



HONEYCOMB™

Expand the Possibilities for Single Cell Transcriptional Profiling with the **HIVE™ scRNAseq Solution**



For research use only. Not for use in diagnostic procedures.

HIVE™ scRNAseq Solution

CAPTURE, STORAGE, & PROCESSING: **ALL IN ONE WORKFLOW**

Biological resolution at the level of individual cells is powering the next phase of precision health. The HIVE™ scRNAseq Solution integrates sample storage and single cell profiling into a complete workflow, solving the issues that limit single cell RNA analysis by:

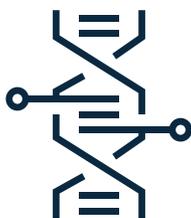
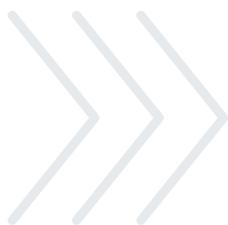
- **Enabling multi-site and multi-timepoint sample collection**
- **Maintaining sample integrity through storage, shipping, and processing**
- **Increasing the recovery rates of fragile cells**
- **Facilitating loading of larger sample volumes**
- **Delivering flexible and scalable workflows by enabling batch processing**
- **Removing the need for specialized instrumentation**

The HIVE™ scRNAseq Solution is a portable, handheld, single-use device that enables gentle capture, robust storage, and easy processing for the analysis of single-cell samples. The HIVE™ scRNAseq Solution will expand single-cell analysis in basic, translational, pre-clinical, and clinical research applications.

THE HIVE™ scRNAseq SOLUTION



**SAMPLE CAPTURE
& STORAGE**



**RNA LIBRARY
PREP**



**DATA
ANALYSIS**

Enabling Multi-site & Multi-timepoint Sample Collection

The HIVE™ scRNAseq solution is a combined sample storage and single-cell profiling system. The HIVE™ device delivers versatility by enabling sample collection at different sites or at different timepoints and sample processing at the same location where they are collected or at a centralized processing laboratory.

Easy to Use

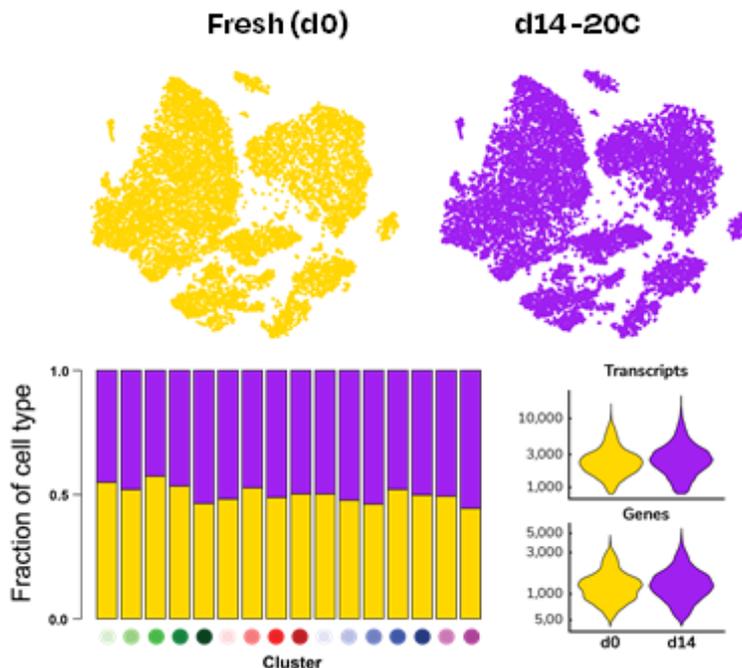
The HIVE™ scRNAseq solution incorporates reagents and a single-use, handheld, shippable HIVE™ device that can be used in almost any lab environment. No specialized equipment is required to process the samples from single cells through library preparation and the workflow can be run in most labs.

With a sample storage solution built into the capture and processing workflows, the HIVE™ devices provide a stable environment to arrest cells in their current states and protect the sample over time.

Maintaining Sample Integrity

Cell quality is not compromised when using the HIVE™ device during storage, shipping or processing. As can be seen in Figure 1, single cell libraries prepared from fresh cells and cells stored at -20°C for 14 days prior to processing have similar profiles, showing no loss of cell population diversity, number of transcripts or genes detected.

Figure 1. Comparison between samples processed while fresh or stored at -20°C for 14 days prior to processing.



Increasing the Recovery Rates of Fragile Cells

Cells isolated using the HIVE™ device settle gently into microwells within a matter of minutes. This change enables the analysis of cells that are typically difficult to analyze either because of their fragile membrane structures or because they have been stimulated or transfected which can induce fragility. Figure 2 shows the HIVE™ scRNAseq workflow is able to recover granulocytes which are difficult to detect with other platforms because of their fragility.

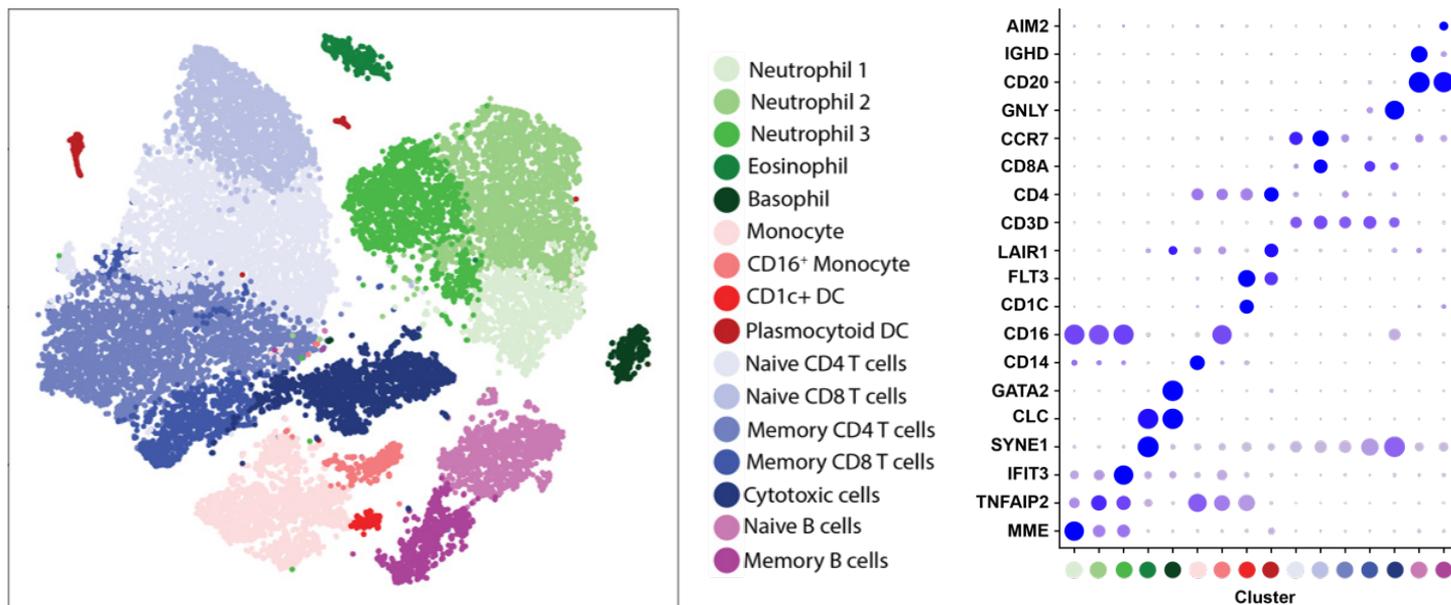


Figure 2. Illustrates 24,720 cells were captured in six HIVE™ devices. The cell types processed include granulocytes such as neutrophils, eosinophils, and basophils.

The HIVE™ scRNAseq solution delivers comprehensive biological representation, including fragile and sparse cells.

Facilitating Loading of Larger Sample Volumes

Other systems for single cell analysis only allow small sample loading volumes, typically around 50 μ L. To ensure you are not missing critical information available in the primary sample, the HIVE™ scRNAseq solution allows you to load much larger volumes of up to 4 mL.

Delivering Flexible & Scalable Workflows

The HIVE™ scRNAseq workflow reduces experimental and inter-site variability seen in other single cell analysis platforms. The workflow also delivers flexibility of processing location and throughput. The samples can be easily processed where they are collected or stored and shipped to a central facility for processing. By allowing safe sample storage, samples can be batched to improve lab efficiency.

START YOUR SOLUTION TODAY

Expand your possibilities with enhanced single cell transcriptional profiling by contacting us at NGS@perkinelmer.com



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