

Supporting Information

Simple and rapid manipulation of a single circulating tumor cell using visualization of hydrogel encapsulation to facilitate single-cell whole-genome amplification

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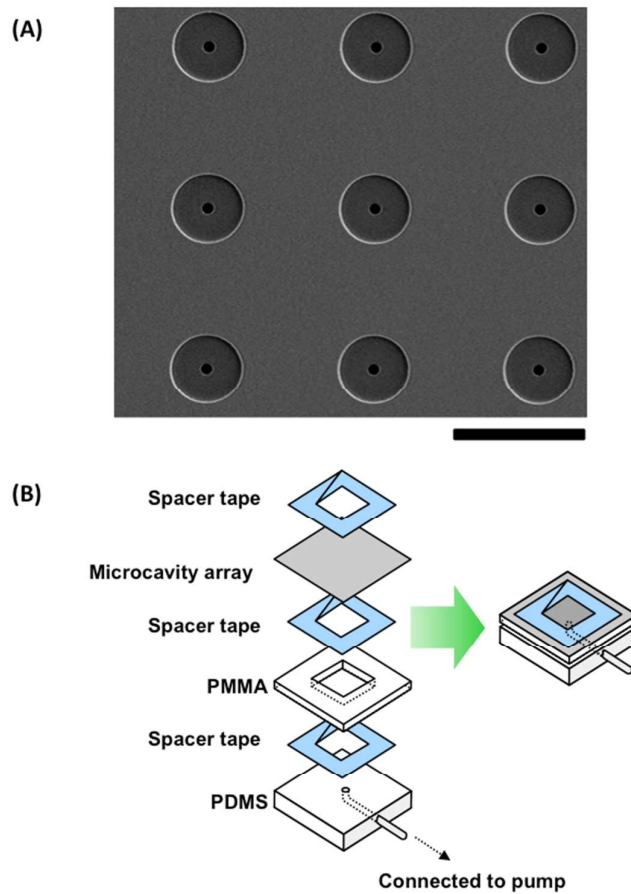


Fig. S1 CTC recovery device equipped with a microcavity array. (A) Scanning electron microscope image of the microcavity array. Scale bar: 100 μm . (B) Schematic image of the CTC recovery device.

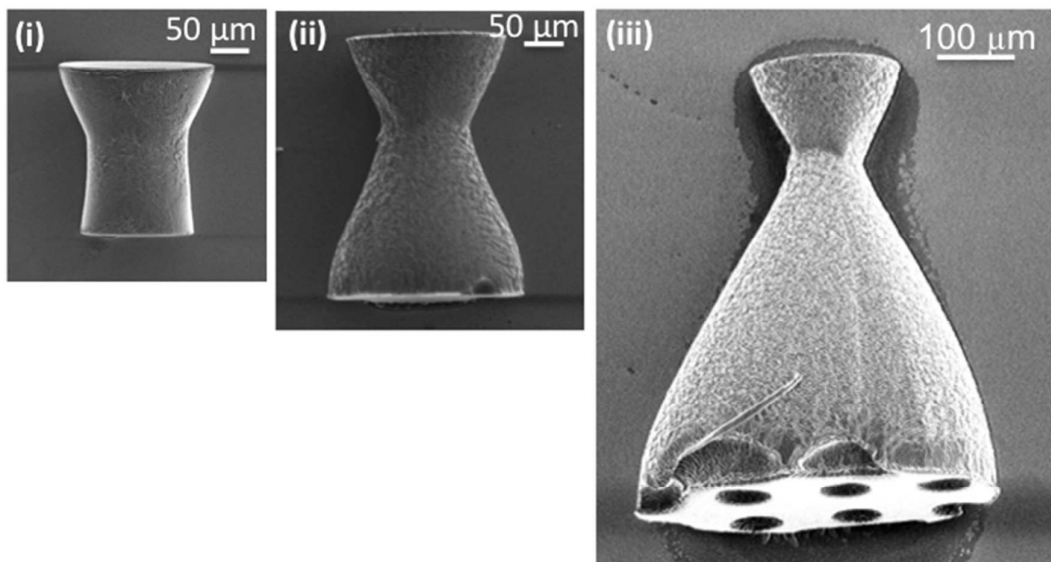


Fig. S2 SEM images of photopolymerized PEGDA hydrogels varying the distance between the cover glass and microcavity array. The heights were (i) 205 μm , (ii) 327 μm , and (iii) 567 μm .

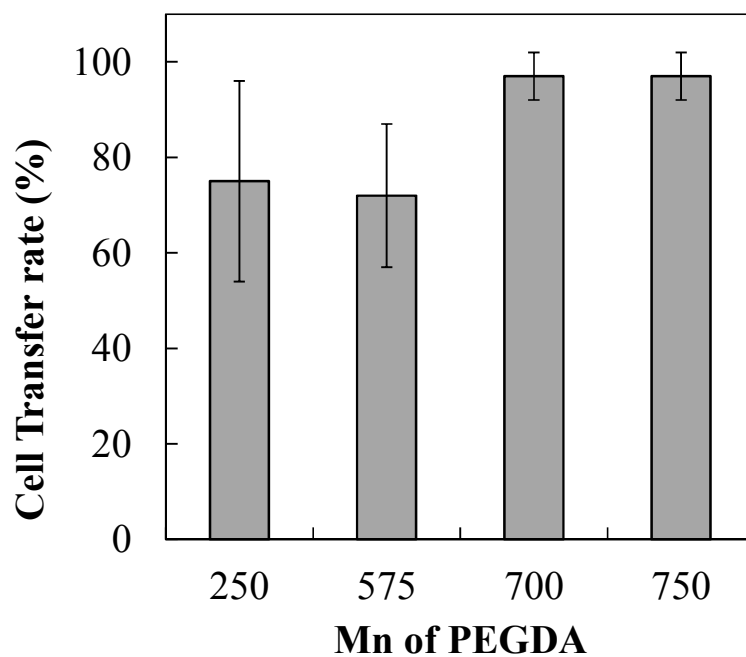


Fig. S3 Cell transfer rate by using different molecular weight of PEGDA.

All values are mean \pm standard deviation of n = 3.

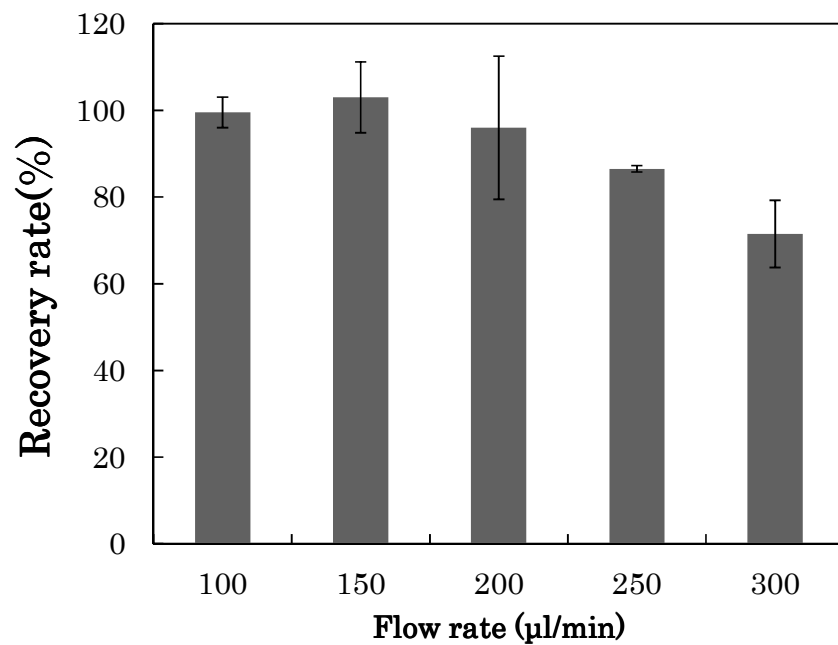


Fig. S4 Recovery rates of CellTracker Orange Stained NCI-H1975 cells from 100 cells spiked whole blood sample per one milliliter when using microcavity array.

All values are mean \pm standard deviation of $n = 3$.

Table S1 Evaluation of whole genome amplification (WGA) bias

Gene name (Chr.)	PIK3CA (3q)	MSH2 (2p)	CAT (11p)	P53 (17p)	ADCYAP1 (18p)	PMS2 (7p)	C6orf195 (6p)	PTEN (10q)	TOP1 (20q)
Single-cell isolated by micromanipulation (Pre amplification : 12 cycles Amplification : 14 cycles)	3/5	1/5	1/5	5/5	5/5	5/5	5/5	5/5	5/5
Single-cell encapsulated "on" hydrogel (Pre amplification : 12 cycles Amplification : 14 cycles)	5/5	0/5	2/5	5/5	4/5	3/5	3/5	4/5	4/5
Single-cell encapsulated "on" hydrogel (Pre amplification : 15 cycles Amplification : 17 cycles)	5/5	0/5	3/5	5/5	5/5	5/5	4/5	4/5	3/5