

SINGLE-CELL TRANSCRIPTOMICS

Apply highest-resolution biology data
to drive your discoveries

Nebion Curates and Integrates Single-Cell RNA-Seq Data

- Compatible** – harmonization of public and private data
- High-quality** – comprehensive QC and peer review
- Systematic** – state of the art processing pipeline for 10x and Smart-Seq
- Competent** – cell-type reference built by domain experts
- Informative** – sub-clustering of main cell-type clusters
- Reliable** – cluster identification and verification on multiple levels
- Analysis-ready** – cross-study integration and cluster assignment evaluation



Key Applications

- ▶ Obtain high-resolution views of single-cell heterogeneity on a global scale
- ▶ Reveal complex and rare cell populations
- ▶ Track the trajectories of distinct cell lineages in development or in response to stimuli
- ▶ Uncover regulatory relationships on the cell-type level for improved target discovery
- ▶ Identify cell-type specific disease associations for biomarker development

Products and Services

- ▶ Analyze and visualize single-cell RNA-Seq data in GENEVESTIGATOR®
- ▶ Test your hypothesis with high-quality compendia of single-cell RNA-Seq data
- ▶ Accurately annotate single-cell studies using the Nebion cell-type references
- ▶ Get harmonized single-cell data sets with our curation services
- ▶ Find relevant public single-cell RNA-Seq studies using our scouting services



500+ Cell types



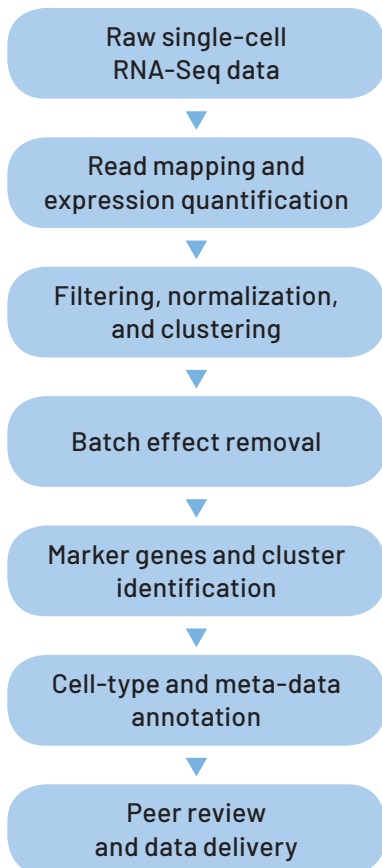
Millions of Cells



GET IN TOUCH!

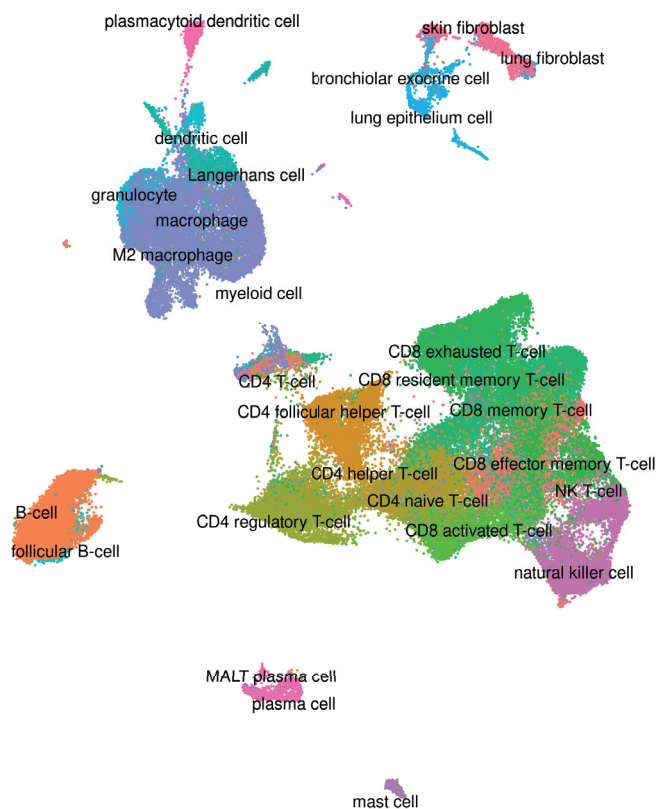
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Our Single-Cell Curation Pipeline



Example of a Cell-Type Reference

6 studies, 134'000 cells, 160 cell types



Left: Pipeline for single-cell curation at Nebion. Right: Integrated multi-study and cell-type reference map for immuno-oncology generated based on six 10x Genomics studies. Data sets were merged using Seurat 3 with the reciprocal PCA integration function and UMAP was used for visualization.

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Want to learn more about our latest developments in single-cell transcriptomics?

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