

Rapid Parallel Generation of a Fluorescently Barcoded Drop Library from a Microtiter Plate Using the Plate-Interfacing Parallel Encapsulation (PIPE) Chip

Journal:	Lab on a Chip
Manuscript ID	LC-ART-09-2022-000909
Article Type:	Paper
Date Submitted by the Author:	28-Sep-2022
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3	Encapsulation (PIPE) Chip†					
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19	experimental details. See DOI: 10.1039/x0xx00000x					
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25 Abstract

In drop-based microfluidics, an aqueous sample is partitioned into drops using individual 26 pump sources that drive water and oil into a drop-making device. Parallelization of drop-making 27 devices is necessary to achieve high-throughput screening of multiple experimental conditions, 28 especially in time-sensitive studies. Here, we present the Plate-Interfacing Parallel Encapsulation 29 (PIPE) chip, a microfluidic chip designed to generate 50- to 90-µm diameter drops of up to 96 30 different conditions in parallel by interfacing individual drop makers with a standard 384-well 31 32 microtiter plate. The PIPE chip is used to generate two types of optically barcoded drop libraries consisting of two-color fluorescent particle combinations: a library of 24 microbead barcodes and 33 a library of 192 quantum dot barcodes. Barcoded combinations in the drop libraries are rapidly 34 35 measured within a microfluidic device using fluorescence detection and distinct barcoded 36 populations in the fluorescence drop data are identified using DBSCAN data clustering. Signal 37 analysis reveals that particle size defines the source of dominant noise present in the fluorescence 38 intensity distributions of the barcoded drop populations, arising from Poisson loading for microbeads and shot noise for quantum dots. A barcoded population from a drop library is isolated 39 using fluorescence-activated drop sorting, enabling downstream analysis of drop contents. The 40 41 PIPE chip can improve multiplexed high-throughput assays by enabling simultaneous encapsulation of barcoded samples stored in a well plate and reducing sample preparation time. 42

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48 Introduction

Drop-based microfluidics technology reduces assay times and increases sample throughput 49 by rapidly creating and analyzing picoliter-sized drops.^{1, 2} Drop-based microfluidics has recently 50 been applied towards combinatorial drug discovery,³ massively multiplexed nucleic acid 51 detection,⁴ and antibiotic susceptibility screening.⁵ In these assays, 10³ to 10⁶ drops are tracked by 52 a unique identifier in each drop, called a "barcode". This is commonly achieved using one of two 53 barcode types: DNA barcodes introduced to tag drop contents as part of a next generation 54 sequencing pipeline;⁶⁻⁹ or fluorescent dyes and particles used to label drops for fluorescence-based 55 assays, such as enzyme activity or dose-response screening.^{3-5, 10-14} DNA barcoding can provide 56 upwards of 10⁷ unique identifiers, enabling large-scale single-cell transcriptomics, but requires 57 coalescing the drop emulsion before sequencing.⁶⁻⁹ Though an advantage in single cell sequencing, 58 drop coalescence prohibits ultrahigh-throughput experiments in which drop contents are assayed 59 60 over time. Fluorescent labeling allows the barcode and fluorescent assay output to be measured 61 simultaneously without coalescing the drops. The resulting collections of either DNA or fluorescent barcodes in drops, known as "libraries", enable multiplexed or combinatorial readouts 62 of the unique components encapsulated within the drops.¹⁰⁻¹³ 63

A typical method for creating a barcode within a drop library is to emulsify a fixed sample volume of that barcode contained within a microtiter plate well or microcentrifuge tube using a single drop-making device. The process rapidly becomes labor- and time-intensive when a single drop-making device is used to generate increasingly large numbers of barcoded drops that are subsequently pooled together. Individual microfluidic drop makers can be run in parallel, but this requires multiple pump sources to emulsify each sample. Alternatively, liquid handling machines or autosamplers can be programmed to sequentially load individual samples from a microtiter plate

into a microfluidic device;¹⁴⁻¹⁷ however, these technologies are costly and cannot create multiple 71 different barcodes simultaneously, which may be necessary for time-sensitive experiments. For 72 example, all samples must be emulsified and processed in parallel to accurately capture the time-73 sensitive kinetics needed for performing comparative rapid enzymatic reaction screening studies.^{18,} 74 ¹⁹ Thus, to perform parallel encapsulation of multiple different barcodes, specialized microfluidic 75 devices actuated using vacuum²⁰ or positive pressure^{7, 8} and containing multiple drop makers have 76 77 been designed to interface with wells on standard microtiter plates. Prior work from Rotem et al. used such a device to encapsulate DNA barcodes to perform single-cell chromatin profiling.^{7, 8} 78 However, the fabrication of this device was not described in detail, nor was the device used to 79 create fluorescently barcoded libraries. Extending the utility of this device for fluorescent 80 barcoding would enable multiplexed assaying, wherein a barcoded signal is simultaneously 81 measured along with an assay output. Additionally, fluorescently barcoded drops enable sample 82 isolation and enrichment of a particular sample using fluorescence-activated drop sorting.^{21, 22} To 83 allow for longer term storage of the drop libraries, fluorescent particles may be used in the place 84 of dyes^{3, 11} to prevent diffusion of barcode labels between drops.²³ 85

Here, we detail the fabrication of a microfluidic device comprised of 96 simultaneously 86 operating drop makers called the Plate-Interfacing Parallel Encapsulation (PIPE) chip that directly 87 interfaces with 96 wells of a standard 384-well microtiter plate. The PIPE chip is operated within 88 a pressure chamber, a modified commercial pressure cooker, wherein pressurized air drives 89 parallelized drop formation across the 96 drop makers on the device. Parallelization enables rapid 90 creation of drop libraries at a total drop throughput of approximately 300 kHz, approximately two 91 orders of magnitude larger than serial drop generation using a single drop-making device, creating 92 a total of approximately 3.6×10^7 drops in 2 min. Drop sizes produced by the PIPE chip are 93

described using a simple drop scaling law, which allows for fine-tuning of drop diameters ranging 94 from approximately 50 - 90 µm. The PIPE chip is used to create two types of optically barcoded 95 drop libraries using two-color combinations of either microbeads or quantum dots (QDs). A 96 quarter of the 96 drop makers on the PIPE chip was used to create a drop library consisting of 24 97 fluorescent microbead combinations. The PIPE chip was also used twice to create a drop library 98 consisting of 192 QD combinations. Fluorescence from each barcoded drop was measured at high 99 speed using a flow-based detection method²² to create a two-color scatter plot for each type of 100 barcode library. A data clustering method, density-based spatial clustering of applications with 101 noise (DBSCAN).²⁴ is used to identify uniquely barcoded concentrations and minimize the signal 102 103 overlap between the combinations. The dominant sources of noise influencing the fluorescence signal overlap between barcode populations arise from Poisson loading for drops containing 104 fluorescent microbeads approximately 1 µm in diameter and shot noise of the photodetector for 105 drops containing ODs approximately 10 nm in diameter. The effect of these noise sources when 106 designing barcode label concentration can be accounted for by scaling the barcode particle 107 concentration with a quadratic function, thereby allowing for quick prototyping of barcode library 108 labels. Finally, we demonstrate the utility of the PIPE chip by sorting and isolating a single 109 fluorescently barcoded sample from a drop library of 24 different barcode combinations.^{21, 22} The 110 ability to sort a specific barcoded sample from a drop library enables further analysis of drop 111 contents using downstream techniques such as PCR amplification and genetic sequencing.²⁵⁻²⁷ 112 Drop libraries created with the PIPE chip can help to streamline existing multiplexed assays, such 113 as combinatorial drug screening³ or high-throughput assaying of protease activity,¹² by enabling 114 simultaneous encapsulation of barcoded samples stored in a well plate. 115

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Materials and Methods

119 **PIPE Chip Design**

The PIPE chip was fabricated from three separate approximately 5-mm thick layers of 120 polydimethylsiloxane (PDMS) plasma bonded on top of one another to form a 3-dimensional 121 network of channels. The top layer of the device (Fig. 1a, i) is comprised of a narrow strip of 122 PDMS containing two long channels that function as a common oil inlet and drop outlet for all 123 124 three layers. Oil inlet and drop outlet channels run perpendicular to the channels in the remaining two PDMS layers, thereby allowing oil and drops to flow throughout the device from a single inlet 125 126 and outlet, respectively. The oil inlet channel (Fig. 1a, i, blue) and drop outlet channel (Fig. 1a, i, 127 yellow) are connected to the rest of the device through a total of nine via holes punched in the middle layer (Fig. 1a, ii), five for oil distribution and four for drop collection, providing a pathway 128 129 for fluids from the top layer through to the bottom layer (Fig. 1a, dashed black lines). The middle 130 layer contains oil distribution and drop collection channels that pass the oil phase to the drop makers and collect produced drops. The bottom layer (Fig. 1a, iii) contains 96 drop makers (Fig. 131 1b), each connected to oil distribution and drop collection channels. Drop maker inlet holes are 132 spaced 4.5 mm apart to match the standard pitch of a 384-well microtiter plate, enabling the PIPE 133 chip to interface directly to ¹/₄ of a 384-well microtiter plate. 134

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136 PIPE Chip Fabrication

Each of the PDMS layers i – iii (Fig. 1a) was cast from a unique master mold and bonded
following standard techniques in soft lithography (see ESI *PIPE Chip Fabrication* for details).^{†22}
Short lengths (22.5 mm) of SAE 304 stainless steel capillary tubes (0.71 mm OD, 0.41 mm ID,

Vita Needle) were fitted into the sample inlet holes of the device to provide a path for fluids from each microtiter plate well to the sample inlet of each drop maker (Fig. 1b). For encapsulating barcoded samples, the device was manually positioned above ¹/₄ of a standard 384-well microtiter plate such that each of the stainless steel inlet capillaries nearly extended to the bottom of a different well (Fig. 1c).



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Fig. 1 PIPE chip design and assembly. (a) The PIPE chip was assembled from three layers: (i) a 146 top layer containing oil distribution (blue) and drop collection (yellow) channels connected to a 147 single inlet and outlet, respectively; (ii) a middle layer which reduces fluidic resistance by 148 providing additional height to the oil and drop collection distribution channels on the bottom layer; 149 and (iii) a bottom layer which contains an array of 96 drop makers (eight rows of twelve drop 150 makers) with channels for oil distribution (five rows, blue) and drop collection (four rows, vellow). 151 (b) Detailed view of one of the 96 drop makers positioned on the bottom layer. Colors are used to 152 distinguish oil inlet (blue), aqueous sample inlet (green), and drop outlet (yellow) channels. (c) 153 Image of a completed device interfaced with $\frac{1}{4}$ of a 384-well plate. Each layer (i – iii) of the fully 154 assembled device from part (a) is indicated using black arrows. Stainless steel sample inlet 155 capillary tubes are visible extending into the microtiter plate wells below. 156

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158 **Pressure Chamber**

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The barcoded samples contained in the wells of the microtiter plate were simultaneously driven into each of the 96 drop makers of the PIPE chip under the uniform pressure within the sealed aluminum interior chamber of a 6-quart pressure cooker (Fig. 2a). Compressed air (approximately 60 psig) supplied both the oil reservoir pressure P_{oil} and chamber pressure P_{water} ,

both adjusted from 0-15 psig using manual regulators (McMaster-Carr 6745K32 0-25 psi) and 163 analog gauges (McMaster-Carr 3850K2 0-15 psi). The oil reservoir was comprised of a pressure-164 rated glass bottle (Sigma Duran Z674397) and a cap fitted with ports for compressed air and oil 165 inlet tubing. Custom-drilled ports in the pressure chamber allowed the passage of oil inlet tubing 166 and drop outlet tubing (Fig. 2a, Side view). The ports were sealed with silicone sealant (DAP Kwik 167 Seal Plus). A viewport was created using a 1.5 mm-thick transparent polycarbonate sheet that was 168 169 affixed and sealed to a fabricated opening in the pressure chamber lid, allowing device operation to be monitored or recorded (Fig. 2a, Top view). A strip of white LEDs (Ledmo SMD 2835) was 170 mounted to the inside of the chamber to provide illumination. 171

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173 Drop Encapsulation

Barcoded samples were pipetted into individual wells of a 384-well microtiter plate and 174 then placed into the pressure chamber apparatus. The PIPE chip was connected to the oil inlet and 175 drop outlet tubing and positioned with the inlet capillaries extending into the wells of the microtiter 176 177 plate containing barcoded samples (Fig. 2b). An oil reservoir was pressurized by house air and was regulated at pressure P_{oil} to control the oil flowrate. The oil reservoir contained Novec 7500 178 fluorinated oil (3M) with 1.5% w/w of a Krytox-PEG surfactant that was synthesized in-house 179 180 following a previously published protocol incorporating Jeffamine ED900 (Huntsman) as the hydrophilic portion of the PTFE-PEG-PTFE triblock perfluorosurfactant.²⁸ The water flowrate 181 was controlled by a second regulator which adjusted P_{water} within the chamber, driving barcoded 182 samples from each microtiter plate well into the PIPE chip to be encapsulated into drops. Barcoded 183 drops were passed through the wall of the pressure chamber before reaching a collection tube to 184

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form a library of drops, each indexed to a unique sample well. Drop collection continued for 2-3 185 min, or until air bubbles were observed in the outlet tubing, indicating sample wells were empty. 186 A detailed schematic summarizes barcoded drop encapsulation within the PIPE chip where 187 barcoding is represented by a unique combination of green and red fluorescent microbead 188 concentrations in each well (Fig. 2c). The encapsulation process is the same when quantum dots 189 are used. Pressurization of the chamber pushes the fluid from these wells into the bottom PIPE 190 191 chip layer (Fig. 2c, iii) where drops are formed at individual drop makers. The drops are then collected in shared drop outlet channels formed from the union of channels in the middle and 192 bottom layer (Fig. 2c, ii and iii, yellow). These shared channels are connected to a perpendicular 193 194 collection channel on the top layer (Fig. 2c, i) through via holes where drops subsequently flow and are collected in a common drop outlet. The flow of oil is the reverse of the flow of drops; a 195 common oil inlet is distributed in the top layer (Fig. 2c, i) to perpendicular channels (Fig. 2c, ii 196 and iii, blue) through via holes until oil reaches the drop makers (Fig. 2c, iii). 197



Fig. 2 PIPE chip operation and barcoded drop library production. (a) Side view and top view 200 profiles of the PIPE chip apparatus and components. (b) PIPE chip operation schematic for the 201 encapsulation of 96 wells from a 384-well microtiter plate. Pressure P_{oil} is applied to an external 202 oil reservoir to provide oil to the device within the pressure chamber while a second pressure P_{water} 203 applied to the chamber pushes fluid from sample wells into the microfluidic device. Barcoded 204 drops travel through tubing past a sealed opening in the wall of the chamber for collection in a 205 drop library. (c) Detailed schematic of the internal channels and flows within the PIPE chip. 206 Samples in wells (indexed A - C and 1 - 2) barcoded with different concentrations of green and 207 red microbeads are encapsulated in layer (iii), collected in large drop channels (yellow) formed 208 from both layers (ii) and (iii) where they are transported to perpendicular drop collection channels 209 in layer (i). The barcoded drops flow out of the device in a shared drop outlet. 210

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212 Drop Size Measurements

To characterize drop formation, the PIPE chip was placed on a petri dish filled with 10 mL 213 of sterile-filtered deionized water (0.2 µm filter) within the pressure chamber and the oil reservoir 214 215 was filled with 100 mL of Novec 7500 (3M) oil with surfactant²⁸ added at 1.5% w/w. Drops were collected across a range of water P_{water} and oil P_{oil} inlet pressure combinations (2-3, 2-6, 2-12, 4-216 3, 6-3, 6-6, 6-12, 8-9, and 8-12 psig, where combinations are denoted as P_{water} - P_{oil}). 217 Approximately 10 µL of drops were placed on an 8-well Teflon printed slide (Electron Microscopy 218 Sciences, Cat. #63422-06) and imaged under an inverted brightfield microscope (Nikon TE2000). 219 The height of the Teflon well was larger than the drop diameter, as drops regularly formed a bilayer 220 during imaging. A custom image processing script in MATLAB (R2019a) was used to measure 221 drop diameter D_{drop} . To convert the water and oil pressure ratios $P_{\text{water}}/P_{\text{oil}}$ to volumetric flowrate 222 ratios $Q_{\text{water}}/Q_{\text{oil}}$, we measured the volumes V of the oil and water phases after t = 0.5-2.5 min of 223 collection for each water and oil pressure condition. In this case, surfactant was not added to the 224 oil phase to allow for drop coalescence and phase separation of oil and water. The volumetric 225 flowrates of each phase were calculated using $Q_i = \frac{V}{t}$ and plotted as $Q_{\text{water}}/Q_{\text{oil}}$ as a function of 226 $P_{\text{water}}/P_{\text{oil}}$ (Fig. S1).† 227

Real-time drop formation within the PIPE chip was visualized through the viewport on the pressure cooker using a high-speed camera (Phantom VEO 710L, Vision Research) attached to a tube lens (Model CFM, ISCO-OPTIC) mounted with a 10× objective (NA 0.25). The underside of the PIPE chip was illuminated by a liquid light guide routed through the side of the pressure cooker and attached to an LED light source (SugarCUBE, Ushio America).

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234 Fluorescent Microbead Barcodes

Microbead barcodes consisted of unique two-color combinations of approximately 1-um 235 diameter green and red microbeads (Thermo Scientific Fluoro-Max G0100 ex. 468 / em. 508 nm 236 237 and R0100 ex. 542 / em. 612 nm). Green and red microbead (stock of 1% solids, approximately 2.5×10^7 microbeads/µL) barcode labels were made from five dilutions in water (5.1 × 10⁵, 1.3 × 238 10^6 , 2.3×10^6 , 3.6×10^6 , 5.1×10^6 beads/µL). The five dilutions of each microbead color were 239 240 mixed equally in a combinatorial manner to create a total of 24 barcode labels. The concentration combinations are detailed in Table S1.[†] Four concentrations of blue microbeads (Thermo 241 242 Scientific Fluoro-Max B0100 ex. 412 / em. 473 nm, 5.1×10^5 , 1.3×10^6 , 2.3×10^6 , 3.6×10^6 microbeads/ μ L from a stock of 1% solids, approximately 2.5 × 10⁷ microbeads/ μ L) were randomly 243 spread across 24 microbead-barcoded wells and used as a mock assay signal. For microbead 244 barcoded drop experiments, the oil pressure was set to 3 psig (P_{oil}) and the chamber pressure was 245 set to 2 psig (P_{water}). For the purpose of collecting 24 samples instead of 96, a modification to the 246 PIPE chip was made to allow drop outlet tubing to be directly connected to the drop collection 247 channels of the second layer of the device. This modification provided separate collection from 248 each quadrant of drop makers on the device where each quadrant is comprised of 24 drop makers. 249 A confocal image of the microbead barcoded drops captured in a drop array device²⁹ is shown in 250

Fig. S2.[†] The drop library was collected and re-injected into a secondary device for use with a custom drop fluorescence detection system (See ESI *Barcoded Drop Detection* and Fig. S3-4 for details).^{†22} The photomultiplier tube (PMT) gain control voltage was set to 0.32 V for microbead barcoded drop detection.

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256 Quantum Dot Barcodes

QDs of two colors (Thermo Scientific QD625 and QD705) were used as barcode labels by 257 preparing 12 QD625 (1.15×10^4 , 9.68×10^3 , 8.00×10^3 , 6.48×10^3 , 5.12×10^3 , 3.92×10^3 , 2.88×10^3 , 2.88×10^3 , 5.12×10^3 , 258 10^3 , 2.00×10^3 , 1.28×10^3 , 7.20×10^2 , 3.20×10^2 , 8.00×10^1 pM) and 16 QD705 (1.02×10^4 , 9.00259 $\times 10^3$, 7.84 $\times 10^3$, 6.76 $\times 10^3$, 5.76 $\times 10^3$, 4.84 $\times 10^3$, 4.00 $\times 10^3$, 3.24 $\times 10^3$, 2.56 $\times 3$, 1.96 $\times 10^3$, 260 1.44×10^3 , 1.00×10^3 , 6.40×10^2 , 3.60×10^2 , 1.60×10^2 , 4.00×10^1 pM) dilutions in water. The 261 12 and 16 dilutions were mixed equally in a combinatorial manner to create a total of 192 barcode 262 labels. The concentration combinations are detailed in Table S2.⁺ For drops containing QD 263 barcodes, the oil pressure (P_{oil}) was set to 8 psig while the chamber pressure (P_{water}) was set to 5 264 psig. The PIPE chip was operated twice to create 192 barcodes (96×2). The PMT control voltage 265 was set to 0.45 V for QD barcoded drop detection. 266

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268 Two-channel Fluorescence-activated Drop Sorting

Barcoded drops were injected into a microfluidic drop sorting device²² at a flowrate of 40 μ L/h and spacer oil (Novec 7500) without surfactant was injected at a flowrate of 800 μ L/h. A sorting electrode driven by a high voltage amplifier (Trek Model 2220-CE) and controlled by a custom LabVIEW program was used to pull drops into a collection channel. The sorting electrode provided a 400 μ s pulse of a 25 kHz, 400 V square wave signal when the drop fluorescence signal fell within the threshold values set for a specific barcode (1 - 1.2 V green channel, 0.15 - 0.25 V)red channel).

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277 **Results and Discussion**

278 **Drop Formation Characterization**

Drops were generated with the PIPE chip under a range of pressures for P_{water} and P_{oil} to 279 identify combinations that produce uniformly-sized drops. We measured D_{drop} and its distribution, 280 as quantified by the coefficient of variation (CV) of D_{drop} , at each pressure combination (Fig. 3a). 281 To observe drop formation across the range of pressures tested, high speed videos of drop 282 283 formation in the PIPE chip were captured at four extreme water and oil pressure combinations. 284 The four combinations are labeled with corresponding symbols in Fig. 3a-c: high water pressure (\blacksquare , $P_{\text{water}} = 6 \text{ psig and } P_{\text{oil}} = 3 \text{ psig}$), low combined pressure (\triangledown , $P_{\text{water}} = 2 \text{ psig and } P_{\text{oil}} = 3 \text{ psig}$), 285 high combined pressure (\blacktriangle , $P_{water} = 8$ psig and $P_{oil} = 12$ psig) and high oil pressure (\blacklozenge , $P_{water} = 2$ 286 psig and $P_{oil} = 12$ psig). Representative images of Videos S1a-d⁺ are presented in Fig. 3b. At high 287 water pressure (**•**), the greater water volume fraction led to each drop filling the full length of the 288 exit channel and partially extending into the collection channel before drop break-up occurred, a 289 phenomenon not seen with the other three combinations. As drop formation is no longer fully 290 constrained by the flow focusing junction, this extension of the drop into the collection channel 291 may explain the greater polydispersity at this condition, where $D_{drop} = 83.9 \pm 12.5 \ \mu\text{m}$. At low and 292 high combined pressure conditions ($\mathbf{\nabla}, \mathbf{A}$, both at $P_{\text{water}}/P_{\text{oil}} = 0.67$), drop formation occurred 293 within the exit channel, creating smaller, more uniform drops at the high pressure condition (\blacktriangle , 294 $D_{\text{drop}} = 56.2 \pm 2.6 \,\mu\text{m}$) than the low pressure condition (∇ , $D_{\text{drop}} = 68.8 \pm 5.0 \,\mu\text{m}$). Drop uniformity 295 did not improve with a higher oil volume fraction (\blacklozenge , CV = 6.0%) when compared to the high 296

combined pressure condition (\blacktriangle , CV = 4.6%). As the oil volume fraction was increased, drop formation was limited by the 50-µm width of the exit channel, a characteristic of drop formation in the dripping regime.^{30, 31} The dripping regime forms highly uniform drops, whose diameters are largely determined by the flowrates and the width of the flow focusing junction.^{30, 32, 33} For all the conditions observed, drop break-up occurred at the flow focusing junction which indicates that drop formation was in the dripping regime.^{30, 32}

The size of drops formed in the dripping regime can be described by a drop scaling law³⁴, thereby providing a predictive drop formation model for the PIPE chip. A drop scaling law³⁴ developed for T-junction geometries, and shown to be applicable for flow focusing geometries³⁵, is fit to the data and defined as:

$$\frac{L_{drop}}{w_{channel}} = 1 + \alpha \frac{Q_{water}}{Q_{oil}}$$
(Eq. 1)

where L_{drop} is defined as the length of a drop in the channel measured end to end, $w_{channel}$ is the 308 width of the channel (50 μ m), $Q_{\text{water}}/Q_{\text{oil}}$ is the volumetric flowrate ratio, and α is a geometric 309 constant of order 1. To apply the scaling law to our data, pressure ratios are converted to flowrate 310 ratios using a standard curve (Fig. S1)[†]. We converted L_{drop} from Eq. 1 to drop volume V_{drop} by 311 approximating the shape of the drop as a capsule geometry when drops are elongated within the 312 microfluidic channel (see ESI PIPE Chip Drop Formation Characterization for details)[†]. The best 313 fit of the drop scaling law with V_{drop} plotted as a function of Q_{water}/Q_{oil} is presented as a dotted line 314 in Fig. 3c with $\alpha = 1.70$ and an $R^2 = 0.793^{34}$ Drops produced using the PIPE chip can be adjusted 315 by tuning the pressures applied to the oil and aqueous phases, thereby adjusting $Q_{\text{water}}/Q_{\text{oil}}$ and 316 enabling the generation of drops within a desired range of diameters (\approx 50-90 µm). 317

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Drop size distribution improved from a CV of 14.9% to 4.6% as $Q_{\text{water}}/Q_{\text{oil}}$ was decreased 319 from 2 to 0.17 (Fig. 3c). When $Q_{\text{water}}/Q_{\text{oil}} < 1$, further reductions in $Q_{\text{water}}/Q_{\text{oil}}$ have diminishing 320 effects on V_{drop} . In this case, the minimum drop volume (65 pL, correlating to $D_{\text{drop}} = 50 \ \mu\text{m}$) is 321 reached as $Q_{\text{water}}/Q_{\text{oil}} \rightarrow 0$ due to the 50-µm width of the drop channel ($L_{\text{drop}} \approx w_{\text{channel}}$ according 322 to Eq. 1). Interestingly, despite the low and high combined pressure conditions having the same 323 pressure ratio and similar measured flowrate ratios ($Q_{\text{water}}/Q_{\text{oil}} = 0.43$ or 0.53, respectively), they 324 produced drops with different V_{drop} , from 173 ± 37 pL to 94 ± 13 pL. The difference in V_{drop} for 325 similar $Q_{\text{water}}/Q_{\text{oil}}$ at higher oil flowrates may be attributed to an increased oil phase capillary 326 number Ca which represents the ratio of the viscous drag to surface tension forces acting on a 327 drop. A higher oil phase Ca corresponds to increased drag at the drop formation junction which 328 leads to faster break-up, resulting in a decreased V_{drop} .^{30, 35} 329



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Fig. 3 Characterization of drop sizes produced by the PIPE chip. (a) Drop diameter average, 331 standard deviation, and CV at various water pressures P_{water} and oil pressures P_{oil} . For additional 332 visualization, the relative size of each open circle corresponds to the relative mean drop diameter 333 measured. Solid shapes indicate conditions used for high-speed image capture in (b). (b) High-334 speed image capture of drop formation, ordered by descending D_{drop} , for high water pressure (\blacksquare , 335 $P_{\text{water}} = 6 \text{ psig and } P_{\text{oil}} = 3 \text{ psig}, P_{\text{water}}/P_{\text{oil}} = 2)$, low combined pressure ($\mathbf{\nabla}, P_{\text{water}} = 2 \text{ psig and } P_{\text{oil}}$ 336 = 3 psig, $P_{\text{water}}/P_{\text{oil}} = 0.67$), high combined pressure (\blacktriangle , $P_{\text{water}} = 8$ and $P_{\text{oil}} = 12$ psig, $P_{\text{water}}/P_{\text{oil}} = 12$ 337 0.67), and high oil pressure (\blacklozenge , $P_{water} = 2$ psig and $P_{oil} = 12$ psig, $P_{water}/P_{oil} = 0.17$) conditions. Scale 338 bars = 100 μ m. (c) Corresponding drop volumes V_{drop} versus the volumetric flowrate ratio 339 340 $Q_{\text{water}}/Q_{\text{oil}}$ (open circles or solid shapes). V_{drop} scales with $Q_{\text{water}}/Q_{\text{oil}}$ following a drop scaling law (dotted black line).³⁴ Error bars represent one standard deviation from the mean. 341

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345 Optimizing Barcode Discrimination in Drop Libraries

Drop libraries barcoded with fluorescence-based barcodes have recently reached a label 346 count of 1,050 unique combinations with the use of four dye colors.⁴ Lanthanide nanophosphors 347 are capable of creating up to 1,023 unique labels with a six-color combination, but have yet to be 348 used in drop libraries.³⁶ However, using a large number of barcode colors may not be 349 advantageous, as the overlap of emission spectra between the fluorescent reporters can limit the 350 practical number of colors that can be used in an assay.^{37, 38} Simply reducing the number of barcode 351 colors to one or two and varying their concentrations can greatly expand the range of usable 352 reporters. Thus, the PIPE chip was used to generate two fluorescently barcoded drop libraries from 353 two-color combinations of either microbeads or QDs. Fluorescent particles were used to prevent 354 diffusion of the barcode labels between drops.²³ The libraries were prepared by mixing different 355 ratios of each color to form distinct combinations on a microtiter plate (see Materials and 356 Methods). The polystyrene microbead drop library was comprised of 24 barcodes made from ratios 357 of green and red fluorescent polystyrene microbeads while the QD drop library was comprised of 358 359 192 barcodes made from ratios of QDs with peak emissions at 625 and 705 nm. The PIPE chip was used to simultaneously encapsulate all the barcoded contents of the plate in 2 min, creating 360 approximately 3.75×10^5 drops ($D_{drop} = 50 \ \mu m$) per barcode. Barcoded drops were reinjected into 361 a microfluidic device for analysis using a laser-induced fluorescence detection system.²² Drop 362 fluorescence was measured as the drops flowed past a laser at approximately 300 Hz. 363

Contributions from spectral crosstalk and sources of noise limit the number of barcodes that can be identified after library reinjection. The narrow emission spectra of QDs leads to less spectral crosstalk between each barcoding color compared to the microbeads. This can be observed in the raw data of the 24 microbead fluorescence intensities (Fig. 4a) compared to the 192 QD

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fluorescence intensities (Fig. 4b). Due to the wide emission spectra of the microbeads, the emission of the green microbeads overlaps with the red microbeads. This causes barcodes with high green intensity to appear more red, skewing the data to the upper right (Fig. 4a). The effect of spectral crosstalk also skews the QD data (Fig. 4b), but due to the narrow emission spectra of the QDs, the effect is lower in magnitude compared to the microbeads.

We applied a clustering algorithm, Density-Based Spatial Clustering of Applications with 373 374 Noise (DBSCAN), to identify and separate "clusters" of specific barcoded drops within the libraries.²⁴ Densely packed data points are assigned to clusters by DBSCAN while outlier data 375 points in low-density regions are marked as noise. When the data are graphed on a linear plot, 376 377 DBSCAN was able to group 70% of the 1.31×10^4 drops containing microbeads into 24 clusters (Fig. 4a, blue dots) and 30% as noise (Fig. 4a, black dots), with a mean of 399 ± 201 drops per 378 barcode (CV = 50.4%). However, DBSCAN was not able to completely identify clusters in the 379 OD raw data (Fig. 4b, blue dots). Of the clusters identified, DBSCAN grouped 76% of the $1.27 \times$ 380 10^5 drops containing ODs with a range of 15 to 6.033 drops per barcode (mean of 508 ± 478 drops 381 and CV = 94.1%). A significant number of clusters were mislabeled as noise (Fig. 4b, upper right 382 black dots) due to the large variability in cluster density. 383

To better understand the variability between barcode clusters, we identify two major sources of variation in our data, both a direct consequence of particle size: *Poisson loading* for microbeads and *shot noise* for QDs. The loading of approximately 1-µm diameter fluorescent microbeads into drops is dependent upon Poisson statistics. The fluorescence signal obtained from drops containing microbeads follows a Poisson distribution due to the discrete nature of particle loading in drops.²² The Poisson distribution is described by the equation:

$$P = \frac{\lambda^k e^{-\lambda}}{k!}$$
(Eq. 2)

where P is the probability distribution of drops that contain k number of particles with a mean 391 number of particles per drop λ . Variability inherent to Poisson loading²² is represented by the 392 standard deviation of the number of particles in drops $\sigma_{\text{narticle}} = \lambda^{1/2}$. We plot a representative subset 393 394 of five red microbead barcodes (Fig. 4c, black dots) corresponding to the clusters in Fig. 4a (dashed red boxes). The subset is compared to estimated Poisson distributions centered around the 395 microbead loading concentrations $\lambda = 33, 83, 149, 232$, and 333 beads/drop where λ is converted 396 397 to voltage using an experimentally verified linear standard curve relating PMT output voltage to microbead concentration (beads/drop, λ) (Fig. S7a).[†] The probability of microbead distributions 398 (Fig. 4c, dashed red line) closely tracks the PMT voltage measurements of the red microbead data 399 (Fig. 4c, black dots) with $R^2 = 0.931$. 400

When the particle size is far below the objective resolution, for example in the case of ODs 401 that are approximately 10 nm in diameter, the variability in drop fluorescence is no longer a 402 function of the number of discrete particles in drops, but is instead governed by the shot noise of 403 the PMT. Shot noise is inherent to counting photons with a PMT and contributes to the 404 fluorescence signal in low light environments such as high-speed detection of drop fluorescence.^{39,} 405 ⁴⁰ We plot the signal distributions of a 12 OD625 barcode subset of the OD barcoded library (Fig. 406 4d, black dots) corresponding to the clusters outlined in Fig 4b (dashed green boxes). The Schottky 407 equation approximates shot noise^{40, 41} in which the standard deviation of the PMT voltage σ_{shot} is 408 proportional to the square root of the mean PMT voltage $\mu_{intensity}$ (see ESI Schottky Equation for 409 details).† The subset of QD data is compared to normal distributions defined by $\mu_{\text{intensity}}$ and σ_{shot} 410 for each QD barcode. The value of $\mu_{intensity}$ is determined by an experimentally verified linear 411 standard curve relating PMT output voltage to QD concentration (nM) (Fig. S7b, Eq. S1)[†]. The 412

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413 probability of QD distributions (Fig 4d, dashed green line) closely tracks the PMT voltage 414 measurements of the QD625 data (Fig 4d, black dots) with $R^2 = 0.852$.

To demonstrate that the remainder of the experimental microbead and QD barcode data 415 follow either Poisson loading or shot noise, barcode clusters are manually grouped and compared 416 to theoretical estimates of σ_{particle} (Fig. 4c-d, inset, dashed red line) and σ_{shot} (Fig. 4c-d, inset, dotted 417 green line, see ESI *Calculation of Noise* for details).[†] Drop library fluorescence data are manually 418 grouped by drawing lines around each cluster by eye (Fig. S8)⁺ to isolate individual barcode signal 419 populations for each PMT channel. The mean μ_{barcode} and standard deviation σ_{barcode} of the 420 manually-segmented 24 microbead and 192 QD signal distributions are calculated for each PMT 421 channel, yielding 48 and 384 values of μ_{barcode} and σ_{barcode} . The σ_{barcode} is plotted against $\mu_{\text{barcode}}^{1/2}$ for 422 423 each grouped microbead and QD barcode population (Fig. 4c-d, inset, black dots). The experimental σ_{barcode} of the microbeads closely follows the theoretical estimate of particle loading 424 noise σ_{particle} (Fig. 4c, inset, dashed red line). The σ_{barcode} is approximately an order of magnitude 425 greater than the theoretical estimate of shot noise σ_{shot} (Fig. 4c, inset, dotted green line). Therefore, 426 across all drops, the discrimination of microbead barcode signals is limited by particle loading 427 noise as the dominant source of variation. By contrast, the experimental σ_{barcode} of the QDs closely 428 follows the theoretical estimate of shot noise σ_{shot} (Fig. 4d, inset, dotted green line) and is 429 approximately an order of magnitude greater than the estimate of particle loading noise σ_{particle} 430 431 (Fig. 4d, inset, dashed red line), indicating the data is shot noise-limited. The narrow emission spectrum of the QDs results in a 1-2 log decrease of σ_{shot} compared to $\sigma_{particle}$. This enables an 8× 432 increase in unique barcode concentrations obtained with QDs compared to microbeads (192 versus 433 434 24).

As signal variation depends upon Poisson loading for microbeads ($\sigma_{\text{particle}} \propto \lambda^{1/2}$) and shot 435 noise for QDs ($\sigma_{\text{shot}} \propto \mu^{1/2}$), scaling the intensity data for both barcode libraries by a square root 436 function linearizes the noise. This scaling spaces each barcode grouping as shown in Fig. 4e-f (Fig. 437 S5-6)[†]. When DBSCAN is applied to the scaled data, the increased spacing allows for improved 438 clustering of each barcode compared to the unscaled raw data (Fig. 4a-b). Of the 1.31×10^4 439 microbead barcoded drops detected, DBSCAN was able to group 74.8% of the data into 24 clusters 440 441 (Fig. 4e, blue dots) and identify 25.2% as noise (Fig. 4e, black dots) with a mean of 408 ± 62 drops per barcode (CV = 15.2%). The CV of clustered square root scaled data is greatly reduced from 442 50.4% with the linearly scaled data (Fig. 4a) to 15.2% with the square root scaled data (Fig. 4e). 443 444 Additionally, a square root scaling of the QD data allows DBSCAN to correctly identify 188 out of the 192 of barcoded drop populations where the missing four populations are due to two clogged 445 drop makers on the PIPE chip and are indicated by the yellow ovals (Fig. 4f). Of the 1.27×10^5 446 447 QD barcoded drops detected, DBSCAN was able to group 85.4% of data into 188 clusters (Fig. 4f, blue dots) and identify 14.6% as noise (Fig. 4f, black dots) with a mean barcode cluster size of 448 576 ± 88 drops (CV = 15.3%). Once again, the CV is greatly reduced from 94.1% with the linearly-449 450 scaled quantum dot data to 15.5% with the square root-scaled data.

Previous examples of drop libraries using one or two fluorescence dye colors have realized up to eight¹⁰ or sixteen¹¹ unique labels. Using the PIPE chip, we achieved a total of 188 discrete barcodes with two-color combinations of QDs. To our knowledge, this is the largest two-color fluorescent barcode combination in drops to date. Additionally, the effect of particle size on signal noise can be described empirically and used for future experiments to inform the selection of barcode concentrations.



Fig. 4 Analysis of microbead and OD barcoded drop libraries. Scatter plots of (a) microbead and 459 (b) QD fluorescence intensity in the drop library. Clusters identified by DBSCAN are indicated in 460 blue while noise is in black. Probability distributions of (c) five red microbead barcoded drop 461 populations (black dots) plotted against the particle loading noise estimate (dashed red line, $R^2 =$ 462 0.931) and (d) twelve QD625 barcoded drop populations (black dots) plotted against the shot noise 463 estimate (dotted green line, $R^2 = 0.852$). Solid black lines guide the eye for the measured microbead 464 and QD625 data. Inset (c-d): standard deviations of each barcode σ_{barcode} (black dots) plotted 465 against $\mu_{\text{barcode}}^{1/2}$ with estimates for σ_{particle} (dashed red line) and σ_{shot} (dotted green line). Scatter 466 plots of (e) microbead and (f) QD drop library data scaled by $V^{1/2}$. Clusters identified by DBSCAN 467 are indicated in blue while noise is in black. Missing clusters in (f) are due to two clogged channels 468 in the PIPE chip and are indicated by dotted yellow ovals. 469 470

471 Sample Isolation Using Fluorescence-activated Drop Sorting

To demonstrate the utility of the PIPE chip, fluorescence-activated drop sorting^{21, 22} was 472 performed to isolate drops of a single barcode population within a drop library of 24 green and red 473 microbead combinations spiked with four concentrations of blue microbeads. We verify that the 474 desired green and red barcode combination was isolated by detecting a single concentration of the 475 blue microbeads. A barcode from the drop library was chosen by designating a box with upper and 476 477 lower fluorescence intensity bounds in the green and red fluorescence channels (Fig. 5a, red box). Recovery of the desired barcode population is confirmed by performing flow-based fluorescence 478 detection on the sorted drops, vielding an isolated barcode cluster with intensity bounds close to 479 480 those originally chosen in the green and red channels (Fig. 5b). However, there is an observed shift in fluorescence signal distribution from pre- to post-sort (Fig. 5a-b) where the post-sort data has 481 shifted by ≈ 0.2 V along the x-axis. This shift is likely caused by run-to-run variation arising from 482 the positioning of the laser in the device channel. Post-processing of the sorted drop data using 483 DBSCAN provides a clear distinction between the target barcode population (Fig. 5b, red dots) 484 and the outlier data points (Fig. 5b, open black circles). The outlier points comprise 7.5% of the 485 drop data. 486

The four populations of blue microbead-barcoded drops were detected in the pre-sort drop library (Fig. 5c). Fluorescence detection of the sorted drops yielded a single blue microbead population with few outliers (Fig. 5d), matching the highest blue microbead concentration (Fig. 5c, arrow). DBSCAN clustering of corresponding green and red fluorescence identifies these outliers (Fig. 5d, black bars) and the target sorted population (Fig. 5d, red bars). The outliers comprise 5.9% of the sorted population, in close agreement with the data corresponding to the green and red barcoded drops (Fig. 5b). These results demonstrate the ability to isolate a single

494 barcoded population from a drop library created using the PIPE chip, critical for performing495 downstream assays.



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Fig. 5 Fluorescence-activated drop sorting of a microbead-barcoded drop library. (a) Fluorescence 497 intensity of barcoded drops before sorting. The sorted region is indicated by the red box. (b) 498 Fluorescence intensity of barcoded drops after sorting. DBSCAN is used to separate the outlier 499 data points (open black circles) from the target barcode population (red dots). (c) Distribution of 500 four concentrations of blue microbead drops within the drop library. (d) Distribution of blue 501 502 microbeads in the sorted barcoded drop population shows a single peak corresponding to the largest concentration of blue microbeads. DBSCAN is used to separate the outliers (black bars) 503 from the target sorted population (red bars). 504

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509 **Conclusions**

510 Here we have demonstrated tunable parallel production of 50 to 90 µm diameter drops containing upwards of 96 different loading conditions from a microtiter plate, improving upon the 511 previously published limit of 24.²⁰ By scaling the signal noise with the square root of the intensity, 512 barcoded drop libraries comprised of 24 microbead barcodes or 192 QD barcodes are 513 distinguishable using DBSCAN.²⁴ Barcode number is ultimately limited by microbead or QD 514 515 signal resolution. As a function of size, signal resolution between larger microbeads was limited by Poisson loading noise while the signals from the smaller QD barcodes were limited by shot 516 noise. This empirical relationship found between signal noise and barcode concentration can be 517 used to quickly prototype barcode label concentrations for future experiments. Utilizing two-color 518 combinations of QDs, we achieved a total of 188 discrete barcodes, the largest two-color 519 fluorescence barcode combination in drops published to date. The addition of a third QD color, 520 offering up to 16 unique concentrations, would enable QDs to easily index multiple 384-well 521 microtiter plates using as many as 3,072 unique barcodes $(12 \times 16 \times 16)$, far surpassing what has 522 been achieved with four color combinations (1,050 labels).⁴ Furthermore, we have shown that 523 barcoded populations can be selectively sorted with minimal error (5.9-7.5%), demonstrating that 524 downstream analysis of a specific sample population is possible. By reducing sample 525 encapsulation time and enabling rapid, parallel generation of a barcoded library directly from a 526 microtiter plate, we envision that the PIPE chip will further advance multiplexed assaying in 527 applications including combinatorial drug screening,^{3, 10} DNA microarray analysis,¹¹ or enzyme 528 activity screening.¹² 529

531 **Conflicts of Interest**

532 There are no conflicts to declare.

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534 Acknowledgments

535 This work was supported by Defense Advanced Research Projects Agency (DARPA) grant

536 W911NF-17-2-0034, National Institutes of Health (NIH) 1R21Al151923, and National Science

537 Foundation (NSF) CAREER DMR-1753352. The work at Harvard was supported in part by the

538 NSF through the Harvard MRSEC (DMR-2011754). We thank, Joshua Ricouvier, Stan Cotreau

539 for help with machining, and Betsey Pitts for help with confocal imaging. R.A.S. gratefully

acknowledges financial support from the German Research Foundation (DFG), grant SP 1282/1-

541 1. G.K.Z. acknowledges financial support from Montana State University Office of the Provost.

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543 Author Contributions

G.K.Z., R.A.S., A.R.A., D.A.W. and C.B.C. designed research; G.K.Z., R.A.S, C.W.H., and R.A.
performed research; G.K.Z. and R.A.S. analyzed data; and G.K.Z., R.A.S., C.W.H., D.A.B., and
C.B.C. wrote the manuscript.

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553 **References**

554 1. J. J. Agresti, E. Antipov, A. R. Abate, K. Ahn, A. C. Rowat, J.-C. Baret, M. Marquez, A. M. Klibanov, A. D. Griffiths and D. A. Weitz, *Proceedings of the National Academy of* 555 Sciences, 2010, 107, 4004-4009. 556 M. T. Guo, A. Rotem, J. A. Heyman and D. A. Weitz, Lab on a Chip, 2012, 12, 2146-557 2. 2155. 558 A. Kulesa, J. Kehe, J. E. Hurtado, P. Tawde and P. C. Blainey, Proceedings of the 559 3. National Academy of Sciences, 2018, 115, 6685-6690. 560 C. M. Ackerman, C. Myhrvold, S. G. Thakku, C. A. Freije, H. C. Metsky, D. K. Yang, H. 561 4. Y. Simon, C. K. Boehm, T.-S. F. Kosoko-Thoroddsen and J. J. N. Kehe, Nature, 2020, 1-562 6. 563 564 5. O. Scheler, K. Makuch, P. R. Debski, M. Horka, A. Ruszczak, N. Pacocha, K. Sozański, O.-P. Smolander, W. Postek and P. J. S. r. Garstecki, Scientific Reports (Nature Publisher 565 Group), 2020, 10, 1-8. 566 A. M. Klein, L. Mazutis, I. Akartuna, N. Tallapragada, A. Veres, V. Li, L. Peshkin, D. A. 567 6. 568 Weitz and M. W. J. C. Kirschner, Cell, 2015, 161, 1187-1201. A. Rotem, O. Ram, N. Shoresh, R. A. Sperling, A. Goren, D. A. Weitz and B. E. 569 7. Bernstein, Nature biotechnology, 2015, 33, 1165-1172. 570 8. A. Rotem, O. Ram, N. Shoresh, R. A. Sperling, M. Schnall-Levin, H. Zhang, A. Basu, B. 571 572 E. Bernstein and D. A. Weitz, *PloS one*, 2015, 10, e0116328. 573 9. E. Z. Macosko, A. Basu, R. Satija, J. Nemesh, K. Shekhar, M. Goldman, I. Tirosh, A. R. Bialas, N. Kamitaki and E. M. Martersteck, Cell, 2015, 161, 1202-1214. 574 E. Brouzes, M. Medkova, N. Savenelli, D. Marran, M. Twardowski, J. B. Hutchison, J. 575 10. M. Rothberg, D. R. Link, N. Perrimon and M. L. Samuels, Proceedings of the National 576 577 Academy of Sciences, 2009, 106, 14195-14200. A. R. Abate, T. Hung, R. A. Sperling, P. Mary, A. Rotem, J. J. Agresti, M. A. Weiner and 578 11. D. A. Weitz, Lab on a Chip, 2013, 13, 4864-4869. 579 12. C. H. Chen, M. A. Miller, A. Sarkar, M. T. Beste, K. B. Isaacson, D. A. Lauffenburger, 580 L. G. Griffith and J. Han, Journal of the American Chemical Society, 2013, 135, 1645-581 1648. 582 13. J. Kehe, A. Kulesa, A. Ortiz, C. M. Ackerman, S. G. Thakku, D. Sellers, S. Kuehn, J. 583 Gore, J. Friedman and P. C. Blainey, Proceedings of the National Academy of Sciences, 584 2019, 116, 12804-12809. 585

586 587 588	14.	O. J. Miller, A. El Harrak, T. Mangeat, J. C. Baret, L. Frenz, B. El Debs, E. Mayot, M. L. Samuels, E. K. Rooney, P. Dieu, M. Galvan, D. R. Link and A. D. Griffiths, <i>Proceedings of the National Academy of Sciences</i> , 2012, 109 , 378-383.
589 590	15.	T. S. Kaminski, S. Jakiela, M. A. Czekalska, W. Postek and P. Garstecki, <i>Lab on a Chip</i> , 2012, 12 , 3995-4002.
591 592	16.	T. D. Rane, H. C. Zec and TH. Wang, <i>Journal of laboratory automation</i> , 2012, 17 , 370-377.
593 594	17.	J. Clausell-Tormos, A. D. Griffiths and C. A. Merten, <i>Lab on a Chip</i> , 2010, 10 , 1302-1307.
595 596	18.	MP. N. Bui, C. A. Li, K. N. Han, J. Choo, E. K. Lee and G. H. Seong, <i>Analytical chemistry</i> , 2011, 83 , 1603-1608.
597 598	19.	J. Lim, O. Caen, J. Vrignon, M. Konrad, V. Taly and JC. Baret, <i>Biomicrofluidics</i> , 2015, 9, 034101.
599 600 601	20.	L. A. Bawazer, C. S. McNally, C. J. Empson, W. J. Marchant, T. P. Comyn, X. Niu, S. Cho, M. J. McPherson, B. P. Binks, A. deMello and F. C. Meldrum, <i>Science Advances</i> , 2016, 2 .
602 603 604	21.	J. C. Baret, O. J. Miller, V. Taly, M. Ryckelynck, A. El-Harrak, L. Frenz, C. Rick, M. L. Samuels, J. B. Hutchison, J. J. Agresti, D. R. Link, D. A. Weitz and A. D. Griffiths, <i>Lab on a Chip</i> , 2009, 9 , 1850-1858.
605 606	22.	L. Mazutis, J. Gilbert, W. L. Ung, D. A. Weitz, A. D. Griffiths and J. A. Heyman, <i>Nature protocols</i> , 2013, 8 , 870-891.
607 608	23.	P. Gruner, B. Riechers, B. Semin, J. Lim, A. Johnston, K. Short and JC. Baret, <i>Nature communications</i> , 2016, 7, 1-9.
609	24.	M. Ester, HP. Kriegel, J. Sander and X. Xu, Portland, OR, 1996.
610	25.	S. W. Lim, T. M. Tran and A. R. Abate, <i>PloS one</i> , 2015, 10, e0113549.
611 612	26.	H. Zhang, S. K. Cockrell, A. O. Kolawole, A. Rotem, A. W. Serohijos, C. B. Chang, Y. Tao, T. S. Mehoke, Y. Han and J. S. Lin, <i>Journal of virology</i> , 2015, 89 , 7722-7734.
613 614	27.	Y. Tao, A. Rotem, H. Zhang, S. K. Cockrell, S. A. Koehler, C. B. Chang, L. W. Ung, P. G. Cantalupo, Y. Ren and J. S. J. C. Lin, <i>ChemBioChem</i> , 2015, 16 , 2167-2171.
615 616 617	28.	C. Holtze, A. C. Rowat, J. J. Agresti, J. B. Hutchison, F. E. Angile, C. H. Schmitz, S. Koster, H. Duan, K. J. Humphry, R. A. Scanga, J. S. Johnson, D. Pisignano and D. A. Weitz, <i>Lab Chip</i> , 2008, 8 , 1632-1639.

618	29.	C. H. Schmitz, A. C. Rowat, S. Köster and D. A. Weitz, <i>Lab on a Chip</i> , 2009, 9, 44-49.
619	30.	T. Cubaud and T. G. Mason, Physics of Fluids, 2008, 20, 053302.
620	31.	J. D. Tice, A. D. Lyon and R. F. Ismagilov, Analytica chimica acta, 2004, 507, 73-77.
621 622	32.	D. Funfschilling, H. Debas, HZ. Li and T. Mason, <i>Physical Review E</i> , 2009, 80 , 015301.
623 624	33.	P. Garstecki, H. A. Stone and G. M. Whitesides, <i>Physical review letters</i> , 2005, 94 , 164501.
625 626	34.	P. Garstecki, M. J. Fuerstman, H. A. Stone and G. M. Whitesides, <i>Lab on a Chip</i> , 2006, 6 , 437-446.
627 628	35.	A. Abate, A. Poitzsch, Y. Hwang, J. Lee, J. Czerwinska and D. Weitz, <i>Physical Review E</i> , 2009, 80 , 026310.
629 630	36.	H. Q. Nguyen, B. C. Baxter, K. Brower, C. A. Diaz-Botia, J. L. DeRisi, P. M. Fordyce and K. S. Thorn, <i>Advanced optical materials</i> , 2017, 5 , 1600548.
631	37.	M. Han, X. Gao, J. Z. Su and S. Nie, Nature biotechnology, 2001, 19, 631.
632	38.	H. Lee, J. Kim, H. Kim, J. Kim and S. Kwon, Nature materials, 2010, 9, 745-749.
633 634	39.	A. Huebner, M. Srisa-Art, D. Holt, C. Abell, F. Hollfelder, A. Demello and J. J. C. c. Edel, <i>Chemical communications</i> , 2007, 1218-1220.
635	40.	R. L. McClain and J. C. Wright, Journal of Chemical Education, 2014, 91, 1455-1457.
636	41.	W. Schottky, Annalen der Physik, 1918, 362, 541-567.
637 638		