

Perturb-seq

Perturb-seq is an advanced single-cell genomics technology that enables high-throughput investigation of gene function by combining CRISPR-based perturbations with single-cell RNA sequencing. By selectively altering gene activity and measuring the resulting cellular responses, Perturb-seq allows researchers to explore gene regulation, biological pathways, and cellular phenotypes at unprecedented scale.

NYGC specializes in VIPerturb-seq, an optimized approach that leverages the scalable 10x Genomics Flex Apex platform to enable genome-scale and genome-wide single-cell perturbation studies with increased throughput and cost efficiency. Our team works with researchers during project planning to design and execute Perturb-seq experiments tailored to their biological questions and study goals.

Due to the project-specific nature of Perturb-seq, project planning typically begins with an initial consultation involving our Perturbation Platform and Project Management teams. Pricing and turnaround times are customized based on the scope and scale of the project and are provided following discussion with our teams.

Submission Requirements

- Specific submission requirements will be confirmed during project planning.

Standard Analysis

- Basic computational analysis including differential expression for perturbed cells, UMAP embedding

Standard Deliverables

- FASTQ files
- Single cell count matrices and basic analyzed objects

Frequently Asked Questions – Perturb-seq

What information is needed to start a project?

To begin planning a library sequencing project, we typically request:

- The size of your targeting library
- What guide expression system is being used, including if VIPerturb barcodes are incorporated in your expressed guides
- Will the cells be fixed before shipment
- Required timeline
- Data delivery requirements
- Any planned downstream analyses

How are projects initiated?

Once project scope and service requirements have been finalized with your NYGC Project Manager, NYGC will provide a formal service quote outlining the agreed-upon deliverables, pricing, and project details. To begin project execution and submit samples, NYGC requires a signed copy of the quote and an approved purchase order (PO). For large-scale projects, additional discussions regarding customized terms and conditions may be accommodated.

What is the expected turnaround time?

All turnaround times can be found on our '[main research services page](#)'.

How should samples be submitted?

For U.S.-based submissions, once a project has been quoted and a purchase order has been received, we provide NYGC-barcoded tubes in a matrix rack, an electronic sample manifest, and an overnight return shipping label for sample submission. Note that the provided tube orientation is critical, and tubes should not be rearranged.

Your Project Manager will coordinate international submissions, including shipping requirements and documentation.

Do you offer downstream alignment and analysis services?

Depending on the library type and species, yes, for an additional cost. See more about Bioinformatics and Data Analysis Services on '[main research services page](#)'.

How is data returned?

We support data delivery to a variety of client-managed endpoints and storage environments. Before delivery, we can perform a test transfer to confirm connectivity and ensure efficient transfer of large sequencing datasets.