cellenion
ENHANCING LIFE

Single cell isolation with cellenONE®

for sequencing applications

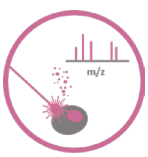
with integrated nanoliter dispenser


scRNA-Seq


scWGS


scATAC-Seq


scMethyl-Seq

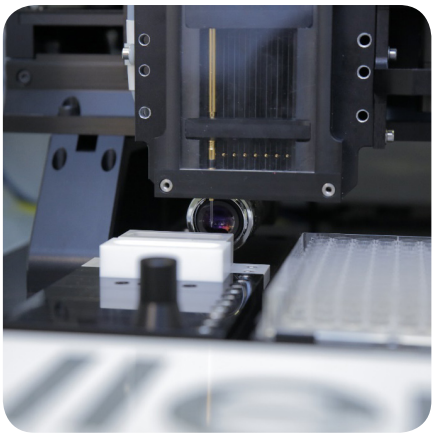


scMS

scYour-Seq

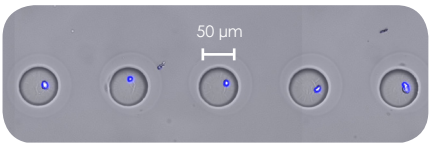
LOW VOLUME, HIGH PRECISION & RECOVERY SINGLE CELL ISOLATION FOR SEQUENCING... AND MUCH MORE

About the technology



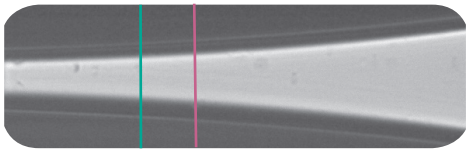
cellenONE, an automated single cell dispensing system based on patented piezo-acoustic technology, allows precise cell deposition on a wide range of microplates (96, 384, 1536) and microwell substrates.

Most dispensing and microfluidic technologies follow Poisson distribution, which leads to multiple cells per position, low efficiency and biased data. cellenONE uses software-integrated visual feedback to ensure only single cells are deposited in every position.

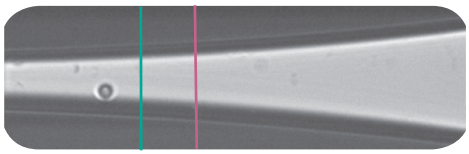


Single cell deposited in 50 µm microwells

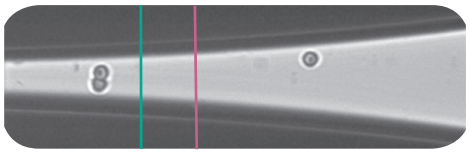
Each drop generated with cellenONE can contain:



(A) no cell



(B) one cell,

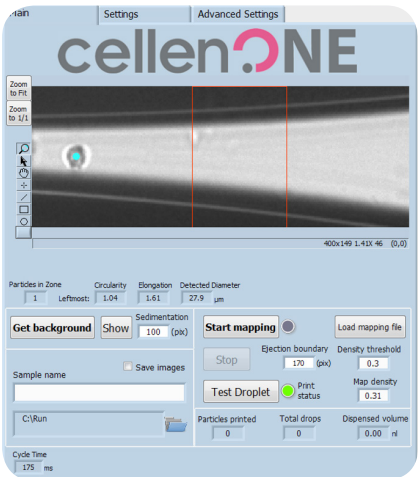


(C) multiple cells.

Thanks to visual feedback, only single cells are dispensed

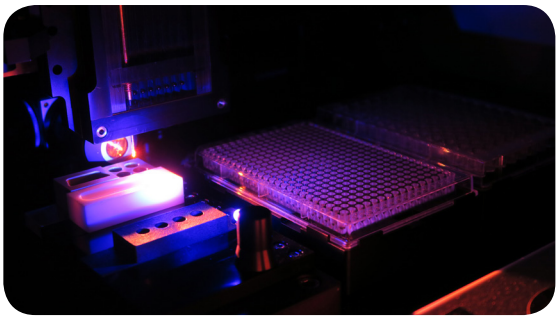
cellenONE only dispenses single-cell containing drops (B) directly into microplates or microwell chips of your choice.

All remaining drops are dispensed into a recovery tube, resulting in none of the cells being lost and leaving the possibility to reprocess those non-isolated cells later.



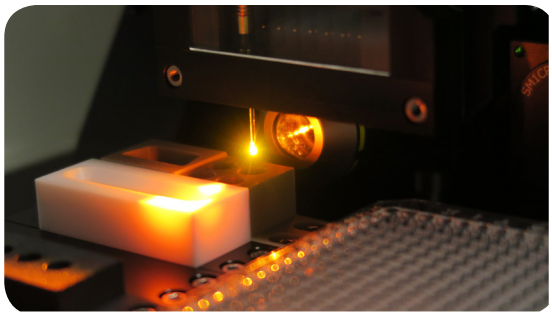
Samples are analyzed live and pictures recorded for post processing analysis

NOW also available with fluorescence detection module



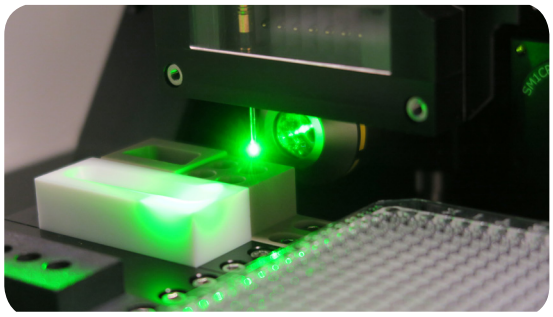
cellenONE can now be ordered with optional fluorescence detection setup which can be used for:

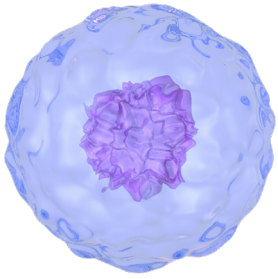
- Isolation of live single cells (Live/Dead)
  Remove dead cells from scRNA-seq libraries
- Isolation of very rare single cells
  Only isolate single cells of interests
- Cloning best expressers
  Boost clonal recovery and expressers levels

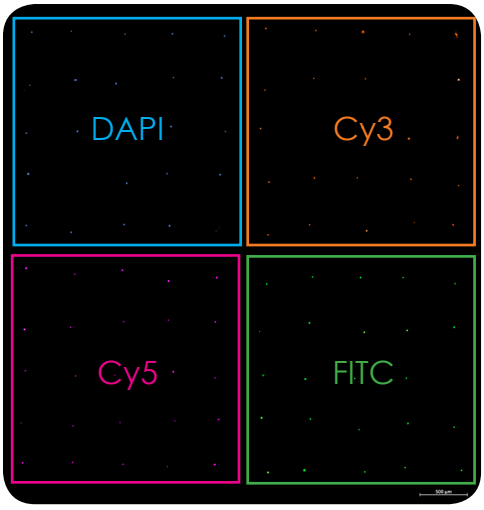


Optional fluorescence detection comes in two levels:

One channel	FITC
Four channels	DAPI
	FITC
	PE
	Cy5







Four arrays of 5x5 single HEK293T cells labeled with DAPI, CellTracker Green, Orange and Deep Red sorted using 4-channels setup.

A mixture of four cell populations were labeled with Hoechst 33342 (DAPI channel), CellTracker Green (FITC channel), CellTracker Orange (Cy3 channel) and CellTracker Deep Red (Cy5 channel).

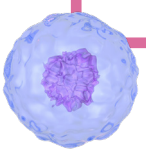
25 single cells from each cell population were successfully isolated on microscope slide with the fluorescence detection module of cellenONE.

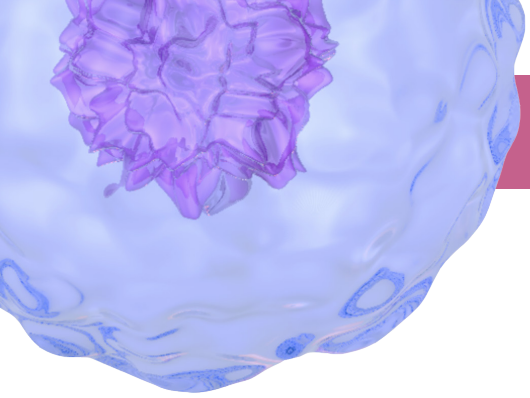
Sorting Features

Live / Dead

Very rare cells

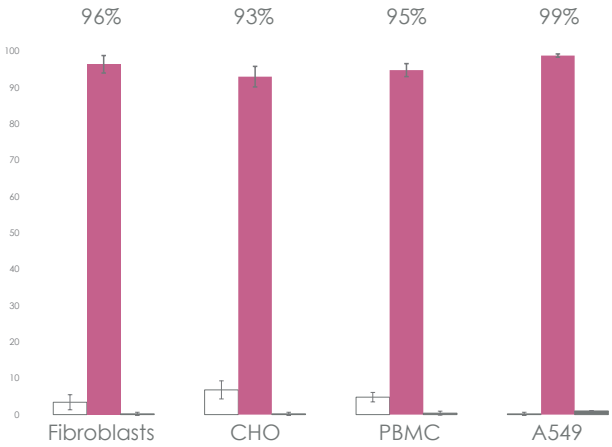
Only isolate single cells of interest





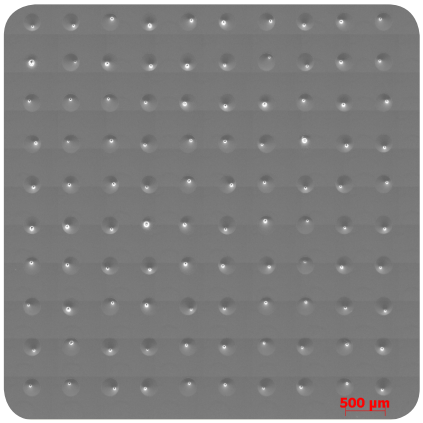
Up to 100% single cells

Outstanding accuracy



Results from 5x100 positions filled with single cells from four different cells samples. Single cells rate is indicated in pink, up to 99% for A549 cells; in white are empty positions and in grey, multiple cells positions.

Unlike other technologies (microdroplet, microfluidic traps), doublets can be completely excluded and only single cells are dispensed.



Single cells from dissociated lung cancer spheroids successfully isolated onto a microscope slide. Every position contains one single cell.

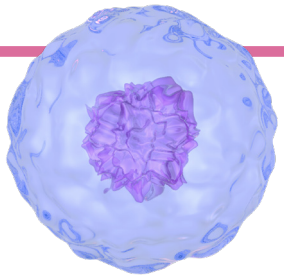
Key Features

cellenONE®

No doublets

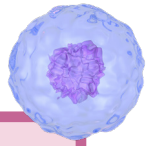
Unseen recovery

Suitable for most cell types



Open and versatile platform

Thanks to high definition optics, cells are individually identified and isolated. These are selected according to their size, geometry and now potentially using fluorescent markers (see page 3). Once selected, cells are dispensed into microplates such as 96, 384, 1536wp or into microwells such as ICELL8™ chip.



Successfully isolated cells and particles so far:

- **cell lines** such as CHO, hybridoma, HEK293T, HeLa, A549, PC3, H1975, HepaRG, Jurkat
- **primary cells** such as PBMC (including B- and T- cell fractions), fibroblasts, keratinocytes, melanocytes, cardiomyocytes, HUVEC, neural stem cells
- **nuclei** from cell line, fresh frozen (FF) and formalin-fixed paraffin-embedded (FFPE) tissue slices
- **microbeads** like PMMA microbeads from 2 to 30µm diameters, TOYOPEARL®, PS microbeads

Cells and particles from 2 to 70 µm

System Set up Workflow

10 min

Cell Sample Preparation

- Prepare a minimum volume of 2 µL, ideally around 10 µL
- Optimal cell concentration below 200 cells/µL

Place sample in holder

Aspirate sample

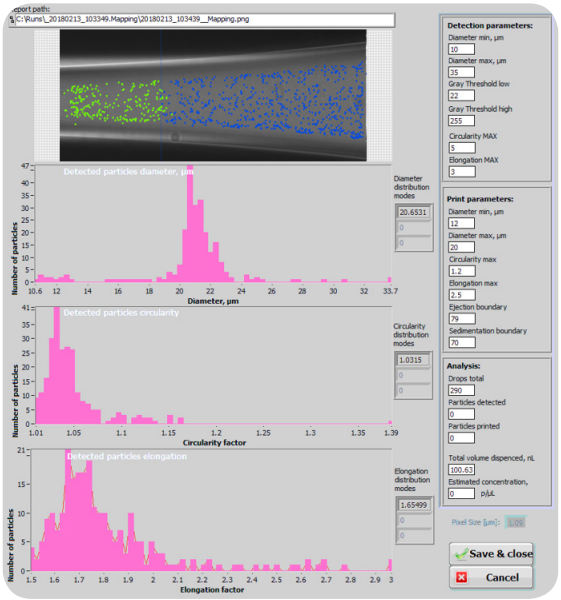
5 min

Cell Mapping

- Automated cell tracking and report generation
- Choose isolation parameters
- Select type of target (96, 384, 1536 wp. ICELL8™ chip)

System setup only takes a few minutes

Users can walk away during isolation process



A mapping report is automatically generated, it contains:

- Evaluation of ejection zone boundary
- Detected cell diameter, elongation and circularity distribution
- Average cell concentration

4 min*

Automated Isolation

- Up to 2 microplates (or equivalent) per run
- 100 cells in 4 min or 1000 cells in less than 45 min*
- Walk-away and easy to operate system
- Temperature control to avoid RNA degradation

* at optimal cell concentration

Open Workflow for Library Preparation

cellenONE is an open platform providing both single cell isolation and nanoliter dispensing.

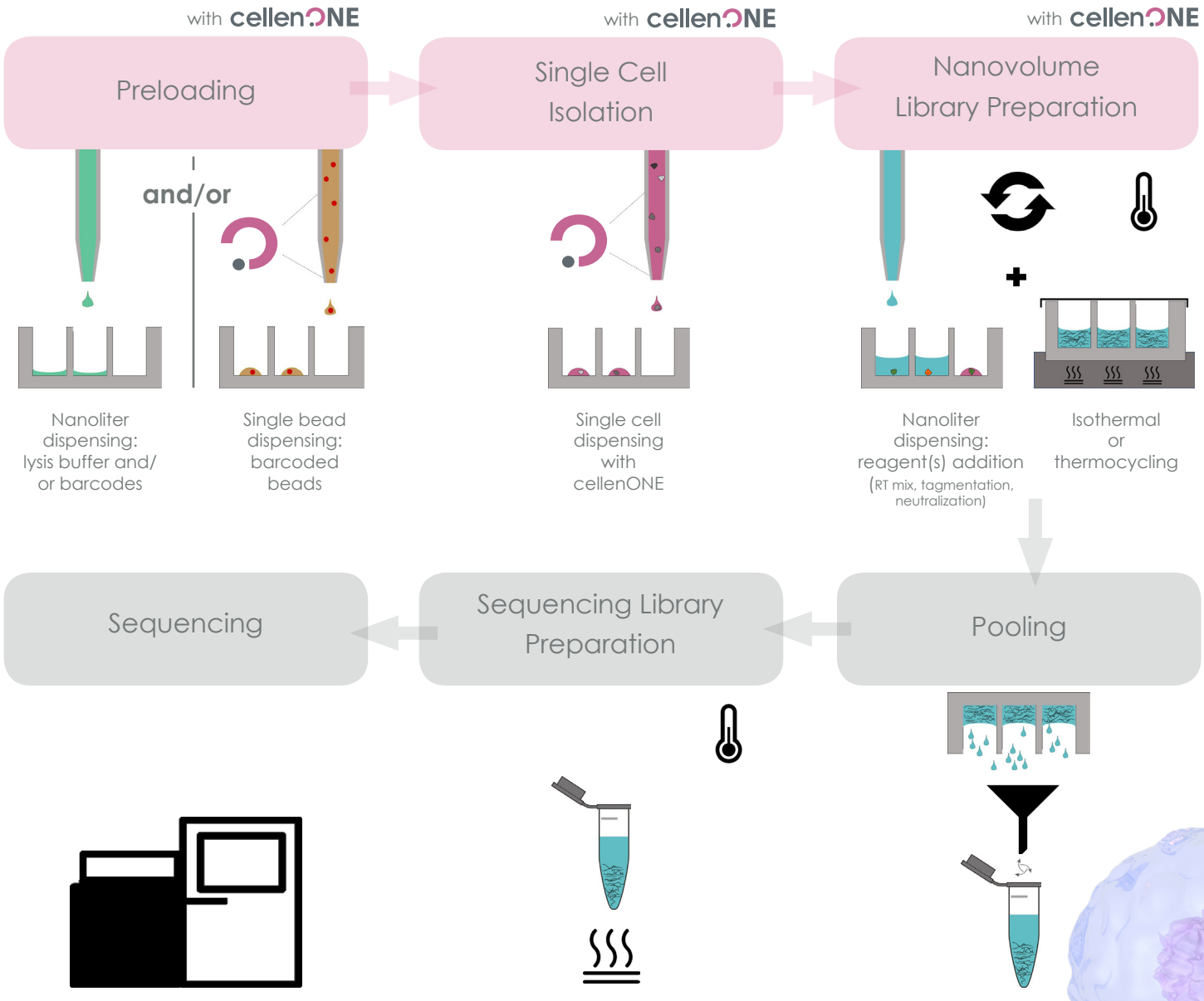
Such versatility allows users to automate many of the crucial steps involved in the ever growing number of single cell library preparation methods available today. Moreover, ability to work in nanovolumes and microwells allows a drastic reduction in reagents consumption and associated costs.

Benefits
cellenONE®

All-in-one device

Low reaction volumes

Low reagent costs



Rare cells isolation from cerebrospinal fluid

Unseen recovery
for low concentration samples
for low volume samples

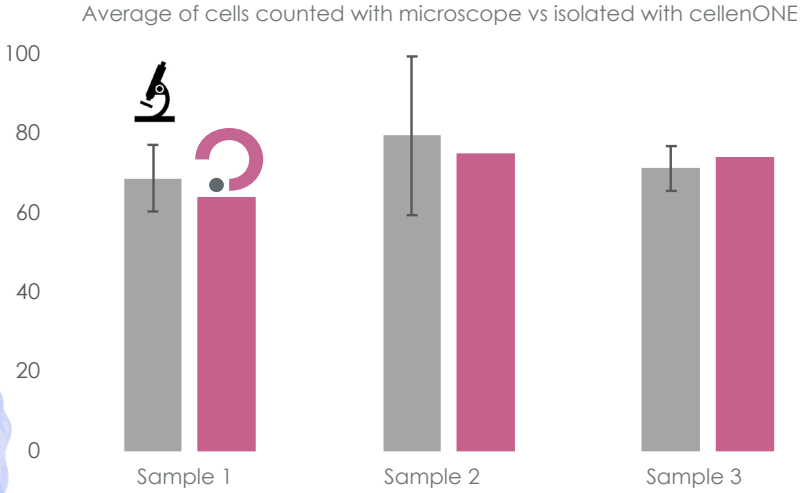
scRNA-Seq

UCSF Department of Neurology
Weill Institute for Neurosciences

In collaboration with the Department of Neurology at Weill Institue in San Francisco, a study performed aiming to isolate single immune cells in multiple sclerosis patient´s cerebrospinal fluid (CSF) samples for subsequent single cell RNA sequencing.
The main challenge associated with such sample is the very low number of cells present in these samples which can vary from only 20 to 500 cells per 20mL of patient's CSF.

To demonstrate achievable cellenONE recovery rates, a proof of concept experiment was undertaken with low concentration PBMC samples (~25 cells/µL).
Three samples of 30µL were prepared, for each sample, 4 aliquots of 5 µL were pipetted into 4 wells of a 1536 wp and the exact number of cells was counted under microscope to calculate starting cell concentrations (average input or).
Finally, for each sample, a 5µL aliquot was processed using cellenONE and as many as possible single cells were isolated into a microwell chip and subsequently counted by microscopy (output or).

On average, recovery reached 95%, meaning most of the cells present in each sample were successfully isolated as single cells (number of single cells successfully isolated with cellenONE over average cell number for each sample).



Benefits
cellenONE®

From minute samples
(from just 2µL)

Recovery up to 95%

No dead volume

DLP+ for Whole Genome Sequencing

scWGS

BC CANCER MOLECULAR ONCOLOGY RESEARCH
Provincial Health Services Authority

THE UNIVERSITY OF BRITISH COLUMBIA

High throughput, versatile and low cost WGS

Scalable whole genome sequencing of 40,000 single cells identifies stochastic aneuploidies, genome replication states and clonal repertoires

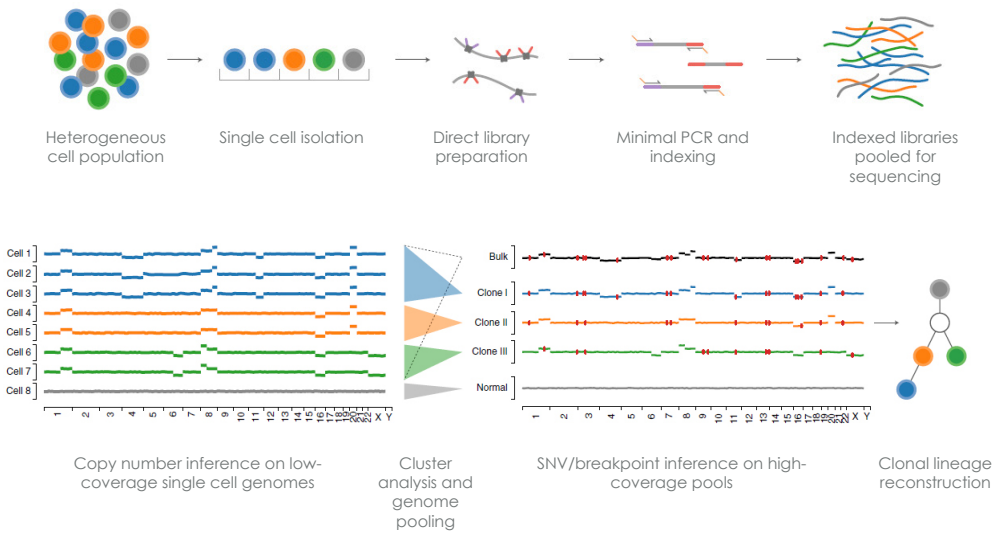
Emma Laks[1] (elaks@bccrc.ca), Hans Zahn[1], Daniel Lai[1], Andrew McPherson[1], Adi Steif[1], Jazmine Brimhall[1], Justina Biele[1], Beixi Wang[1], Tehmina Masud[1], Diljot Grewal[1], Cydney Nielsen[1], Samantha Leung[1], Viktoria Bojilova[1], Maia Smith[1], Oleg Golovko[1], Steven Poon[1], Peter Eirew[1], Farhia Kabeer[1], Teresa Ruiz de Algara[1], So Ra Lee[1], M. Jafar Taghiyar[1], Curtis Huebner[1], Jessica Ngo[1], Tim Chan[1], Spencer Vatrt-Watts[1], Pascale Walters[1], Nafis Abrar[1], Sophia Chan[1], Matt Wiens[1], Lauren Martin[1], R. Wilder Scott[1], Michael T. Underhill[2], Elizabeth Chavez[1], Christian Steidl[1], Daniel Da Costa[1], Yusanne Ma[3], Robin J. N. Coope[3], Richard Corbett[3], Stephen Pleasance[3], Richard Moore[3], Andy J. Mungall[3], CRUK IMAXT Consortium[4], Marco A. Marra[5], Carl Hansen[5], Sohrab Shah[1] (sshah@bccrc.ca) and Samuel Aparicio[1] (saparicio@bccrc.ca)

[1]BC Cancer Research Centre; [2]Michael Smith Laboratories; [3]Michael Smith Genome Sciences Centre; [5]University of British Columbia

doi: https://doi.org/10.1101/411058

Single cell WGS study performed jointly at UBC and BCCRC aimed to analyze genome heterogeneity, mutational process and clonal evolution over tens of thousands of single cells or single nuclei from a variety of tissues. The author developed DLP+, a fully integrated pipeline from wet bench to analysis platform.

Direct Library Preparation (DLP+) is a new single cell tagmentation-based WGS method without preamplification which includes an analysis pipeline and allows clustering of thousands of cells at once



DLP protocol, adapted from Zahn et al., Nature Methods 2017

The platform was successfully used to study lineages and tissue heterogeneity according to parameters such as genome state, ploidy, copy number alteration and single nucleotide variant.

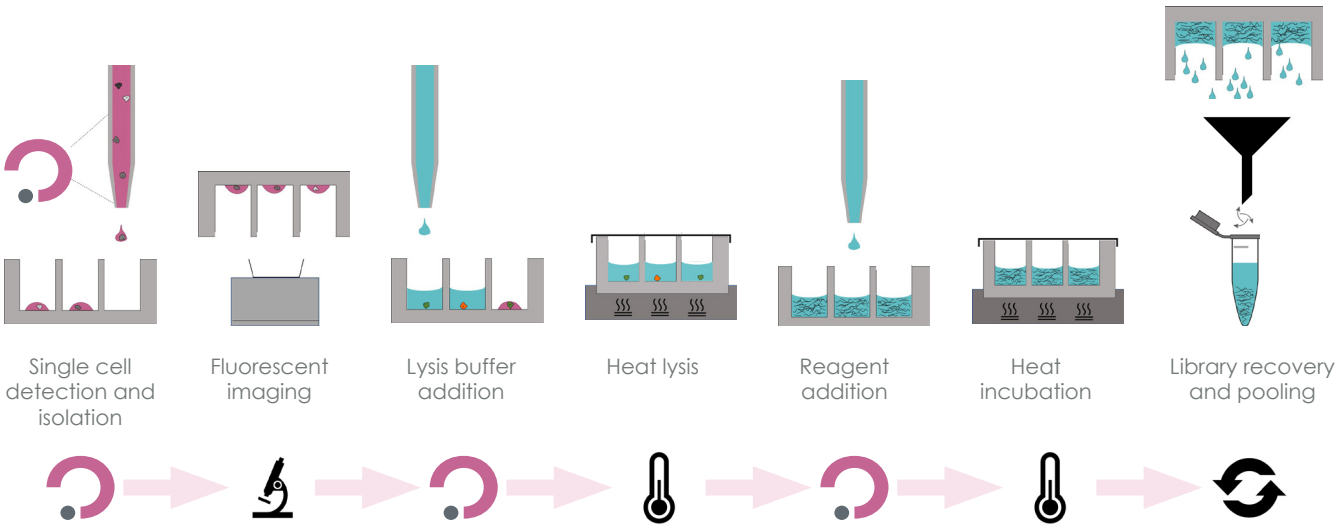
DLP+ for efficient Whole Genome Sequencing

scWGS

BC CANCER MOLECULAR ONCOLOGY RESEARCH
Provincial Health Services Authority

THE UNIVERSITY OF BRITISH COLUMBIA

Direct Library Preparation Method



DLP+ protocol, adapted from Laks et al., BioRxiv 2018

Benefits

cellenONE®

Low volume & reagent costs

0,27 US$/cell

High quality library

Versatile: cell and nuclei

from 5 to 80µm

Open and high throughput

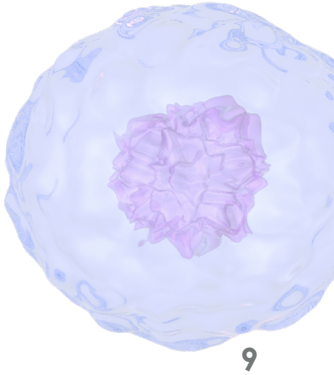
1000's cell/experiments

Results

- Compatible with cell line, dissociated mouse and human tissues and nuclei from FF human breast cancer PDX tissue
- Optimized WGS protocol for nanovolume library preparation
- Open-source cloud computing pipeline for single-cell genome analytics (http://www.cellmine.org)
- Pseudobulk sequence from assembled single cell genomes successfully used as reference for clustering the same single cells
- Level genome ploidies, cell specific mitotic error rates, and cell specific replication status were successfully obtained from single cell data

"cellenONE technology enables the work we are doing: isolating cell and then dispensing a few nanoliters from various reagents. The system is spatially and volumetrically accurate and is able to spot each cell, one after another, into each well."

Dr. Robin Coope,
British Columbia Cancer Genome Sciences Centre



Specifications

Technical information

Dispensing technology: piezo acoustic drop-on-demand

Dispense volume: 50-800 pL per drop

Linear drives for X/Y and spindle drive for Z

Resolution: 1 µm

Accuracy (Absolute Position): < 10 µm

Precision (Repeat Position): < 3 µm

HD camera for detection of cells or particles from 2µm

Max. speed: 100 cm/sec

Isolation area (mm): x=180; y=120 (2 microtiter plates)

Dimensions LxWxH (mm): 650 x 700 x 1590

-> including monitor's arm L = 1300 mm

-> with door open H = 2050 mm

Weight: 205 kg

Voltage: 110 V; 220 V

Options & Software

Temperature, humidity and dew point control

2nd channel for nanoliter dispensing

Fluorescence module up to 4 channels (DAPI, FITC, Cy3 or Cy5)

Customized holders for microwells chips

Fiducial recognition and automated target alignment

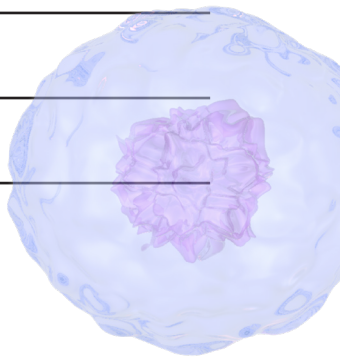
Related Products & Services

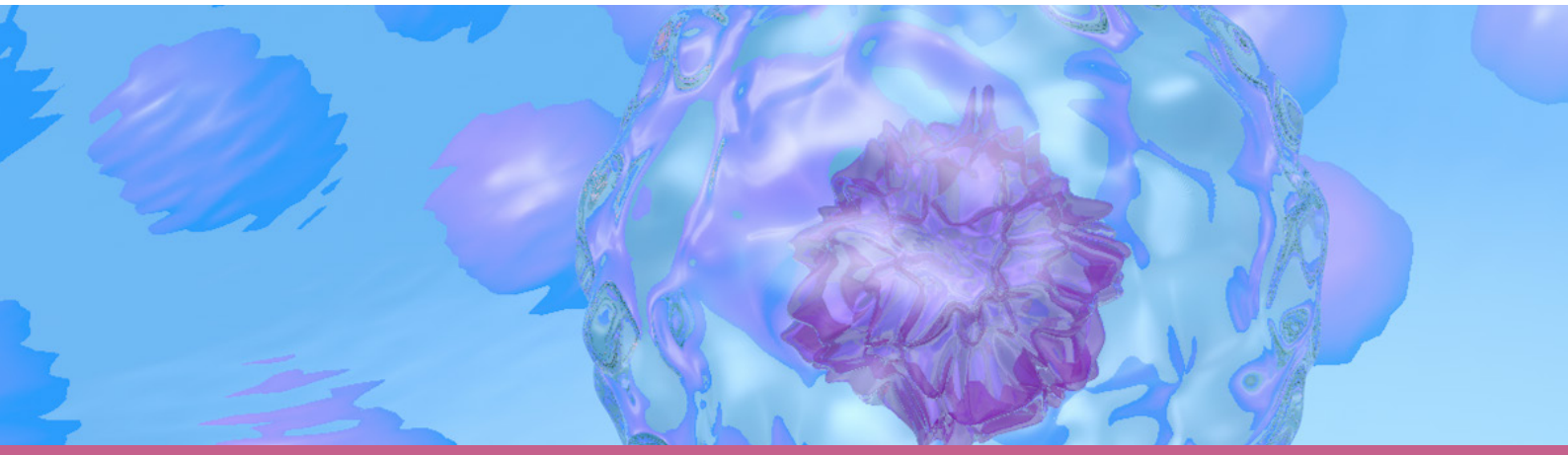
cellenBEADS for calibration

cellenWASH for sterilization

cellenVIALS for recovery

cellenSERVICEs for application support





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