

Lab on a Chip

Accepted Manuscript



This is an *Accepted Manuscript*, which has been through the Royal Society of Chemistry peer review process and has been accepted for publication.

Accepted Manuscripts are published online shortly after acceptance, before technical editing, formatting and proof reading. Using this free service, authors can make their results available to the community, in citable form, before we publish the edited article. We will replace this *Accepted Manuscript* with the edited and formatted *Advance Article* as soon as it is available.

You can find more information about *Accepted Manuscripts* in the [Information for Authors](#).

Please note that technical editing may introduce minor changes to the text and/or graphics, which may alter content. The journal's standard [Terms & Conditions](#) and the [Ethical guidelines](#) still apply. In no event shall the Royal Society of Chemistry be held responsible for any errors or omissions in this *Accepted Manuscript* or any consequences arising from the use of any information it contains.

Size and Deformability based Separation of Circulating Tumor Cells from Castrate Resistant Prostate Cancer Patients using Resettable Cell Traps

Xi Qin^a, Sunyoung Park^a, Simon P. Duffy^a, Kerryn Matthews^a, Richard R. Ang^a, Tilman Todenhöfer^b, Hamid Abdi^b, Arun Azad^c, Jenny Bazov^b, Kim N. Chi^{abc}, Peter C. Black^{ab}, and Hongshen Ma^{ab}

a Department of Mechanical Engineering, University of British Columbia, 2054-6250 Applied Science Lane, Vancouver, BC, Canada V6T 1Z4

b Vancouver Prostate Centre, Vancouver General Hospital, Vancouver, BC, Canada

c BC Cancer Agency – Vancouver Cancer Centre, Vancouver General Hospital, Vancouver, BC, Canada

ABSTRACT

The enumeration and capture of circulating tumor cells (CTCs) are potentially of great clinical value by offering a non-invasive means to access tumor materials to diagnose disease and monitor treatment efficacy. Conventional immunoenrichment of CTCs may fail to capture cells with low surface antigen expression. Micropore filtration presents a compelling label-free alternative that enriches for CTCs using their biophysical rather than biochemical characteristics. However, this strategy is prone to clogging of the filter microstructure, which dramatically reduces selectivity after processing large numbers of cells. Here, we use the resettable cell trap (RCT) mechanism to separate cells based on their size and deformability using an adjustable aperture that can be periodically cleared to prevent clogging. After separation, the output sample is stained and analyzed using multi-spectral analysis, which provides a more sensitive and unambiguous method to identify CTC biomarkers than traditional immunofluorescence. We tested the RCT device using blood samples obtained from 22 patients with metastatic castrate-resistant prostate cancer while comparing the results with the established CellSearch[®] system. The RCT mechanism was able to capture ≥ 5 CTCs in 18/22 (82%) patients with a mean count of 257 in 7.5 ml of whole blood, while the CellSearch system found ≥ 5 CTCs in 9/22 (38%) patients with a mean count of 25. The $\sim 10X$ improvement in CTC capture rate provides significant more materials for subsequent analysis of these cells such as immunofluorescence, propagation by tissue culture, and genetic profiling.

31 INTRODUCTION

32 Circulating tumor cells (CTCs) are cells from primary or metastatic tumor sites that are shed into the
33 peripheral blood circulation. The enumeration and capture of CTCs in blood potentially has clinical value
34 by offering a non-invasive means to diagnose the presence of tumors, to monitor treatment efficacy and
35 to study evolving molecular alterations under therapy¹⁻³. Correlation between CTC counts and both
36 progression and overall survival have been reported in patients with various metastatic cancers⁴⁻⁸.
37 Current CTC separation platforms can be stratified into methods that involve biochemical selection and
38 biophysical selection⁹. Biochemical methods typically discriminate tumor cells from leukocytes based on
39 the expression of surface antigens such as the epithelial cell adhesion molecule (EpCAM). This approach
40 is currently employed by the CellSearch system (Janssen Diagnostics, USA), the only FDA-approved
41 commercial system for CTC enumeration, as well as many research systems currently in development¹⁰⁻
42¹³. A key limitation of this approach is the potential to miss CTCs because of the variability in the cell
43 surface markers for positive selection that prevent the efficient capture of CTCs. This loss can arise in
44 two ways: first, the heterogeneity of CTCs results in different expression levels of surface markers
45 among different cancer types and even within the same patient^{1,14}. Second, due to the epithelial to
46 mesenchymal transition (EMT), a subpopulation of CTCs, which are potentially highly aggressive, are
47 thought to lose expression of epithelial antigens¹⁵.

48 To compensate for this potential loss, recent research in this field has focused on label-free separation
49 of CTCs, based on differences in their biophysical properties relative to leukocytes. One approach is
50 micropore filtration which separates CTCs from hematological cells based on differences in size and
51 deformability^{16,17}. A key challenge of this approach is clogging of the filter microstructures, which occurs
52 after processing a large number of cells. Clogging causes unpredictable changes of the hydrodynamic
53 resistance of the filter resulting in reduced selectivity. Additionally, the retrieval of isolated CTCs is often
54 difficult or impossible since these methods typically trap and identify the captured cells on-chip, but
55 cannot release them for subsequent analysis¹⁶⁻¹⁹.

56 We previously developed a mechanism for chromatographic separation of cells based on their physical
57 differences using the transit speed of cells through a textured microfluidic²⁰. We then generalized this
58 method to create the resettable cell trap (RCT) mechanism, which uses an adjustable aperture to
59 capture cells based on their size and deformability, and can be periodically cleared to prevent clogging²¹.
60 Here, we developed an enhanced multiplexed version of this mechanism with improved selectivity and

61 throughput. This new chip successfully demonstrates high-sensitivity separation of CTCs from whole
62 blood of patients with metastatic castration-resistant prostate cancer (mCRPC). Unlabeled and viable
63 CTCs separated from patient blood samples were retrieved, identified via immunostaining, and could be
64 extracted for downstream analysis.

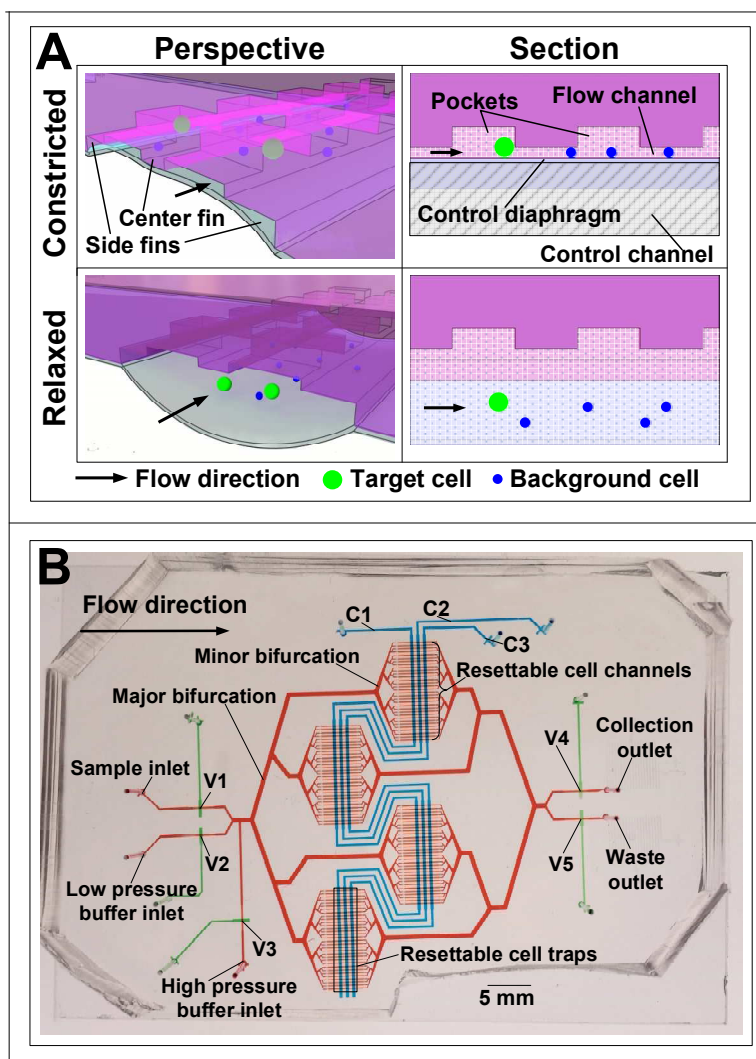
65

66 **DESIGN**

67 **Resettable Cell Trap Mechanism**

68 The resettable cell trap is a two-layer PDMS structure comprising a sample-carrying upper flow channel
69 and a lower fluid-filled control channel. Separating these two layers is a thin flexible diaphragm that can
70 be inflated by applying an external pneumatic pressure to control the geometry of the two
71 microchannels. Opposing the diaphragm, the surface of the flow channel is textured with two rows of
72 micro-pockets and a protruding center fin (Figure 1A). These microstructures and the diaphragm
73 combines to create an adjustable aperture that selectively traps and releases target cells. The position of
74 the diaphragm can be considered to have two states: a constricted state, where the diaphragm is in
75 contact with the textured surface to reduce the aperture of the flow channel; as well as a relaxed state,
76 where the diaphragm is deflected away from the textured surface to enlarge the aperture of the flow
77 channel (Figure 1A).

78



79

80 *Figure 1: The resettable cell trap. A: In the constricted state, the flow channel and diaphragm form an*
 81 *aperture to capture the more rigid target cells. In the relaxed state, target cells can be released and*
 82 *collected and the device is reset to its original state. B: Photograph of the multiplexed microfluidic device.*
 83 *The red filled channels are flow and resettable cell channels carrying sample. The blue filled channels (C1-*
 84 *C3) are the adjustable control diaphragms that trap the cells in the resettable cell traps (darker blue).*
 85 *The green filled channels (V1-V5) form the on/off valves that control the flow of sample.*

86 In the constricted state, the pressure in the control channel is greater than the flow channel and the
 87 diaphragm is deflected to come into contact with the center and side fins of the flow channel. The
 88 center fin and the two side fins act as the mechanical stop to limit the movement of the diaphragm and
 89 flatten it to create an approximately rectangular channel on either side of the center fin with a minimum
 90 size of 5 μm . Since the top and bottom boundary of the aperture is the most parallel at the center of the

91 channel, a flow focuser is used to center the cells upstream in the flow channels to provide a consistent
92 filtration aperture for the incoming cell stream ²¹. Furthermore, multiple micro-pockets at the trap area
93 line both sides of the center fin and temporarily hold the larger and more rigid cells to prevent them
94 from blocking the flow channel. This structure is capable of selectively capturing cells based on their
95 phenotypically distinct size and deformability.

96 In the relaxed state, the pressure in the control channel is less than the flow channel and the diaphragm
97 is deflected away from the textured surface of the flow channel. The aperture in this state is large
98 enough for all cells to pass through freely. By simply relaxing the diaphragm, the micro-pockets filled
99 with captured cells can be purged to empty the recesses and the channels are reset. This ability to
100 refresh the flow channel on demand is important to release captured cells and prevent clogging.

101 One of the key advantages of the RCT mechanism is its ability to create an adjustable aperture with well-
102 controlled geometry inside a microchannel. Previous adjustable mechanisms have employed only the
103 basic structure of the conventional rectangular membrane micro-valves, ²² which, when the diaphragm
104 is inflated, form two triangular openings at the two upper corners of the flow channel to close it off.
105 These triangular pores do not provide a well-controlled shape and therefore cannot provide a precisely
106 controlled aperture for separating cells. Consequently, these mechanisms have been restricted to the
107 separation of particles from suspension ²³. The RCT mechanism enables a precisely controlled separation
108 aperture by adding a center fin and two side fins to a rectangular microchannel. When deflected, the
109 flexible diaphragm is bisected by the center fin and flattens to make two rectangular channels with a
110 rectangular aperture that could be used to specifically select cells based on a combination of size and
111 deformability. Previously, we showed that this mechanism is capable of separating polymer microbeads
112 with less than 1 μm resolution and that whole blood could be filtered with a throughput of $\sim 900,000$
113 nucleated cells per hour ²¹.

114

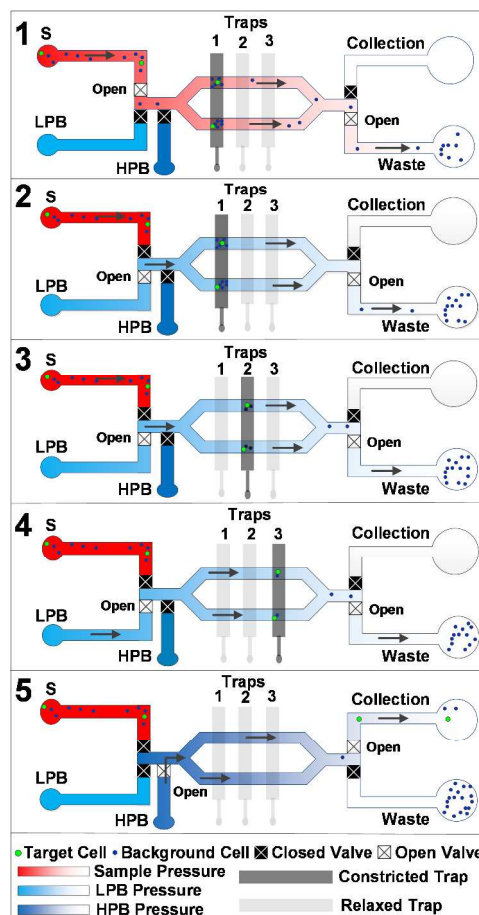
115 **Device Operation**

116 As shown in Figure 1B, the improved RCT device consists of 4 groups of 32 parallelized (128 channels in
117 total) resettable cell channels (shown in red) with 3 control diaphragm channels (C1-C3, shown in blue)
118 that make up 3 x 128 resettable cell traps (shown in darker blue). Bifurcation channels (minor and major)
119 are designed to connect the 128 channels and to evenly distribute cells into each cell trap channel²⁴. Five

120 on/off valves (V1-V5, shown in green) route the sample and buffers from inlet reservoirs into the
121 collection and waste reservoirs as required²².

122 Cell separation using this device involves a three-step cycle of filtration, purging, and collection. The
123 filtration step (Figure 2, Step 1) involves infusing cells from the sample inlet into the constricted cell trap.
124 The cell traps catch the larger and more rigid target cells while the smaller and less rigid leukocytes
125 traverse through to the waste reservoir. The purging step (Figure 2, Step 2) involves infusing buffer fluid
126 at a modest pressure while the cell trap is constricted. This process washes away the contaminant
127 leukocytes remaining in the cell traps. The collection step (Figure 2, Step 5) involves infusing buffer fluid
128 at a higher pressure with all the cell traps opened. All of the cells that are captured are released and
129 directed into the collection reservoir. This releasing flow is much faster than the filtration and purging
130 flow so as to produce high shear forces to remove cells that may have adhered to the walls of the cell
131 traps^{25,26}. The filtration step lasts 10 minutes, the purging step takes 5-10 seconds and the collection
132 step lasts 2-3 seconds. After the collection step, all cells are removed from the trap area and the device
133 is reset back to its initial state. This periodic refresh process prevents clogging and fouling to maintain
134 selectivity of the separation mechanism, and thereby allowing the filtration process to continue
135 perpetually.

136



137

138 *Figure 2: Cells from the inlet are filtered through three resettable cell traps before being flowed to the*
 139 *collection outlet. Captured cells are purged using a low-pressure buffer (LPB) flow, and collected with*
 140 *high-pressure buffer (HPB) flow. Step 1 is the initial filtration. Step 2 is the purging step. Step 3 & 4 are*
 141 *the 2x re-filtration steps and Step 5 is the collection step.*

142

143 Multi-filtration

144 In early experiments it was observed that cancer cells were primarily captured in the micro-pockets at
 145 the beginning of the constricted trap while white blood cells (WBCs) were captured on surfaces
 146 throughout the micro-pockets in the entire cell trap microstructure. This behavior suggests that cancer
 147 cells are captured because of mechanical constraint while leukocytes are captured because of non-
 148 specific adsorption. Interestingly, leukocytes that have adsorbed onto the walls of the cell traps can be
 149 released using greater shear stress applied through increased flow rate in the collection step, which
 150 suggests the potential to improve selectivity by filtering a sample multiple times. To investigate this

151 possibility, we cascaded three identical resettable cell traps in series (Figure 1B, shown in darker blue).
152 Cells captured in the first trap will be released, filtered again using the second trap, and again using the
153 third trap as shown in Figure 2 (Steps 1-4). Finally, all the trapped cells will be collected under high-
154 pressure buffer flow when all the traps are opened (Figure 2, Step 5).

155

156 RESULTS AND DISCUSSION

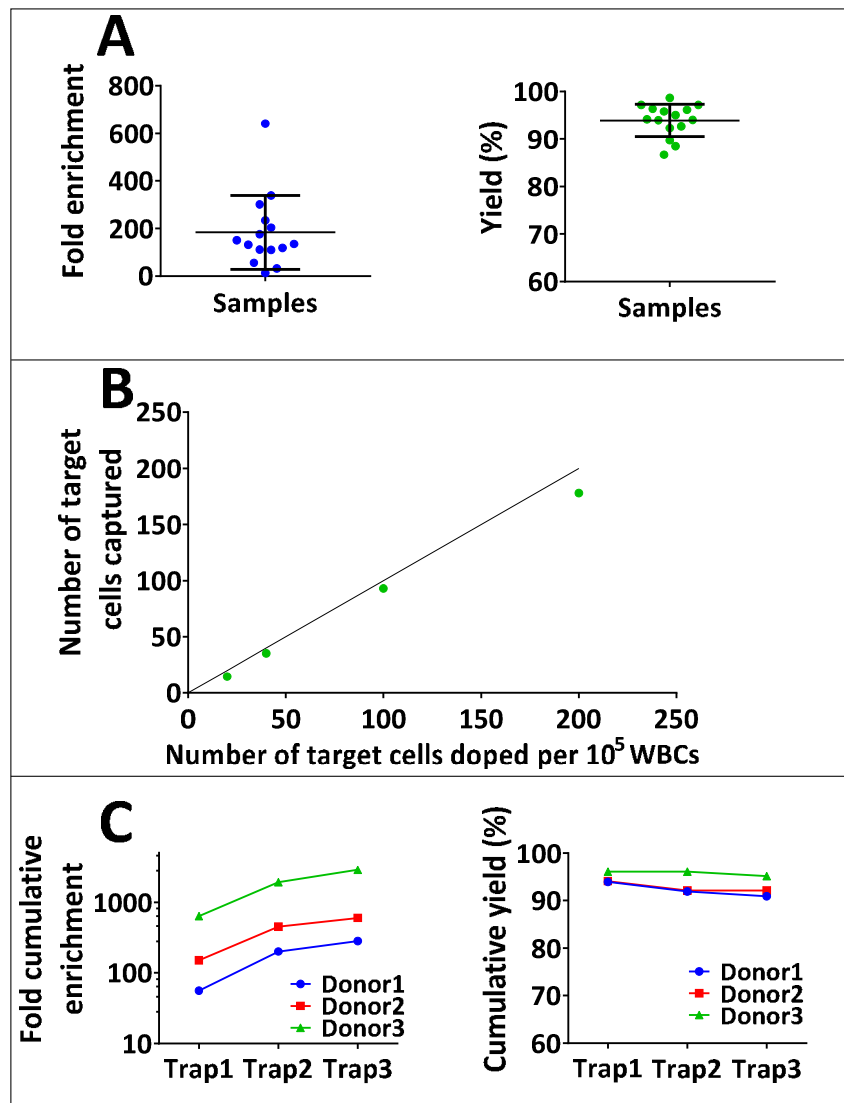
157 **Device Characterization using UM-UC13 cells.** We used UM-UC13 bladder cancer cells doped into whole
158 blood from healthy donors to characterize device performance and optimize process parameters. UM-
159 UC13 cells and leukocytes have an overlapping size distribution, but significantly different
160 deformabilities²¹. While the overlapping size-distribution limits the performance of size-only separation
161 mechanisms, the RCT mechanism separates cells based on size and deformability. Thus, UM-UC13 cells
162 are a good phenotype for validating the device by offering the distinct difference in deformability
163 compared to leukocytes. Previously, we found that leukocyte contamination can be reduced by
164 increasing the flow rate. However, at a flow rate of 4 mm s^{-1} , there appears to be irreversible damage to
165 the trapped cancer cells because of the shear force applied to the cell membrane from the fluid²¹.
166 Therefore, to minimize the potential damage to target cells, cell separation was performed at a flow rate
167 of 2.5 mm s^{-1} .

168 For multi-filtration using three identical cell traps in parallel, the first trap acts as the initial filtration trap.
169 To validate the multi-filtration process, cells filtered away during each filtration step and cells collected
170 in the final collection step were directed and collected into different wells. The numbers of UM-UC13
171 cells and leukocytes in each well were counted to calculate the enrichment and yield of our RCT device
172 at each step.

173 Figure 3A shows the enrichment and yield from a single filtration step. UC13 cells were doped into
174 diluted whole blood at 1:1000 ratio to leukocytes. After processing a total of 15 samples, we found that
175 that the first trap processed 2×10^6 nucleated cells/hour with an average of 183-fold enrichment and 93.8%
176 yield (Figure 3A). The yield results for doped UC13 cells are shown as a calibration curve in Figure 3B.
177 Figure 3C shows results from a separate experiment to measure the enrichment and yield from multiple
178 filtration steps. UC13 cells were doped at 1:1000 ratio to leukocytes too. Cells captured in the first trap
179 were released and re-filtered through the second and third traps. The second and third traps together

180 provided an additional enrichment of ~5X without additional change in the yield (Figure 3B). The
 181 average enrichment of the third trap was 1.4. The enrichment performance of the RCT device was highly
 182 donor dependent but the trend of improvement was the same for each donor. These results show that
 183 the leukocytes that are captured in our device because of non-specific adhesion can be depleted by
 184 multiple re-filtrations. We achieved an average enrichment of ~900 after three filtrations, which rival
 185 previously reported label-free separation techniques²⁷⁻³⁰.

186



187

188 *Figure 3: Performance of resettable cell traps in enrichment and retention of UM-UC13 cells relative to*
189 *leukocytes. A: results of main filtration step from 15 samples (mean \pm standard deviation). B: Calibration*
190 *curve for the RCT mechanism. C: cumulative enrichment and yield results of 3-trap serial filtrations.*

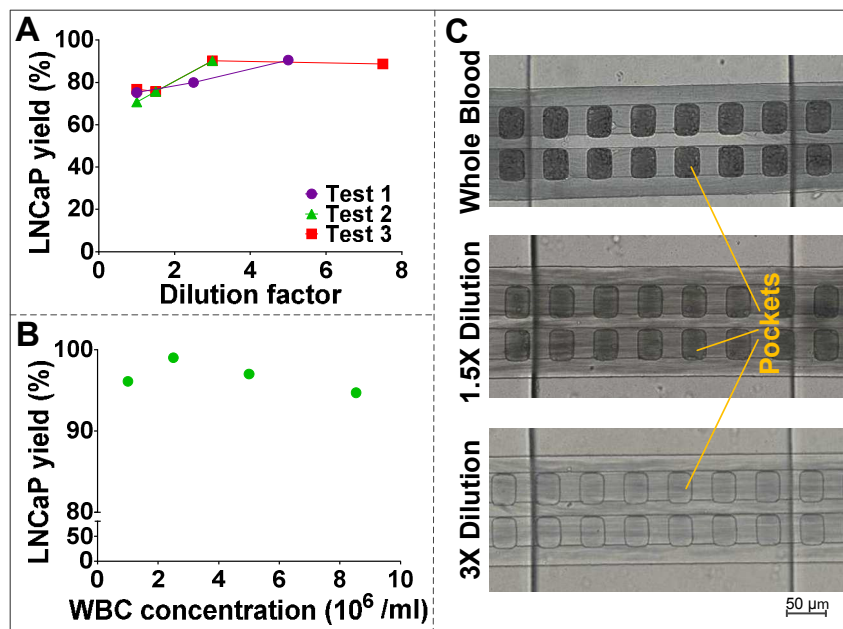
191 **Device Characterization using LNCaP Cells.** To further optimize parameters for processing samples from
192 patients with prostate cancer, androgen-sensitive human prostate adenocarcinoma cells were used to
193 characterize the device. Although cultured LNCaP cells have similar size distributions as the cultured
194 UM-UC13 cells, they required a smaller trap opening, obtained through the application of a higher
195 pressure across the diaphragm, to achieve the same retention ratio as UM-UC13 cells during processing.
196 Furthermore, the flow speed limit that they can withstand before they are damaged is 1.5 mm s^{-1} , much
197 less compared to the limit of 4 mm s^{-1} for UM-UC13 cells. This implies that LNCaP cells are more
198 deformable than UM-UC13 cells. Multiple filtrations for LNCaP cells worked the same as for UM-UC13
199 cells. The only difference was that the average enrichment of the initial filtration step was much lower
200 (83-fold) due to the slower flow speed and smaller channel openings. Extra filtrations gave an average
201 enrichment improvement of $\sim 5X$, as before. Purity of enriched doping samples can be calculated from
202 the enrichment. We hypothesized that CTCs from patients with metastatic castration-resistant prostate
203 cancer (mCRPC) would be more deformable than cultured cancer cells. Previous studies have correlated
204 greater deformability with greater invasiveness^{31,32}. CTCs are highly invasive, and are therefore likely to
205 be more deformable. As we have showed, LNCaP cells are more deformable than UM-UC13 cells, and
206 are likely to better mimic CTCs. The parameter settings described for processing LNCaP cells were
207 therefore applied to the processing of patient samples.

208

209 **Working with Whole Blood.** In early experiments, the yield of doped cancer cells was low when whole
210 blood was processed directly. Whole blood was thus diluted in buffer to reduce the sample cell density,
211 which improved the yield, as shown in Figure 4A. To determine whether this improvement was caused
212 by the diluted leukocyte concentration or diluted red blood cell (RBC) concentration, the relationship
213 between the yield and leukocyte concentration was investigated first. We separated leukocytes from
214 whole blood, re-suspended them at various concentrations and added LNCaP cells to each suspension at
215 a ratio of 1 LNCaP cell to 1000 leukocytes. The lack of correlation between the yield and leukocyte
216 concentration indicates that the performance is not necessarily related to leukocyte concentration
217 (Figure 4B). It was therefore determined that high concentrations of red blood cells (RBCs) negatively
218 influence the yield of target cells trapped. RBCs aggregate in the storing pockets (Figure 4C) and prevent

219 incoming target cells from getting trapped. Therefore, to balance the overall yield and throughput,
 220 which are sacrificed with dilution, we implemented a 2 times dilution for processing samples.

221



222

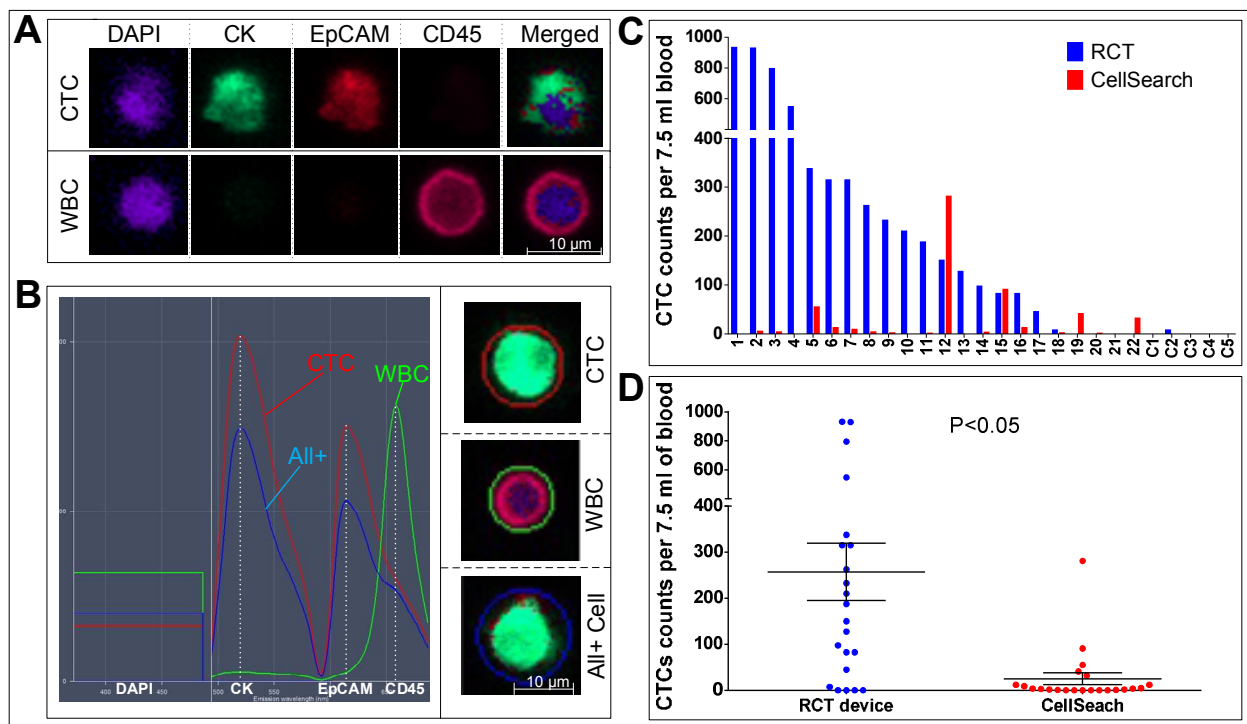
223 *Figure 4: Parameter optimization of RCT devices for patient sample processing. A: LNCaP yield improved*
 224 *when whole blood was diluted. B: There was no correlation between the yield of LNCaP cells and the*
 225 *concentration of leukocytes. C: RBCs occupy the pockets at different densities when diluted.*

226 **Enrichment and identification of candidate CTCs from patients with mCRPC**

227 Blood samples from 22 patients with mCRPC and 5 healthy controls were processed using the RCT
 228 device. After immunostaining and single-cell spectral analysis using the Zeiss LSM 780 system, enriched
 229 CTCs were defined as DAPI+ CK+ EpCAM+/- and CD45- while leukocytes were identified as DAPI+ CK-
 230 EpCAM- and CD45+ as represented in Figure 5A. The LSM 780 confocal microscopy system can
 231 simultaneously collect a 34-channel spectrum on each pixel of the image including a bright-field image,
 232 as well as a low wavelength channel for imaging the DAPI signal. Compared to standard fluorescent
 233 microscopy, which use individual color filters, this system provides greatly improved discrimination of
 234 overlapping emissions from multiple fluorophores. Our immunofluorescence system for CTC
 235 identification includes CK-Alexa 488 (emission peak at 529 nm), EpCAM-Alexa 594 (617 nm), and CD45-
 236 APC (660 nm). CTCs are distinguished from leukocytes based on the shape of their spectra. Typical CTCs
 237 and WBCs are shown in Figure 6B. A typical CTC spectrum has two distinct peaks: one for CK at 525 nm

238 and one for EpCAM at 617 nm. A typical spectrum of a leukocyte has only one clear peak for CD45 at 660
 239 nm. A small amount of cells in the enriched samples were found to be positive for all 4 immunostains
 240 (Figure 5B) as reported previously by others³³. The merged images of these cells look similar to CTCs, but
 241 can be distinguished by their spectral curves. As the nature of these cells is not yet established, they
 242 were not counted as CTC. The RCT device identified 81.8% (18/22) patients with >5 CTCs per 7.5ml of
 243 blood. The numbers varied between patients, from 0 to 930, with a mean of 257 per 7.5ml of blood.
 244 Within the same patient group, CellSearch analysis revealed ≥ 5 CTCs in 40.9% (9/22) patients. The
 245 numbers ranged from 0 to 281 with a mean of 25 CTCs per 7.5 ml of blood. Control samples from five
 246 healthy donors were also processed with the RCT device. Scanned images of sorted cells of the healthy
 247 controls were mixed blindly with the images of patient samples and counted. Among the five healthy
 248 blind tests, only one donor had a count of 7.5 CTC per 7.5 ml of blood. The purity of enriched patient
 249 samples varies significantly since the number of CTCs varies dramatically from patient to patient. The
 250 number of leukocytes captured from 22 patient samples ranges from $\sim 1,300$ to $\sim 18,000$ per ml blood
 251 processed.

252



253

254 *Figure 5: Enumeration of CTCs derived from CRPC patient samples. A: Micrographs of a CTC and*
 255 *leukocyte stained with fluorescent markers. B: Merged images of a CTC, a leukocyte and an all-positive*

256 cell with their corresponding spectral curves. C: Number of CTCs identified following resettable cell trap
257 (RCT) or CellSearch® enrichment. D: Grouped results of RCT device and CellSearch System. Data is
258 displayed with mean \pm standard deviation. P value is calculated by parametric paired T-test analysis. C1-
259 C5 are normal controls.

260 As shown in Figure 5C and 5D, significantly more CTCs were identified using our approach compared to
261 the CellSearch platform ($p=0.0056$). This improved capability derives from a combination of enhanced
262 ability to capture CTCs, as well as a more sensitive an imaging system that permitted single cell spectral
263 analysis. While these two aspects are necessarily coupled, we observe strong evidence that both
264 contribute significantly to the overall increased sensitivity. Specifically, previous biomechanical (size and
265 deformability) based separation approaches have demonstrate the ability to capture more CTCs
266 compared to the EpCAM affinity capture method of the CellSearch System^{33,34}. The discordance that we
267 observed between the number of CTCs reported by CellSearch and the number reported by our
268 enumeration system further suggests that our system is able to capture cells with low levels of EpCAM
269 expression. From our single-cell spectral analysis, we also found high heterogeneity of expression levels
270 (intensity of the spectrum) of markers for CTCs between patients. In 2/22 patient samples, EpCAM
271 expression was much weaker than CK while the opposite was true for 3 of the other samples. There
272 were also 4/22 patient samples with both weak CK and weak EpCAM expression. Interestingly, however,
273 all CK+ CTCs identified using the RCT device were also EpCAM+, which likely arises from the greater
274 sensitivity of the single cell spectral analysis technique. Previous reports affirmed that heterogeneity of
275 biological properties (expression level of surface antigens) exist in CTCs from diverse cancer origins,
276 different subtypes, and even the CTCs in the same patient^{1,35}. The epithelial-to-mesenchymal transition
277 (EMT) that occurs with dissemination of cancer cells into the blood stream results in down-regulation of
278 EpCAM on the CTC surface^{36,37}. For those samples with inadequate EpCAM expression, successful
279 capture of CTCs may be impossible with the CellSearch system.

280 Coupling CTC enrichment using the RCT device with a single cell spectral analysis system provided both
281 more sensitive and more objective discrimination of CTCs from contaminating leukocytes. This increased
282 sensitivity derived in part from its spectral sensor, which has 1.8-fold higher quantum efficiency
283 compared to conventional PMT detectors. This system is also more objective because it could accurately
284 differentiate overlapping spectra. Classification of captured cells with the CellSearch system relies on an
285 operators' judgment of the fluorescent images, where inconsistencies in the image interpretation may
286 lead to incorrect identification of CTCs³⁸.

287 One potential concern for filtration-based separation of CTCs is the potential loss of smaller CTCs.
288 Coumans and colleagues reported that the ideal diameter of a microsieve is 5 μm , which corresponds to
289 the aperture adopted in this study³⁹. However, these researchers and others have observed that CTC
290 size varies from one tumor type to another^{39,40}. A key advantage of the RCT mechanism is that the
291 aperture of the device can be adapted dynamically altered to accommodate different tumor types. It
292 would require further experimentation to determine the optimal aperture for CTCs derived from each
293 tumor type but it is conceivable that careful optimization could enhance the performance of the device
294 beyond what is presented in this report. The potential loss of smaller CTCs could result in an
295 underestimation of the tumor cells in patient blood. However, prostate cancer has been reported to
296 involve CTCs that are relatively small in size^{39,40} and the observed sensitivity of RCT enrichment likely
297 reflects the fact that even these small CTCs are significantly less deformable than contaminating
298 leukocytes.

299 Overall, the performance of the RCT device competes well with other reported methods that process
300 CRPC samples and the CellSearch system. Other methods are either based on EpCAM affinity capture⁴¹⁻
301⁴³ using EpCAM coated micro-structures which increase contact between CTC and surface and thereby
302 improve efficiency, or are label-free methods based on the physical properties of CTCs^{34,44} or even
303 hybrid methods that combine both EpCAM affinity and the physical properties⁴⁵. Unlike most label-free
304 microfluidics chips, our RCT device can process whole blood samples with a dilution factor of only 2^{29,46}.
305 There is no further processing of the blood sample such as lysis of RBCs^{33,47} or fixation^{34,48} where the
306 addition of chemical buffers might affect the viability of the CTCs. Captured CTCs are easily retrieved
307 from the collection reservoirs of the device for easy enumeration or further downstream analysis.

308

309

310 **CONCLUSIONS**

311 The RCT mechanism is a separation tool that enriches for CTCs from 2 x diluted whole blood with high
312 throughput, sensitivity and selectivity. Furthermore, the RCT avoids the issue of clogging by the periodic
313 resetting of its microstructures. We demonstrated the separation of viable, label-free CTCs from mCRPC
314 patients, which were amenable to further standard cellular analysis methods, such as immunostaining.
315 The RCT device presents a compelling and more sensitive alternative for the enrichment of CTCs based

316 on size and deformability that may enable better risk stratification and monitoring of treatment
317 response in cancer patients.

318

319 **MATERIALS AND METHODS**

320 **Fabrication and Set-up**

321 The resettable cell trap (RCT) device was fabricated using standard multilayer soft lithography
322 techniques using polydimethylsiloxane (PDMS)^{22,49}. Master wafers for the control and flow layers are
323 patterned through photolithography. Molds for the flow layer devices were fabricated using
324 polyurethane and a master PDMS replica against the flow layer wafer. PDMS replicas against the master
325 molds yielded the flow channels. The control channels were fabricated by coating a thin PDMS layer on
326 the control layer wafers. These two layers were plasma bonded after they were separately oxidized in an
327 oxygen plasma chamber (Harrick Plasma, Ithaca, NY). A 0.5 mm OD punch (Harris Unicore, Ted Pella Inc.,
328 Redding, CA) was used to create the inlet and outlet ports on-chip. Finally the device was plasma
329 bonded to a 25x75 mm glass slide (Fisher Scientific).

330 Fluids flow into the device from 15 ml polypropylene falcon tubes (BD Biosciences, Mississauga, Canada)
331 through Tygon microbore tubing with 0.02 inch inner diameter (ID) (Cole-Parmer, Montreal, Canada)
332 and then a 0.017 inch ID stainless steel needle (New England Small Tube, Litchfield, NH) which is
333 connected to the device. An external pneumatic pressure actuates the flow through custom machined
334 caps fitted to the falcon tubes. The pneumatic pressure sources for sample and buffer infusion are
335 offered by a 4-channel microfluidic flow control system (MCFS-Flex, Fluigent, France). The control valves
336 on the device chip are activated by a custom designed system consisting of on-off pressure valves and a
337 MSP430 microprocessor (Texas Instruments), which provides easy and flexible programming ability to
338 meet different automation requirements. Prior to use, device channels were slowly flushed for 20
339 minutes with 0.2% Pluronic F-127 (Sigma-Aldrich, St. Louis, Missouri, USA) in PBC for surface passivation.
340 Fluid outlets can be customized by either punching with a 6 mm outer diameter (OD) punch to form an
341 on-chip reservoir or by punching with a 0.5 mm OD punch to lead out the fluids through needle and
342 tubing to either a 96-well plate (Thermo Fisher Scientific, Rochester, NY, USA) or 15 ml tube.

343 The optimal trapping pressure for target cells was determined by following the target cells through a
344 constricted trap and increasing the trapping pressure until over 90% of the target cells were captured.

345 The optical trapping pressure determined were 150 mbar for UC13 cells and 350 mbar for LNCaP cells
346 (LNCaP cells are much softer than UC13 cells). For the validation experiments, where target cell
347 concentration is specific, the processed volume in the first filtration step was based on a total of 100
348 target cells captured in the 128 channels or a total of 100,000 cells processed. This was to prevent
349 obstruction of the flow channel, which will dramatically decrease the filtration ability. For processing
350 patient samples, where the CTC and leukocytes concentration is unknown, conservative estimates are
351 made to determine the length/volume of the main filtration. Patient samples processing utilizes the
352 same parameter settings described for processing LNCaP cells: 350 mbar trapping pressure and 1.5 mm
353 s^{-1} flow rate. This flow rate will yield a volumetric flow rate of 600 μ l/h. Throughput is increased by
354 further parallelization.

355 **Sample Preparation**

356 Device validation was performed using whole blood doped with UM-UC13 (provided by the Pathology
357 Core of the Bladder Cancer SPORE at MD Anderson Cancer Center) bladder cancer cells and LNCaP
358 prostate cancer cells (American Type Culture Collection (ATCC), Manassas, VA, USA). UC13 bladder
359 cancer cells were cultured in complete minimal essential medium (CMEM): minimum essential medium
360 Eagle (MEM) (Life Technology, Carlsbad, CA, USA) supplemented with 10% (v/v) fetal bovine serum (Life
361 Technology), 1% sodium pyruvate (Invitrogen), 1% L-glutamine (Life Technology), 1% MEM non-essential
362 amino acids (Life Technology), and 1% penicillin streptomycin (Fisher Scientific). LNCaP cells were
363 cultured in RPMI 1640 media (Life Technology) containing 10% (v/v) fetal bovine serum, 2mM L-
364 glutamine and 1% penicillin/streptomycin. Both cell lines were incubated in a humidified environment at
365 37°C and 5% CO₂. When needed, cells were trypsinized, washed and resuspended at the desired
366 concentration for experiments.

367 After informed consent was received from healthy donors (n=20), whole blood was drawn into 6 ml
368 EDTA collection tubes (Becton-Dickinson, Franklin Lakes, NJ, USA). Leukocytes in the whole blood were
369 stained with Hoechst 33342 (Invitrogen, Carlsbad, CA, USA), which emits a blue fluorescence, and were
370 further diluted to 2 million leukocytes per ml with phosphate buffered saline (PBS, Gibco).

371 For validation experiments, cancer cells, stained with Calcein AM (Invitrogen), which emits a green
372 fluorescence, were doped into the whole blood which was diluted to 2×10^6 leukocytes/ml. The mixed
373 sample that was processed in each cell separation trial for validation experiments contained a minimum

374 of 100 cancer cells at different doping ratios. Each sample was processed in multiple full device
375 operation cycles with each cycle processing ~100,000 leukocytes.

376 **Experimental Characterization of the Device Performance**

377 The yield and enrichment are the two main characteristics used to measure the performance of the RCT
378 device. The yield is defined as the retention rate of target cells. The enrichment is defined as the ratio of
379 target cancer cells to background cells in the collection reservoir divided by the same ratio of the input
380 sample. To get these results, we counted the number of cancer cells in both collection and waste
381 reservoirs and leukocytes (background cells) in the collection reservoir after each experiment. Cancer
382 cells were identified by the green fluorescence of the Calcein AM stain and the leukocytes were blue
383 from the Hoescht 33342 stain. Images were taken using an inverted microscope with fluorescent
384 capabilities (Nikon ECLIPSE Ti) and camera (QImaging, Surrey, BC, Canada). The numbers of cells in the
385 images were manually counted.

386 **Patient Blood Sample Acquisition, Separation, Immunofluorescence, and Enumeration**

387 Patients with metastatic castrate resistant prostate cancer (n=22) were recruited at the BC Cancer
388 Agency. This study was approved by the institutional review board (protocol H13-00870). After informed
389 consent was obtained, blood samples were collected in 6 ml EDTA tubes (BD). The CRPC patients in this
390 study ranged in age from 49–88 years, had PSA levels between 0.05 and 12,840 µg/L. Each 1 ml of blood
391 was diluted 1:1 with PBS in a 15 ml falcon tube. The diluted sample was directly processed with the RCT
392 device. A parallel sample of 7.5 ml of blood was analyzed using the Veridex CellSearch™ system.

393 The cells were collected into a 15 ml falcon tube through needle and microbore tubing. The enriched cell
394 fraction was washed with 1 x PBS, centrifuged at 400 g for 5 min and then fixed in 3% paraformaldehyde
395 (PFA, Sigma, USA) for 15 min. After fixation, the cells were permeabilized in 0.5% Tween20 for 10 min,
396 washed in PBS, and blocked by incubation with 3% BSA (Sigma-Aldrich, St. Louis, Missouri, USA) in PBS
397 for 30 min and washed a final time in PBS. Every step was conducted at room temperature. Cells were
398 stained with antibodies for cytokeratin (CK) using Pan-Keratin (C11) Mouse mAb-Alexa Fluor® 488 (Cell
399 Signaling Technology, Danvers, Massachusetts, USA), EpCAM (VU1D9) Mouse mAb-Alexa Fluor® 594
400 (Cell Signaling Technology), and anti-human CD45-APC (Biolegend, San Diego, California, USA) at 0.625
401 µg/ml, 0.525 µg/ml, 0.36 µg/ml respectively in PBS/3% BSA at 4°C overnight.

402 Stained cells were washed 3 times with PBS to remove floating superfluous antibodies. After the last
403 centrifuge, cells were suspended in 40ul PBS and stained with DAPI using VECTASHIELD® Mounting
404 medium with DAPI (Vector Laboratories, Burlingame, CA, USA) at a concentration of 0.075 µg/ml. All
405 cells were transferred to a single well of a Corning® 384-well high content image plate (Sigma-Aldrich)
406 and centrifuged at 400 g for 2 min. The well was automatically scanned at 40X magnification with a
407 confocal microscope (LSM 780, Carl Zeiss, Oberkochen, Germany) and Zen software (Carl Zeiss).
408 Spectrum analysis of single cells was manually conducted to identify the presence of CTCs candidates.
409 DAPI+/CK+/EpCAM+or-/CD45- enriched cells were considered CTCs while DAPI+/CK-/EpCAM-/CD45+
410 enriched cells were considered WBCs. CTCs counts from the RCT device were scaled to numbers per 7.5
411 ml to compare with the CellSearch system.

412

413 **ACKNOWLEDGEMENT**

414 This work was made possible by grants from Natural Sciences and Engineering Research Council of
415 Canada Canadian Institutes of Health Research, Prostate Cancer Canada, Vancouver Prostate Centre's
416 Translational Research Initiative for Accelerated Discovery and Development, C.J. Martin Biomedical
417 Overseas Fellowship from the National Health and Medical Research Council of Australia, and Engineers-
418 in-Scrubs training program at UBC.

419

420 **REFERENCES**

- 421 1 A. van de Stolpe, K. Pantel, S. Sleijfer, L. W. Terstappen and J. M. J. den Toonder, *Cancer Res.*, 2011,
422 **71**, 5955–5960.
- 423 2 E. S. Lianidou, A. Strati and A. Markou, *Crit. Rev. Clin. Lab. Sci.*, 2014, **51**, 160–171.
- 424 3 A. E. Dago, A. Stepansky, A. Carlsson, M. Luttmann, J. Kendall, T. Baslan, A. Kolatkar, M. Wigler, K.
425 Bethel, M. E. Gross, J. Hicks and P. Kuhn, *PLoS One*, 2014, **9**, e101777.
- 426 4 D. F. Hayes, M. Cristofanilli, G. T. Budd, M. J. Ellis, A. Stopeck, M. C. Miller, J. Matera, W. J. Allard, G. V.
427 Doyle and L. W. Terstappen, *Clin. Cancer Res.*, 2006, **12**, 4218–4224.
- 428 5 J. S. de Bono, H. I. Scher, R. B. Montgomery, C. Parker, M. C. Miller, H. Tissing, G. V. Doyle, L. W.
429 Terstappen, K. J. Pienta and D. Raghavan, *Clin. Cancer Res.*, 2008, **14**, 6302–6309.
- 430 6 S. J. Cohen, C. J. Punt, N. Iannotti, B. H. Saidman, K. D. Sabbath, N. Y. Gabrail, J. Picus, M. Morse, E.
431 Mitchell and M. C. Miller, *J. Clin. Oncol.*, 2008, **26**, 3213–3221.
- 432 7 X.-L. Ma, Y.-Y. Li, J. Zhang, J.-W. Huang, H.-Y. Jia, L. Liu and P. Li, *Asian Pac. J. Cancer Prev. APJCP*, 2014,
433 **15**, 6015–6020.
- 434 8 A. Kulasinghe, C. Perry, L. Jovanovic, C. Nelson and C. Punyadeera, *Int. J. Cancer J. Int. Cancer*, 2015,
435 **136**, 2515–2523.
- 436 9 C. Jin, S. M. McFaul, S. P. Duffy, X. Deng, P. Tavassoli, P. C. Black and H. Ma, *Lab. Chip*, 2014, **14**, 32–44.

- 437 10 S. Riethdorf, H. Fritsche, V. Müller, T. Rau, C. Schindlbeck, B. Rack, W. Janni, C. Coith, K. Beck, F.
438 Jänicke, S. Jackson, T. Gornet, M. Cristofanilli and K. Pantel, *Clin. Cancer Res. Off. J. Am. Assoc. Cancer*
439 *Res.*, 2007, **13**, 920–928.
- 440 11 S. Nagrath, L. V. Sequist, S. Maheswaran, D. W. Bell, D. Irimia, L. Ulkus, M. R. Smith, E. L. Kwak, S.
441 Digumarthy, A. Muzikansky, P. Ryan, U. J. Balis, R. G. Tompkins, D. A. Haber and M. Toner, *Nature*,
442 2007, **450**, 1235–1239.
- 443 12 M. Lin, J.-F. Chen, Y.-T. Lu, Y. Zhang, J. Song, S. Hou, Z. Ke and H.-R. Tseng, *Acc. Chem. Res.*, 2014, **47**,
444 2941–2950.
- 445 13 V. Murlidhar, M. Zeinali, S. Grabauskiene, M. Ghannad-Rezaie, M. S. Wicha, D. M. Simeone, N.
446 Ramnath, R. M. Reddy and S. Nagrath, *Small Weinh. Bergstr. Ger.*, 2014, **10**, 4895–4904.
- 447 14 A. A. Powell, A. H. Talasaz, H. Zhang, M. A. Coram, A. Reddy, G. Deng, M. L. Telli, R. H. Advani, R. W.
448 Carlson, J. A. Mollick, S. Sheth, A. W. Kurian, J. M. Ford, F. E. Stockdale, S. R. Quake, R. F. Pease, M. N.
449 Mindrinos, G. Bhanot, S. H. Dairkee, R. W. Davis and S. S. Jeffrey, *PLoS One*, 2012, **7**, e33788.
- 450 15 N. Krawczyk, F. Meier-Stiegen, M. Banys, H. Neubauer, E. Ruckhaeberle and T. Fehm, *BioMed Res. Int.*,
451 2014, **2014**, 415721.
- 452 16 S. J. Tan, R. L. Lakshmi, P. Chen, W.-T. Lim, L. Yobas and C. T. Lim, *Biosens. Bioelectron.*, 2010, **26**,
453 1701–1705.
- 454 17 S. Zheng, H. Lin, J.-Q. Liu, M. Balic, R. Datar, R. J. Cote and Y.-C. Tai, *J. Chromatogr. A*, 2007, **1162**,
455 154–161.
- 456 18 Y. Tang, J. Shi, S. Li, L. Wang, Y. E. Cayre and Y. Chen, *Sci. Rep.*, 2014, **4**, 6052.
- 457 19 R. A. Harouaka, M.-D. Zhou, Y.-T. Yeh, W. J. Khan, A. Das, X. Liu, C. C. Christ, D. T. Dicker, T. S. Baney, J.
458 T. Kaifi, C. P. Belani, C. I. Truica, W. S. El-Deiry, J. P. Allerton and S.-Y. Zheng, *Clin. Chem.*, 2014, **60**,
459 323–333.
- 460 20 T. Gerhardt, S. Woo and H. Ma, *Lab. Chip*, 2011, **11**, 2731–2737.
- 461 21 W. Beattie, X. Qin, L. Wang and H. Ma, *Lab. Chip*, 2014, **14**, 2657–2665.
- 462 22 M. A. Unger, H. P. Chou, T. Thorsen, A. Scherer and S. R. Quake, *Science*, 2000, **288**, 113–116.
- 463 23 S.-B. Huang, M.-H. Wu and G.-B. Lee, *Sens. Actuators B Chem.*, 2009, **142**, 389–399.
- 464 24 L. Saias, J. Autebert, L. Malaquin and J.-L. Viovy, *Lab. Chip*, 2011, **11**, 822–832.
- 465 25 A. Jain and L. L. Munn, *PLoS ONE*, 2009, **4**, e7104.
- 466 26 S. K. Murthy, A. Sin, R. G. Tompkins and M. Toner, *Langmuir ACS J. Surf. Colloids*, 2004, **20**, 11649–
467 11655.
- 468 27 J. Sun, M. Li, C. Liu, Y. Zhang, D. Liu, W. Liu, G. Hu and X. Jiang, *Lab. Chip*, 2012, **12**, 3952–3960.
- 469 28 H. S. Moon, K. Kwon, K. A. Hyun, T. Seok Sim, J. Chan Park, J. G. Lee and H. I. Jung, *Biomicrofluidics*,
470 2013, **7**, 14105.
- 471 29 S. Zheng, H. K. Lin, B. Lu, A. Williams, R. Datar, R. J. Cote and Y.-C. Tai, *Biomed. Microdevices*, 2011, **13**,
472 203–213.
- 473 30 S. C. Hur, A. J. Mach and D. Di Carlo, *Biomicrofluidics*, 2011, **5**, 22206.
- 474 31 V. Swaminathan, K. Myhre, E. T. O'Brien, A. Berchuck, G. C. Blobe and R. Superfine, *Cancer Res.*,
475 2011, **71**, 5075–5080.
- 476 32 J. Guck, S. Schinkinger, B. Lincoln, F. Wottawah, S. Ebert, M. Romeyke, D. Lenz, H. M. Erickson, R.
477 Ananthakrishnan, D. Mitchell, J. Käs, S. Ulvick and C. Bilby, *Biophys. J.*, 2005, **88**, 3689–3698.
- 478 33 B. L. Khoo, M. E. Warkiani, D. S.-W. Tan, A. A. S. Bhagat, D. Irwin, D. P. Lau, A. S. T. Lim, K. H. Lim, S. S.
479 Krishna, W.-T. Lim, Y. S. Yap, S. C. Lee, R. A. Soo, J. Han and C. T. Lim, *PLoS ONE*, 2014, **9**, e99409.
- 480 34 H. K. Lin, S. Zheng, A. J. Williams, M. Balic, S. Groshen, H. I. Scher, M. Fleisher, W. Stadler, R. H. Datar,
481 Y.-C. Tai and R. J. Cote, *Clin. Cancer Res.*, 2010, **16**, 5011–5018.
- 482 35 A. M. Sieuwerts, J. Kraan, J. Bolt, P. van der Spoel, F. Elstrodt, M. Schutte, J. W. M. Martens, J.-W.
483 Gratama, S. Sleijfer and J. A. Foekens, *J. Natl. Cancer Inst.*, 2009, **101**, 61–66.

- 484 36 C. G. Rao, D. Chianese, G. V. Doyle, M. C. Miller, T. Russell, R. A. Sanders and L. W. M. M. Terstappen,
485 *Int. J. Oncol.*, 2005, **27**, 49–57.
- 486 37 O. Gires and N. H. Stoecklein, *Cell. Mol. Life Sci. CMLS*, 2014, **71**, 4393–4402.
- 487 38 J. Kraan, S. Sleijfer, M. H. Strijbos, M. Ignatiadis, D. Peeters, J.-Y. Pierga, F. Farace, S. Riethdorf, T.
488 Fehm, L. Zorzino, A. G. J. Tibbe, M. Maestro, R. Gisbert-Criado, G. Denton, J. S. de Bono, C. Dive, J. A.
489 Foekens and J. W. Gratama, *Cytometry B Clin. Cytom.*, 2011, **80B**, 112–118.
- 490 39 F. A. W. Coumans, G. van Dalum, M. Beck and L. W. M. M. Terstappen, *PLoS One*, 2013, **8**, e61770.
- 491 40 S. T. Ligthart, F. A. W. Coumans, F. C. Bidard, L. H. J. Simkens, C. J. A. Punt, M. R. de Groot, G. Attard, J.
492 S. de Bono, J.-Y. Pierga and L. W. M. M. Terstappen, *PLoS One*, 2013, **8**, e67148.
- 493 41 S. Wang, K. Liu, J. Liu, Z. T.-F. Yu, X. Xu, L. Zhao, T. Lee, E. K. Lee, J. Reiss, Y.-K. Lee, L. W. K. Chung, J.
494 Huang, M. Rettig, D. Seligson, K. N. Duraiswamy, C. K.-F. Shen and H.-R. Tseng, *Angew. Chem. Int. Ed.*,
495 2011, **50**, 3084–3088.
- 496 42 T. W. Friedlander, V. T. Ngo, H. Dong, G. Premasekharan, V. Weinberg, S. Doty, Q. Zhao, E. G. Gilbert,
497 C. J. Ryan, W.-T. Chen and P. L. Paris, *Int. J. Cancer J. Int. Cancer*, 2014, **134**, 2284–2293.
- 498 43 S. L. Stott, C.-H. Hsu, D. I. Tsukrov, M. Yu, D. T. Miyamoto, B. A. Waltman, S. M. Rothenberg, A. M.
499 Shah, M. E. Smas, G. K. Korir, F. P. Floyd, A. J. Gilman, J. B. Lord, D. Winokur, S. Springer, D. Irimia, S.
500 Nagrath, L. V. Sequist, R. J. Lee, K. J. Isselbacher, S. Maheswaran, D. A. Haber and M. Toner, *Proc. Natl.*
501 *Acad. Sci.*, 2010, **107**, 18392–18397.
- 502 44 F. Farace, C. Massard, N. Vimond, F. Drusch, N. Jacques, F. Billiot, A. Laplanche, A. Chauchereau, L.
503 Lacroix, D. Planchard, S. Le Moulec, F. André, K. Fizazi, J. C. Soria and P. Vielh, *Br. J. Cancer*, 2011, **105**,
504 847–853.
- 505 45 E. Ozkumur, A. M. Shah, J. C. Ciciliano, B. L. Emmink, D. T. Miyamoto, E. Brachtel, M. Yu, P. Chen, B.
506 Morgan, J. Trautwein, A. Kimura, S. Sengupta, S. L. Stott, N. M. Karabacak, T. A. Barber, J. R. Walsh, K.
507 Smith, P. S. Spuhler, J. P. Sullivan, R. J. Lee, D. T. Ting, X. Luo, A. T. Shaw, A. Bardia, L. V. Sequist, D. N.
508 Louis, S. Maheswaran, R. Kapur, D. A. Haber and M. Toner, *Sci. Transl. Med.*, 2013, **5**, 179ra47–
509 179ra47.
- 510 46 E. Sollier, D. E. Go, J. Che, D. R. Gossett, S. O’Byrne, W. M. Weaver, N. Kummer, M. Rettig, J. Goldman,
511 N. Nickols, S. McCloskey, R. P. Kulkarni and D. Di Carlo, *Lab. Chip*, 2014, **14**, 63–77.
- 512 47 L. T. D. Chinen, C. A. L. Mello, E. A. Abdallah, L. M. Ocea, M. E. Buim, N. M. Breve, J. L. Gasparini, M. F.
513 Fanelli and P. Paterlini-Bréchet, *OncoTargets Ther.*, 2014, **7**, 1609–1617.
- 514 48 R. RIAHI, P. GOGOI, S. SEPEHRI, Y. ZHOU, K. HANDIQUE, J. GODSEY and Y. WANG, *Int. J. Oncol.*, 2014,
515 **44**, 1870–1878.
- 516 49D. C. Duffly, J. C. McDonald, O. J. A. Schueller and G. M. Whitesides, *Anal. Chem.*, 1998, **70**, 4974–4984.
- 517