healthy, CD\_inflamed and CD\_non\_inflamed





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# Explore differentially activated regulons between health and UC or CD in epithelial cells

Gene Expression Profile  
Regulon Activity Profile  
Gene Expression Comparison  
**Regulon Activity Comparison**  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

Select dataset

Major cluster	Epithelial	Minor cluster	Goblet, Tuft, Paneth, Enteri	Location	duodenum, ileum, jejunum	Disease state	CD_PBMC, CD_inflamed, I	Sample	GSM3140593, GSM3140	Submit
Transcript factor	AR	Tissue	smallint, largeint, blood, ly	Development stage	fetal, pediatric, adult	Study	AlisonSimmons_2018Cell	Color profile	Reds	GO

Select Epithelial as major cluster to explore differentially activated regulons between health and UC or CD in epithelial cells.

Compare regulons between healthy and UC

Show 10 entries	Search:				
gene	UC_inflamed	Healthy	FoldChange	p.value	p.adjust
All	All	All	All	All	All
RFX5	0.042718	0.016440	2.449472	0.000000	0.000000
NFE2L3	0.073421	0.032640	2.182573	0.000000	0.000000
ZBTB40	0.013699	0.005331	2.163928	0.000000	0.000000
EGR4	0.010417	0.005158	1.691655	0.000000	0.000000
ZNF436	0.007414	0.003458	1.663145	0.000000	0.000000
PITX1	0.027530	0.016265	1.594513	0.000000	0.000000
RUNX3	0.006697	0.003253	1.574623	0.000000	0.000000
KDM4A	0.005257	0.002432	1.531633	0.000000	0.000000
HOXD13	0.099801	0.064639	1.520456	0.000000	0.000000
TBX10	0.086436	0.056469	1.504046	0.000000	0.000000

The value in the second and the third column represents the average regulon activity in inflamed tissue of CD, UC patients or healthy individuals.

# Compare regulon activity of PITX1 between healthy individuals and patients with UC or CD in epithelial cells

Gene Expression Profile  
Regulon Activity Profile  
Gene Expression Comparison  
**Regulon Activity Comparison**  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

Select dataset

Major cluster: Epithelial (highlighted with red arrow)

Minor cluster: Goblet, Tuft, Paneth, Entero (highlighted with red arrow)

Location: duodenum, ileum, jejunum

Disease state: CD\_inflamed, CD\_non\_infl

Sample: GSM3140593, GSM3140 (highlighted with red arrow)

Submit: GO

Transcript factor: PITX1 (highlighted with red arrow)

Tissue: smallInt, largeInt, blood, ly

Development stage: adult (highlighted with red arrow)

Study: AlisonSimmons\_2018Cell

Color profile: RdPu

Violin plot of regulon activity

Group by: disease

Relative regulon activity: 0.00, 0.05, 0.10, 0.15

Activity scale: 0.0175, 0.0200, 0.0225, 0.0250, 0.0275

CD\_inflamed (pink), CD\_non\_inflated (light orange), Healthy (light orange), UC\_inflamed (dark purple)

Download

Cells in each group

Select value to display: Number

Number of cells: 0, 20000, 40000, 60000

CD\_inflamed (red), CD\_non\_inflated (green), Healthy (teal), UC\_inflamed (purple)

Download

# Compare regulon activity of PITX1 between healthy individuals and patients with UC in DUOX2+ epithelial cells in colorectum

Gene Expression Profile  
Regulon Activity Profile  
Gene Expression Comparison  
**Regulon Activity Comparison**  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

→

Select dataset

Major cluster	Minor cluster	Location	Disease state	Sample	Submit
Epithelial	DUOX2+ epithelial	colon, rectum	Healthy, UC_inflamed, UC	GSM3140593, GSM3140	GO
PITX1	smallInt, largeInt, blood, ly	adult	AlisonSimmons_2018Cell	RdPu	

Violin plot of regulon activity

Group by: disease

Relative regulon activity

Activity scale: 0.00 to 0.15

Groups: Healthy, UC\_Inflamed, UC\_non\_inflamed

Download

Cells in each group

Select value to display: Number

Number of cells

Group	Number of cells
Healthy	~10
UC_Inflamed	~3200
UC_non_inflamed	~1500

Download

# Compare regulon activity of PITX1 between colon and rectum in DUOX2+ epithelial cells in patients with UC

Gene Expression Profile  
Regulon Activity Profile  
Gene Expression Comparison  
**Regulon Activity Comparison**  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
GWAS-implicated Risk Genes  
Meta Data Exploration

→

Select dataset

Major cluster	Minor cluster	Location	Disease state	Sample	Submit
Epithelial	DUOX2+ epithelial	colon, rectum	UC_inflamed	GSM3140593, GSM3140	GO
PITX1	smallInt, largeInt, blood, ly	adult	AlisonSimmons_2018Cell	RdPu	

Transcript factor

Tissue

Development stage

Study

Color profile

Violin plot of regulon activity

Group by

tissue.sub

Relative regulon activity

Activity

colon

rectum

Download

Cells in each group

Select value to display

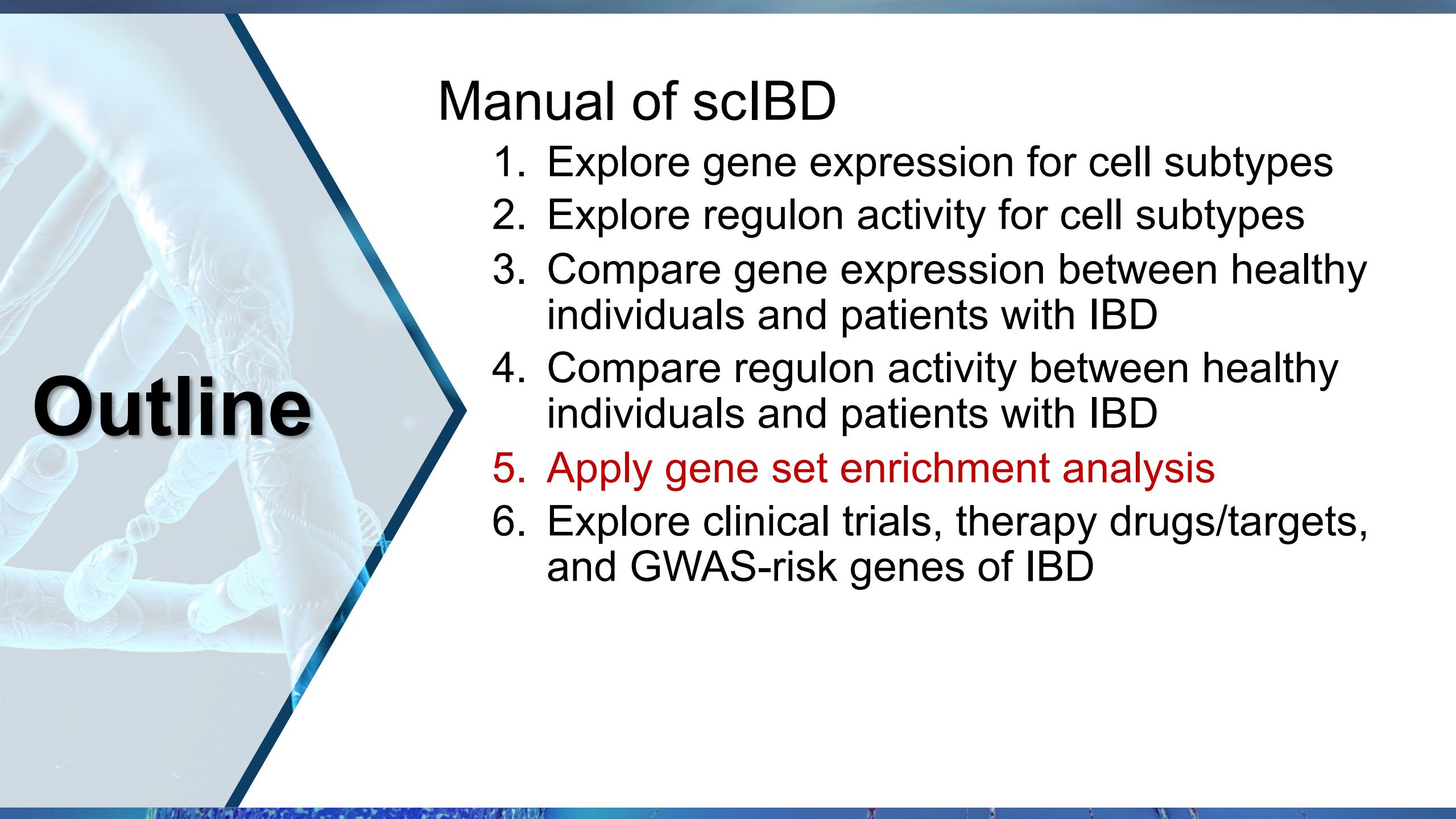
Number

Number of cells

colon

rectum

Download



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4. Compare regulon activity between healthy individuals and patients with IBD
5. **Apply gene set enrichment analysis**
6. Explore clinical trials, therapy drugs/targets, and GWAS-risk genes of IBD

# Apply gene set enrichment analysis

Three ways to input a gene set

Input gene set

Genes Upload Select

Check genes in selected studies:

- ALK
- AMZ1
- ANO6
- ARL14
- ARSB
- ATOH8
- BRMS1L
- BTG3
- C3orf49
- CACNB2
- CARD9

Pre-defined gene sets

- Ellinghaus D (2016) Nat Genet,GCST005537,Chronic inflammatory diseases
- Anderson CA (2011) Nat Genet,GCST000964,UC
- Liu JZ (2015) Nat Genet,GCST003045,UC
- de Lange KM (2017) Nat Genet,GCST004133,UC
- Jostins L (2012) Nature,GCST001728,UC
- McGovern DP (2010) Nat Genet,GCST000624,UC
- de Lange KM (2017) Nat Genet,GCST004132,CD
- Liu JZ (2015) Nat Genet,GCST003044,CD
- Franke A (2010) Nat Genet,GCST000879,CD
- Barrett JC (2008) Nat Genet,GCST000207,CD
- Jostins L (2012) Nature,GCST001729,CD
- de Lange KM (2017) Nat Genet,GCST004131,IBD
- Jostins L (2012) Nature,GCST001725,IBD
- Liu JZ (2015) Nat Genet,GCST003043,IBD

 GO

Input gene set

Genes Upload Select

Input a gene set:

- ALK
- AMZ1
- ANO6
- ARL14
- ARSB
- ATOH8

 GO

Input gene set

Genes Upload Select

Check genes in uploaded file:

Select a txt file:

No file selected

 GO

- In the “Gene Enrichment Analysis” panel, you can choose one or more pre-defined risk gene sets from different studies.
  - Here, we choose all pre-defined risk genes of UC
- After selection, gene list would be generated automatically in the box.
- Similarly, you can define your interested gene set in the same format (one gene per line) or upload a txt file containing your gene set.

# Apply gene set enrichment analysis to risk genes of UC

- After applying gene set enrichment analysis on the risk genes of UC, the enrichment of them in each cell types are shown.

Output of enrichment analysis			
Show 10 entries	Search:		-
Cell type	P-value	Adjusted P-value	Odds ratio
CD4+ Th17	0.00037	0.03590	3.00651
cDC2	0.00092	0.04409	2.97863
Inflammatory monocyte	0.00241	0.07720	3.10887
Stromal 1	0.00375	0.08995	2.75181
pDC	0.02694	0.33825	2.03900
LAMP3+ DC	0.03024	0.33825	2.29128
CD4+ Tem	0.06734	0.33825	2.02992
CD4+ Tfh	0.05789	0.33825	1.99352
CD4+ Treg	0.05051	0.33825	2.34485
CD8+ Tem	0.04858	0.33825	2.36889
Showing 1 to 10 of 96 entries	Previous	1	2 3 4 5 ... 10 Next

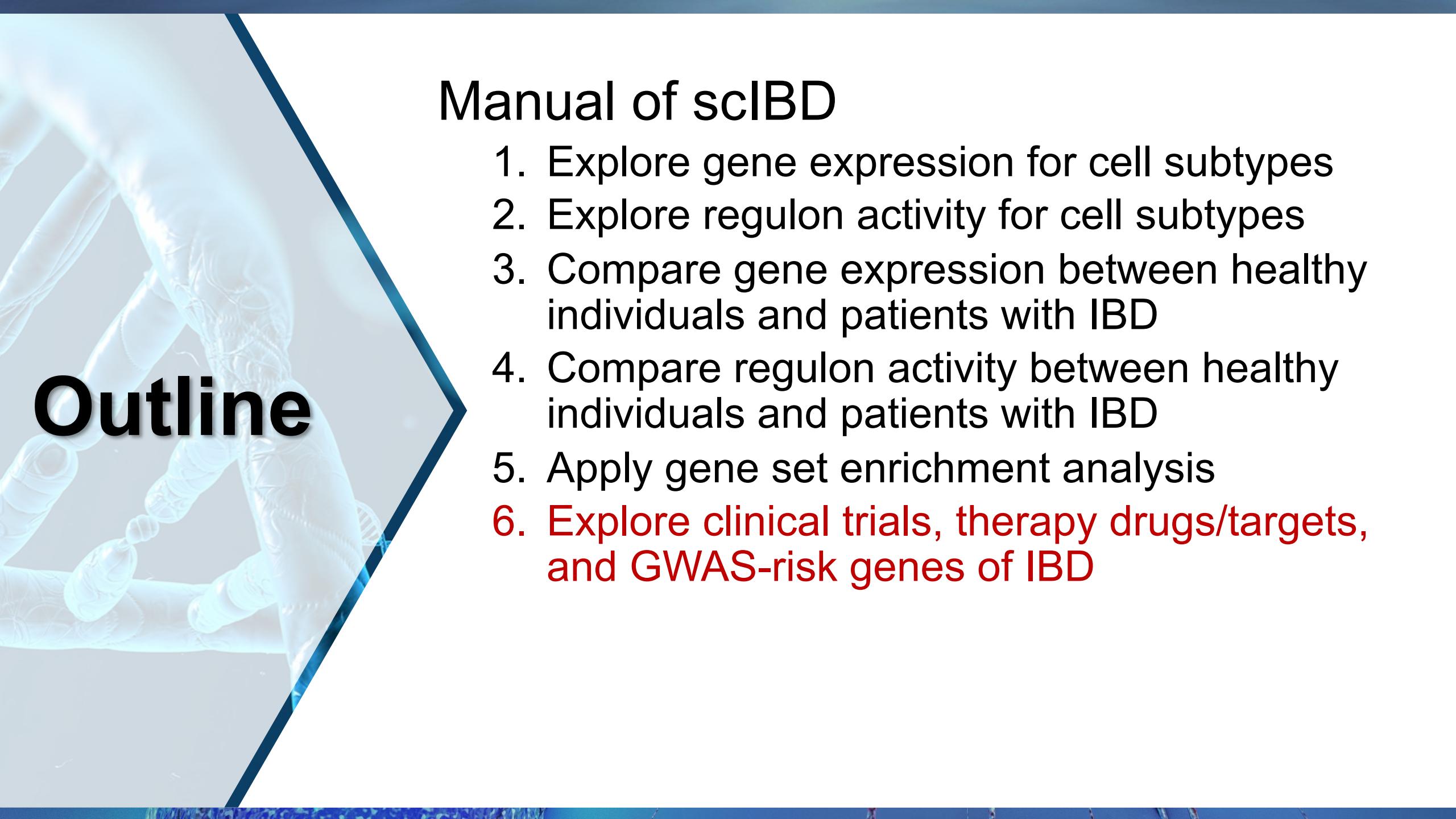
- Odds ratio indicates how likely an outcome is to occur in one context relative to another.

# Heatmap to show gene expression of each GWAS-risk genes in each cell subtypes

Input gene list:

ACTA2  
ARL14  
BTG3  
CD226  
CD40  
CDC37  
CPEB4  
DNER  
EDNRB  
ENC1  
HADH  
HHEX  
ID4  
IL1RL1  
IRF8  
ITGB8  
ITLN1  
KCTD12  
LRRC32  
LY75  
MAP1B  
NDFP1  
NFKB1  
NOS2  
NTM  
PARK7  
PDGFB  
PITX1  
PLCG2  
PROX1  
PTGER3  
RNF186  
RSPO3  
SLC26A3  
SLT3  
TNFAIP3  
TNFSF11  
TSPAN5  
ZBTB3  
BTG3  
CDC37





# Outline

## Manual of scIBD

1. Explore gene expression for cell subtypes
2. Explore regulon activity for cell subtypes
3. Compare gene expression between healthy individuals and patients with IBD
4. Compare regulon activity between healthy individuals and patients with IBD
5. Apply gene set enrichment analysis
6. **Explore clinical trials, therapy drugs/targets, and GWAS-risk genes of IBD**

# Explore clinical trials of IBD

- You can explore FDA approved drugs in the “Current Therapy Strategy” panel.
- Clinical trial information can be reached through the “View” button.

The image shows two panels from the scIBD web application. The left panel, titled 'FDA approved drugs for IBD', lists ten drugs with their details and a 'View' button. The right panel, titled 'Clinical trials for Infliximab', lists 12 clinical trials with their details and a 'View' button. A blue arrow points from the 'View' button in the first row of the left panel to the second row of the right panel.

**FDA approved drugs for IBD**

Compound INN	Compound design	Target	GeneName	Route	CD	UC	Clinical trials
Infliximab	chimeric	TNF $\alpha$	TNF	iv or sc	x	x	<button>View</button>
Adalimumab	human	TNF $\alpha$	TNF	sc	x	x	<button>View</button>
Golimumab	human	TNF $\alpha$	TNF	sc		x	<button>View</button>
Certolizumab	pegylated Fab	TNF $\alpha$	TNF	sc		x	<button>View</button>
Ustekinumab	humanized	IL12/23 p40	IL12B	iv or sc	x	x	<button>View</button>
Natalizumab	humanized	$\alpha 4$ integrin	ITGA4	iv	x		<button>View</button>
Vedolizumab	humanized	$\alpha 4\beta 7$ integrin	ITGA4, ITGB7	iv or sc	x	x	<button>View</button>
Tofacitinib	NA	JAK 1+3	JAK1, JAK2, JAK3	po		x	<button>View</button>
Daravatstrocel	NA	NA	NA	Injection next to fistula canal			<button>View</button>
Ozanimod	NA	S1PR1,5	S1PR1, S1PR5	po		x	<button>View</button>

Showing 1 to 10 of 10 entries

**Clinical trials for Infliximab**

Trial acronym	Clinical trial	Stage	Year	Reference	More
N/A	N/A	N/A	1997	<a href="#">PMID: 9321530</a>	<button>View</button>
N/A	N/A	N/A	1999	<a href="#">PMID: 10228190</a>	<button>View</button>
ACCENT-1	<a href="#">NCT00207662</a>	III	2002	<a href="#">PMID: 12047962</a>	<button>View</button>
ACCENT-2	<a href="#">NCT00207766</a>	III	2004	<a href="#">PMID: 14985485</a>	<button>View</button>
ACT-1	<a href="#">NCT00036439</a>	III	2005	<a href="#">PMID: 16339095</a>	<button>View</button>
ACT-1	<a href="#">NCT00096655</a>	III	2005	<a href="#">PMID: 16339095</a>	<button>View</button>
TAILORIX	<a href="#">NCT01442025</a>	IV	2018	<a href="#">PMID: 29317275</a>	<button>View</button>
STORI	<a href="#">NCT00571337</a>	III	2012	<a href="#">PMID: 21945953</a>	<button>View</button>
SONIC	<a href="#">NCT00094458</a>	III	2010	<a href="#">PMID: 20393175</a>	<button>View</button>
UC SUCCESS	<a href="#">NCT00537316</a>	III	2014	<a href="#">PMID: 24512909</a>	<button>View</button>

Showing 1 to 10 of 12 entries

[Previous](#) [1](#) [2](#) [Next](#)

[Close](#)

# Explore clinical trials for infliximab

- The clinical trial information for each drug includes the clinical stage, year of publication, and links for study record of clinical trial, PubMed page for the reference and more detailed clinical information.

## Study record detail of clinical trial

This screenshot shows the ClinicalTrials.gov study record detail page for a trial titled "Efficacy & Safety of Infliximab Monotherapy Vs Combination Therapy Vs AZA Monotherapy in Ulcerative Colitis (Part 1) Maintenance Intermittent Therapy for Maintaining Remission (Part 2)(Study #04807)". The page includes a summary of the study, sponsor information (Merck Sharp & Dohme LLC), and tabs for Study Details, Tabular View, Study Results, Disclaimer, and How to Read a Study Record. A red arrow points from this page to the Clinical trials for Infliximab table below.

## Reference

This screenshot shows the PubMed page for a study titled "Combination therapy with infliximab and azathioprine is superior to monotherapy with either agent in ulcerative colitis". The page includes the abstract, background & aims, methods, results, and conclusions. A red arrow points from this page to the Detailed clinical information table below.

## Detailed clinical information

This screenshot shows a detailed clinical information table for the UC SUCCESS trial. It includes fields for Drug (Infliximab), Trial acronym (UC SUCCESS), Clinical trial (NCT00537316), Stage (III), Year (2014), Reference (PMID: 24512909), Description (N/A), Indication (Moderate to severe UC naïve to anti-TNF), Design (Randomized double-blind trial), and Main Purpose (Comparing Infliximab monotherapy, azathioprine monotherapy and combination therapy in the treatment of UC). A red arrow points from the Clinical trials for Infliximab table above to this detailed information table.

# Explore therapy drugs/targets of IBD

- You can also explore drugs or targets under clinical trials in this panel.
- Click “View” button for clinical trial information.

Therapy targets and drugs for IBD									
disease Name	drugName	type	mechanism of action	action type	symbol	name	phase	clinical trail	Search:
Crohn's disease	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA1	adenosine A1 receptor	1	<a href="#">View</a>	
ulcerative colitis	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA1	adenosine A1 receptor	4	<a href="#">View</a>	
Crohn's disease	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA1	adenosine A1 receptor	4	<a href="#">View</a>	
ulcerative colitis	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA1	adenosine A1 receptor	1	<a href="#">View</a>	
Crohn's disease	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA2A	adenosine A2a receptor	1	<a href="#">View</a>	
ulcerative colitis	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA2A	adenosine A2a receptor	4	<a href="#">View</a>	
Crohn's disease	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA2A	adenosine A2a receptor	4	<a href="#">View</a>	
ulcerative colitis	CAFFEINE	Small molecule	Adenosine receptor antagonist	Antagonist	ADORA2A	adenosine A2a receptor	1	<a href="#">View</a>	
Crohn's disease	PENTOXIFYLLINE	Small molecule	Adenosine A2 receptor antagonist	Antagonist	ADORA2A	adenosine A2a receptor	0	<a href="#">View</a>	
Crohn's disease	PENTOXIFYLLINE	Small molecule	Adenosine A2 receptor antagonist	Antagonist	ADORA2B	adenosine A2b receptor	0	<a href="#">View</a>	

Clinical trial information

NIH U.S. National Library of Medicine  
**ClinicalTrials.gov**

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1 Study found for: "NCT02953275"

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Status Recruitment

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Row	Saved	Status	Study Title	Conditions	Interventions	Locations
1	<input type="checkbox"/>	Completed	Synergistic Effect of Vedolizumab and Pentoxifylline	• Crohn Disease	• Drug: vedolizumab • Drug: Pentoxifylline • Drug: placebo	• University of Miami Crohn's and Colitis Center Miami, Florida, United States

# Explore GWAS-risk genes of IBD

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Gene Expression Profile  
Regulon Activity Profile  
Gene Expression Comparison  
Regulon Activity Comparison  
Cellular composition  
Gene Enrichment Analysis  
Current Therapy Strategy  
**GWAS-implicated Risk Genes**  
Meta Data Exploration

Major GWAS study on IBD

Show 10 entries

Catalog	Study	Disease	PubMed ID	# Loci	# Prioritised Genes
All	All	All	All	All	All
<a href="#">GCST005537</a>	Ellinghaus D (2016) Nat Genet	Chronic inflammatory diseases	<a href="#">PMID:26974007</a>	153	119
<a href="#">GCST000964</a>	Anderson CA (2011) Nat Genet	UC	<a href="#">PMID:21297633</a>	163	98
<a href="#">GCST003045</a>	Liu JZ (2015) Nat Genet	UC	<a href="#">PMID:26192919</a>	109	69
<a href="#">GCST004133</a>	de Lange KM (2017) Nat Genet	UC	<a href="#">PMID:28067908</a>	65	40
<a href="#">GCST001728</a>	Jostins L (2012) Nature	UC	<a href="#">PMID:23128233</a>	25	17
<a href="#">GCST000624</a>	McGovern DP (2010) Nat Genet	UC	<a href="#">PMID:20228799</a>	14	7
<a href="#">GCST004132</a>	de Lange KM (2017) Nat Genet	CD	<a href="#">PMID:28067908</a>	104	68
<a href="#">GCST003044</a>	Liu JZ (2015) Nat Genet	CD	<a href="#">PMID:26192919</a>	174	114
<a href="#">GCST000879</a>	Franke A (2010) Nat Genet	CD	<a href="#">PMID:21102463</a>	68	50
<a href="#">GCST000207</a>	Barrett JC (2008) Nat Genet	CD	<a href="#">PMID:18587394</a>	28	20

Showing 1 to 10 of 14 entries

Previous 1 2 Next

Open Targets Genetics

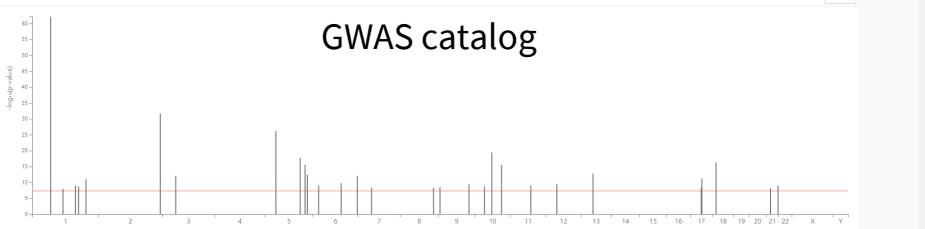
Crohn's disease  
GWAS Catalog: GCST000207

Study summary

Author: Barrett JC  
Year: 2008  
PubMed: 18587394  
Has summary stats: No

Independently-associated loci  
Found 29 loci with genome-wide significance ( $p$ -value < 5e-8) out of 29

GWAS catalog



National Library of Medicine  
National Center for Biotechnology Information

PubMed.gov

Meta-Analysis > Nat Genet, 2008 Aug;40(8):955-62. doi: 10.1038/ng.175. Epub 2008 Jun 29.

Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease

Jeffrey C Barrett<sup>1</sup>, Sarah Hansoul<sup>1</sup>, Dan L Nicolae<sup>1</sup>, Judy H Cho<sup>1</sup>, Richard H Duerr<sup>1</sup>, John D Rioux<sup>1</sup>, Steven R Brant<sup>2</sup>, Mark S Silverberg<sup>2</sup>, Kent D Taylor<sup>3</sup>, M Michael Barnada<sup>4</sup>, Alan Bitton<sup>5</sup>, Themistocles Assopoulas<sup>6</sup>, Lisa Wu Datta<sup>7</sup>, Todd Green<sup>8</sup>, Anne M Griffiths<sup>9</sup>, Emily O Kistner<sup>10</sup>, Michael T Murtha<sup>11</sup>, Miguel D Regueiro<sup>12</sup>, Jerome I Rotter<sup>13</sup>, Philip Schramm<sup>14</sup>, Hillary Steinhardt<sup>15</sup>, Stephan R Targan<sup>16</sup>, Ramnik J Xavier<sup>17</sup>, NIDDK IBD Genetics Consortium<sup>18</sup>, Cécile Liblauille<sup>19</sup>, Cynthia Sandor<sup>20</sup>, Mark Lathrop<sup>21</sup>, Jacques Belachiche<sup>22</sup>, Olivier Dewit<sup>23</sup>, Ivo Gut<sup>24</sup>, Simon Heath<sup>25</sup>, Debby Lakenius<sup>26</sup>, Myriam Mni<sup>27</sup>, Paul Rutgeerts<sup>28</sup>, André Van Gossum<sup>29</sup>, Diana Zelenika<sup>30</sup>, Denis Franchimont<sup>31</sup>, Jean-Pierre Hugot<sup>32</sup>, Martine de Vos<sup>33</sup>, Séverine Vermeire<sup>34</sup>, Edouard Louis<sup>35</sup>, Belgian-French IBD Consortium<sup>36</sup>, Wellcome Trust Case Control Consortium<sup>37</sup>, Lon R Cardon<sup>38</sup>, Carl A Anderson<sup>39</sup>, Hazel Drummond<sup>40</sup>, Elaine Nimmro<sup>41</sup>, Tariq Ahmad<sup>42</sup>, Natalie J Prescott<sup>43</sup>, Clive M Onnie<sup>44</sup>, Sheila A Fisher<sup>45</sup>, Jonathan Marchini<sup>46</sup>, Jilur Ghori<sup>47</sup>, Suzannah Bumpstead<sup>48</sup>, Rhan Gwilliam<sup>49</sup>, Mark Tremelling<sup>50</sup>, Panos Deloukas<sup>51</sup>, John Mansfield<sup>52</sup>, Derek Jewell<sup>53</sup>, Jack Satsangi<sup>54</sup>, Christopher G Mathew<sup>55</sup>, Miles Parkes<sup>56</sup>, Michel Georges<sup>57</sup>, Mark J Daly<sup>58</sup>

Affiliations + expand  
PMID: 18587394 PMCID: PMC2574810 DOI: 10.1038/ng.175  
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# Risk genes of adult IBD

Risk genes of IBD patients												
Show 10 entries	ensembl_gene_id	gene_biotype	chromosome_name	start_position	end_position	description	Search:					
All	All	All	All	All	All	All	All					
AAMP	ENSG00000127837	protein_coding	2	218264129	218270178	angio associated migratory cell protein						
ACTA2	ENSG00000107796	protein_coding	10	88935074	88991339	actin alpha 2, smooth muscle						
ADAM30	ENSG00000134249	protein_coding	1	119893533	119896515	ADAM metallopeptidase domain 30						
ADCY3	ENSG00000138031	protein_coding	2	24819169	24920237	adenylate cyclase 3						
ADCY7	ENSG00000121281	protein_coding	16	50246137	50318135	adenylate cyclase 7						
AHR	ENSG00000106546	protein_coding	7	16916359	17346152	aryl hydrocarbon receptor						
AKAP11	ENSG0000023516	protein_coding	13	42272152	42323261	A-kinase anchoring protein 11						
ALK	ENSG00000171094	protein_coding	2	29192774	29921586	ALK receptor tyrosine kinase						
AMZ1	ENSG00000174945	protein_coding	7	2679522	2775500	archaeolysin family metallopeptidase 1						
ANKRD55	ENSG00000164512	protein_coding	5	56099680	56233330	ankyrin repeat domain 55						
Showing 1 to 10 of 318 entries				Previous	1	2	3	4	5	...	32	Next

The risk genes of adult IBD were retrieved from these studies listed in the table of “Major GWAS study on IBD”

# Risk genes of pediatric IBD

Risk genes of pediatric patients												
Show 10 entries		Search: <input type="text"/>										
hgnc_symbol	ensembl_gene_id	gene_biotype	chromosome_name	start_position	end_position	description						
1	ABCB10	ENSG00000135776	protein_coding	1	229516582	229558707	ATP binding cassette subfamily B member 10					
2	ACSM1	ENSG00000146743	protein_coding	16	20623235	20698890	acyl-CoA synthetase medium chain family member 1					
3	ACSM2A	ENSG00000183747	protein_coding	16	20451461	20487669	acyl-CoA synthetase medium chain family member 2A					
4	ACSM2B	ENSG00000066813	protein_coding	16	20536226	20576427	acyl-CoA synthetase medium chain family member 2B					
5	ACSM5	ENSG00000183549	protein_coding	16	20409534	20441336	acyl-CoA synthetase medium chain family member 5					
6	ACSM6	ENSG00000173124	protein_coding	10	95194200	95228928	acyl-CoA synthetase medium chain family member 6					
7	ADAM10	ENSG00000137845	protein_coding	15	58588809	58749791	ADAM metallopeptidase domain 10					
8	ADAMTS1	ENSG00000154734	protein_coding	21	26835755	26845409	ADAM metallopeptidase with thrombospondin type 1 motif 1					
9	ADAMTS5	ENSG00000154736	protein_coding	21	26917922	26967088	ADAM metallopeptidase with thrombospondin type 1 motif 5					
10	AKIRIN2	ENSG00000135334	protein_coding	6	87674860	87702233	akirin 2					
Showing 1 to 10 of 225 entries				Previous	1	2	3	4	5	...	23	Next

The risk genes of pediatric IBD were retrieved from this paper:

B. Huang *et al.*, Mucosal profiling of pediatric-onset colitis and IBD reveals common pathogenics and therapeutic pathways. *Cell* **179**, 1160-1176 e1124 (2019).

**Thank you !**