

AI-assisted data analysis for target-biomarker discovery and mechanistic insights

Omics data mining without bioinformatics expertise

MetaDB

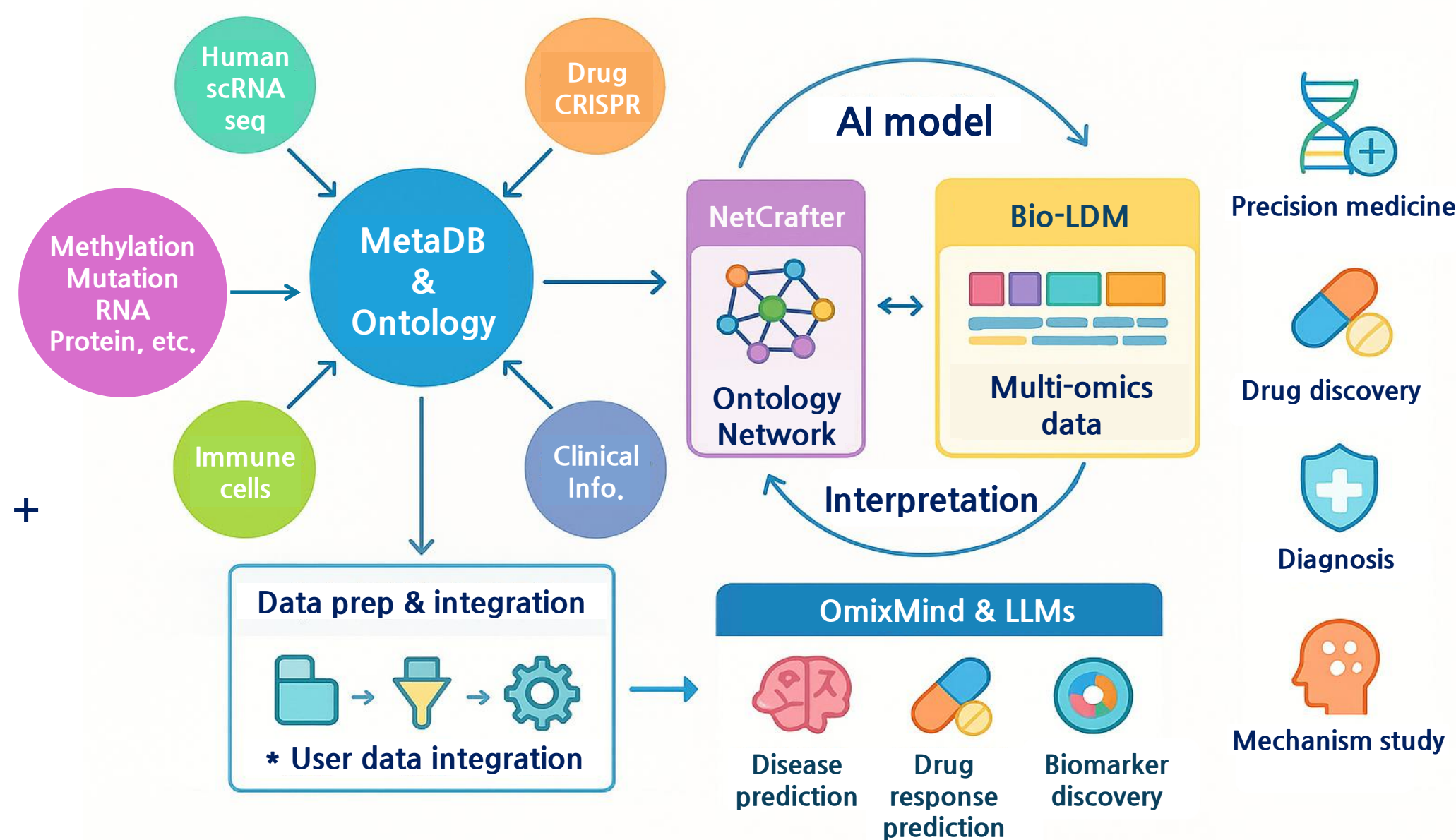
Over 1 billion multi-omics data point
30 billion cross-associations reinforced by consensus scores.

Bio-LDM (Biological Large Data Model)

A breakthrough AI model trained on NetCrafter knowledge graphs (Omics data + Ontology), discovers **hidden gene-gene interaction** and **mechanisms**.

OmixMind & LLMs

Text-to-Data mining automatically generating research trends, data analysis workflows and interpretations from natural-language queries.



Meta DB prioritizes reproducible targets and biomarkers

- ✓ **Consensus scoring** on >30 billion associated data pairs in **MetaDB** → **Reliable targets and biomarkers across lineages and subtypes**

Lineage and sampling consensus analysis of PD-1 expression associated with patient survival

• PD-1 expression was significantly associated with patient survival in 28 of 34 TCGA cancer types (p-values < 0.001). Each lineage's result is itself backed by many sampling conditions.

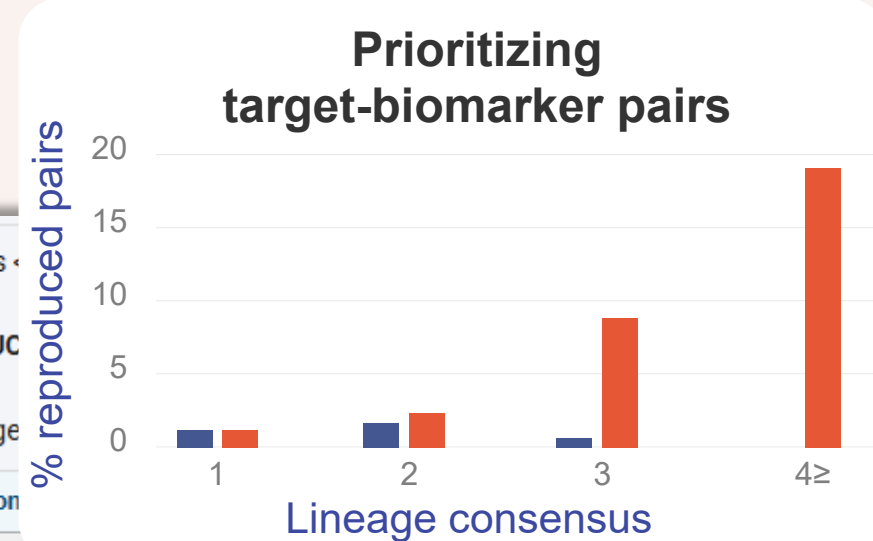
• Higher PD-1 was favorable across these lineages, holding up best in SKCM (135 of 216 conditions), then UCEC 92 and UVM at 88.

Next step: Open the Consensus view to see where the signal holds, or draw a Kaplan-Meier plot for a specific gene.

Lineage	Measure	Sample split	Gender	Stage	Period	AUC ...	AUC ...	p-value	Sampling con
SKCM ...	OS	Median	All	All	Extend...	0.433	0.260	< 0.001	135
UCEC (...)	DFS	Median	All	All	Extend...	0.756	0.507	< 0.001	92
UVM (...)	OS	Median	All	All	Extend...	0.424	0.759	< 0.001	88
HNSC ...	DFS	Median	Male	All	Extend...	0.464	0.261	< 0.001	74
KIRP (...)	OS	Quartile	All	All	Extend...	0.591	0.836	0.001	61
STAD (...)	OS	Quartile	All	III,IV	Extend...	0.609	0.203	0.007	58
LGG (B...)	OS	Median	All	All	Extend...	0.380	0.508	< 0.001	51
LAML (...)	DFS	Tertile	All	All	3-year	0.430	0.730	< 0.001	40
CESC (...)	OS	Tertile	All	All	5-year	0.870	0.721	0.004	32
KIRC (...)	DFS	Quartile	All	All	5-year	0.750	0.855	0.005	32

Hit selection: p-values < 0.05 & min. sample number = 11
What is AUC (Area Under Curve)?

[Kaplan Meier plot](#) [Consensus samplings](#)



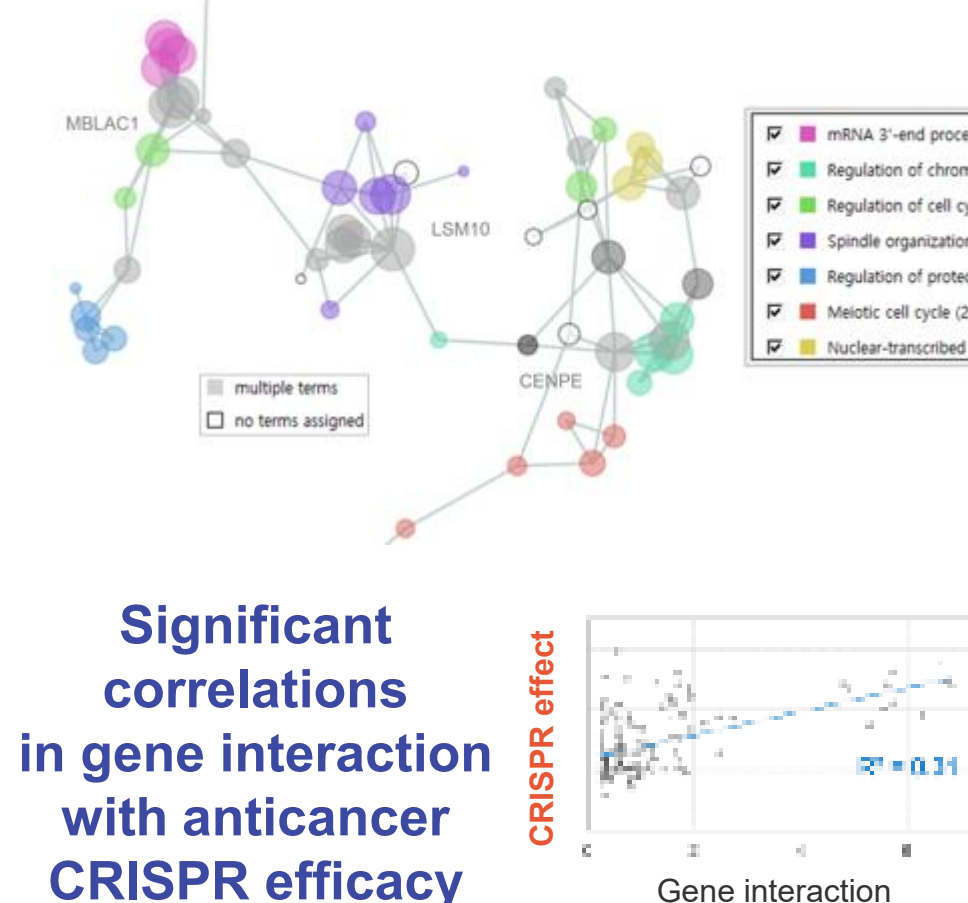
Lineage consensus of associations between **CRISPR** efficacy and RNA expression

→ Gene pairs with high consensus showed stronger reproducibility in independent shRNA screens.

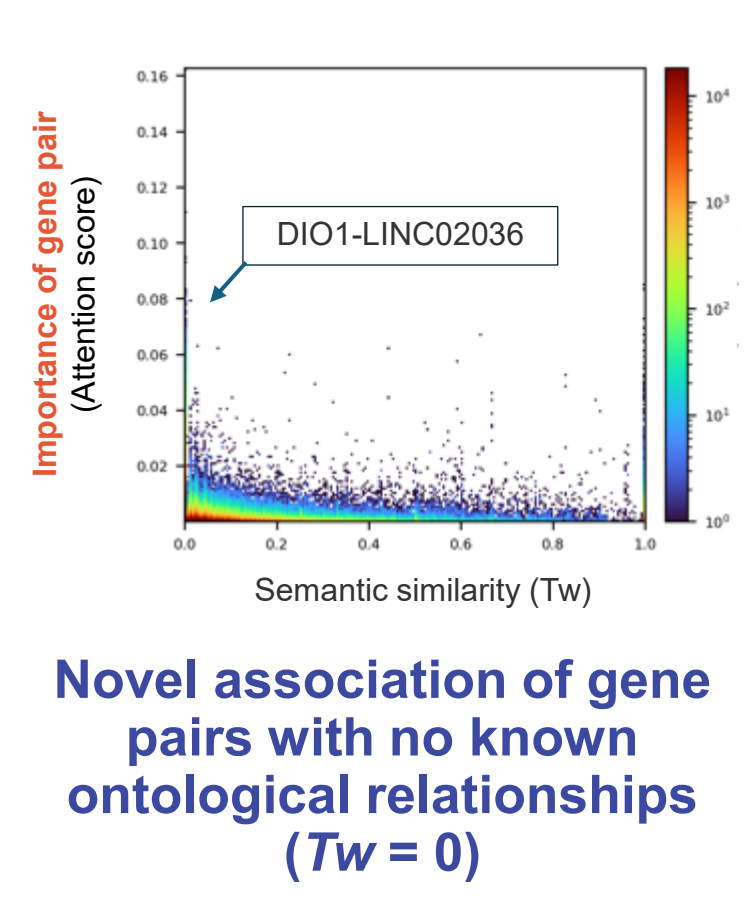
AI interprets omics data

- ✓ **NetCrafter**: Ontology-derived sample-specific gene network modeling
- ✓ **Bio-LDM**: Novel foundation model for predicting hotspots and gene-gene interactions

Predicting anticancer hotspots (targets)



Predicting tumor-specific gene-gene interaction



Text-to-Data mining

Executable Insights

User query: **synthetic lethal gene pairs**

Research digest - Essential findings & trends from recent literature

AI-assisted Research Summary

Keywords: Knowledge graphs, Graph neural networks, Transcriptomic buffering, Multi-omics integration, Genetic dependency

Summary: Advanced computational models, particularly knowledge graph-based neural networks and multi-omics integration, have revealed potential synthetic lethal vulnerabilities specific to BRCA1-deficient breast cancers. These candidate dependencies are consensus-validated within the breast cancer lineage to ensure technical reproducibility across various cell line sampling conditions.

Sample split: Median, Tertile, Quartile

Group 1: # samples: 37, Low (<25%) expression of PSMC3IP

Group 2: # samples: 52, Low (<25%) expression of PSMC3IP

Group 3: # samples: 93, Low (<25%) expression of PSMC3IP

Survival rate (DFS) vs Months

Survival - OS, expression

Survival - OS, mutation

Tumor vs normal - mRNA

Drug: paclitaxel (mut)

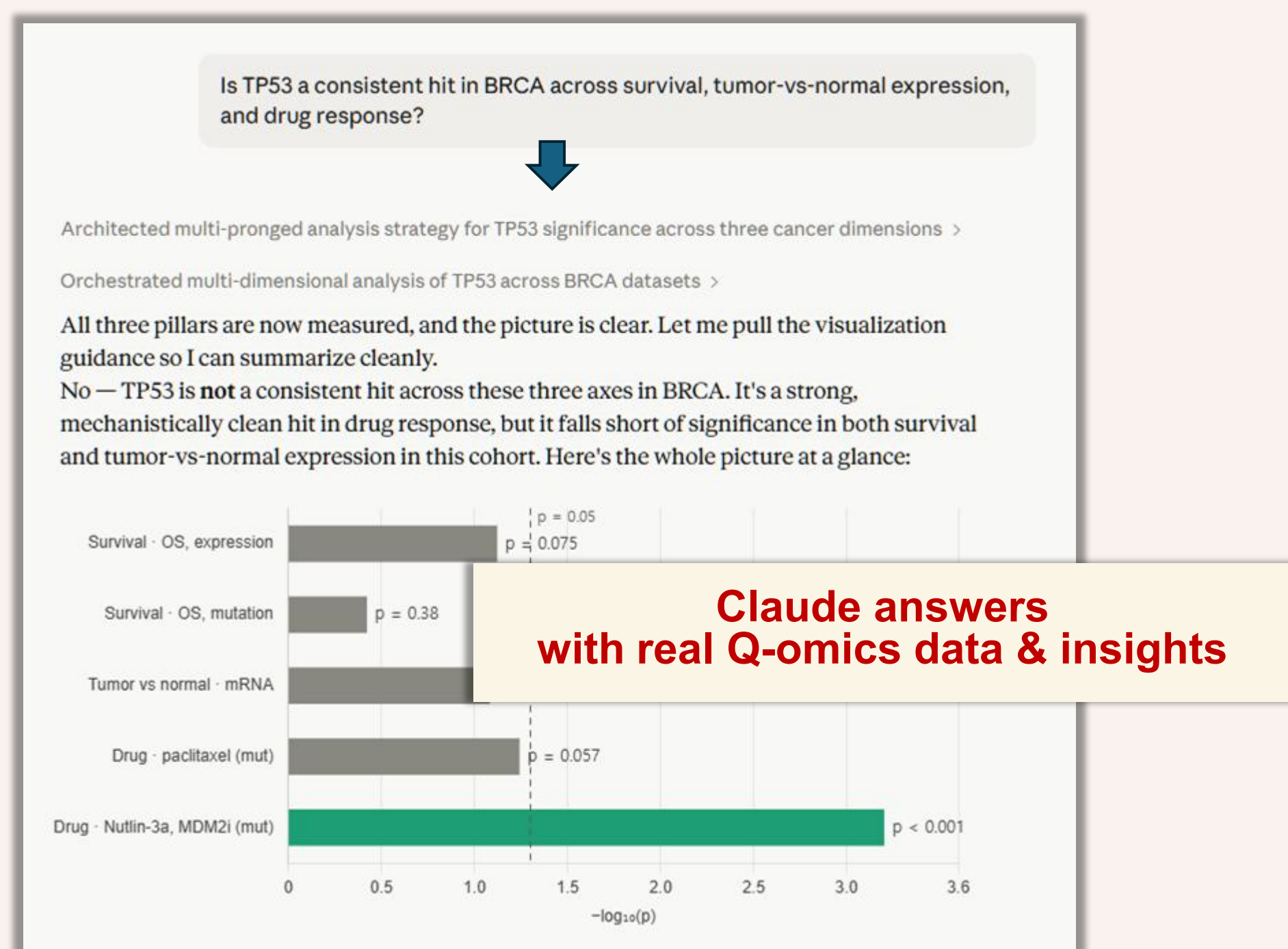
Drug: Nutlin-3a, MDM2i (mut)

Data mining & explanation

This box plot compares CIP2A abundance between normal and tumor tissue in BRCA. Abundance was measured in 111 normal and 111 tumor samples and compared by t-test. CIP2A abundance was significantly higher in tumor tissue than in normal tissue, with a log2 fold-change of 1.39 ($p < 0.001$).

Connect LLMs with Q-omics

Your AI agents for research & drug discovery pipelines



Diverse applications including:

- Drug target and biomarker discovery
- Functional interpretation for underlying mechanisms and disease phenotypes
- Biomarkers in immunotherapy response
- Synthetic lethal gene pairs
- Tumor- antigen discovery
- Undruggable targets and new modalities in drug discovery
- AI-assisted analysis of user data

Availability & Collaboration

- Explore Q-omics **SaaS** at <https://qomics.ai>, AWS Cloud and via **MCP** on **Claude** and **ChatGPT**
- For collaboration, we offer partner-specific **Evident Sprint**, **cloud/API integration** and confidential **PoC** options