

HIVE CLX: An end-to-end solution for single-cell RNAseq.

Key features

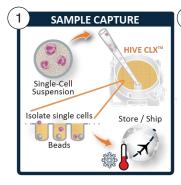
- Detect rare cells
- Recover fragile cells
- Stable storage and shipping
- Instrument-free workflow

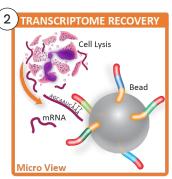
For research use only. Not for use in diagnostic procedures

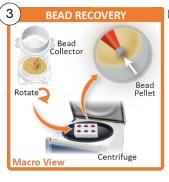
Introduction

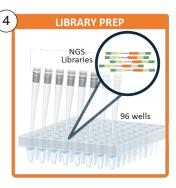
Gently capture and stabilize single-cells in your sample for RNAseq with the HIVE CLX single-cell solution. Use handheld HIVE devices to process minimally invasive biopsies without any specialized instrumentation then ship the loaded devices to a central lab for processing, greatly simplifying your collection logistics.

Unlock access to single-cell RNAseq for new people, places, and projects across your institution's footprint to resolve biological diversity in your samples, uncover rare cell-types, and discover new biomarkers.









Access to new frontiers in single-cell biology

RECOVER ANY CELL-TYPE AND GAIN NEW INSIGHTS WITH COMPLETE ACCESS TO YOUR SAMPLE BIOLOGY

- Access more cell-types, including rare and fragile cells: neutrophils, eosinophils, basophils, mast cells
- Example applications: inflammation, autoimmune diseases, asthma and allergies, dermatitis, rheumatoid arthritis (RA), eosinophilic esophagitis, leukemia (AML/ CML), and other cancers

COLLECT SAMPLES IN ANY SETTING WITH THE INSTRUMENT-FREE WORKFLOW

- Support your longitudinal studies, time-courses, end-ofday collections, and sporadic samples
- Blood, bone marrow, swabs, fine needle aspirates, freshly dissociated tissues, and other biopsies

REACH REMOTE AND LOW RESOURCE LOCATIONS WITH BUILT-IN STORAGE AND GLOBAL SHIPPING

 Emerging and evolving infectious diseases: HBV/HCV, HIV, malaria, tuberculosis, and SARS-CoV-2

Features and benefits of the HIVE CLX single-cell solution

DETECT RARE CELLS

- High single-cell capacity with ~160,000 picowells in every device
- Load 500-60,000 cells per device and pool devices if needed

RECOVER FRAGILE CELLS

- Use gravity or a brief spin to load single-cells into the HIVF
- No microfluidic systems that expose your samples to stress

PROCESS SINGLE-CELL SAMPLES AT THE COLLECTION SITE

- No specialized instruments needed
- No sample damage from cryopreservation

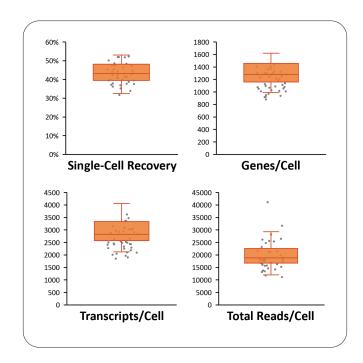
STABILIZE SINGLE-CELLS IN THE HIVE

- Cell and RNA preservation included with every device
- 9-month stability for V1 technology; CLX expected to match

Performance of the HIVE CLX single-cell solution

REPRODUCIBLE PERFORMANCE ACROSS ALL TEST CONDITIONS

- Loaded 500-60,000 human PBMCs (peripheral blood mononuclear cells) with 90% viability
- Processed all samples with the standardized HIVE CLX workflow



Technical specifications

Metric	Performance		
HIVE CLX Picowells	55 µm size, ~160,000 per device		
Sample Type	Single-cell suspensions		
Cell loading range	500-60,000 cells		
Sample volume	1-4 mL		
Cell Recovery	~44%		
Genes/Cell	~1,300		
Transcripts/Cell	~3,000		

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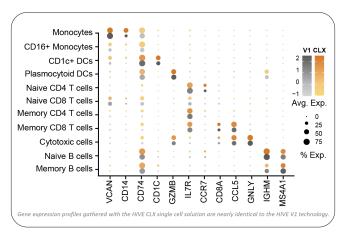
HIVE CLX single-cell sequencing for human PBMCs

Cell Input	Double Rate ¹	Single-cell Recovery ¹	Reads/ Sample ²	# HIVEs per NovaSeq SP flow cell ³
500	0%	220	7 M	>>8
2,000	2%	850	27 M	>8
7,500	5%	3,000	100 M	8
15,000	9%	6,000	200 M	4
30,000	14&	11,000	400 M	2
60,000	36%	17,000	800 M	1

- 1. Performance metrics estimated from experimental data using human PBMCs.
- Recommendations for reads/sample balance the amount of biological information gathered with sequencing costs and should achieve 80% recovery of cells, genes, and transcripts. These are recommended starting points for most applications, but you may need to tailor sequencing depths for your specific experiments.
- 3. *The nominal NovaSeg SP flow cell offers 800 M reads.

EXPERIMENTAL DESIGN

- Processed the same human PBMC sample with multiple devices for the first-generation HIVE V1 and HIVE CLX single cell solutions
- Loaded 8,000 cells with ≥90% viability and followed the standardized HIVE protocol in all cases
- Filtered lower quality data from cells with <300 genes and <600 transcripts



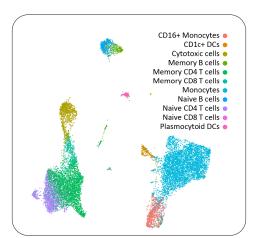
Gene expression profiles gathered with the HIVE CLX single cell solution are nearly identical to the HIVE V1 technology.

Reproducible gene expression profiling

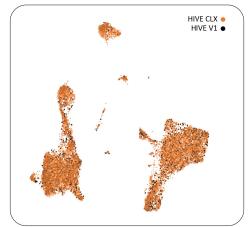
RELIABLY COMBINE DATA WITH THE ESTABLISHED HIVE V1 TECHNOLOGY

- Seamlessly combine RNAseq data with standard integration tools
- The HIVE CLX single-cell solution accommodates 2× more sample, recovers 4× more cells, and detects 20% more genes/transcripts per cell with improved usability and chemistry

Single-cell transcriptomes



HIVE sequencing offers unbiased biological coverage and preserves rare and fragile cells.



Transcriptomes derived from both HIVE configurations show nearly complete overlap.



