

# Insights into Spatial transcriptome via Qiagen Ingenuity Pathway analysis



**Cleo Hsi**資深業務專員

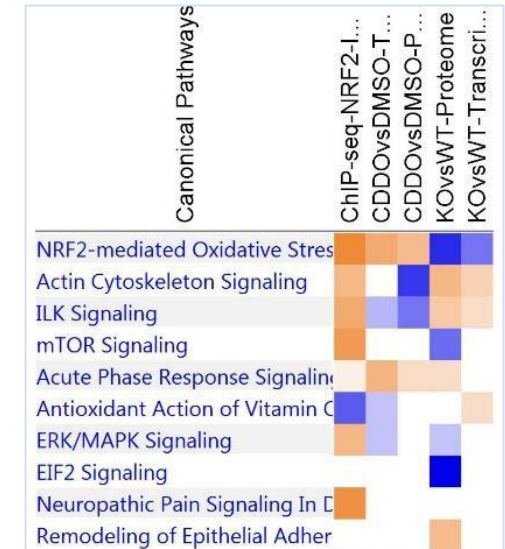
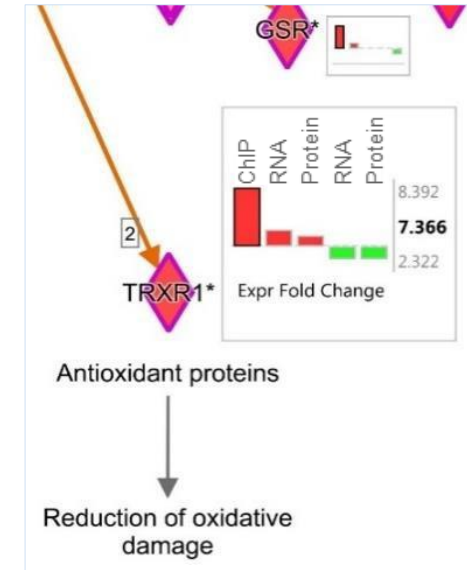
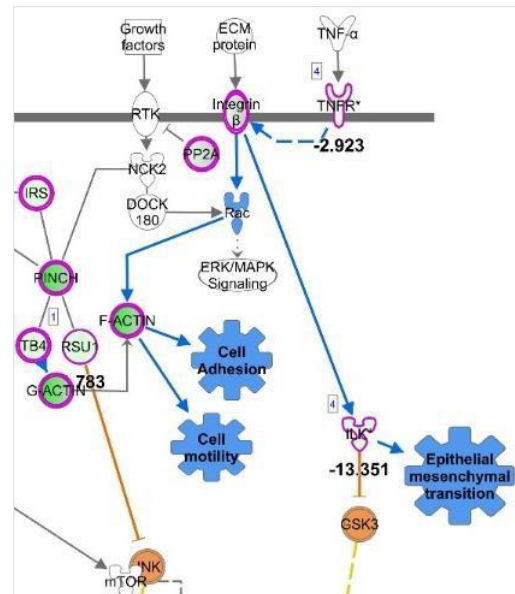
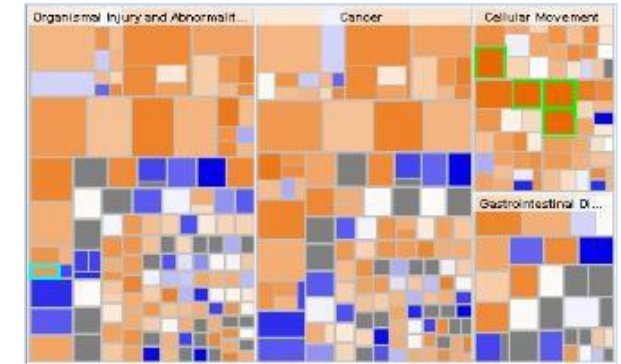
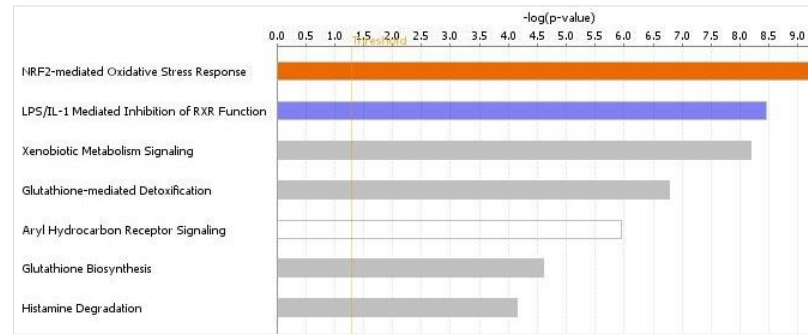
**Christine Hsiung** 熊嘉妮 專案主任

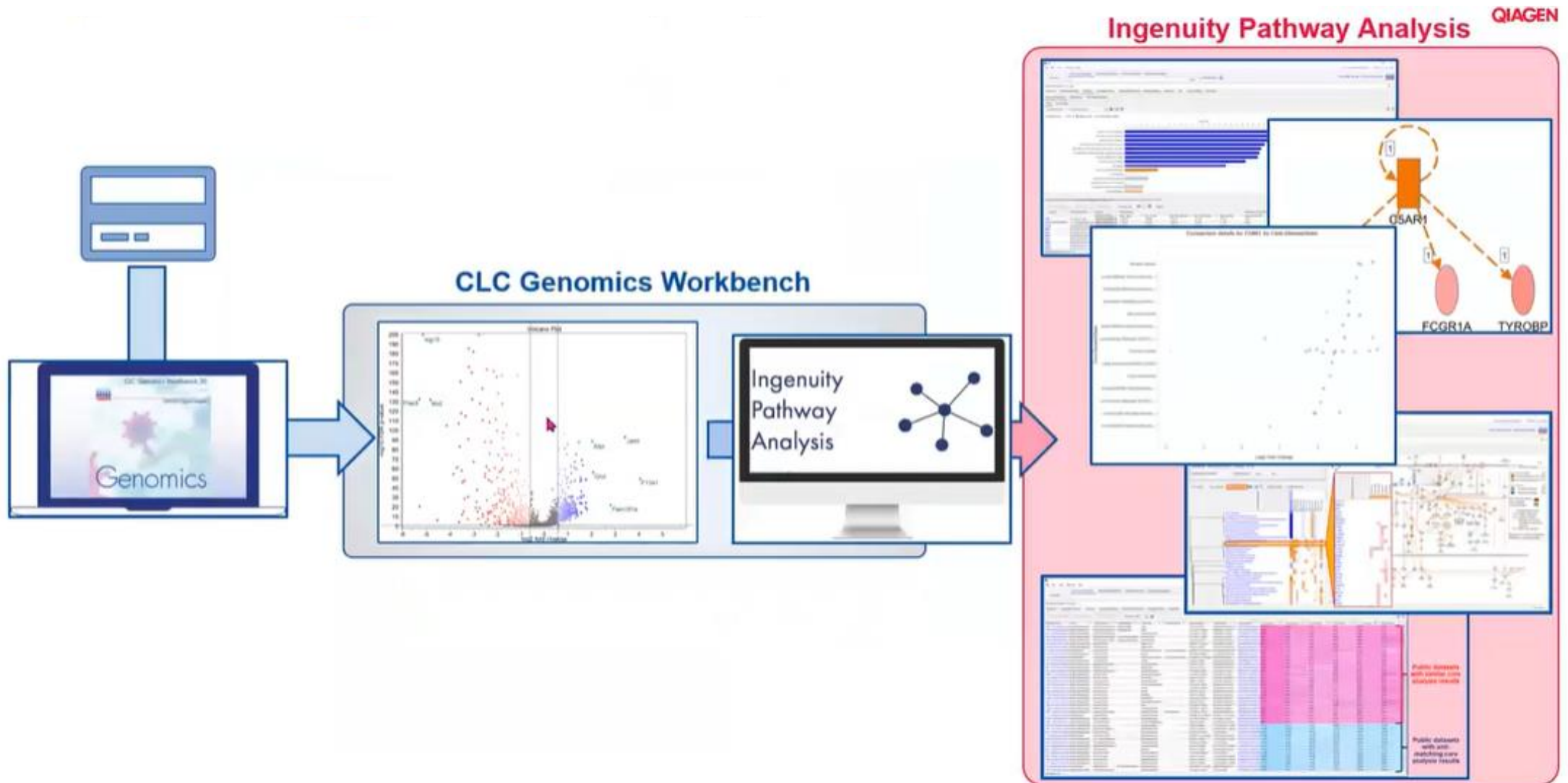
**Bioinfo@GGA.ASIA**

- How to analysis Omics by QIAGEN Ingenuity Pathway Analysis
- Insights into biological function
  - Data format
  - Data upload and analysis setup
  - Comparing cell type-specific biomarker and regulators/targets
- Summary

## Omics data type

- RNA-seq
- scRNA-seq
- Microarray
- Nanostring
- qPCR
- ChIP-seq
- Proteomics
- Metabolomics
- RNAi
- CRISPR
- WGS/WES etc.







約有 2,690 項結果 (0.08 秒)

Article

## Disease-associated astrocyte epigenetic memory promotes CNS pathology

<https://doi.org/10.1038/s41586-024-07187-5>  
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 Check for updates

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Disease-associated astrocyte subsets contribute to the pathology of neurologic diseases, including multiple sclerosis and experimental autoimmune encephalomyelitis<sup>1–8</sup> (EAE), an experimental model for multiple sclerosis. However, little is known about the stability of these astrocyte subsets and their ability to integrate past stimulation events. Here we report the identification of an epigenetically controlled memory astrocyte subset that exhibits exacerbated pro-inflammatory responses upon rechallenge. Specifically, using a combination of single-cell RNA sequencing, assay for transposase-accessible chromatin with sequencing, chromatin immunoprecipitation with sequencing, focused interrogation of cells by nucleic acid detection and sequencing, and cell-specific in vivo CRISPR-Cas9-based genetic perturbation studies we established that astrocyte memory is controlled by the metabolic enzyme ATP-citrate lyase (ACLY), which produces acetyl coenzyme A (acetyl-CoA) that is used by histone acetyltransferase p300 to control chromatin accessibility. The number of ACLY<sup>+</sup>p300<sup>+</sup> memory astrocytes is increased in acute and chronic EAE models, and their genetic inactivation ameliorated EAE. We also detected the pro-inflammatory memory phenotype in human astrocytes in vitro; single-cell RNA sequencing and immunohistochemistry studies detected increased numbers of ACLY<sup>+</sup>p300<sup>+</sup> astrocytes in chronic multiple sclerosis lesions. In summary, these studies define an epigenetically controlled memory astrocyte subset that promotes CNS pathology in EAE and, potentially, multiple sclerosis. These findings may guide novel therapeutic approaches for multiple sclerosis and other neurologic diseases.

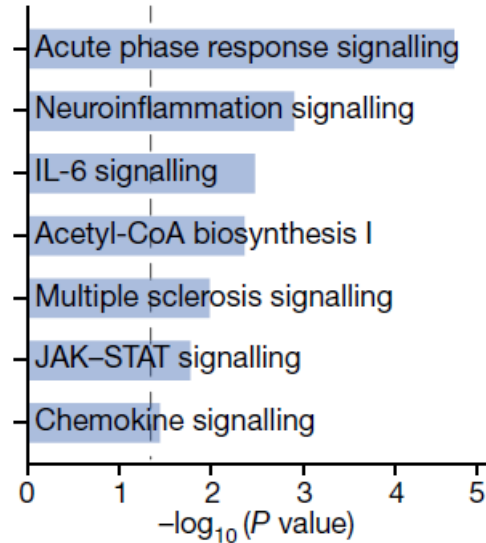
Astrocytes are abundant non-haematopoietic cells of the central nervous system (CNS) that have important functions in health and disease<sup>1–4</sup>. Astrocytes participate in key processes that are relevant to CNS development and homeostasis<sup>5</sup>. In addition, cytokines, interactions with CNS-resident and CNS-recruited immune cells, and other factors trigger astrocyte responses with important roles in CNS pathology<sup>6,7,12,13</sup>. Indeed, several astrocyte subsets have been described in neurologic diseases<sup>14–16</sup>. For example, we and others have interrogated astrocyte functional heterogeneity in multiple sclerosis and EAE<sup>17</sup>. However, the stability of these disease-associated astrocyte subsets is unclear, an important point when considering lifelong chronic neurologic diseases such as multiple sclerosis.

Immunological memory, the generation of faster and stronger responses upon repeated antigenic stimulation, is a classic hallmark

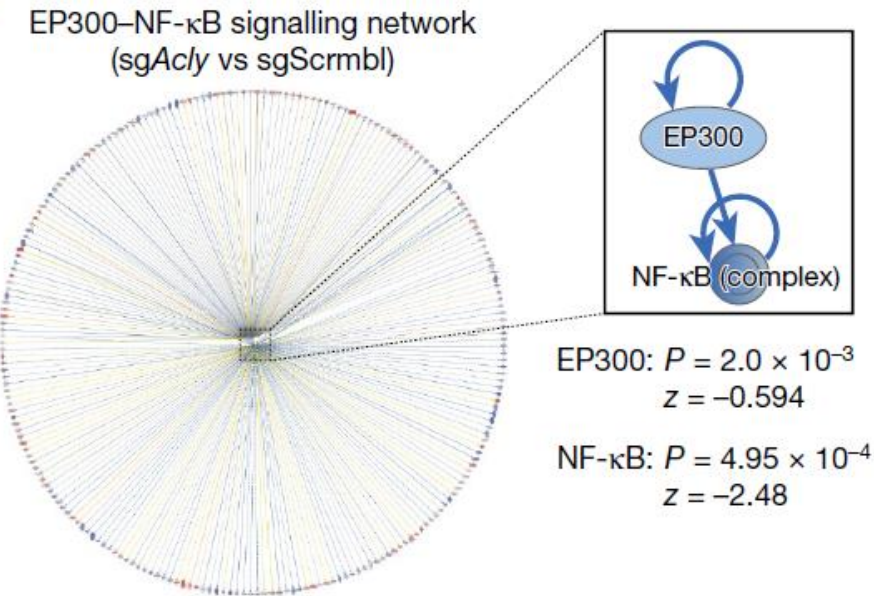
of adaptive immunity driven by long-lived antigen-specific T cells and B cells<sup>18</sup>. In addition, innate immune cells including myeloid cells<sup>19,20</sup> and other cell types<sup>20,21</sup> undergo metabolic, epigenetic and transcriptional adaptations upon stimulation that alter their subsequent responses, boosting protective immunity against pathogens but also contributing to pathogenic inflammation<sup>22</sup>. Although memory T cells and B cells have been identified, our understanding of innate immune or non-haematopoietic cell memory subsets remains limited. In this context, it is still unknown whether astrocytes display altered responses to repeated stimulation, how these responses are regulated, and whether specific astrocyte subsets are involved.

Here we describe a memory astrocyte subset controlled by epigenetic changes driven by ACLY- and p300-dependent histone acetylation, which, following an initial stimulation, display faster and stronger

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UCLA Health Jonsson Comprehensive Cancer center also use Qiagen IPA to interpreted spatial transcriptome

<https://www.uclahealth.org/cancer/researchers/shared-resources/genomics>

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nature communications



Article

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## Spatial transcriptomics reveals distinct and conserved tumor core and edge architectures that predict survival and targeted therapy response

Received: 31 October 2022

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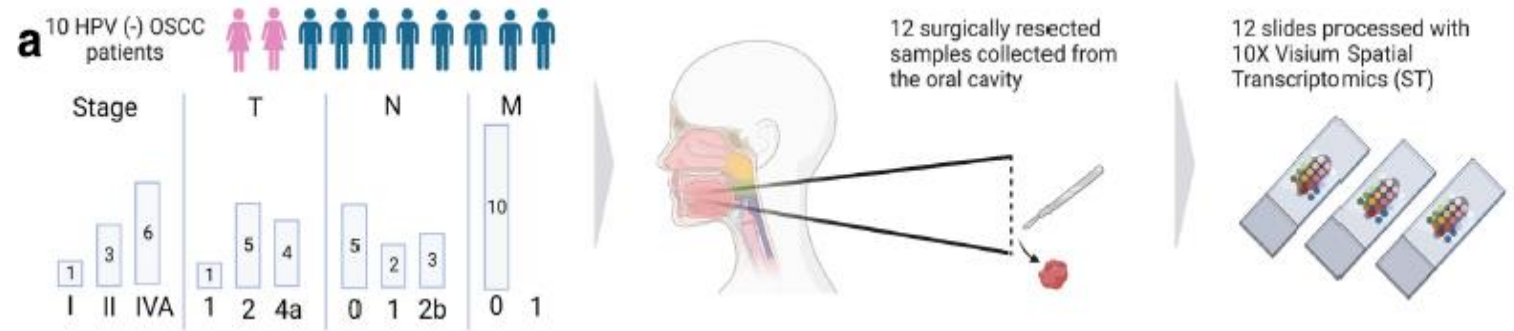
Published online: 18 August 2023

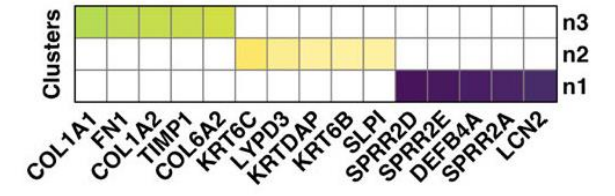
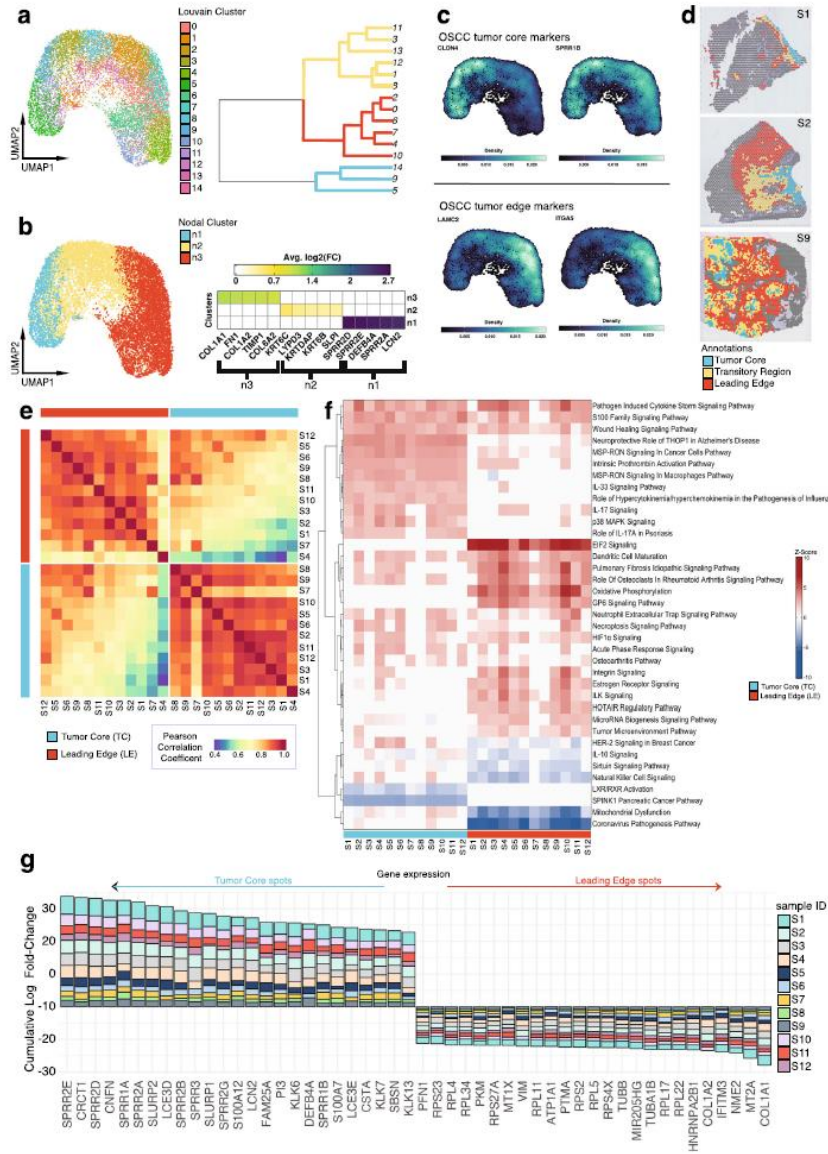
[Check for updates](#)

Rohit Arora<sup>1,16</sup>, Christian Cao<sup>2,16</sup>, Mehul Kumar<sup>1,3</sup>, Sarthak Sinha<sup>4</sup>, Ayan Chanda<sup>5,3</sup>, Reid McNeil<sup>1,3</sup>, Divya Samuel<sup>1,3</sup>, Rahul K. Arora<sup>5,6</sup>, T. Wayne Matthews<sup>7,8</sup>, Shamir Chandarana<sup>7,8</sup>, Robert Hart<sup>7,8</sup>, Joseph C. Dort<sup>3,7,8,9</sup>, Jeff Biernaskie<sup>4,10,11,12</sup>, Paola Neri<sup>3,13</sup>, Martin D. Hryczka<sup>3,14</sup> & Pinaki Bose<sup>1,3,6,15</sup> ✉

The spatial organization of the tumor microenvironment has a profound impact on biology and therapy response. Here, we perform an integrative single-cell and spatial transcriptomic analysis on HPV-negative oral squamous cell carcinoma (OSCC) to comprehensively characterize malignant cells in tumor core (TC) and leading edge (LE) transcriptional architectures. We show that the TC and LE are characterized by unique transcriptional profiles, neighboring cellular compositions, and ligand-receptor interactions. We demonstrate that the gene expression profile associated with the LE is conserved across different cancers while the TC is tissue specific, highlighting common mechanisms underlying tumor progression and invasion. Additionally, we find our LE gene signature is associated with worse clinical outcomes while TC gene signature is associated with improved prognosis across multiple cancer types. Finally, using an in silico modeling approach, we describe spatially-regulated patterns of cell development in OSCC that are predictably associated with drug response. Our work provides pan-cancer insights into TC and LE biology and interactive spatial atlases ([http://www.pboselab.ca/spatial\\_OSCC/](http://www.pboselab.ca/spatial_OSCC/); [http://www.pboselab.ca/dynamo\\_OSCC/](http://www.pboselab.ca/dynamo_OSCC/)) that can be foundational for developing novel targeted therapies.

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gene	avg_log2FC	p_val_adj
SPRR2D	2.706423338	0
SPRR2E	2.654346543	0
DEFB4A	2.579461176	0
SPRR2A	2.520689273	0
LCN2	2.449394678	0
CRCT1	2.414710712	0
SLURP2	2.390169921	0
CNFN	2.342349982	0
SLURP1	2.340477642	0
S100A7	2.260580342	0
SPRR3	2.194651151	0
SPRR2B	2.173298475	0
KLK13	2.097040487	0
LCE3D	2.082024046	0
KLK6	2.027716246	0
SPRR1A	2.017865872	0

gene	avg_log2FC	p_val_adj
COL1A1	1.119188557	0
FN1	1.077456695	0
COL1A2	1.047688083	0
TIMP1	1.040462139	0
COL6A2	0.98234798	0
COL3A1	0.916656628	0
SPARC	0.902377431	0
VIM	0.87526439	0
HMGN2	0.791542974	0
TNC	0.778830913	0
IGFBP7	0.716862936	0
FTL	0.653061976	0
MT2A	0.612219081	0
PFN1	0.546409497	0
FBLN2	0.472353201	0
LGALS1	0.668868409	9.25E-299

1

File Edit View Window Help

Genes and Chemicals Diseases and Functions Pathways and Lists Datasets and Analyses

Create New...

- Core Analysis...
- Comparison Analysis...
- Biomarker Filter...
- Biomarker Comparison Analysis...
- MicroRNA Target Filter...
- BioProfiler
- IsoProfiler
- My Pathway
- Path Designer
- Filter Dataset
- Upload Dataset...
- Advanced Search
- Project...
- Compare
- Import Pathway

A-Z Sort Refresh

Create Core Analysis

Upload

My Projects

- genome > case\_study
- 2024- > CGUST
- 4-05-16 > CCGH\_2
- lc - 202 > CCGH
- 4-26 02 > smh\_miRBA
- RNA\_mf > CMU\_Hung\_RNAseq
- \_mRNA - > 長庚ARDS
- 2024-04 > exosome miRNA 2
- 4hrs - 2l > exosome miRNA
- trama\_data\_unique - 2024-0 > 2023-demo
- GSE73661-UC VDZ with pval > Isoform
- Nature\_comm\_2020 germlin > HTCH\_Dr.Liu\_2022-12-16
- Nature\_comm\_2020 germlin > NDMC1020
- > CGU\_20221018
- TMU0816
- > BIONET
- > CMUHuag
- > Alpharm
- NDMC

Top help articles and FAQs

Contacting Support

Shortcuts

Don't Show at Startup

2

3

Dataset Upload - Tumor\_core\_spatial\_genome\_DEG.xlsx

- Select File Format: Flexible Format
- Contains Column Header:  Yes  No
- Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s). Assign additional columns as ID to improve mapping coverage if desired.
- Array platform used for experiments: Not specified/applicable
- Use the dropdown menus to specify the column names that contain identifiers and observations. For observations, select the appropriate measurement value type.

Raw Data (363) Dataset Summary (360) Metadata

Edit Observation Names Infer Observations

ID/Observation Name	ID	avg_log2FC	avg_log2FC
Measurement/Annotation	Gene Symb...	Expr Log Ra...	Expr p-value
1	gene	avg_log2FC	p_val_adj
2	SPRR2D	2.706423338	0
3	SPRR2E	2.6543465429999999	0
4	DEFB4A	2.5794611760000001	0
5	SPRR2A	2.5206892729999999	0
6	LCN2	2.449394678	0
7	CRCT1	2.4147107120000002	0
8	SLURP2	2.390169921	0
9	CNFN	2.342349982	0
10	SLURP1	2.3404776420000002	0
11	S100A7	2.2605803419999999	0
12	SPRR3	2.194651151	0
13	SPRR2B	2.1732984750000002	0
14	KLK13	2.0970404870000001	0
15	LCE3D	2.0820240459999999	0
16	KLK6	2.0277162459999998	0
17	SPRR1A	2.0178658719999998	0
18	S100A12	1.9998280559999999	0
19	LCE3E	1.829669684	0
20	CSTA	1.789919528	0
21	SLC6A14	1.7496272260000001	0
22	S100A9	1.737970397	0
23	KLK12	1.7283063970000001	0
24	KLK7	1.726511224	0
25	SPRR2F	1.7137438540000001	0
26	SPRR2G	1.7127803829999999	0
27	HOPX	1.688770675	0
28	PI3	1.653903093	0
29	PRSS27	1.6356224720000001	0
30	ECM1	1.6081023320000001	0



IPA
Provide Feedback | Support
Gene Chen
Close IPA

Genes and Chemicals
Diseases and Functions
Pathways and Lists
Datasets and Analyses

Create New...

## Create Core Analysis

Selected Dataset: Tumor\_core\_spatial\_genome\_DEG

Based on this dataset, which Core Analysis type would you like to run?

Expression Analysis

Symbol: A2ML1 - EHF (1/4)

On which measurement type would you like to base the analysis?

Expr Log Ratio

This measurement will be used to calculate directionality (z-scores) in the analysis and will be displayed in color on pathways and networks. If you choose a non-directional measurement (e.g. p-value) then z-scores will not be calculated.

Back

Next

1.109	0.00E00								
0.480	4.91E-2i								
0.397	0.00E00								
0.290	1.26E-14								
0.348	1.91E-2s								
0.327	2.73E-2t								
0.472	4.95E-14								
0.606	3.63E-2s								
0.995	0.00E00								
0.439	3.52E-24								
0.647	2.37E-2t								
0.576	0.00E00								
0.365	1.18E-2z								
0.539	0.00E00								
0.319	4.66E-1s								
0.252	3.13E-2s								
1.029	0.00E00								
1.604	0.00E00								
0.477	5.78E-1t								
0.387	3.42E-2i								
1.047	0.00E00								
0.802	0.00E00								
0.552	1.96E-2k								
0.435	0.00E00								
0.261	5.90E-1c								
0.344	6.94E-2k								
0.307	0.00E00								
0.409	2.11E-1t								
0.828	0.00E00								
0.367	6.97E-2s								
0.500	5.59E-2k								
0.555	1.77E-2s								
0.314	7.11E-1t								
0.806	9.86E-2t								
0.545	6.52E-2k								
0.660	1.30E-2k								
0.639	6.68E-29s	C6orf132	C6orf132	chromosome 6 open reading frame 132	Other				
0.611	4.61E-243	CALML3	CALML3	calmodulin like 3	Cytoplasm				
1.520	0.00E00	CALML5	CALML5	calmodulin like 5	Cytoplasm				
0.812	0.00E00	CARHSP1	CARHSP1	calcium regulated heat stable protein 1	Cytoplasm				
0.528	0.00E00	CCL20	CCL20	C-C motif chemokine ligand 20	Extracellular Space				
0.561	0.00E00	CENGL2	CENGL2	cyclin G2	Nucleus				
0.525	0.00E00	CD177	CD177	CD177 molecule	Cytoplasm				
1.243	0.00E00	CD24	CD24	CD24 molecule	Plasma Membrane				
0.494	1.73E-241	CD55	CD55	CD55 molecule (Cromer blood group)	Plasma Membrane				
0.316	1.29E-133	CD68	CD68	CD68 molecule	Plasma Membrane				
0.356	2.26E-156	CDA	CDA	cytidine deaminase	Nucleus				

Flags:

"D" - Duplicates. Gene/Protein/Chemical identifiers marked with an asterisk indicate that multiple identifiers in the dataset file map to a single gene/chemical in the Global Molecular Network.

"O" - Override molecules. Gene/Protein/Chemical identifiers marked as "Override" are displayed with italic text.

"A" - Gene/Protein/Chemical ID marked as Absent. The gene/protein/chemical will not be used as a focus molecule or appear in networks unless you also explicitly override this flag with the Override column.

Edit Dataset Settings
Analyze/Filter Dataset
Close

Create Expression Analysis - [analysis : Tumor\_core\_spatial\_genome\_DEG]

Set Cutoffs Biological Filters

Use cutoffs to select a set of molecules from your dataset to analyze. Ideally choose between 100 and 3000 significantly regulated molecules, and not more than 8000. Include *both* up-regulated and down-regulated, if possible, to obtain causal predictions.

Set Cutoffs

Dataset Column	Measurement Value Type	Range	Cutoff
----------------	------------------------	-------	--------

## Three Step

1. Set Cutoff
2. Biological Filter
3. Run Analysis

Create Expression Analysis - [analysis : Tumor\_core\_spatial\_genome\_DEG]

Set Cutoffs Biological Filters

- > General Settings ?
- Networks Interaction & Ca... ?
- Node Types biologic drug... ?
- Data Sources All ?
- miRNA Confidence Experi... ?
- Species Human ?
- Tissues & Cell Lines ?
- Mutation All ?

Population of genes to consider for p-value calculations:

Reference Set Ingenuity Knowledge Base (Genes Only) v

Relationships to consider:

Affects networks and upstream regulator analysis

Direct and Indirect Relationships

Direct Relationships

Save As Default

Optional Analyses:

- My Project
  - My Pathways
  - My Lists

Advanced

Recalculate

359 analysis-ready molecules (0 Down and 359 Up)

Run Analysis



# Tumor Core Analysis Result Overview



Expression Analysis - Tumor\_core\_spatial\_genome\_DEG - 2024-06-14 06:24 下午

Summary Graphical Summary Pathways Upstream Analysis Diseases & Functions Regulator Effects Networks Lists Analysis Match Molecules

Export:

> Experiment Metadata

> Analysis Settings

> Top Canonical Pathways

Name	p-value	Overlap
Keratinization	1.66E-30	18.7 % 40/214
Neuroprotective Role of THOP1 in Alzheimer's Disease	3.36E-14	16.8 % 19/113
Neutrophil degranulation	3.94E-10	6.3 % 30/476
SPINK1 Pancreatic Cancer Pathway	1.30E-09	20.0 % 11/55
Intrinsic Prothrombin Activation Pathway	1.78E-08	22.0 % 9/41

> Top Upstream Regulators

> Upstream Regulators

Name	p-value	Predicted Activation
EHF	8.15E-29	Activated
TNF	6.90E-25	Activated
IgG	4.60E-22	Inhibited
KRT14	2.98E-21	
FOXC1	3.67E-20	Inhibited

> Causal Network

Name	p-value	Predicted Activation
EHF	3.90E-32	Activated
HCK	4.05E-31	Activated
JAK (family)	1.02E-29	Activated
EHF	1.25E-27	Activated
IKBKG	8.92E-27	Activated

> Top Diseases and Bio Functions

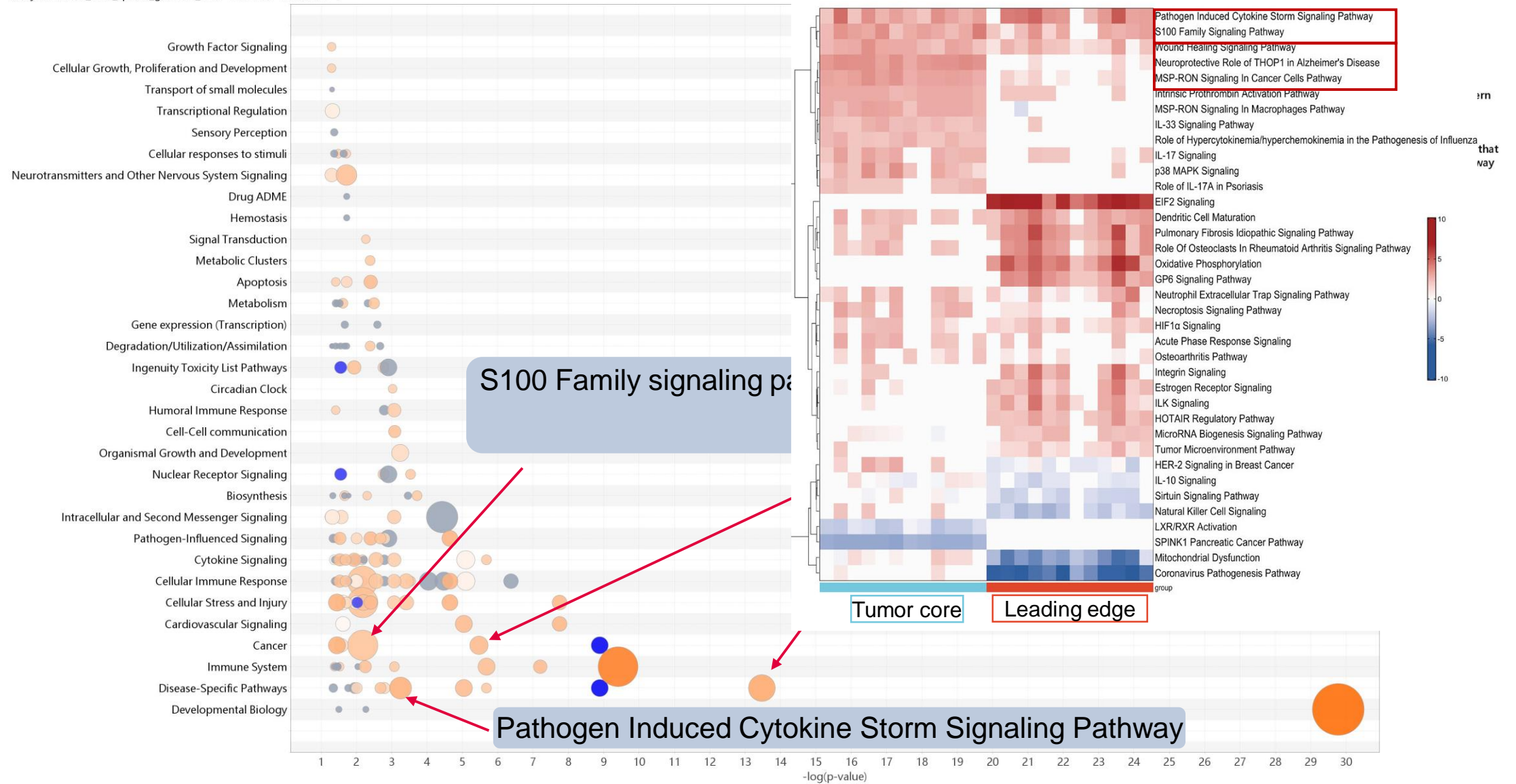
> Diseases and Disorders

Name	p-value range	# Molecules
Dermatological Diseases and Conditions	1.65E-02 - 1.47E-67	287
Organismal Injury and Abnormalities	1.65E-02 - 1.47E-67	354
Inflammatory Disease	1.65E-02 - 1.73E-23	137
Inflammatory Response	1.65E-02 - 1.73E-23	121
Immunological Disease	1.65E-02 - 3.25E-18	124

> Molecular and Cellular Functions

Name	p-value range	# Molecules
Cellular Development	1.65E-02 - 2.92E-17	143
Post-Translational Modification	1.65E-02 - 6.33E-15	27
Cellular Movement	1.65E-02 - 7.21E-09	109
Cell-To-Cell Signaling and Interaction	1.65E-02 - 7.74E-09	75
Cellular Assembly and Organization	1.65E-02 - 7.74E-09	40

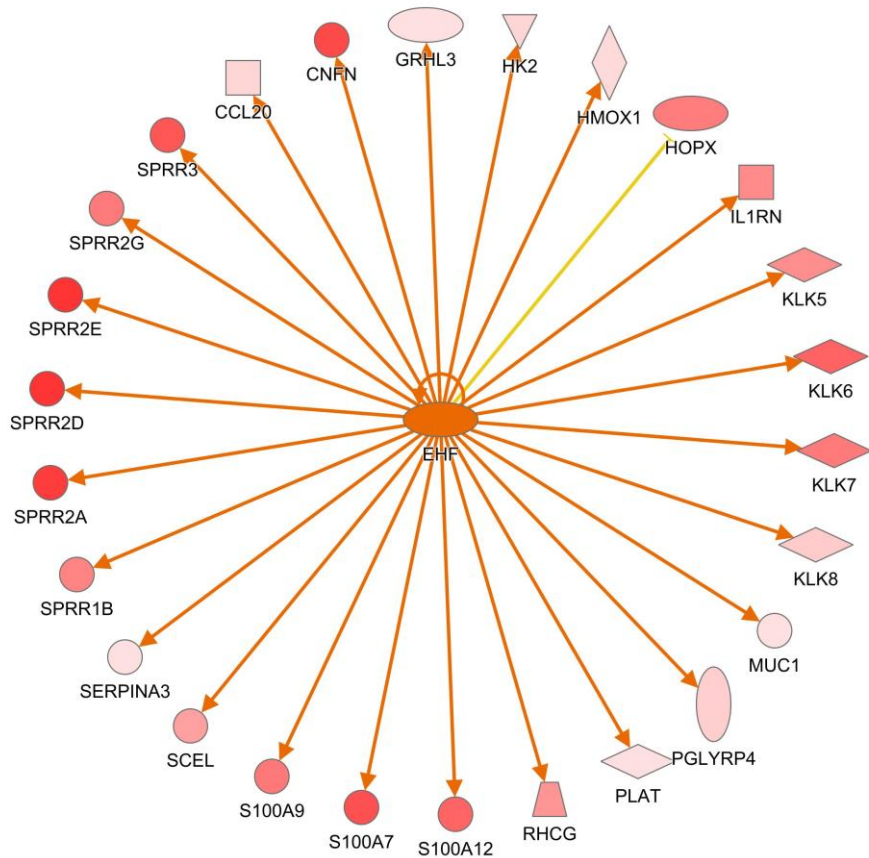
Analysis: Tumor\_core\_spatial\_genome\_DEG - 2024-06-14 06:24 下午





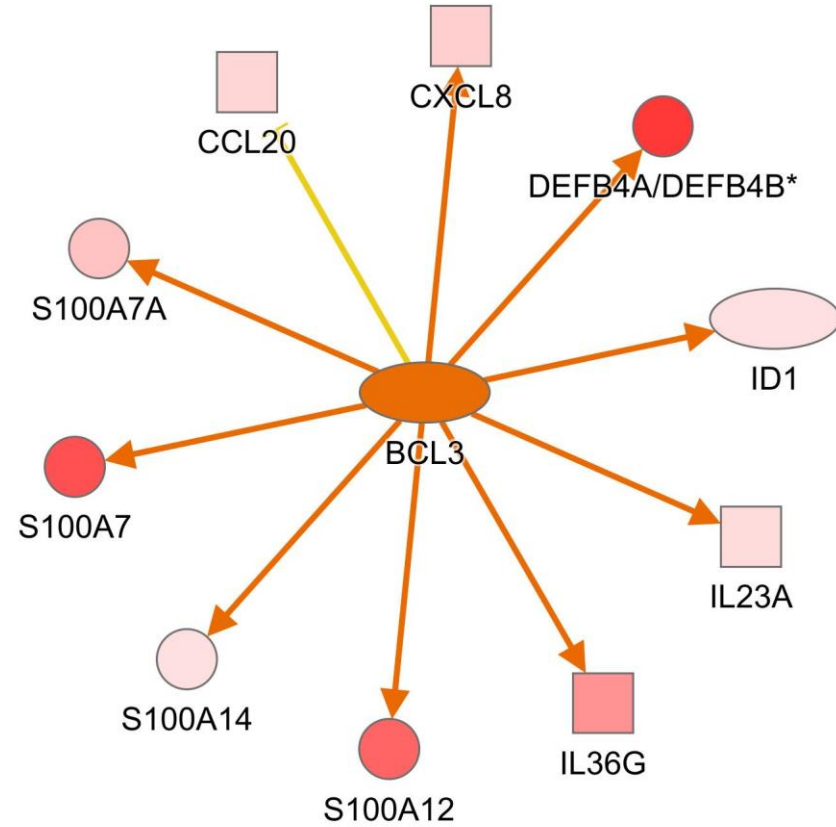
## Proto-Oncogene transcription factor

EHF 1

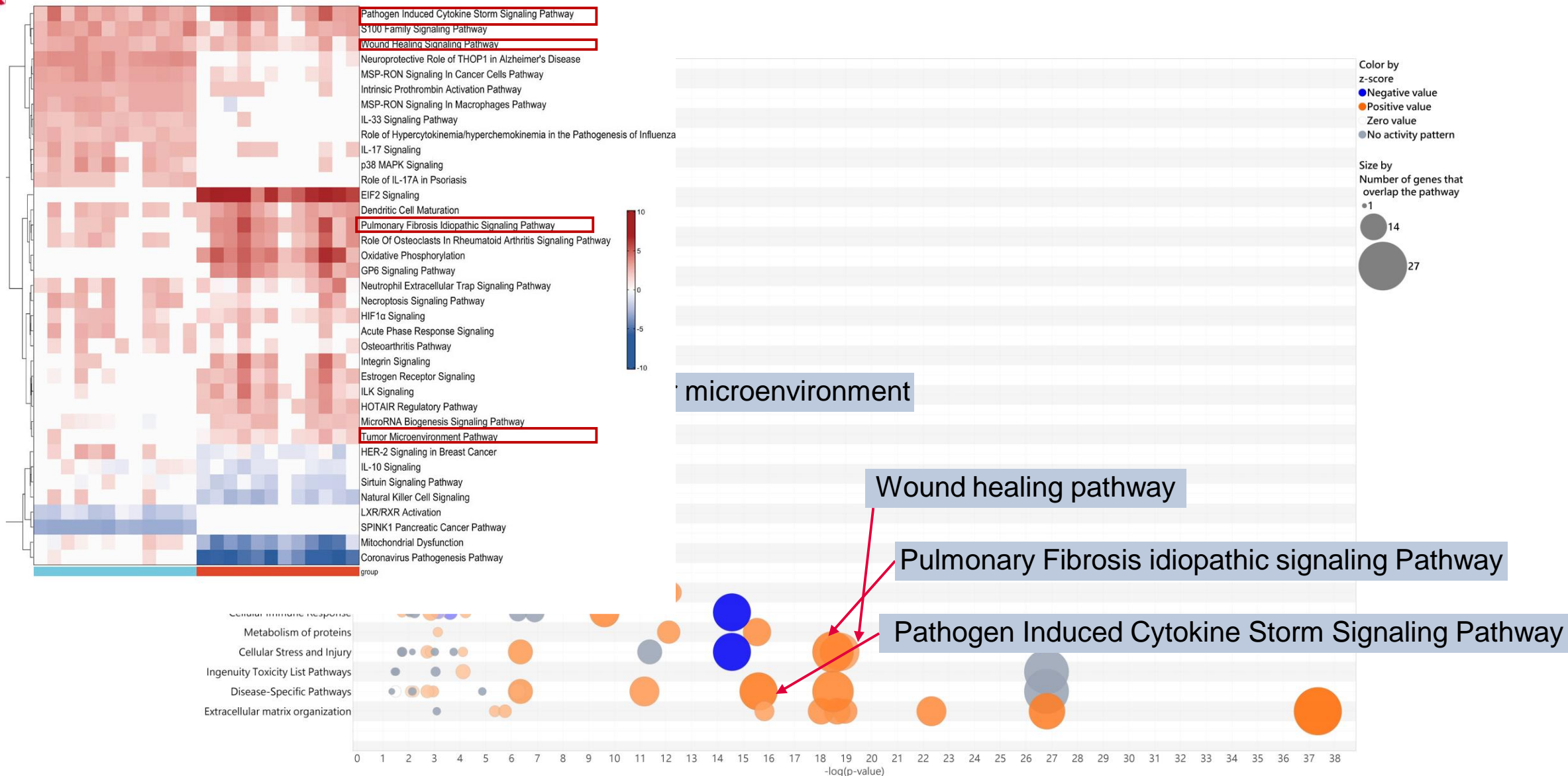


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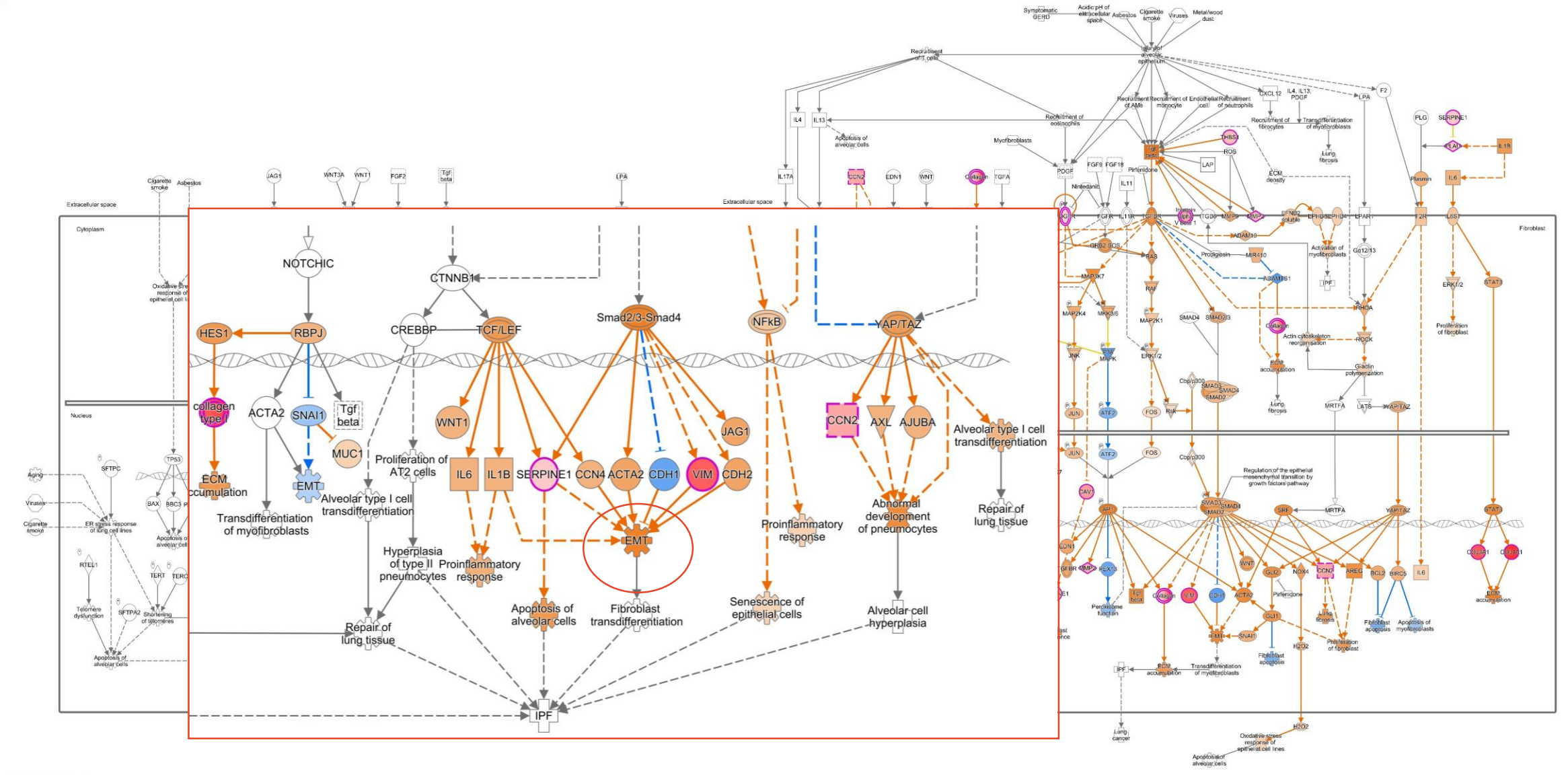
BCL3 2



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# Pulmonary Fibrosis idiopathic signaling Pathway

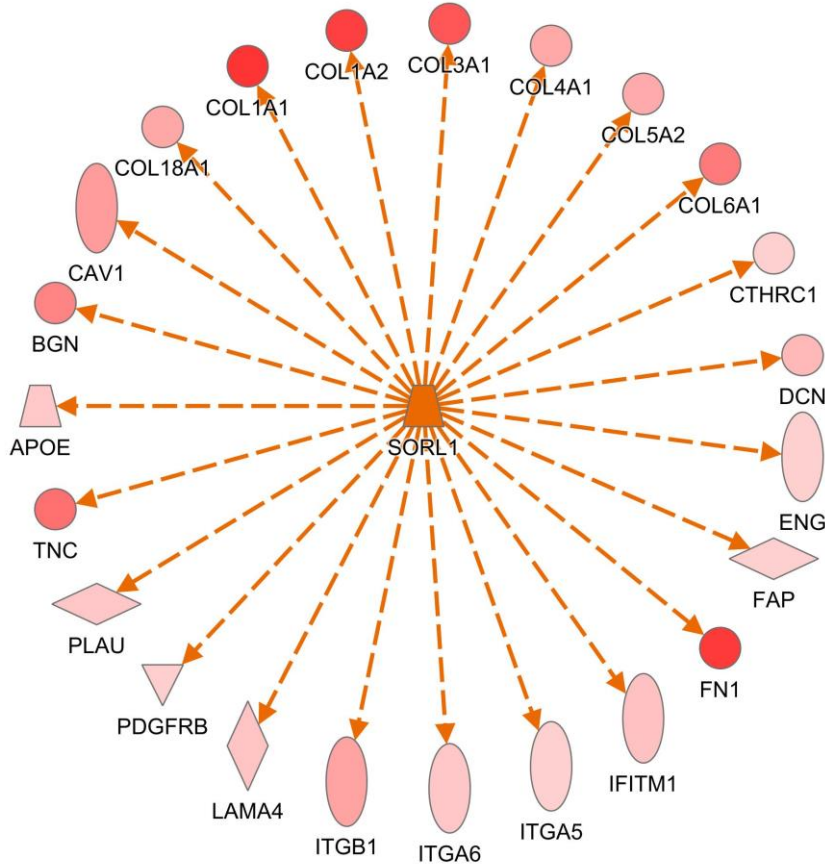


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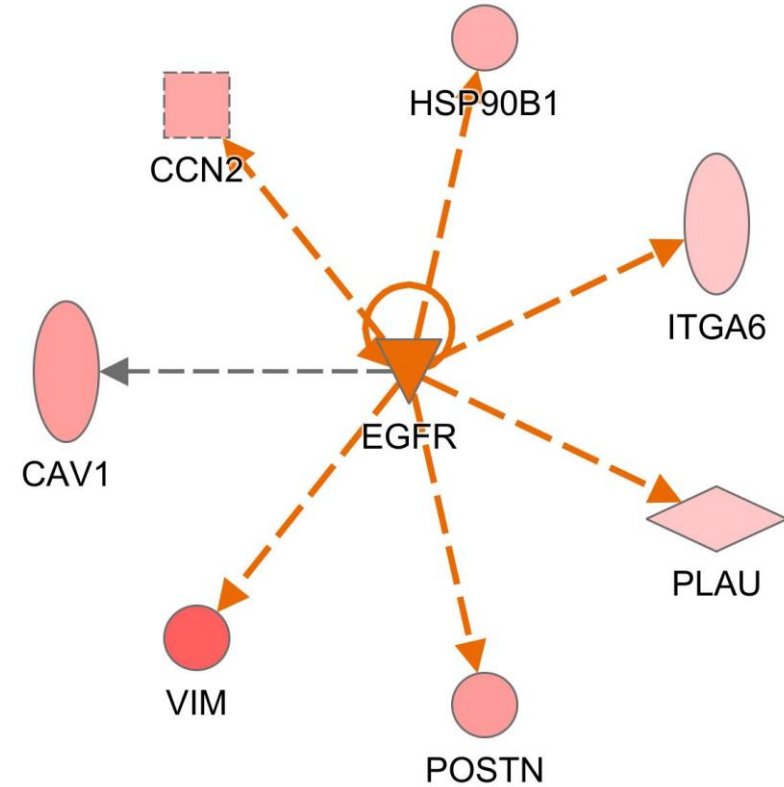
## EMT regulator

SORL1 3



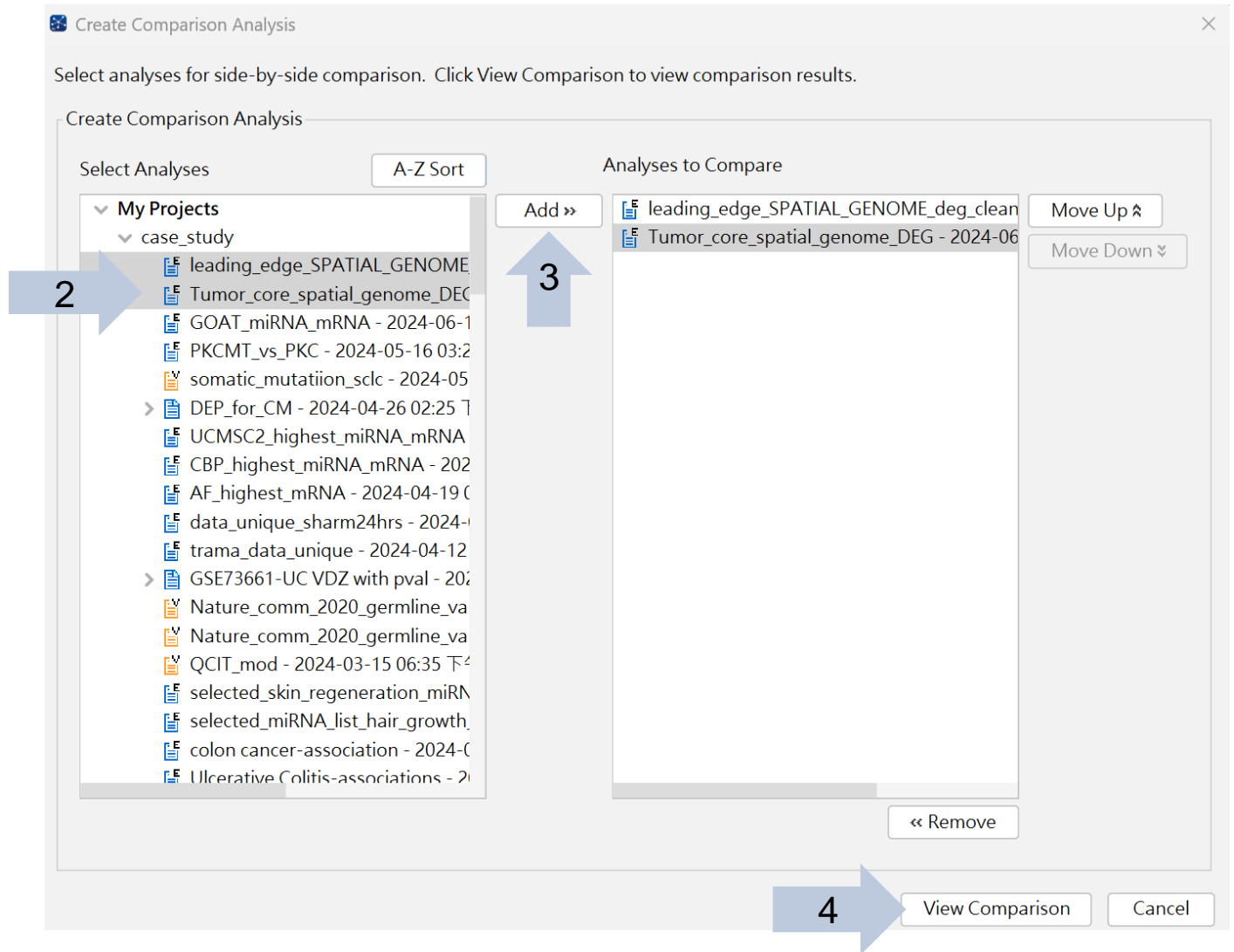
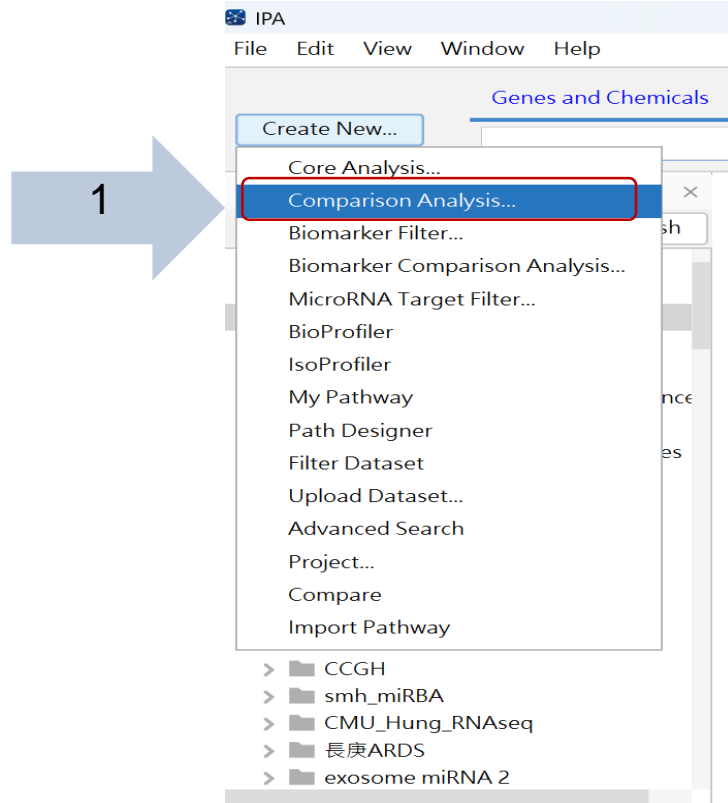
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EGFR 4



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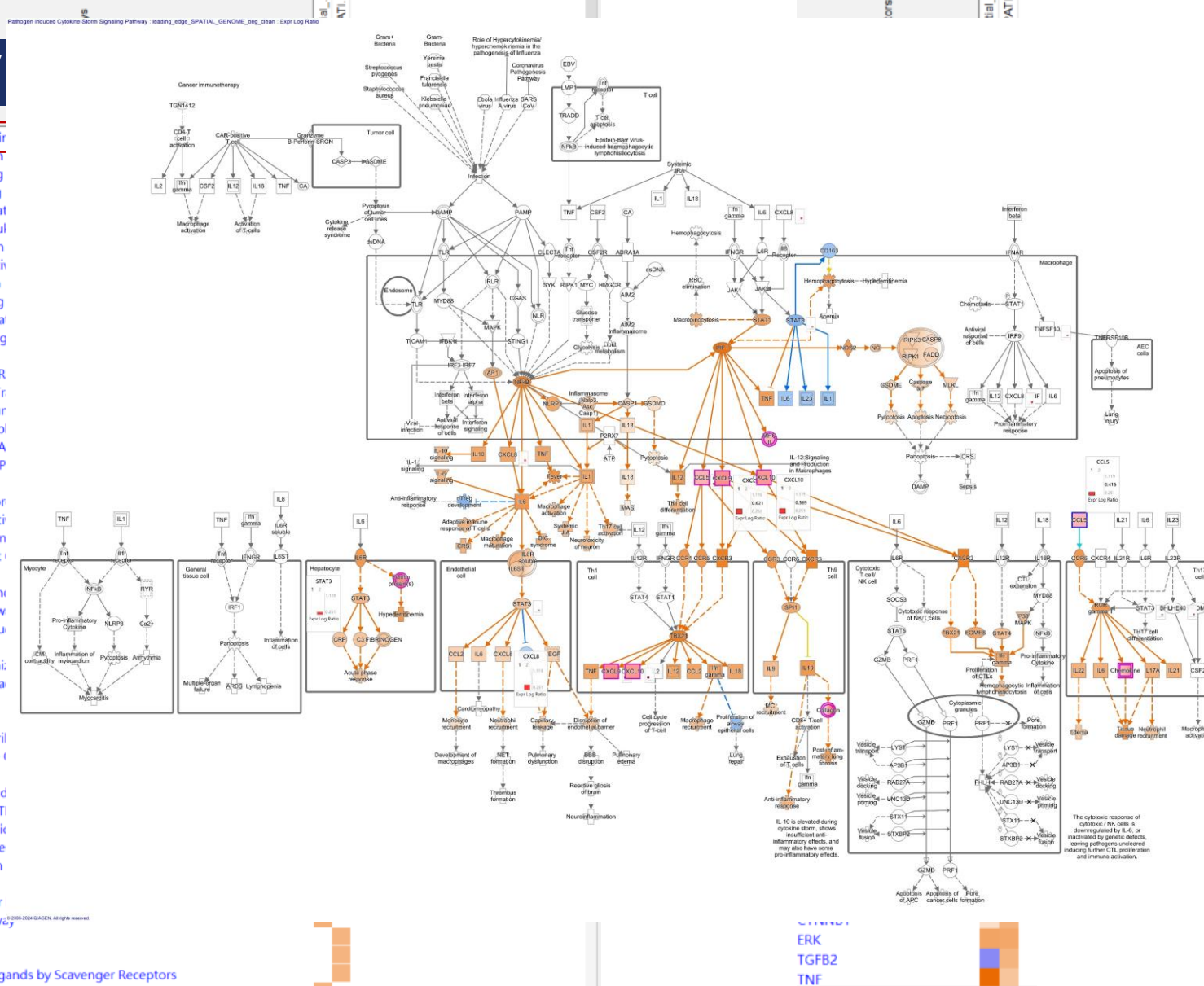
## Step for You to do your compared analysis



## Canonical pathway

### Pathogen Induced Cytokir

- Neutrophil degranulation
- Wound Healing Signaling
- Atherosclerosis Signaling
- Cell surface interactions at Interleukin-4 and Interleu
- Cell junction organization
- Intrinsic Prothrombin Acti
- Dendritic Cell Maturation
- Hepatic Fibrosis Signaling
- Pulmonary Fibrosis Idiopa
- Acute Phase Response Sig
- FAK Signaling
- Role of Chondrocytes in R
- Neutrophil Extracellular Tr
- Sertoli Cell-Sertoli Cell Jur
- IL-17A Signaling in Fibro
- Macrophage Alternative A
- Activin Inhibin Signaling P
- Osteoarthritis Pathway
- Role of Macrophages, Fibr
- Macrophage Classical Acti
- Multiple Sclerosis Signalin
- HER-2 Signaling in Breast
- ID1 Signaling Pathway
- Sertoli Cell-Germ Cell Jun
- HOTAIR Regulatory Pathw
- IL-12 Signaling and Produ
- Keratinization
- Extracellular matrix organi
- Integrin cell surface intera
- GP6 Signaling Pathway
- IL-4 Signaling
- Assembly of collagen fibril
- Regulation of Insulin-like I
- Collagen degradation
- Collagen biosynthesis and
- Neuroprotective Role of T
- Collagen chain trimerizati
- Role of Osteoclasts in Rhe
- Post-translational protein
- Signaling by MET
- SPINK1 Pancreatic Cancer
- Cachexia Signaling Pathway
- Syndecan interactions
- Signaling by PDGF
- Binding and Uptake of Ligands by Scavenger Receptors
- MSP-RON Signaling in Macrophages Pathway



## compared\_TC\_LE



Upstream Regulators

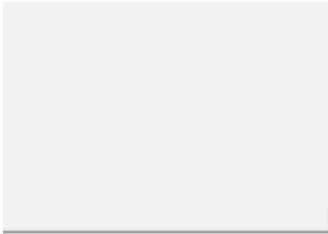
Tumor\_core\_spatial\_ge...  
leading\_edge\_SPATIA...

EGFR  
SORL1  
EHF  
BCL3

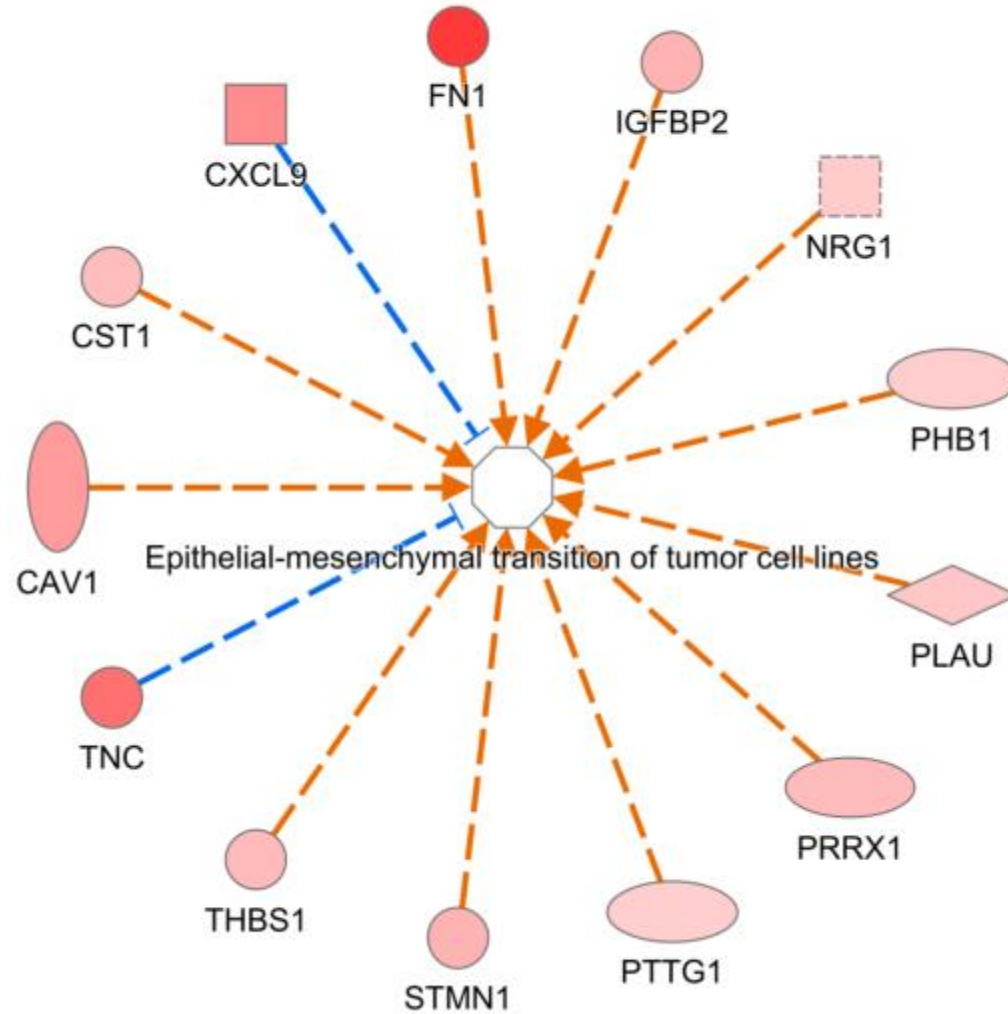
Leading Edge

Tumor core

## EMT signaling



Epithelial-mesenchymal transiti  
 Epithelial-mesenchymal transiti  
 Epithelial-mesenchymal transiti  
 Epithelial neoplasm  
 Epithelial-mesenchymal transiti  
 Epithelial to mesenchymal trans



Cell proliferation of breast cancer cell lines  
 Binding of tumor cell lines  
 Sphere formation of carcinoma cell lines  
 Cell proliferation of colorectal cancer cell lines

## QIAGEN IPA – access to manually-curated knowledge base

- **Perform expression analysis and compare cell clusters**
  - Discover novel biological mechanisms
  - Identify cell type-specific biomarkers and key regulators/targets



Better Care with Better Knowledge

若有需要進一步的資訊或在使用軟體上遇到問題歡迎聯繫以下窗口：  
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