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Olink Explore HT

Capture true biological insights with proven specificity. At any scale.

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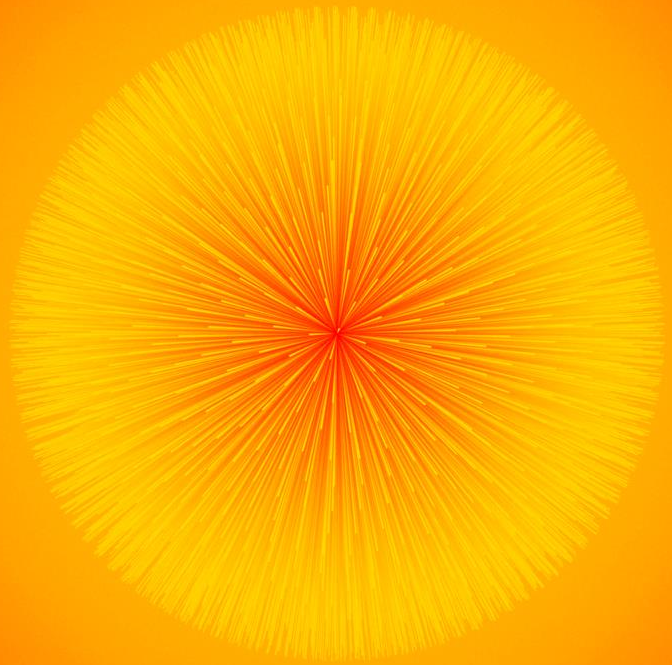

Olink Explore HT

5,400+ protein biomarkers

- Increased library
- Simplified workflow
- Higher throughput
- Automated data processing

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Unprecedented power

Explore thousands of proteins with high specificity, minimal sample consumption, and user-friendly data tools for projects of any size

Proteins

5,400+

with proven specificity

Sample

2 µL

Plasma, serum & more

Throughput

4x

Increase

Dynamic range

fg-mg/mL

10 logs

Runs on

NGS

Automated workflow

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Measure proteins with confidence, obtaining reproducible results

Mean intra-CV
(within run)

<11%

Mean inter-CV
(between runs)

<9%

Per-assay correlation coefficient (R)
between Olink Explore 3072 and Olink Explore HT

0.88 median

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Components

6x fewer

saves time and resources

Boxes

10x fewer

benefits the environment and saves freezer space

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Significant workflow cost savings

~20%
reduction in workflow cost per sample

4x
reduction in labor cost

4x
reduction in consumables cost

Compared to Olink Explore 3072. The exact cost reduction varies depending on the labor cost.

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80% more data at same sequencing cost/sample

Runs on Illumina® NovaSeq 6000

344 biological samples per run (two S4 flow cells)

Compared to Olink Explore 3072

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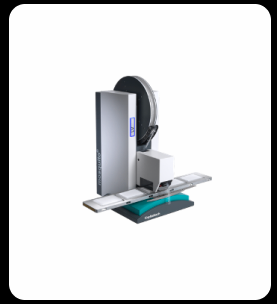
Re-imagine your workflow, not your lab

No new instrumentation required

dragonfly® discovery
SPT Labtech

F.A.S.T.
FORMULATRIX®

or



mosquito® LV
SPT Labtech

Microlab STAR
Hamilton

or

epMotion® 5075lc
Eppendorf®

Compared to Olink Explore 3072

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Flexible access to high-quality data via kits and services

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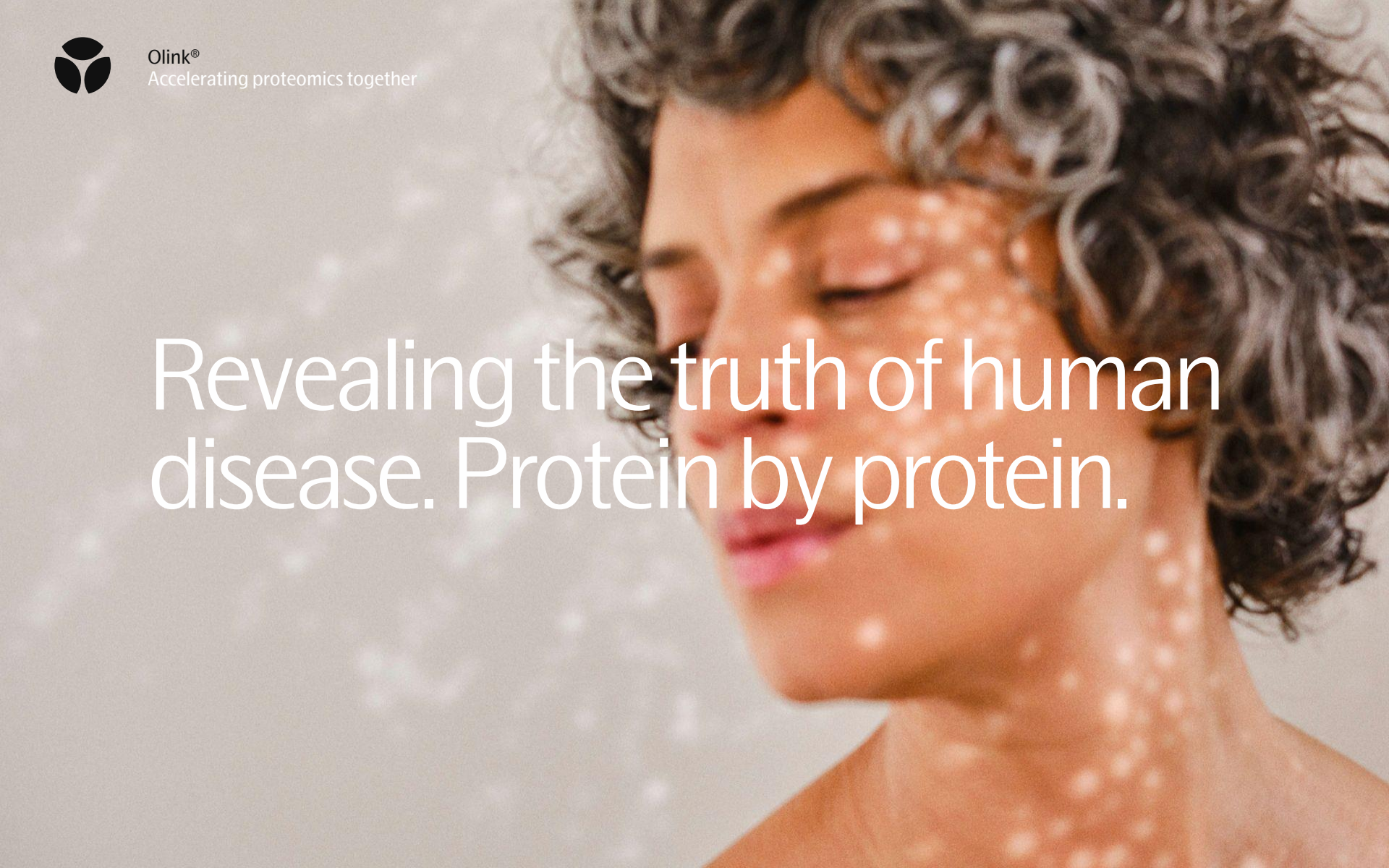

Revealing the truth of human disease. Protein by protein.

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Protein profiling of ovarian cancer with Olink Explore HT

Background

Unmet need: Accurate early diagnosis of ovarian cancer (OvCa)

Study design: Profile plasma proteins in women with OvCa or benign ovarian tumors using Olink Explore HT and its predecessor, Olink Explore 3072

Study objectives:

1) Validate Olink Explore HT's performance by comparing it to Olink Explore 3072
2) Investigate the potential of Olink Explore HT to identify a novel OvCa protein signature for more precise diagnostic tests

Ulf Gyllensten, PhD
Professor
Dept of Immunology, Genetics, & Pathology
Uppsala University, Sweden

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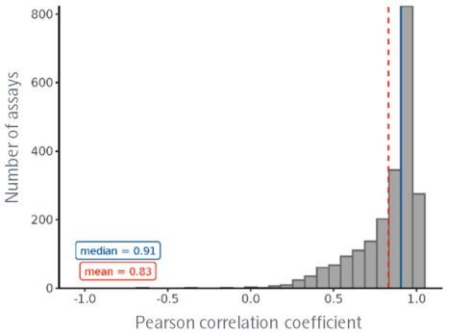
Expanded proteome coverage without compromising performance

Technical performance

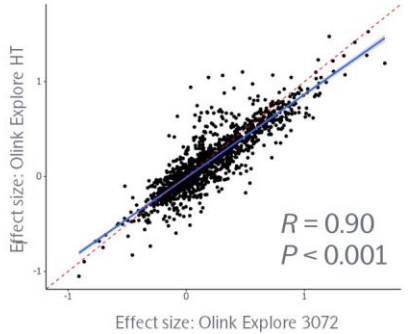
Compared data from ~2,800 overlapping assays between Olink Explore HT and Olink Explore 3072

Achieved expanded proteome coverage while retaining high data quality

Correlation of Normalized Protein eXpression units (NPX)



Correlation of ΔNPX (effect size) between benign & OvCa groups



Correlation across ~2800 overlapping assays measured by Olink Explore HT and Olink Explore 3072. In the right figure, each data point represents a protein biomarker.

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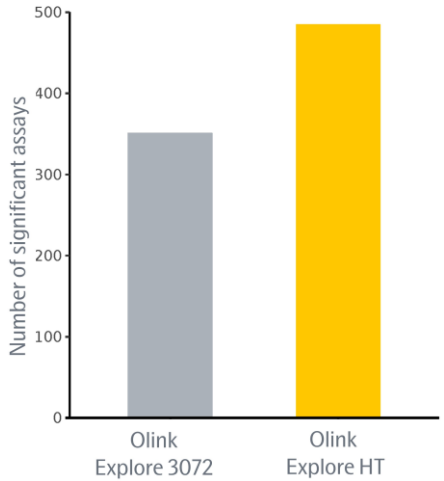
Expanded coverage yields a significant enrichment of OvCa biomarkers

OvCa-associated proteins

485 proteins biomarkers identified (Discovery Cohort, n=233)

128 biomarkers replicated (Validation Cohort, n =171)



OvCa biomarkers identified in the discovery cohort with Olink Explore platforms

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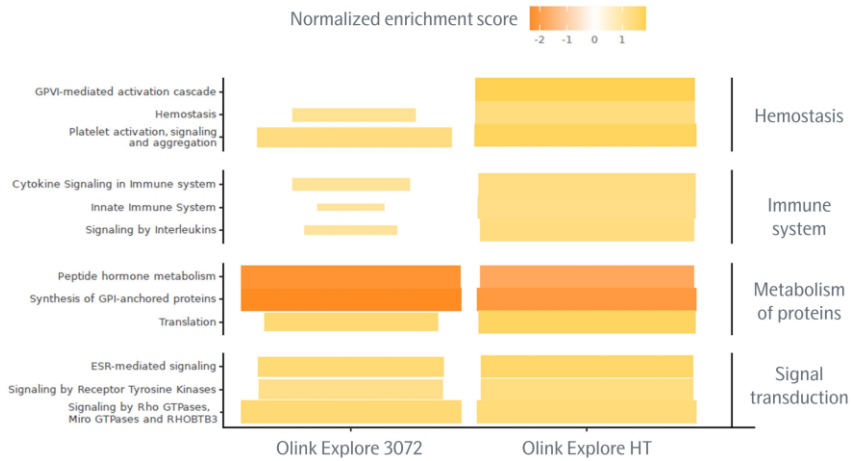
Increased confidence in biological insights with deeper pathway coverage

Pathway analysis

Higher statistical significance obtained for multiple biological pathways*, providing greater confidence in disease insights.

* Reactome database, https://reactome.org



Snippet from gene set enrichment analysis.

Color indicates direction of pathway alterations; color intensity indicates strength of alterations; size of each tile indicates statistical significance

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Revealed a novel protein signature that outperformed clinical biomarker

Diagnostic model

Preliminary 19-protein model identified with Olink Explore HT discriminated OvCa from benign samples better than the clinical marker MUC16

3 of these proteins were newly added to the Olink library

Prediction	Signature	Correctly diagnosed
Benign	MUC16	79.1% (68/86)
	19-protein	89.5% (77/86)
OvCa	MUC16	81.2% (69/85)
	19-protein	84.7% (72/85)

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Olink Explore HT: Biomarker discovery with high data quality, throughput, & coverage

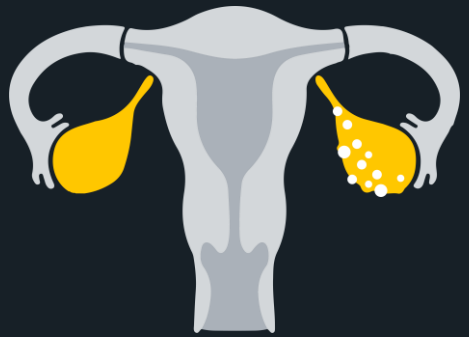
Conclusions

High-quality data, yielding similar results as Olink Explore 3072

Expanded proteome coverage, enabling the discovery of additional OvCa biomarkers

Deeper pathway coverage, enhancing statistical confidence in pathway analysis

Superior multi-protein signature than current biomarker, paving the way for improved early OvCa diagnosis



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Protein profiling of cell lysate using Olink Explore HT

Study objectives

1. Evaluate data correlation between Olink Explore HT and its predecessor, Olink Explore 3072
2. Verify the biological relevance of data acquired with Olink Explore HT by comparing protein profiles across different tissues and cancers

Rationale

Cell culture is an excellent model to study biology

Samples

164 cell culture lysate samples: 45 cancers & 22 tissues *

Study performed by the Broad Institute (Cambridge, MA; USA). * Cancer Dependency Map Cell Lysate Project (DepMap), target-discovery.depmap.org

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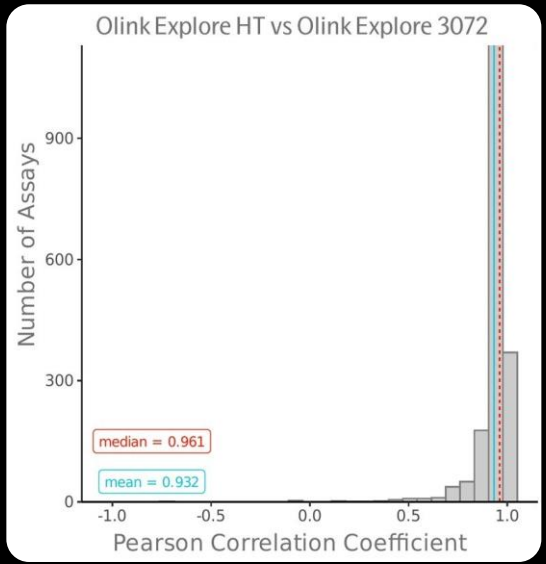
Excellent correlation across Olink Explore platforms with cell lysate

Technical performance

Compared data between Olink Explore HT and Olink Explore 3072

Analyzed ~2,800 overlapping assays across 28 samples at 3 dilutions (1:1, 1:10, 1:100)

Median correlation coefficient (R) = 0.96



Correlation of overlapping protein assays across all sample dilutions of cell lysate measured with Olink Explore HT and Olink Explore 3072

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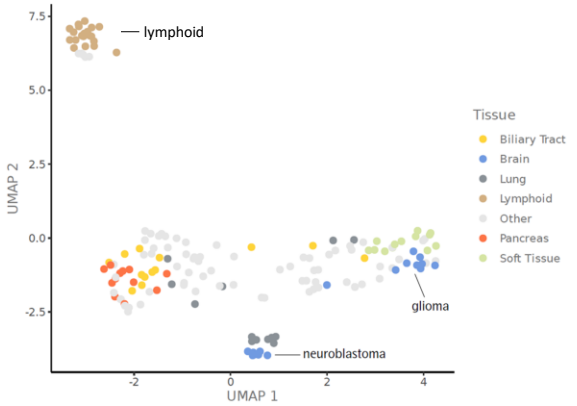
Cellular protein profiles accurately reflect tissue- & disease-specific biology (1/2)

UMAP analysis of tissue proteomes

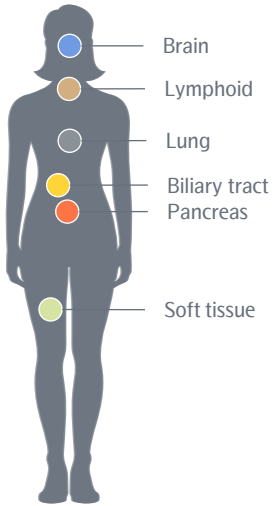
Protein profiles form tissue-specific clusters

Different brain tumors clustered separately

Lymphoid tumors clustered separately from other tissue types



UMAP analysis of Olink Explore HT data. Like PCA analysis, UMAP is a dimensionality reduction method to visualize complex data.



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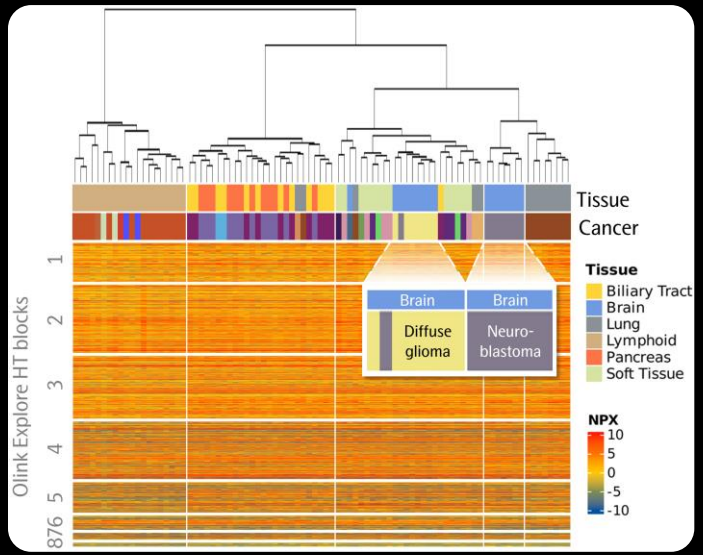
Cellular protein profiles accurately reflect tissue- & disease-specific biology (2/2)

Hierarchical clustering

6 tissues represented with at least 10 samples included in analysis

Distinct clustering of protein profiles demonstrates tissue and disease discrimination at the cellular level



Hierarchical clustering heatmap of protein profiles from cell cultures representing different tissues and cancers. NPX = Normalized Protein eXpression

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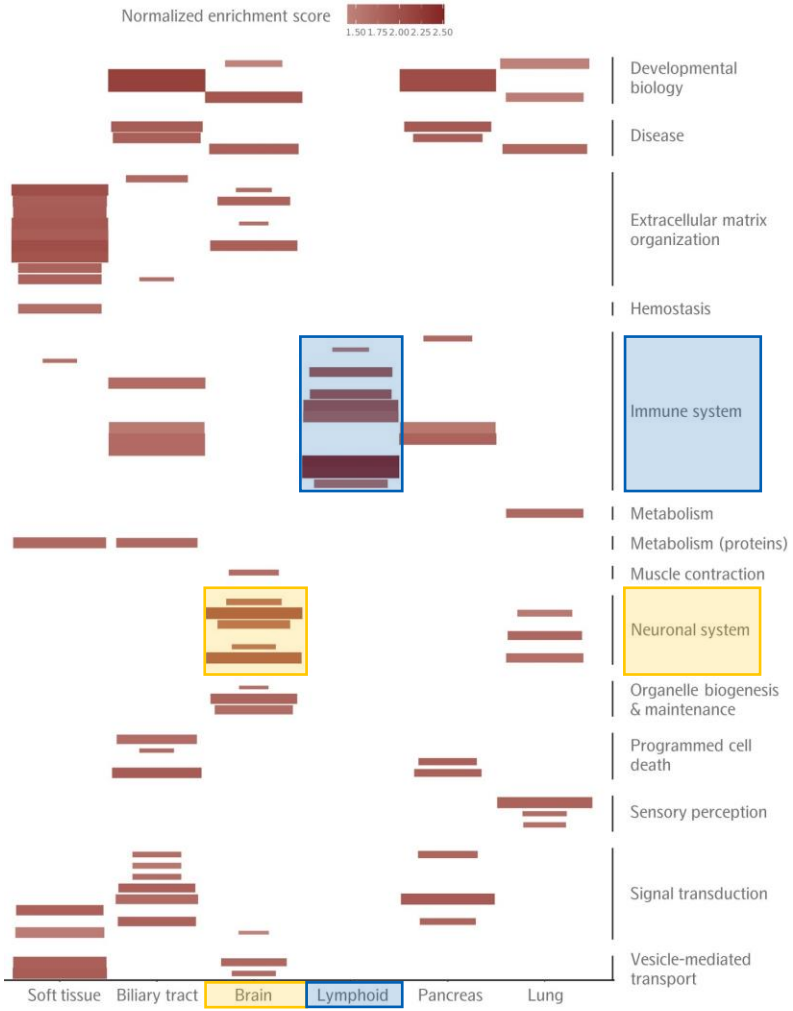
Enriched pathways represent biology of the tissue-of-origin

Pathway analysis

Cellular protein profiles reflect tissue-specific biological pathways

Example: Brain tissue is enriched in neuronal system pathways (yellow), whereas the lymphoid is enriched in immune system pathways (blue)



Enriched pathways for tissue-enriched assays. Color intensity indicates strength of alterations; size of each tile indicates statistical significance.

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Olink Explore HT: A powerful tool to reveal true biological insights

Conclusions

Ensures uncompromised performance, maintaining the same high-quality data as its predecessor

Offers versatile capabilities, enabling high-throughput protein profiling across a wide range of sample types

Facilitates accurate protein measurements, promoting a deeper biological understanding to advance biomarker discovery and drug development