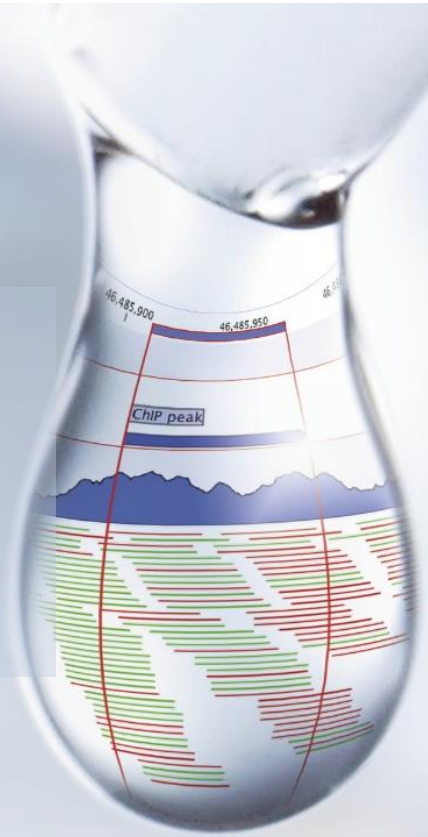
Insights into Spatial transcriptome via Qiagen Ingenuity Pathway analysis



Cleo Hsi資深業務專員

Christine Hsiung　熊嘉妮 專案主任　**Bioinfo@GGA.ASIA**

Agenda

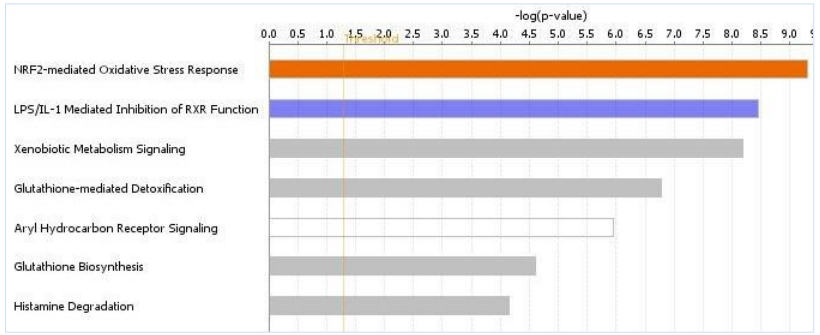
- How to analysis Omics by QIAGEN Ingenuity Pathway Analysis
- Insights into biological function
  - Data format
  - Data upload and analysis setup
  - Comparing cell type-specific biomarker and regulators/targets
- Summary

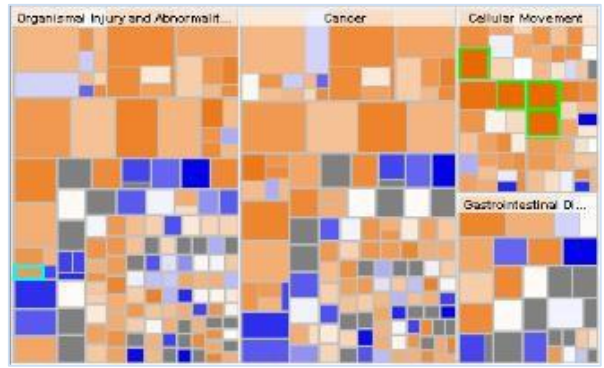
Omics data analysis using QIAGEN IPA

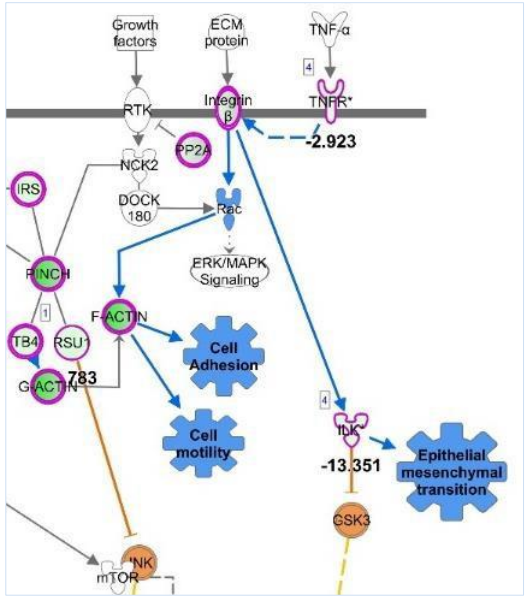
Omics data type

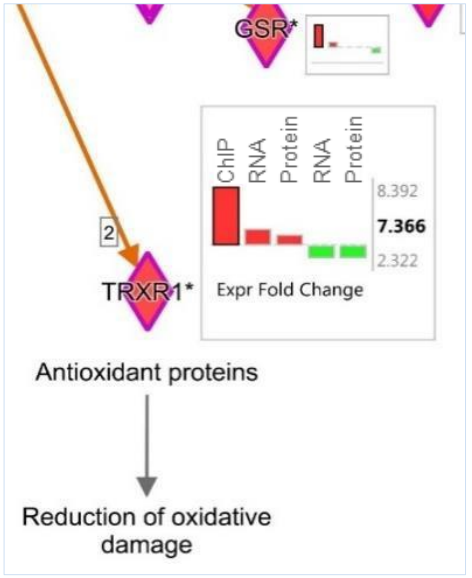
- RNA-seq
- scRNA-seq
- Microarray
- Nanostring
- qPCR
- ChIP-seq
- Proteomics
- Metabolomics
- RNAi
- CRISPR
- WGS/WES etc.

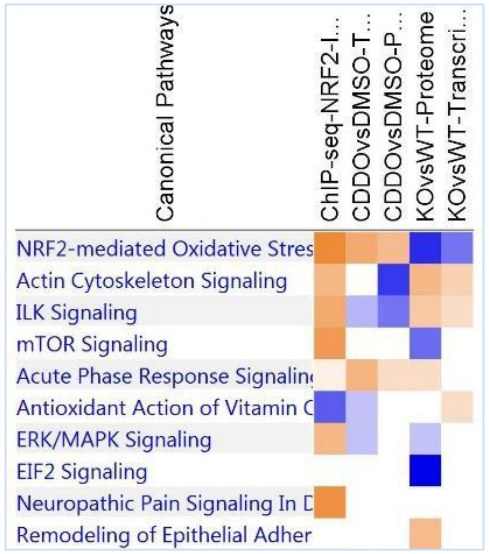
QIAGEN IPA



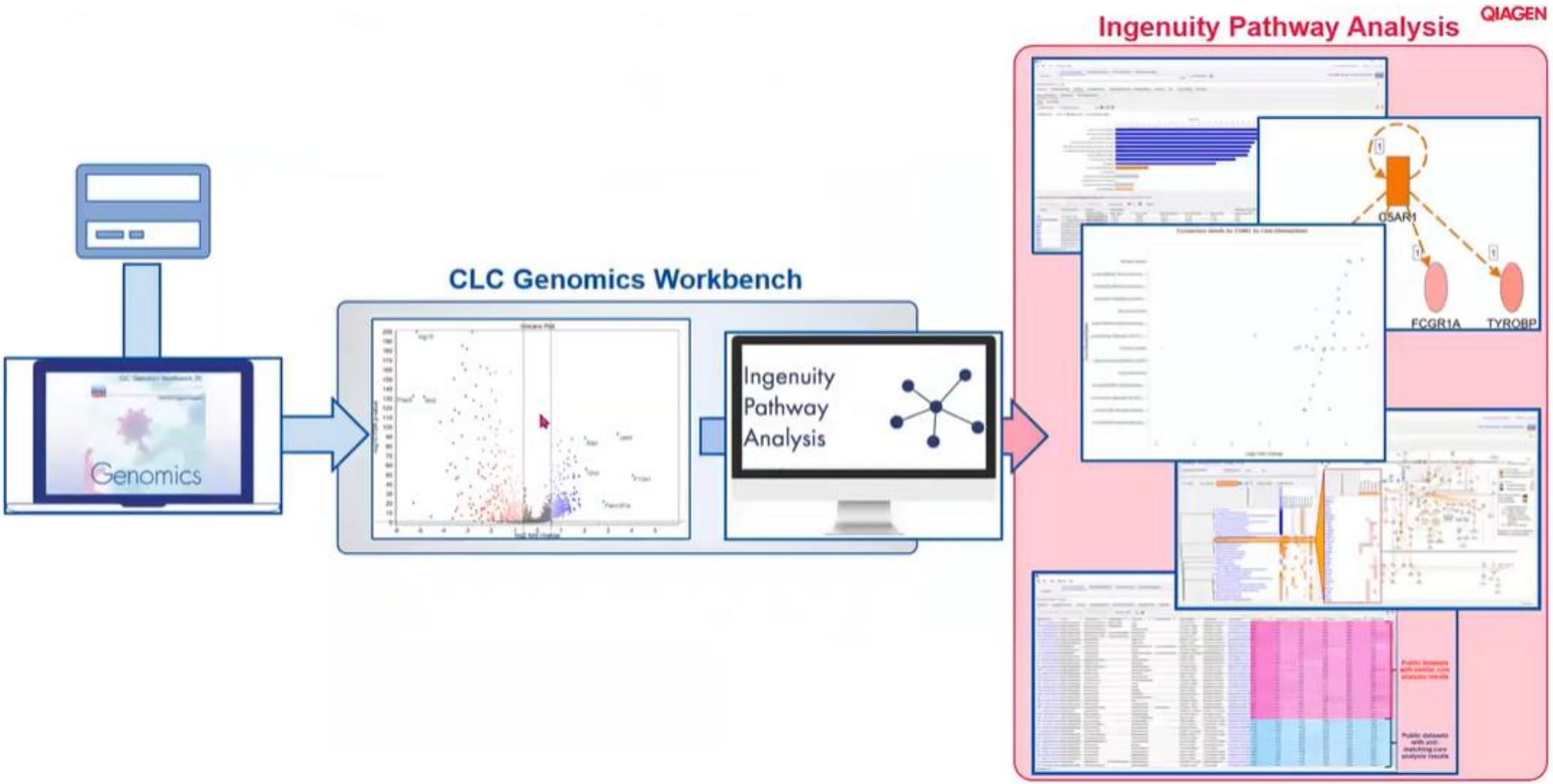








Comprehensive single-cell RNA-seq analysis with Qiagen Digital Insights



Publication of Single-cell RNA Seq and Qiagen IPA

Google 學術搜尋

"single cell RNA seq" "ingenuity pathway analysis"

約有 2,690 項結果 (0.08 秒)

Article

Disease-associated astrocyte epigenetic memory promotes CNS pathology

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Check for updates

Hong-Gyun Lee[1], Joseph M. Rone[1], Zhaorong Li[1,2], Camilo Faust Akl[1], Seung Won Shin[3], Joon-Hyuk Lee[1], Lucas E. Flausino[1], Florian Pernin[4], Chun-Cheih Chao[1], Kilian L. Kleemann[5], Lena Srun[1], Tomer Illouz[1], Federico Giovannoni[1], Marc Charabati[1], Liliana M. Sanmarco[1], Jessica E. Kenison[1], Gavin Piester[1,6], Stephanie E. J. Zandee[7], Jack P. Antel[4], Veit Rothhammer[1,8], Michael A. Wheeler[1,2], Alexandre Prat[7], Iain C. Clark[3] & Francisco J. Quintana[1,2,9]✉

Disease-associated astrocyte subsets contribute to the pathology of neurologic diseases, including multiple sclerosis and experimental autoimmune encephalomyelitis[1–8] (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$^+$p300$^+$ 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$^+$p300$^+$ 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[9–11]. Astrocytes participate in key processes that are relevant to CNS development and homeostasis[9]. In addition, cytokines, interactions with CNS-resident and CNS-recruited immune cells, and other factors trigger astrocyte responses with important roles in CNS pathology[10,12,13]. Indeed, several astrocyte subsets have been described in neurologic diseases[14–16]. For example, we and others have interrogated astrocyte functional heterogeneity in multiple sclerosis and EAE[1–8]. 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[17]. In addition, innate immune cells including myeloid cells[18,19] and other cell types[20,21] undergo metabolic, epigenetic and transcriptional adaptations upon stimulation that alter their subsequent responses, boosting protective immunity against pathogens but also contributing to pathogenic inflammation[22]. 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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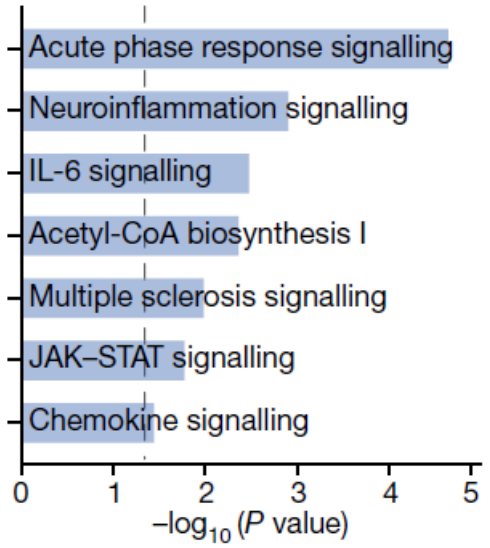

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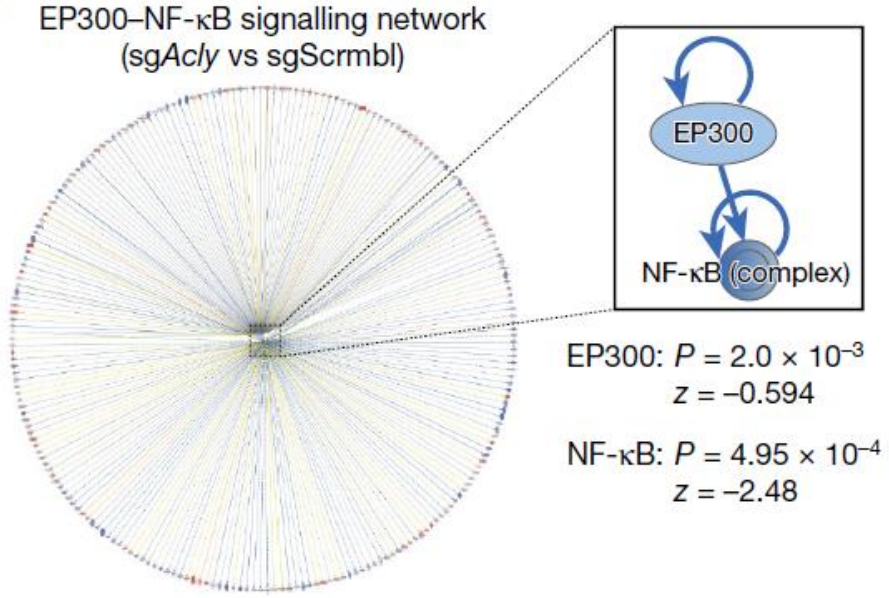

UCLA Health Jonsson Comprehensive Cancer center also use Qiagen IPA to interpreted spatial transcriptome

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

Use Case

nature communications

Article

https://doi.org/10.1038/s41467-023-40271-4

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

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Check for updates

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

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/dynamo_OSCC/) that can be foundational for developing novel targeted therapies.

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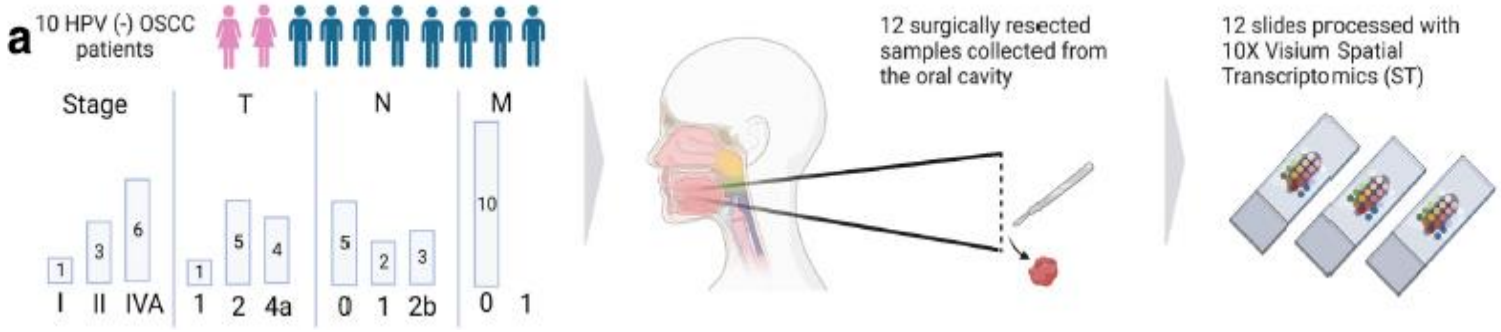
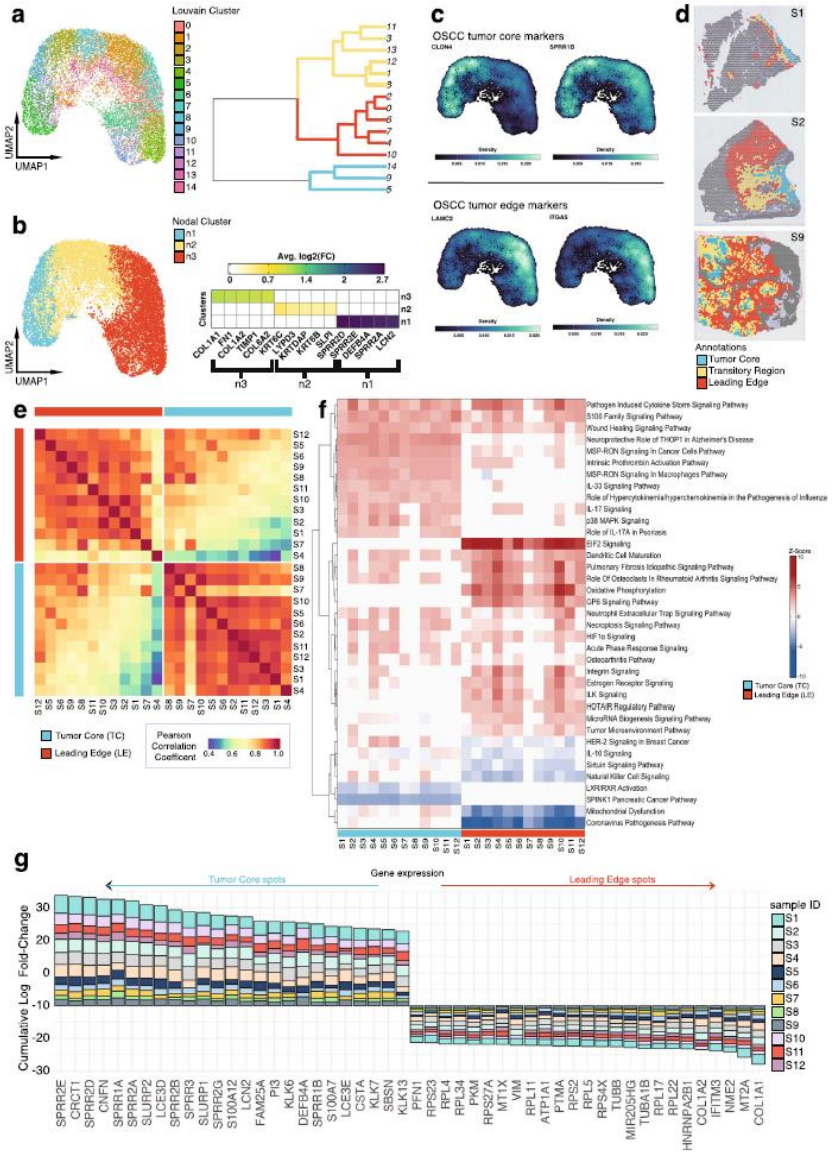
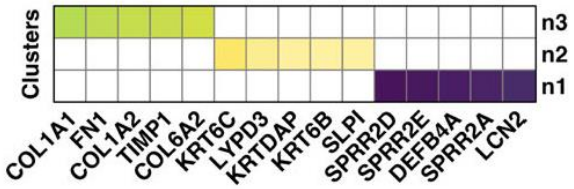


Data Format





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
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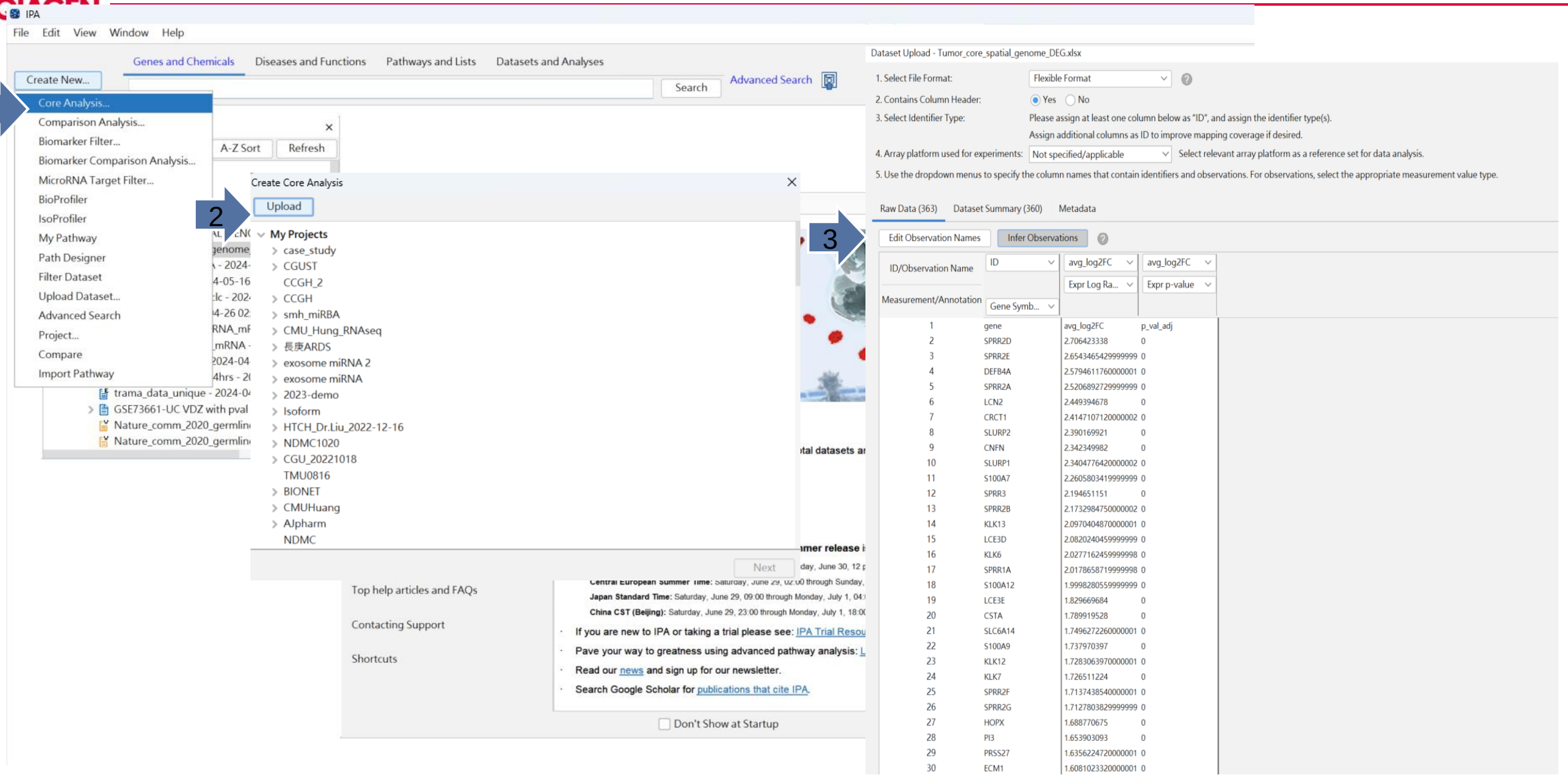
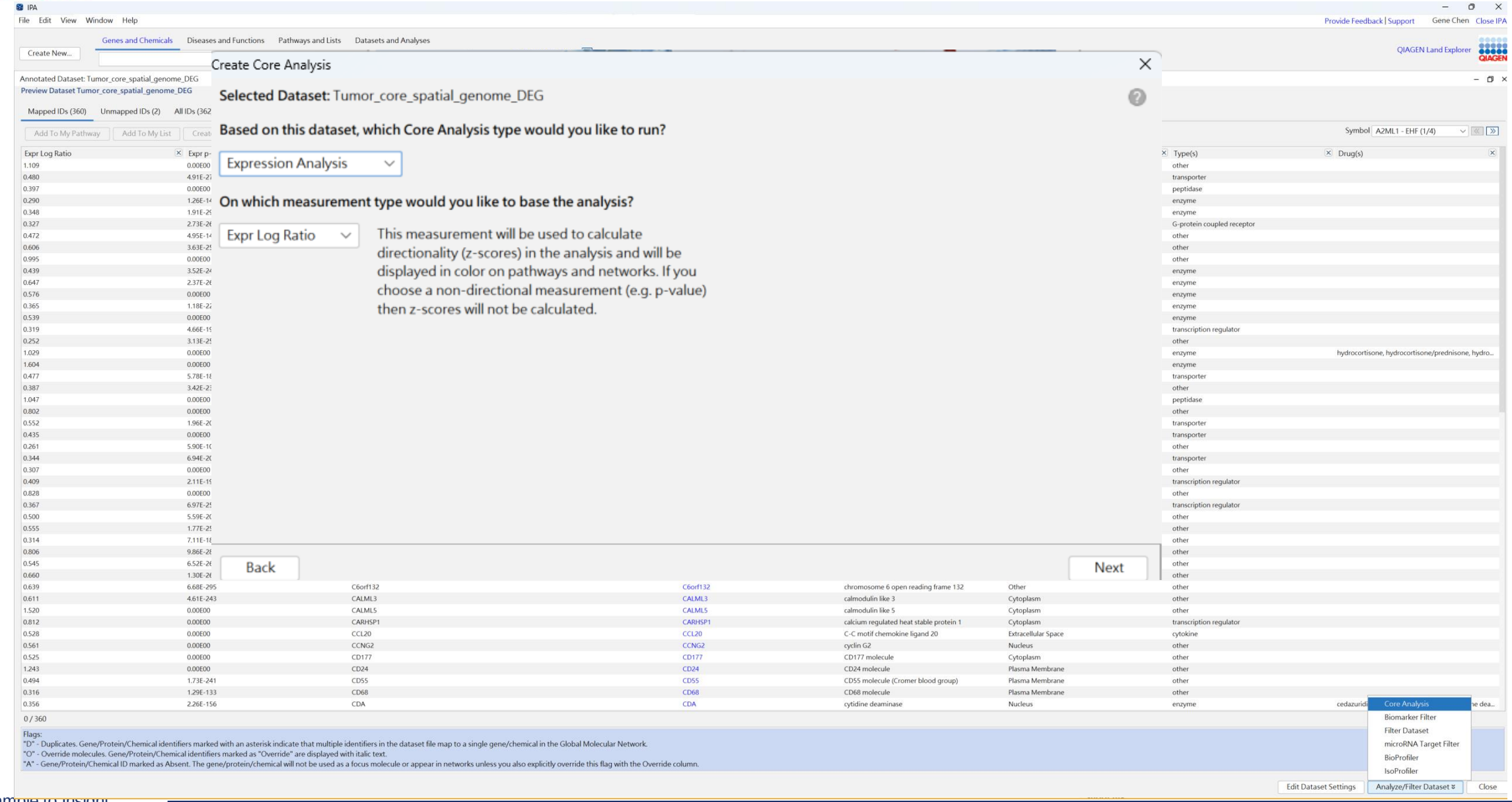
FBLN2	0.472353201	0
LGALS1	0.668868409	9.25E-299

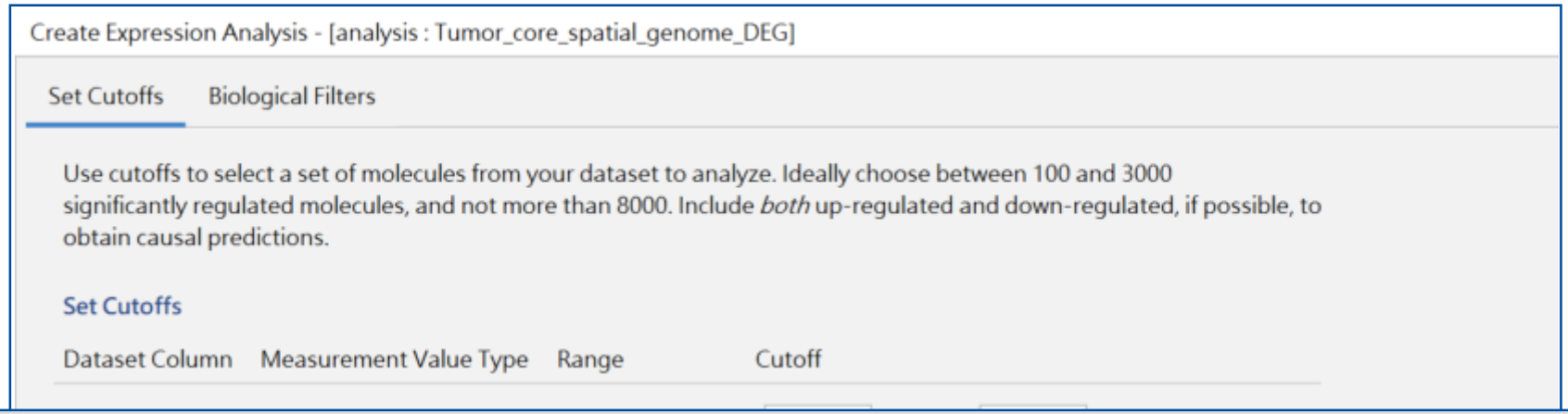
Upload dataset



Core Analysis

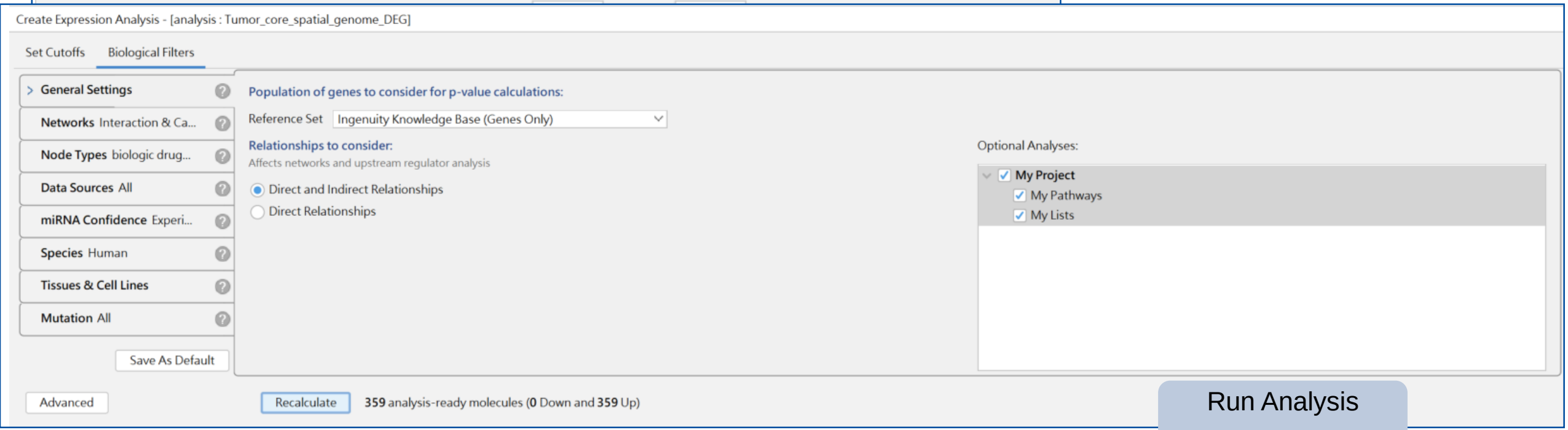


Core Analysis –Set Up



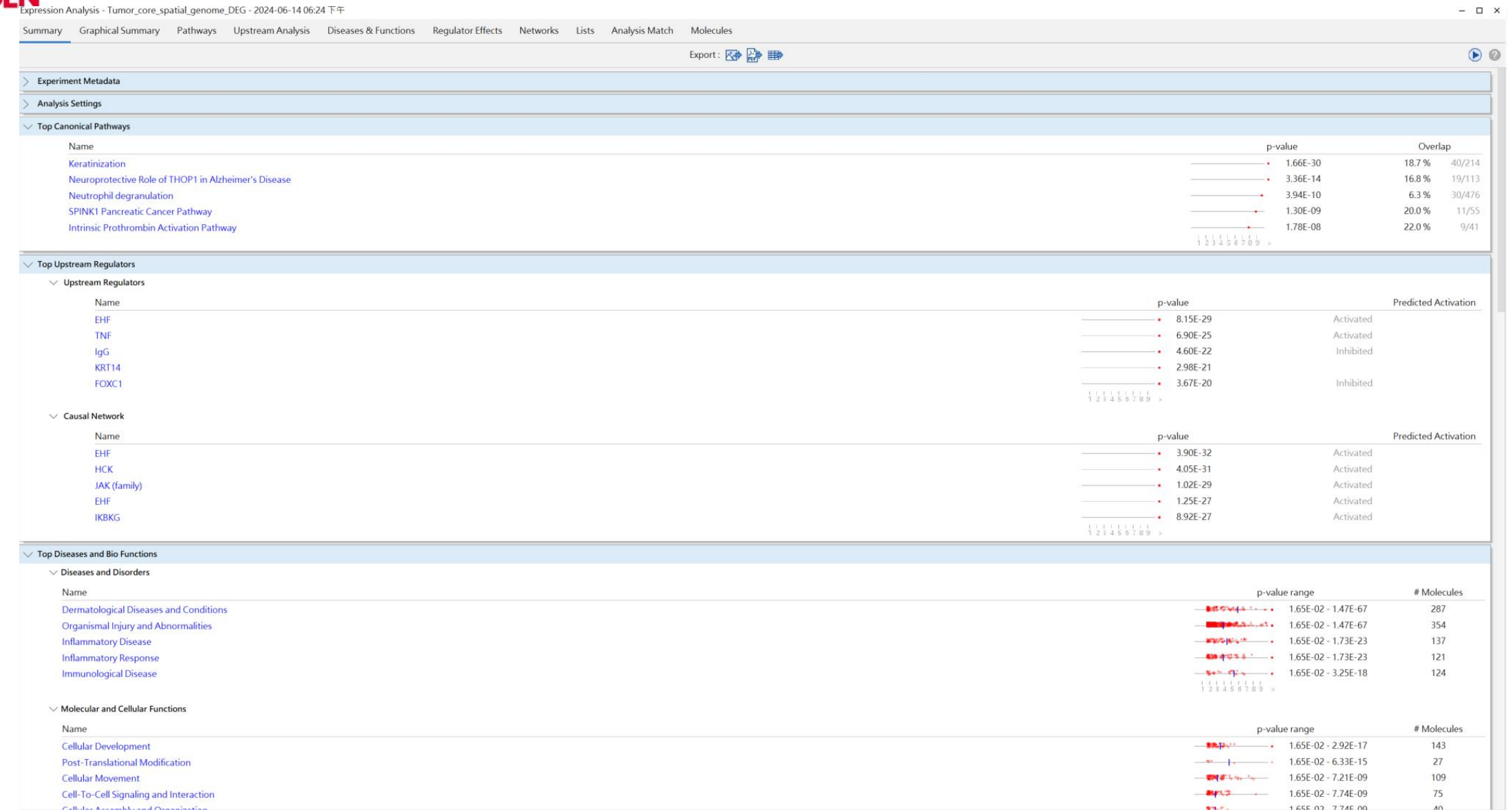
Three Step

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

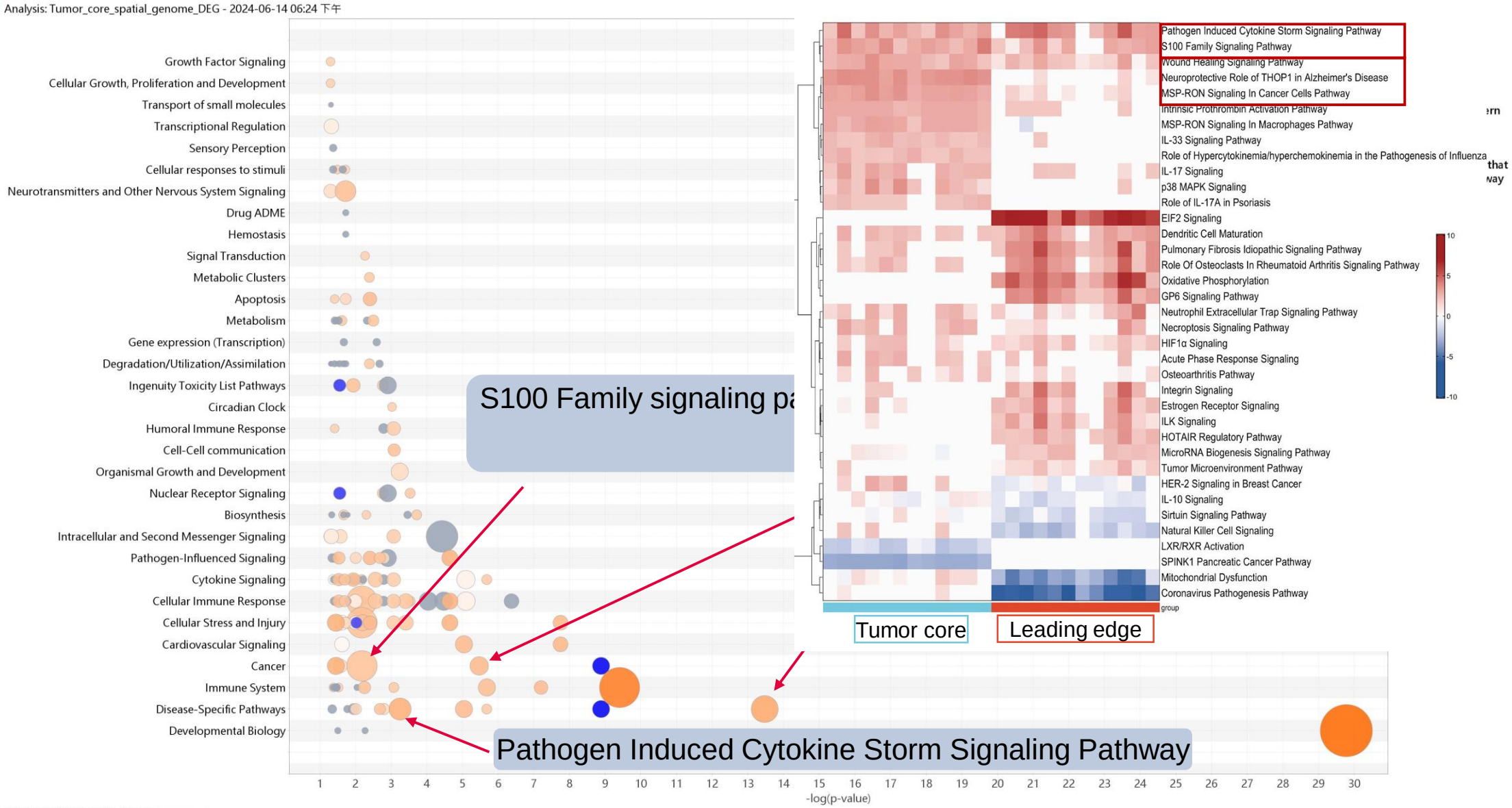


Run Analysis

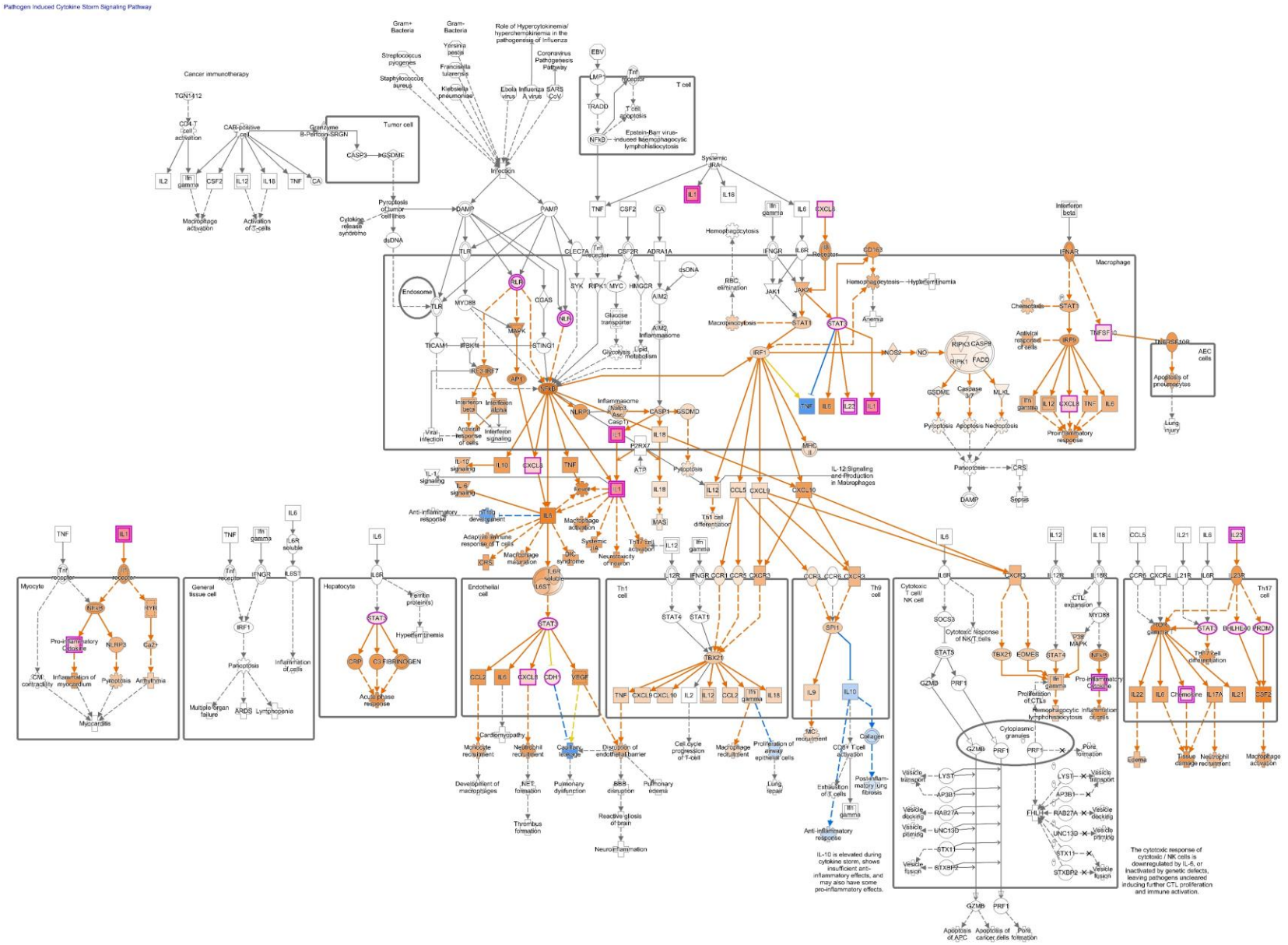
Tumor Core Analysis Result Overview



Tumor Core Bubble Plot

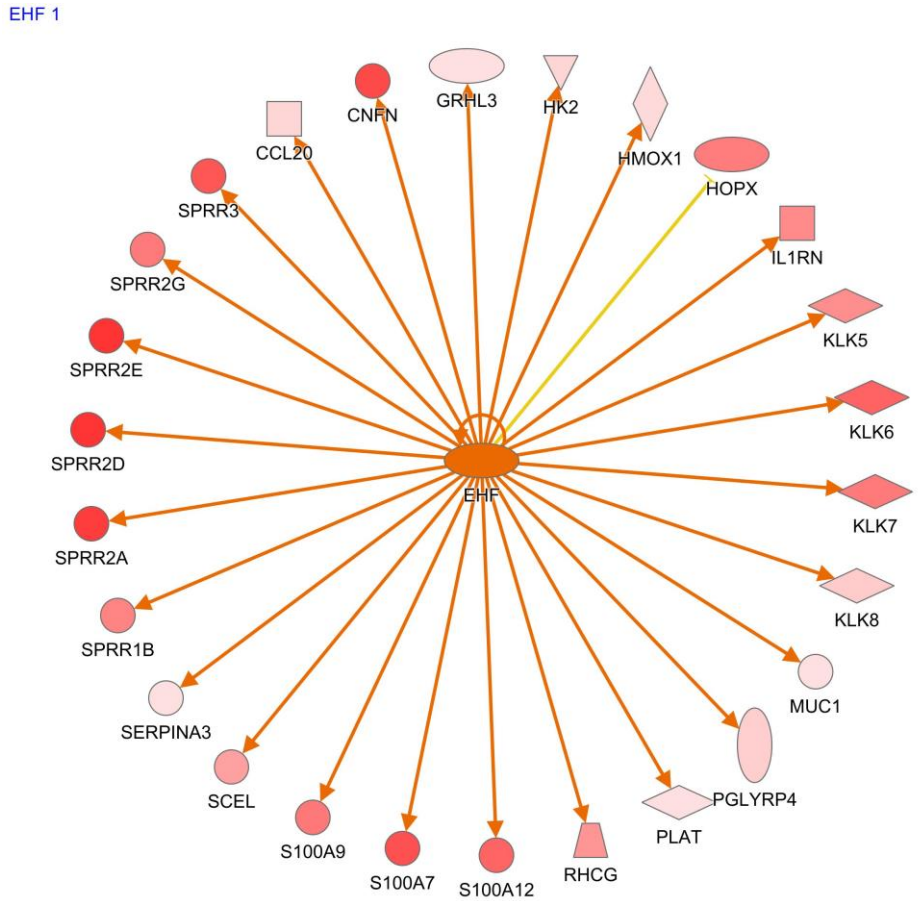


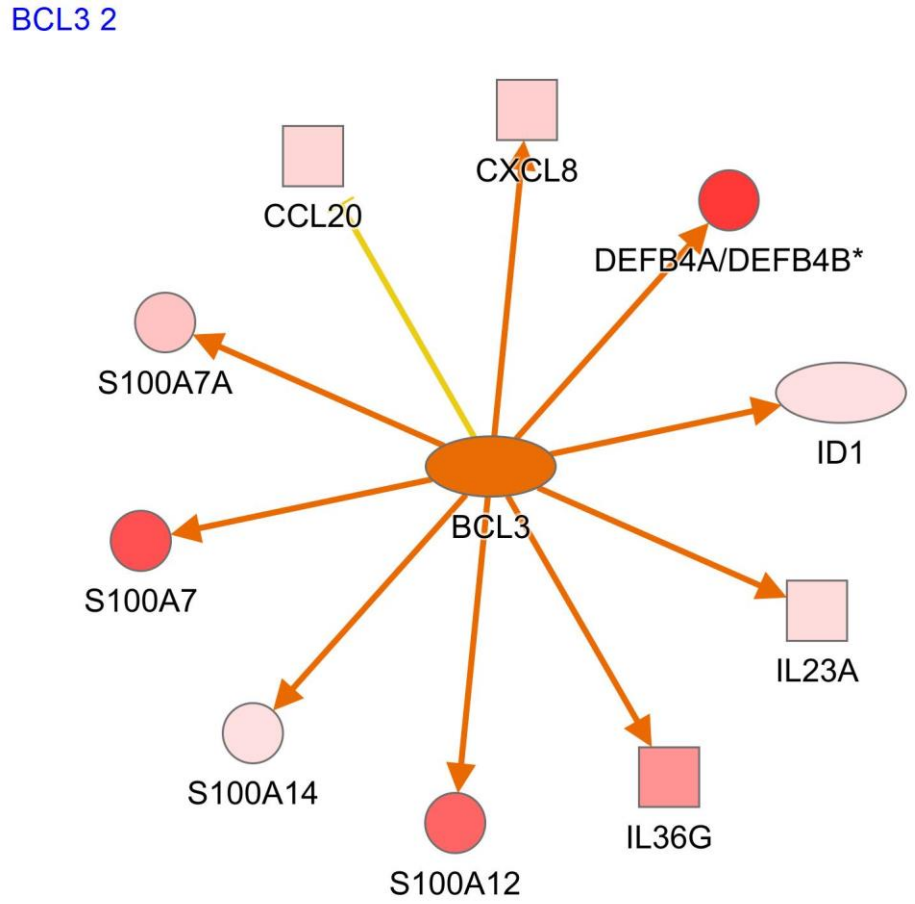
Pathogen Induced Cytokine Storm Signaling Pathway



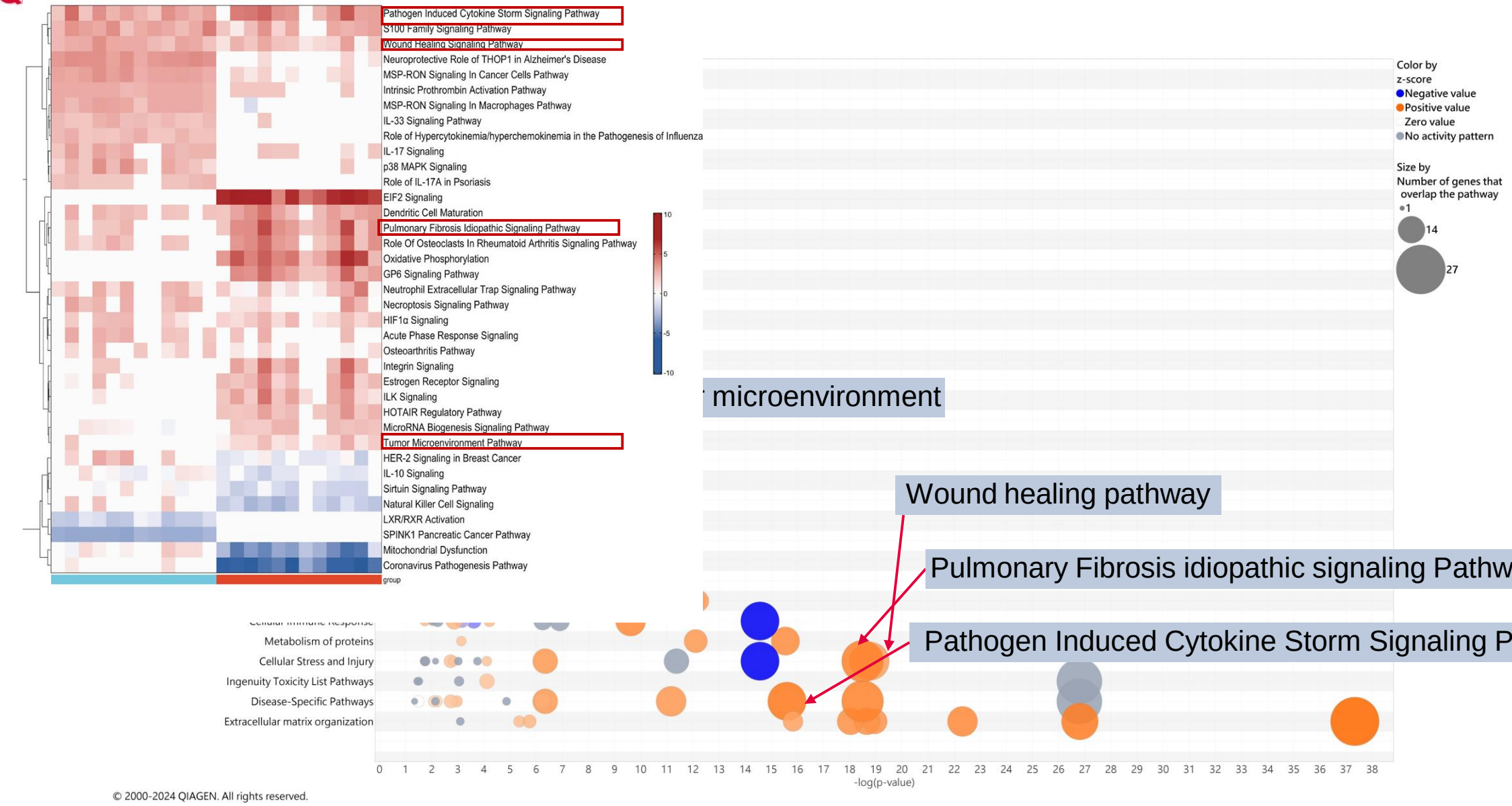
Upstream analysis in Tumor Core

Proto-Oncogene transcription factor

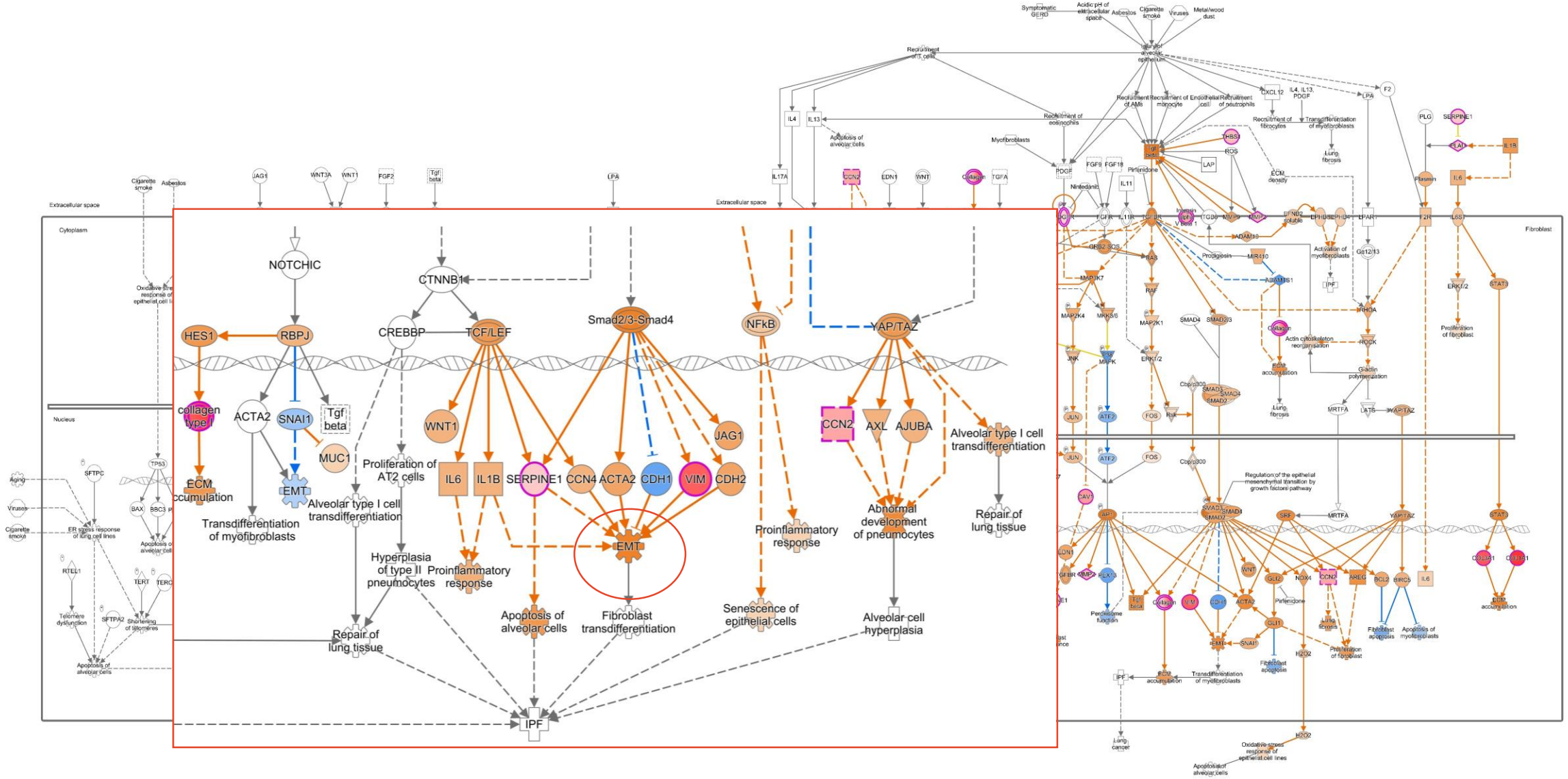




Leading Edge Bubble Plot



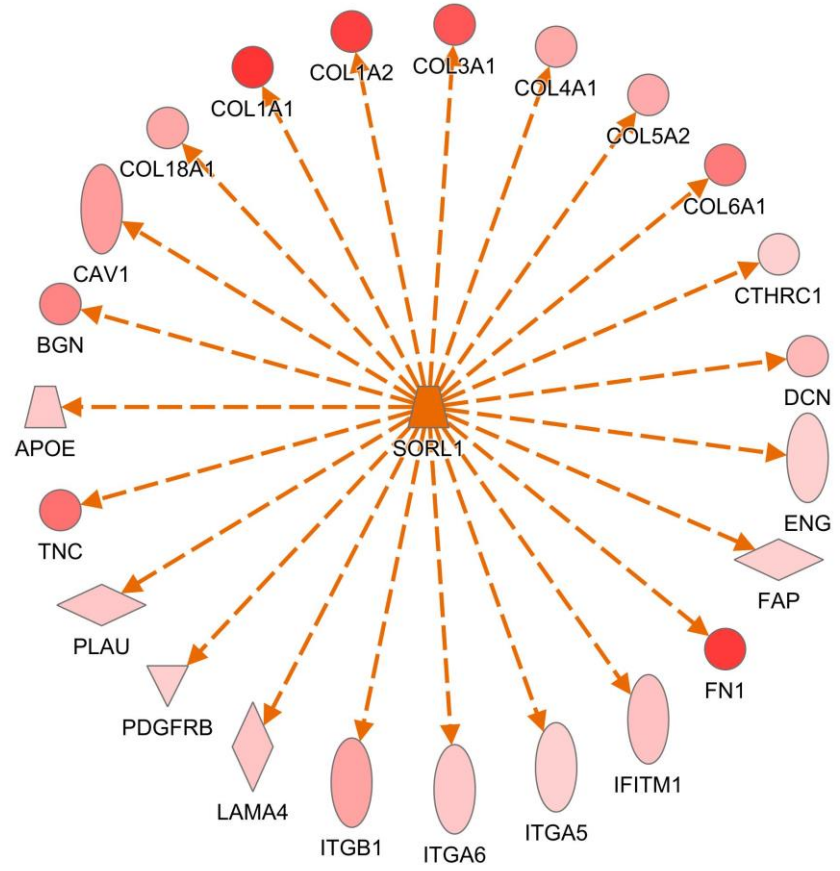
Pulmonary Fibrosis idiopathic signaling Pathway



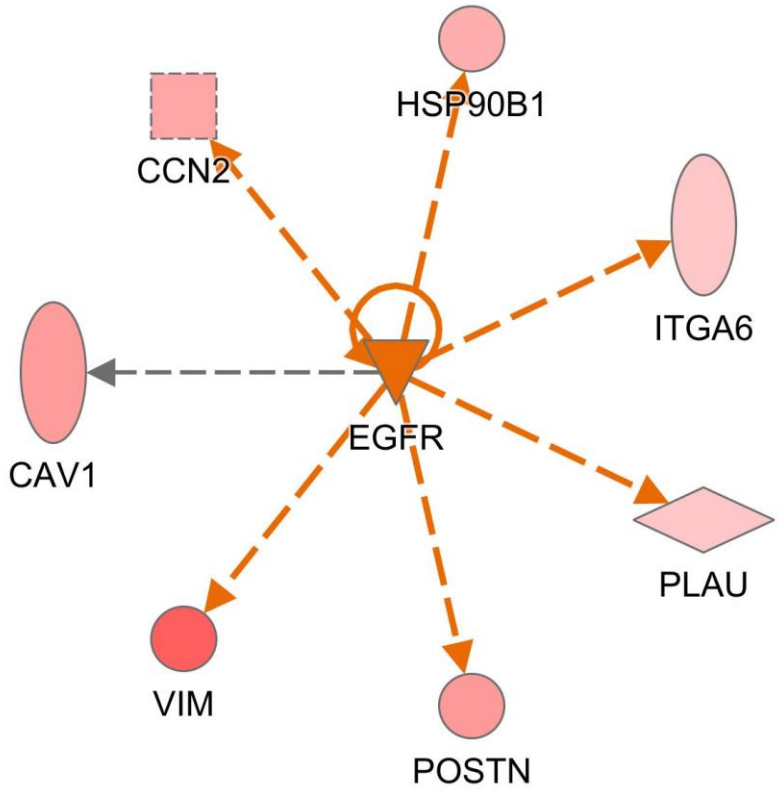
Upstream analysis in Leading Edge

EMT regulator

SORL1 3

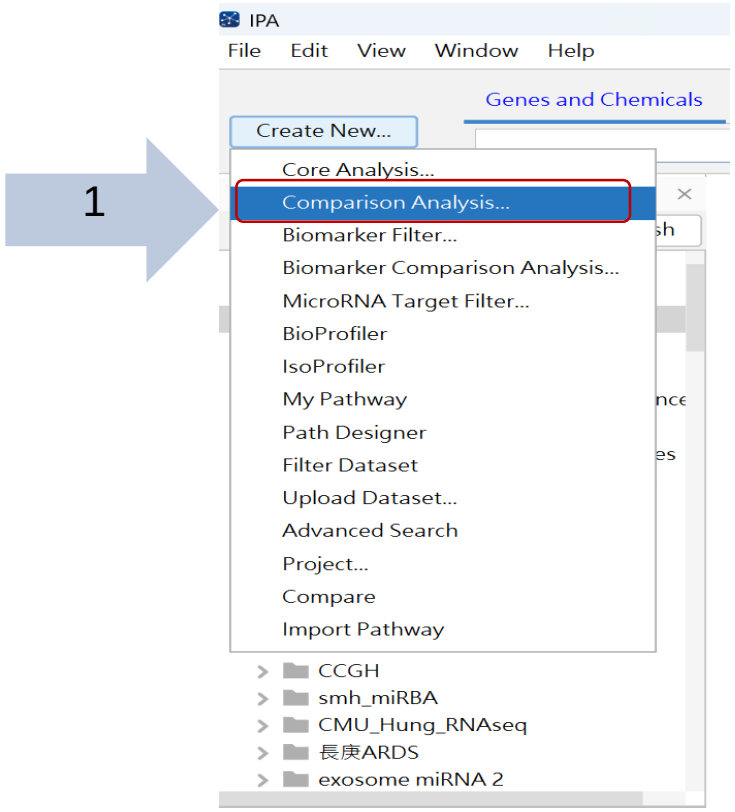


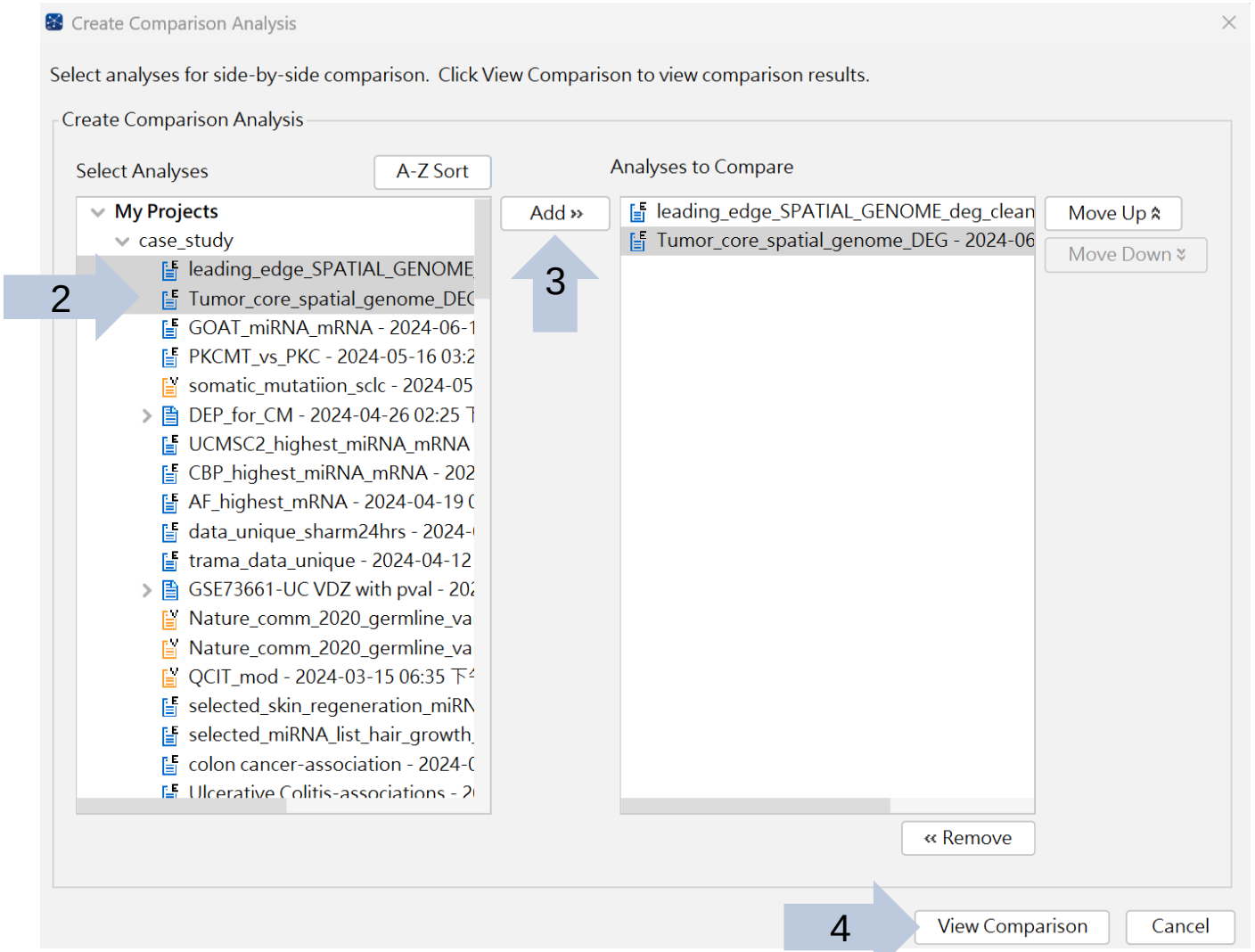
EGFR 4



Compare Analysis

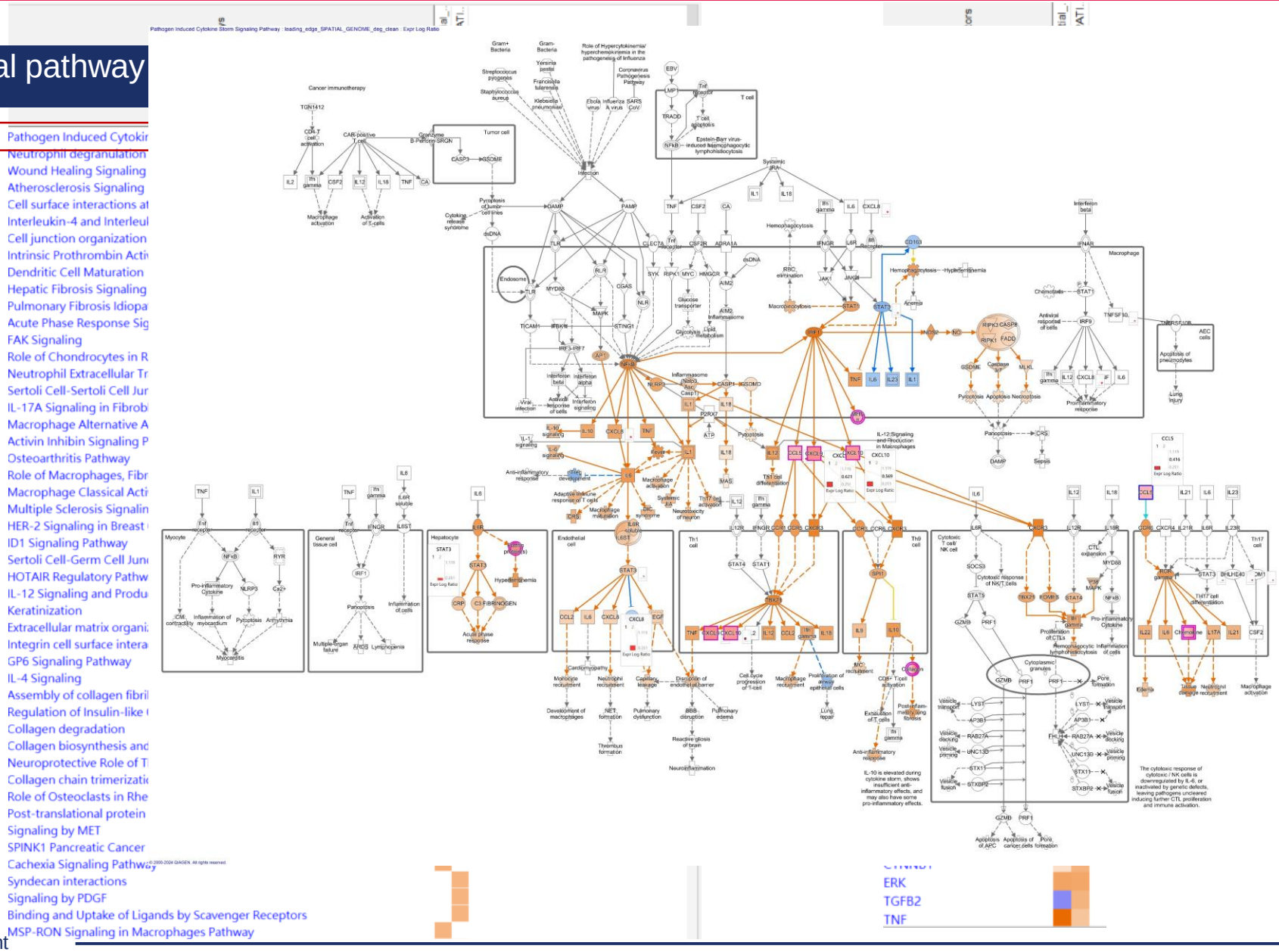
Step for You to do your compared analysis





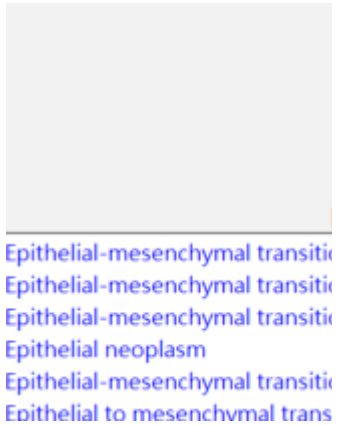
Compare Analysis Result

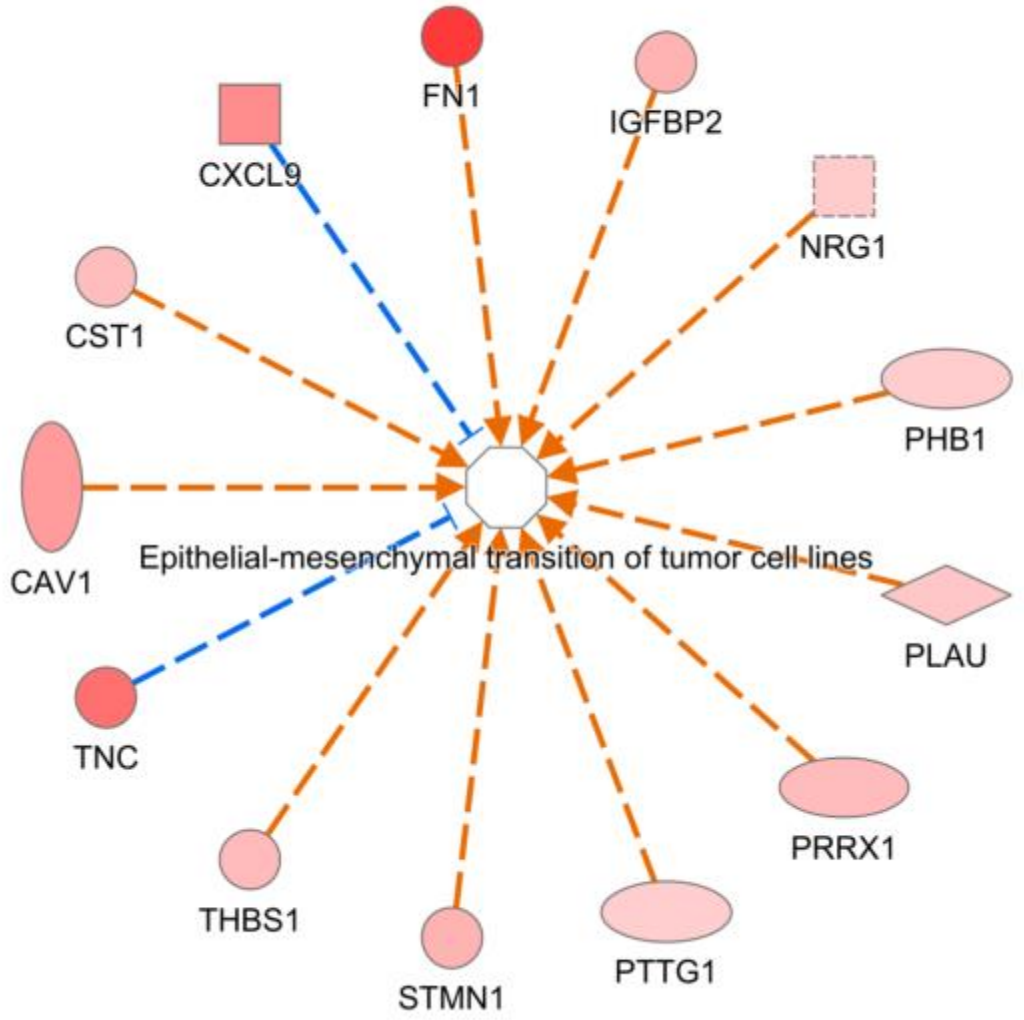
Canonical pathway

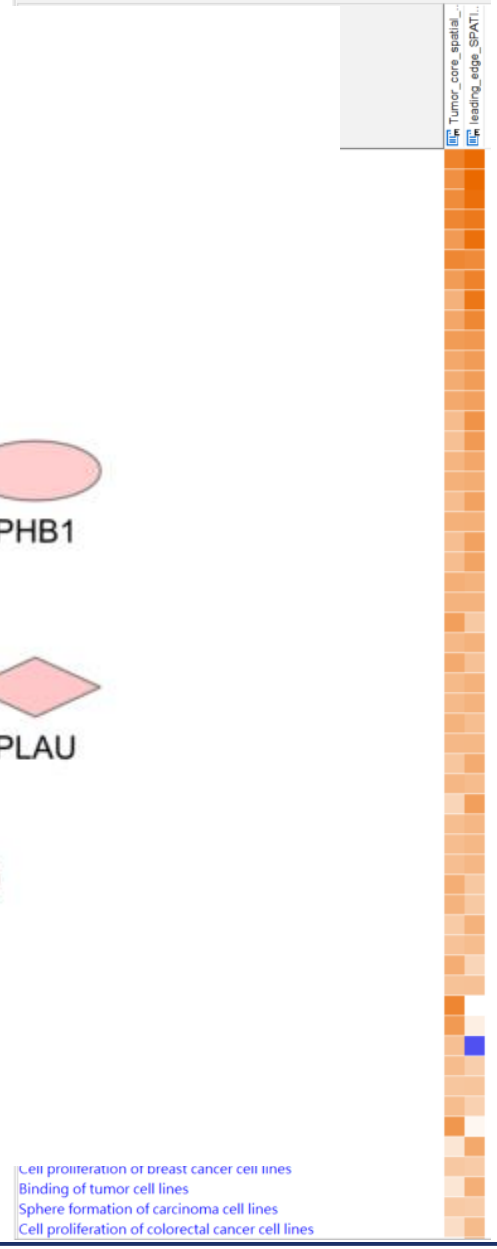


Compare Analysis Result

EMT signaling







Summary

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:
席佩妤 資深業務專員 CleoHsi@gga.asia 02-2795 1777 #3014
熊嘉妮 專案主任 ChristineHsiung@gga.asia 02-2795 1777 #3028
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