

# INGENUITY<sup>®</sup> PATHWAY ANALYSIS

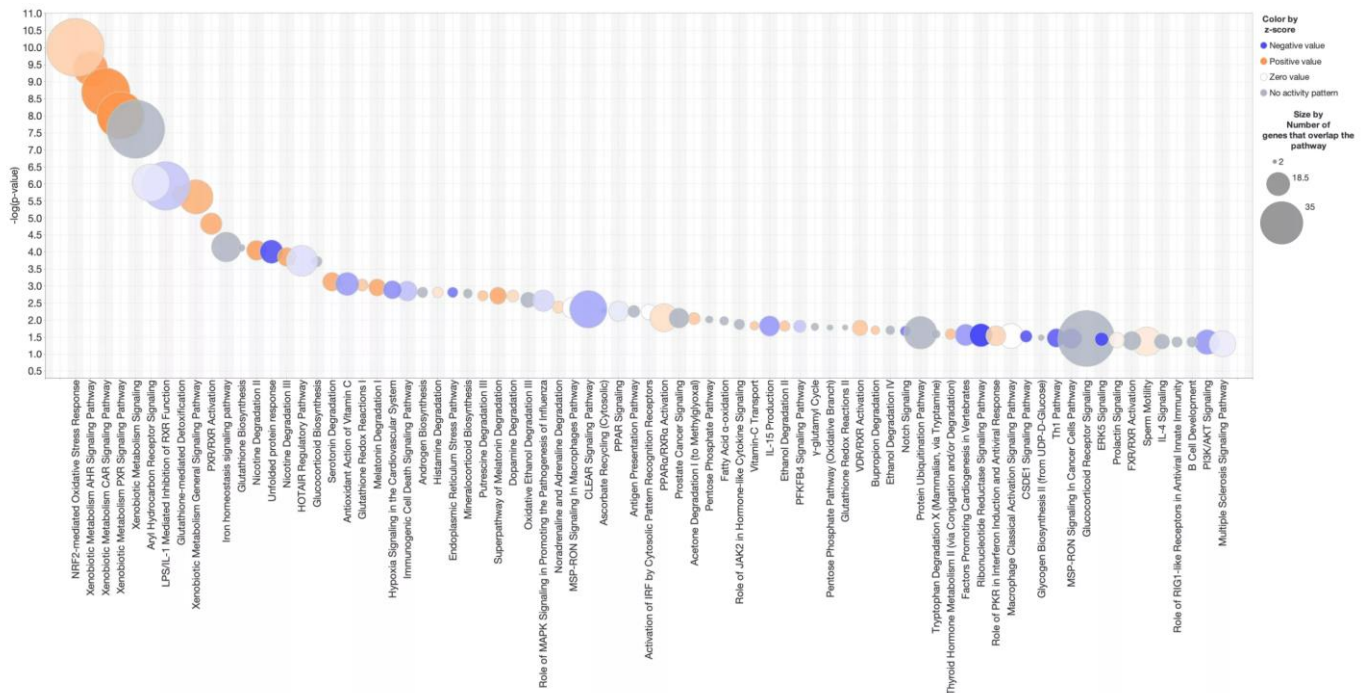
## QIAGEN IPA Fall Release (2022 秋季更新)

### 1. Canonical Pathway 新增泡泡圖功能

泡泡圖可以幫助 Canonical Pathway 有更好的視覺化呈現。泡泡圖能將多種參數同時顯示，並透過泡泡的大小、顏色以及重疊程度提供不同的訊息以解釋您的實驗資料。

圖一顯示的泡泡圖繪製了 Nrf2 活化化合物對小鼠腎臟中 Canonical Pathway 活化的預測影響。這些路徑按顯著性 ( $-\log(p\text{-value})$ ) 排序並根據活化或抑制的預測 (z-score) 進行著色。氣泡的大小隨著與每個路徑重疊的基因數量的增加而增加。

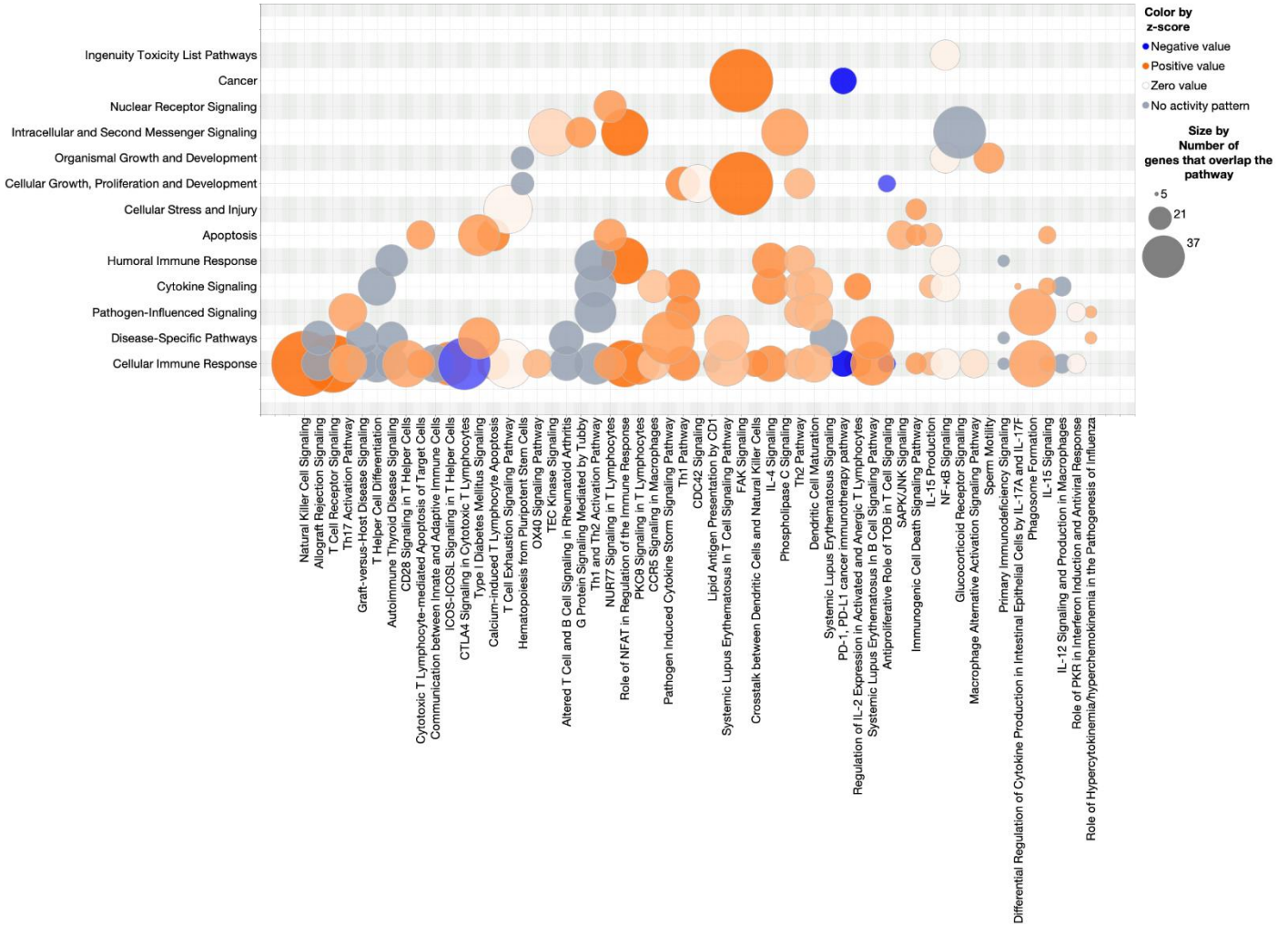
最顯著的路徑位於 x 軸的左側，並且在該路徑大部分被活化，並且與數據集重疊的基因數量最多（如氣泡大小所示）。



圖一、利用路徑名稱與顯著性繪製的 Nrf2 活化子 Canonical Pathway。

顏色表示 z-score（參見右上角的圖例），氣泡的大小隨著重疊基因的數量而增加。因此，圖表左側的大橙色氣泡表示具有統計顯著性、預測會被活化並且與數據集有許多重疊基因的路徑。

還有其他方法可以繪製泡泡圖，例如，您可以繪製一個強調路徑分類的泡泡圖（參見圖二）。

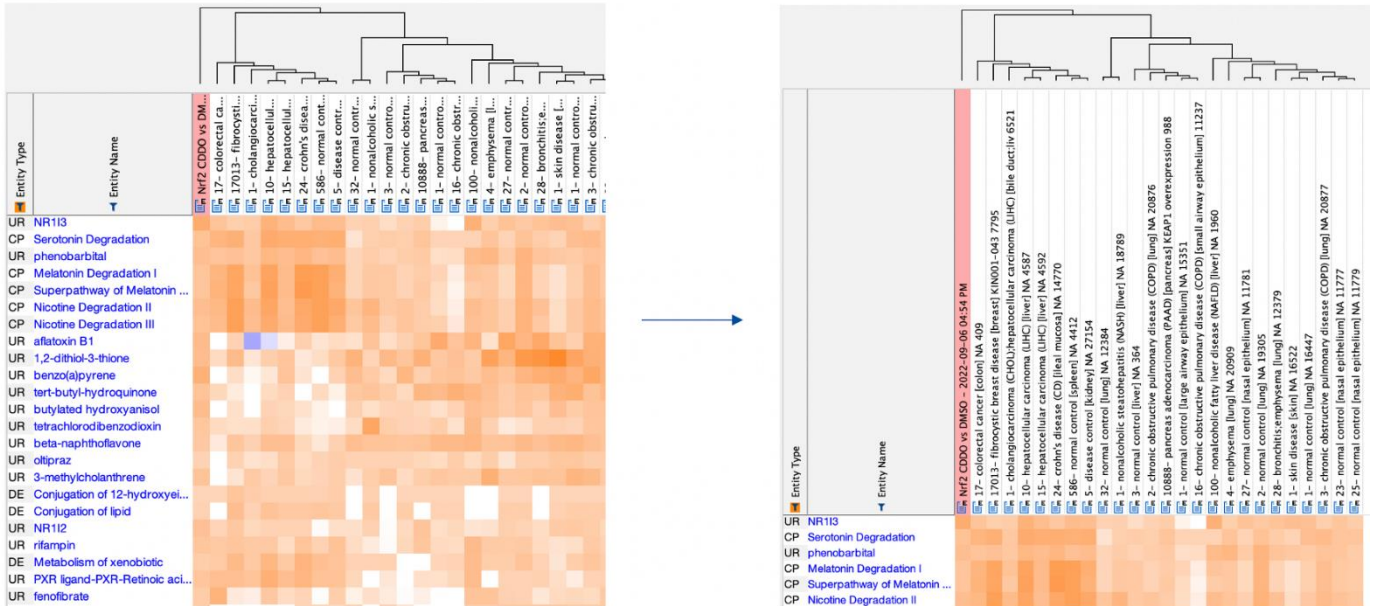


圖二、利用路徑名稱與路徑類別繪製單細胞數據的 Canonical Pathway。

此泡泡圖可幫助您了解路徑及其分數如何歸類到不同類別中。分析的數據來自發育中的人類肝臟的自然殺手 (NK) 細胞群。如圖例 (右上角) 中所列，氣泡根據 z-score 著色，氣泡大小根據  $-\log(p\text{-value})$ ，其中最大的氣泡具有最顯著的分數。例如，左下角的自然殺傷細胞信號傳遞路徑和 T 細胞受體信號傳遞路徑預測會在這些 NK 細胞中被活化。這些路徑被歸類在細胞免疫反應類別 (如 y 軸所示)。

## 2. 改善了 Comparison Analysis heatmaps 中分析名稱的顯示

您現在可以切換熱圖中標題的高度以顯示完整的分析名稱，如圖三所示。較高的標題也出現在匯出的圖片中。



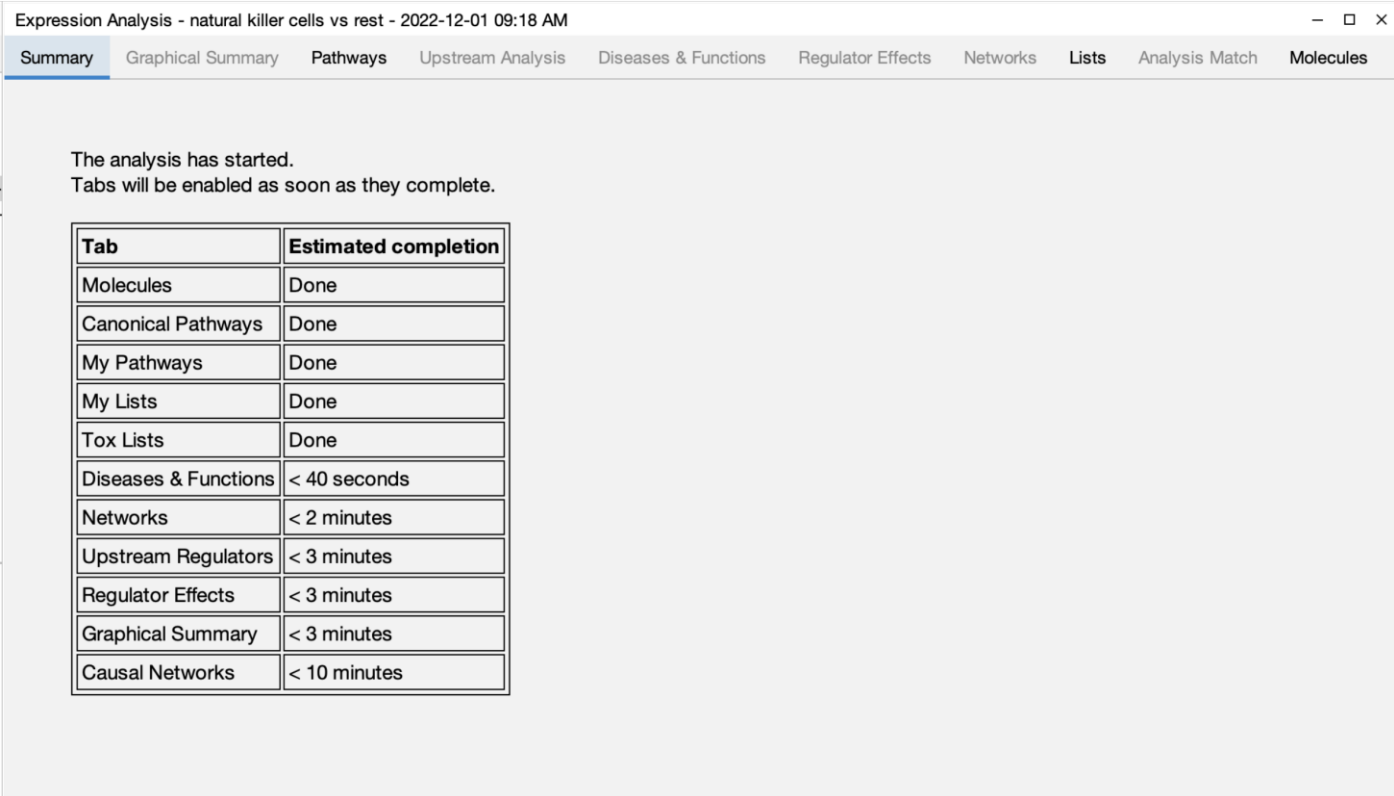
圖三、展開熱圖中的標題以查看完整的分析名稱。

此功能適用於 Comparison Analysis heatmaps 和 Analysis Match heatmaps。

## QIAGEN IPA Fall Release (2022 冬季更新)

### 3. 更快查看 Core Analysis 的結果

現在您可以在 Core Analysis 開始處理後立即打開它並在分析結果可開啟時立即查看。當數據進行 Core Analysis 分析後，就可以馬上在 Project Manager 點擊查看。如果分析的圖標有一個時鐘(🕒)，則表示該分析正在排隊等待處理，並且當您打開它時，您會看到它在排隊中的位置。一旦開始分析，圖標會逐漸充滿綠色(🟢)表示完成進度。這時會出現單獨的分析分頁，例如 Canonical Pathways 等等，一旦完成分析，這些分頁名稱將會從灰色字體變成黑色字體。這時就可以開始查看您的分析結果。



Expression Analysis - natural killer cells vs rest - 2022-12-01 09:18 AM

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

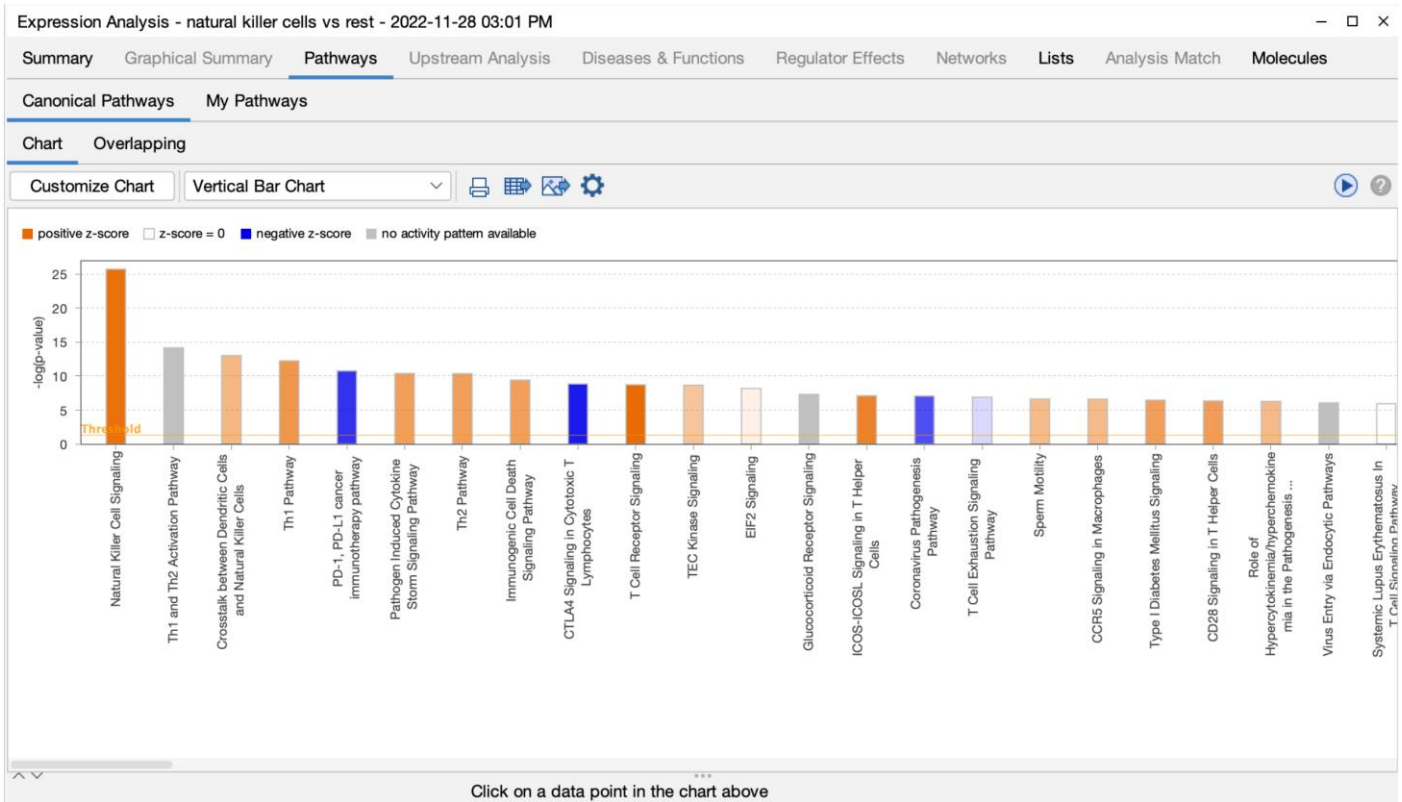
The analysis has started.  
Tabs will be enabled as soon as they complete.

Tab	Estimated completion
Molecules	Done
Canonical Pathways	Done
My Pathways	Done
My Lists	Done
Tox Lists	Done
Diseases & Functions	< 40 seconds
Networks	< 2 minutes
Upstream Regulators	< 3 minutes
Regulator Effects	< 3 minutes
Graphical Summary	< 3 minutes
Causal Networks	< 10 minutes

圖四、在 Core Analysis 正在分析中時立即查看結果。

上排不同的分析分頁顯示它們目前的狀態。分析完成後會由灰色字體變為黑色字體。



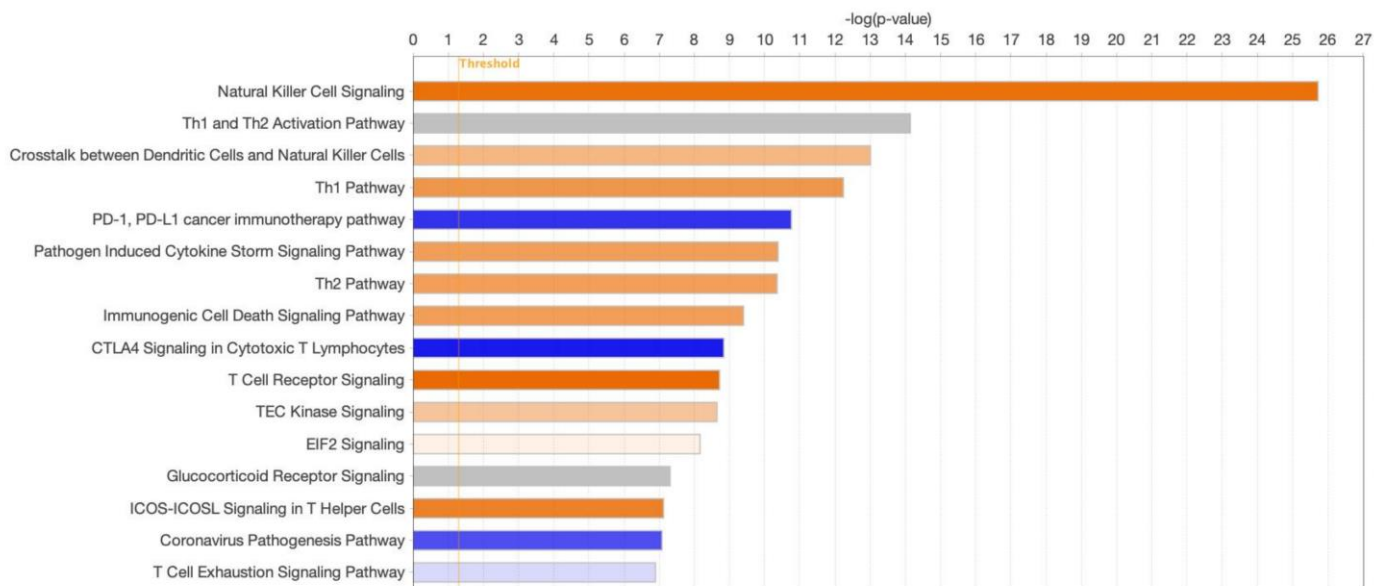


圖五、完成分析的 Core Analysis 分頁。

可以立即查看已分析好的分頁資訊，即使其他分頁的分析還沒完成(呈現灰色字體)。

#### 4. 改善了水平直條圖以用於發表

期刊發表更喜歡數據的緊密呈現以節省期刊中的頁面空間。現在，當直條圖以水平方向呈現時，直條的間隔顯示得更緊密，如圖六所示。



圖六、水平直條圖的新緊密呈現。

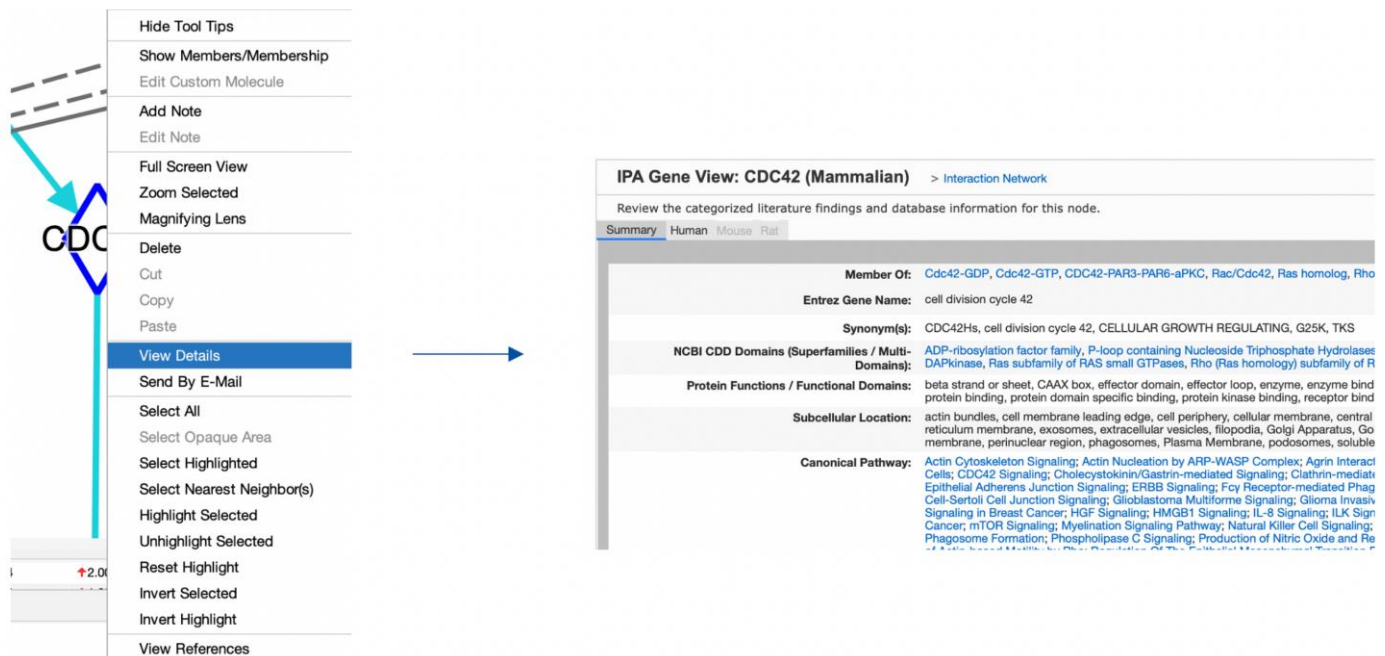
## 5. Core Analysis 分頁的節省空間排列

在此版本中，Core Analysis 中的某些分頁已得到整合，更加直觀和節省空間。Canonical Pathways 分頁和 My Pathways 分頁已作為子分頁匯集到一個新的“Pathways”分頁，Molecules 分頁已移至最右側。現在在預設的情況下不需要放大就可以看到所有的 Core Analysis 分頁。

## 6. 更快地從網絡圖和路徑圖連結至 Gene Views, Chem Views, and Disease

### Views

現在您可以右鍵點擊路徑圖或網絡圖中的任何節點以查看其相應的 Gene Views, Chem Views, and Disease Views 網頁。圖七顯示了右鍵點擊基因節點並選擇“View Details”。這將在您的預設網絡瀏覽器中顯示其 Gene View 頁面。



圖七、右鍵點擊網路圖或路徑圖中的節點以查看基因、化學物、疾病或功能的詳細資訊。

## 7. 資料庫更新

### New pathways

- Chaperone Mediated Autophagy Signaling Pathway
- IL-33 Signaling Pathway
- Myelination Signaling Pathway
- NOD1/2 Signaling Pathway

### Existing pathways updated to include an activity pattern

- Adipogenesis pathway
- Chronic Myeloid Leukemia Signaling
- IL-12 Signaling and Production in Macrophages
- Mitochondrial Dysfunction

### Addition of ~120,000 new findings (bringing the total in IPA to over 12 million)

~96,000 Expert findings ~10,000 protein-protein interaction findings from BioGrid

~8,000 cancer mutation findings from ClinVar

~4,000 Gene Ontology findings

~1,200 target-to-disease findings from ClinicalTrials.gov

~1,200 drug-to-disease findings from ClinicalTrials.gov

~150 gene to disease or phenotype associations from the Mouse Genome Database (MGD or "Jax")

~200 newly mappable chemicals

### Identifier mapping support added for two new species

- Atlantic Salmon (*Salmo salar*)
- Sheep (*Ovis aries*)

### 124,927 expression datasets will be available in early January 2023 (3,177 added)

Land	Repository	Datasets Q3 2022	Datasets Q4 2022	Increase
DiseaseLand	HumanDisease	31,041	32,092	1,051
	MouseDisease	24,411	24,506	95
	RatDisease	7,900	7,900	
	LINCS	28,234	28,234	
OncoLand	OncoHuman (Formerly OncoGEO)	13,360	14,131	771
	OncoMouse	1,054	1,054	
	TCGA	4,438	4,438	
	MetastaticCancer	81	81	
	Hematology	4,267	4,267	
	Pediatrics	444	444	
	ENCODE RNA Binding	486	486	
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	2056	2056	
	SingleCellHumanUmiLite	603	603	
	SingleCellHumanHCL	1,476	1,476	
	SingleCellMouse	81	81	
	SingleCellMouseUmi	1,457	1,457	
	SingleCellMouseUmiLite	115	115	
Normal Cells and Tissues	Human Tissues (GTEx)	52	1,312	1,260

## Breakdown of the OmicSoft datasets by Land (early January 2023)

DiseaseLand	OncoLand	Mouse Single Cell Land	Human Single Cell Land	Normal Cells & Tissues
<b>HumanDisease (32,092)</b> <ul style="list-style-type: none"> <li>684 diseases</li> <li>378 tissues</li> <li>76 expression platforms</li> <li>10,267 RNA-seq datasets</li> </ul>	<b>OncoHuman (14,131)</b> <ul style="list-style-type: none"> <li>245 cancer types</li> <li>117 tissues</li> <li>63 expression platforms</li> <li>4,880 RNA-seq datasets</li> </ul>	<b>SingleCellMouse (81)</b> <ul style="list-style-type: none"> <li>143 cluster cell types</li> <li>7 diseases</li> <li>15 tissues</li> <li>8 projects</li> </ul>	<b>SingleCellHuman (194)</b> <ul style="list-style-type: none"> <li>67 cluster cell types</li> <li>23 diseases</li> <li>22 tissues</li> <li>24 projects</li> </ul>	<b>GTEX (1,312)</b> <ul style="list-style-type: none"> <li>52 tissues</li> <li>Comparisons of <ul style="list-style-type: none"> <li>Age and gender</li> <li>Single tissue vs others</li> <li>Subtissues in same tissue</li> </ul> </li> </ul>
<b>MouseDisease (24,506)</b> <ul style="list-style-type: none"> <li>410 diseases</li> <li>300 tissues</li> <li>57 expression platforms</li> <li>12,828 RNA-seq datasets</li> </ul>	<b>TCGA (4,438)</b> <ul style="list-style-type: none"> <li>33 cancer types</li> <li>27 tissues</li> <li>366 different mut. statuses / clinical signs</li> </ul>	<b>SingleCellMouseUmi (1,457)</b> <ul style="list-style-type: none"> <li>194 cluster cell types</li> <li>15 diseases</li> <li>144 tissues</li> <li>28 projects</li> </ul>	<b>SingleCellHumanUmi (2,056)</b> <ul style="list-style-type: none"> <li>217 cluster cell types</li> <li>106 diseases</li> <li>136 tissues</li> <li>70 projects</li> </ul>	
<b>RatDisease (7,900)</b> <ul style="list-style-type: none"> <li>58 diseases</li> <li>86 tissues</li> <li>1,927 RNA-seq datasets</li> </ul>	<b>OncoMouse (1,054)</b> <ul style="list-style-type: none"> <li>49 cancer types</li> <li>37 tissues</li> <li>21 expression platforms</li> <li>351 RNA-seq datasets</li> </ul>	<b>SingleCellTypeUmiLite (115)</b> <ul style="list-style-type: none"> <li>14 cluster cell types</li> <li>(normal tissues, non diseased)</li> <li>9 tissues</li> <li>1 project</li> </ul>	<b>SingleCellHumanUmiLite (603)</b> <ul style="list-style-type: none"> <li>175 cluster cell types</li> <li>1 disease</li> <li>28 tissues</li> <li>3 projects (includes Tabula Sapiens)</li> </ul>	
<b>LINCS (28,234)</b> <ul style="list-style-type: none"> <li>23 cell lines</li> <li>374 chemical treatments or gene overexpression</li> <li>226 different targets (or groups of target genes)</li> </ul>	<b>Hematology (4,267)</b> <ul style="list-style-type: none"> <li>66 cancer types</li> <li>20 tissue types</li> <li>99 cell types</li> <li>1,148 RNA-seq datasets</li> </ul>		<b>SingleCellHumanHCL (1,476)</b> <ul style="list-style-type: none"> <li>16 diseases</li> <li>56 tissues</li> </ul>	
	<b>Pediatrics (444)</b> <ul style="list-style-type: none"> <li>47 cancers</li> <li>23 tissues</li> </ul>			
	<b>Metastatic Cancer (81)</b> <ul style="list-style-type: none"> <li>27 cancer types</li> <li>18 tissues</li> </ul>			
	<b>ENCODE RNA Binding (486)</b> <ul style="list-style-type: none"> <li>2 cell lines</li> <li>261 shRNA treatments</li> </ul>			

## Gene model source versions

Hg38/mm38	
Ensembl Human	Homo_sapiens.GRCh38.106.gff.gz
Ensembl Mouse	Mus_musculus.GRCm38.106.gff.gz
RefSeq human	GCF_000001405.39_GRCh38.p13
RefSeq mouse	GCF_000001635.25_GRCm38.p4
Hg19/mm10 from UCSC	
Ensembl Human	April 7 <sup>th</sup> , 2014 (/usr/local/idm/instances/ci/data/download/ucsc/store/19_/ensGene.txt.gz)
Ensembl Mouse	Feb 6 <sup>th</sup> , 2019
RefSeq Human	Aug 28 <sup>th</sup> , 2019
RefSeq Mouse	Aug 28 <sup>th</sup> , 2019



## Version and/or date of third-party databases (update until 2022/12/20)

Source name	Latest version number, download date, or Knowledge Base import date
An Open Access Database of Genome-wide Association Results	February-2009
APPRIS	human, refseq: rs109_v46 (February 22, 2022) human, ensembl: GRCh38 (August 3, 2022) mouse, refseq: rs106v29 (February 22, 2022) mouse, ensembl: GRCm39 (August 3, 2022)
BIND	December-2008
BioGRID	Version 4.4.214, October 6, 2022
Chemical Carcinogenesis Research Information System (CCRIS)	October-2006
Clinical Trials	October 25, 2022
ClinGen	April 17, 2022
ClinVar	October 14, 2022
Cognia	October 11, 2007
Conserved Domain Database	Version 3.2, September 20, 2022
COSMIC	Version 95
DIP	October 14, 2008
DrugBank	April 27, 2016
Entrez Gene	February 22, 2022
Gene Ontology (GO)	October 16, 2022
GVK Biosciences	September 31, 2017
Hazardous Substances Data Bank (HSDB)	April 2007
HUGO Gene Nomenclature Committee (HGNC)	August 30, 2022
Human Metabolome Database (HMDB)	v5.0, October 2021
Human Phenotype Ontology (HPO)	October 20, 2022
HumanCyc	Version 16.0, February-2012
IntAct	October 6, 2022
Interactome studies	2008
MGI gene IDs	August 30, 2022
MIPS	April 2008
miRBase	September 22, 2018
miRecords	April 8, 2011
Mouse Genome Database (MGD)	October 17, 2022
NCI Thesaurus	October 5, 2022
Obesity Gene Map Database	December 2006
OncoTree	oncotree_2019_03_01
Online Mendelian Inheritance in Man (OMIM)	October 5, 2022
Orphanet	May 7, 2019
PubChem	July 13, 2022
TarBase	September 18, 2011
TargetScan Human	Version 8.0, September 2022
TargetScan Mouse	Version 8.0, September 2022
The Human Protein Atlas (THPA)	20.1

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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