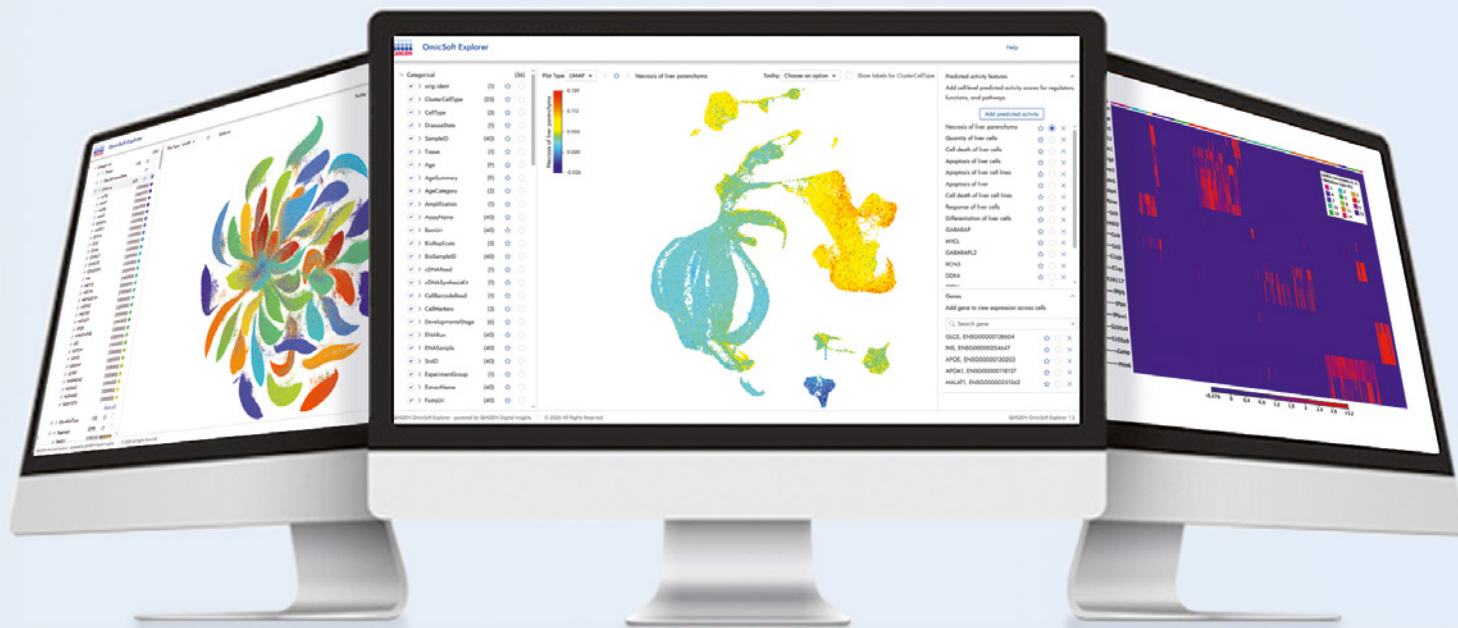




QIAGEN Digital Insights

Single-cell expression analysis for biologists



Turn complexity into clarity

Single-cell experiments generate unprecedented resolution – but also overwhelming complexity.

While open-source tools are powerful, they're often code-centric, fragmented and reliant on in-house expertise. This means they fall short when it comes to biological interpretation and enterprise-scale governance.

Instead of getting bogged down in scripts and pipelines, find the biologically relevant answers you need with pathway-level context. Our intuitive tools support you every step of the way, from quality control to discovery.

Interactive

Explore cell populations, markers and heterogeneity in your samples with responsive cell-level visualizations.

Insightful

Investigate activation patterns, immune responses, mechanisms and more hidden in your gene lists with pathway analysis.

Trusted

Get biologically meaningful results based on our expert-curated biological knowledge

Sample to Insight

The insights you need, **without coding expertise**

We support you every step of the way, from sample to discovery.



Your single-cell **analysis toolkit**

Scale your workflows with intuitive interfaces and flexible transcriptome technology.



QIAGEN CLC Genomics Workbench Premium

Process single-cell data in one environment, without coding expertise. Analyze scRNA-seq, scATAC-seq, immune repertoire and multimodal data from Parse Biosciences, 10x Genomics and more with QC, cell type prediction and differential expression.



QIAGEN Ingenuity Pathway Analysis (IPA)

Uncover biological mechanisms, identify activated or inhibited pathways, predict upstream regulator activity and more with advanced pathway analysis based on expert-curated knowledge from public and proprietary data.



IPA with QIAGEN OmicSoft Explorer

OmicSoft Explorer fills one of the biggest gaps in research: context. Data scientists and discovery biologists can explore, harmonize and compare their findings against millions of cells from curated datasets with interactive visualizations.

Parse Biosciences

Go beyond the limits of previous scRNA-seq technologies with Evercode Whole Transcriptome. Scale up to millions of cells at once, across hundreds of samples, and detect more genes per cell in every experiment, no specialized instrument required.

Go beyond surface-level analysis with QIAGEN Digital Insights. Instead of generating clusters, make data-driven decisions based on the underlying biology – and uncover the insights that move your research forward.



Everything you need for single-cell analysis. Discover more at:
digitalinsights.qiagen.com/single-cell



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