Electronic Supplementary Material (ESI) for Lab on a Chip.

Supplemental information for:

Hydroporator: A hydrodynamic cell membrane perforator for high-throughput vector-free nanomaterial intracellular delivery and DNA origami biostability evaluation

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Supplemental Figure

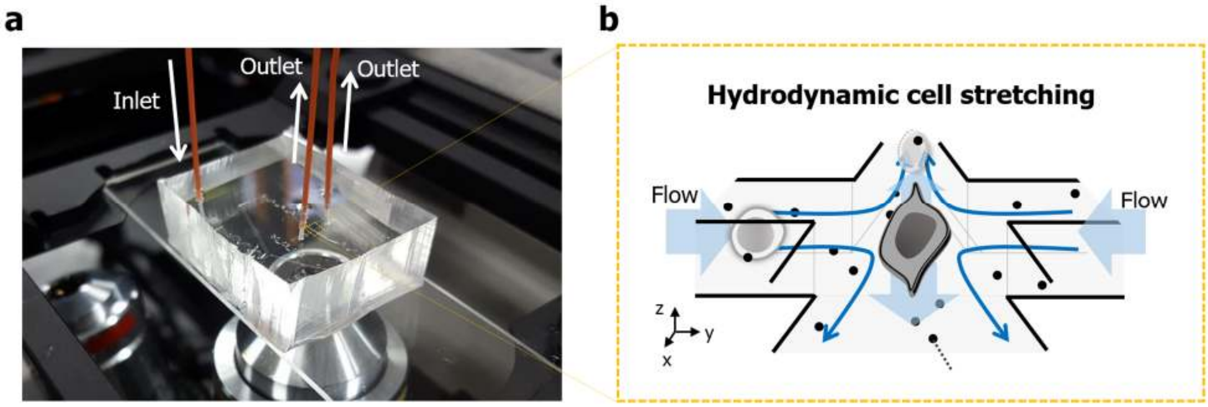

Figure S1. Platform layout. (a) A photograph of a microfluidic device which consists of a standard single-layer PDMS and a 3”x1” glass slide, and (b) A schematic of the design and operating principles for hydrodynamic cell deformation.

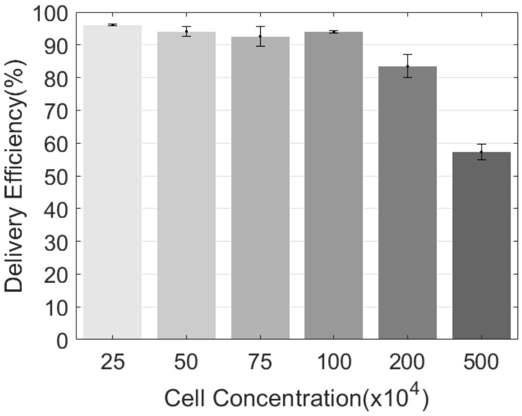

Figure S2. Delivery efficiency as a function of sample concentration. The delivery efficiency decreased as the sample concentration increased to greater than 100 × 10^4 cells/mL. All error bars indicate standard deviations (*N* = 3).

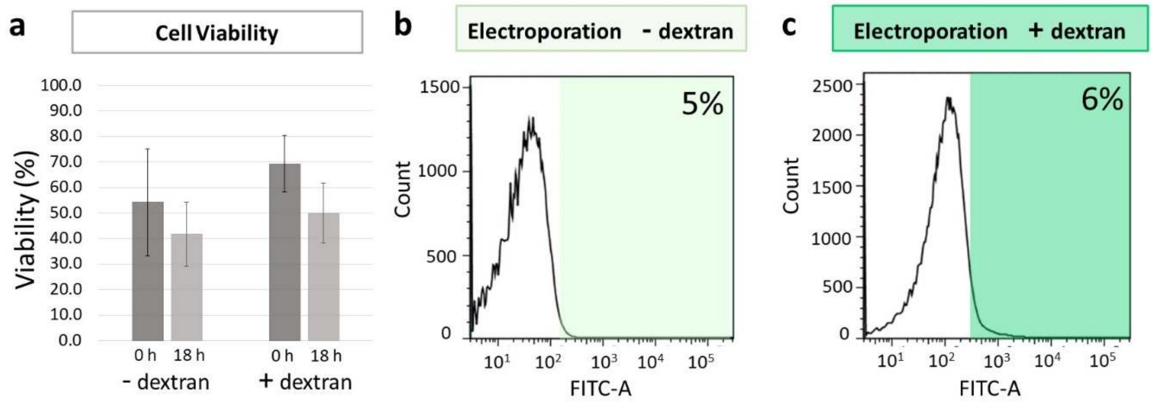

Figure S3. Delivery efficiency and cell viability of electroporation of K562 cells with 3–5 kDa FITC-dextran. (a) Cell viability is shown for electroporated K562 cells with and without FITC-dextran at 0 and 18 h. All error bars indicate standard deviations (*N* = 3). (b) Threshold of electroporated K562 cells without FITC-dextran. The top 5% threshold is shaded in light green. (c) Efficiency of electroporation of K562 cells with FITC-dextran. Efficiency is shaded in darker green.

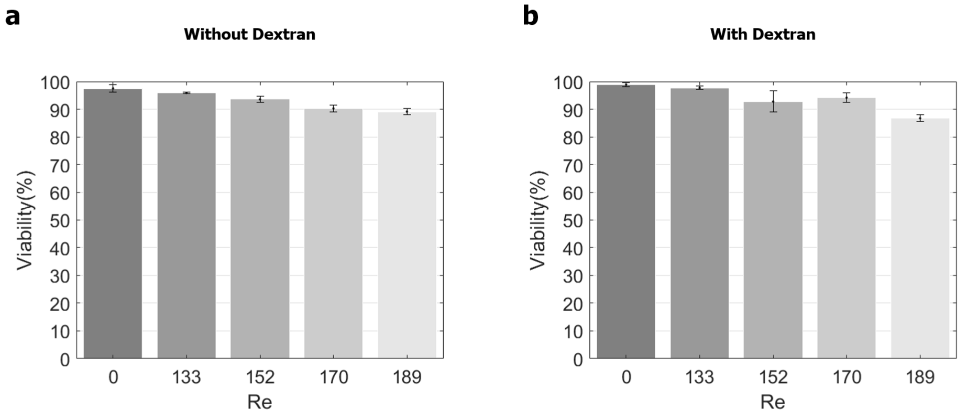

Figure S4. Cellular viability *vs.* Reynolds numbers tested (a) without dextran and (b) with dextran. All error bars indicate standard deviations (N = 3).

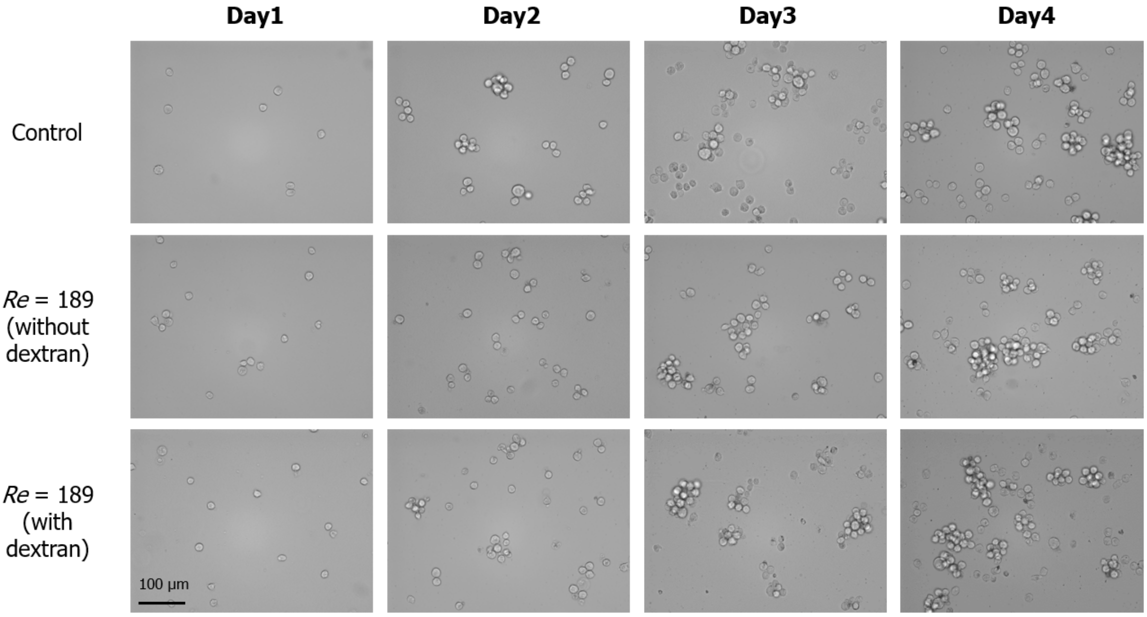

Figure S5. Cell (K562) viability. (Top row) Control cells and **(middle row)** cells collected after processing without dextran and **(Bottom row)** with dextran after processing using the presented platform at *Re* = 189. For all cases, the cells were cultured up to day 4.

Supplemental Tables

Table S1. Sequence of M13mp18 scaffold DNA (7249 bases, 5’ -> 3’).

1	AATGCTACTACTATTAGTAGAATTGATGCCACCTTTTCAGCTCGCGCCCCAAATGAAAAT
61	ATAGCTAAACAGGTTATTGACCATTTGCGAAATGTATCTAATGGTCAAACTAAATCTACT
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241	TCCGCAAAAATGACCTCTTATCAAAAGGAGCAATTAAAGGTACTCTCTAATCCTGACCTG
301	TTGGAGTTTGCTTCCGGTCTGGTTCGCTTTGAAGCTCGAATTAAAACGCGATATTTGAAG
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421	CAGGGTAAAGACCTGATTTTTGATTTATGGTCATTCTCGTTTTCTGAACTGTTTAAAGCA
481	TTTGAGGGGGATTCAATGAATATTTATGACGATTCCGCAGTATTGGACGCTATCCAGTCT
541	AAACATTTTACTATTACCCCCTCTGGCAAAACTTCTTTTGCAAAAGCCTCTCGCTATTTT
601	GGTTTTTATCGTCGTCTGGTAAACGAGGGTTATGATAGTGTTGCTCTTACTATGCCTCGT
661	AATTCCTTTTGGCGTTATGTATCTGCATTAGTTGAATGTGGTATTCCTAAATCTCAACTG
721	ATGAATCTTTCTACCTGTAATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATTTT
781	TCTTCCCAACGTCCTGACTGGTATAATGAGCCAGTTCTTAAAATCGCATAAGGTAATTCA
841	CAATGATTAAAGTTGAAATTAAACCATCTCAAGCCCAATTTACTACTCGTTCTGGTGTTT
901	CTCGTCAGGGCAAGCCTTATTCACTGAATGAGCAGCTTTGTTACGTTGATTTGGGTAATG
961	AATATCCGGTTCTTGTCAAGATTACTCTTGATGAAGGTCAGCCAGCCTATGCGCCTGGTC
1021	TGTACACCGTTCATCTGTCCTCTTTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTGACC
1081	GTCTGCGCCTCGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTCGACACAATTTAT
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1261	GTGGCATTACGTATTTTACCCGTTTAATGGAAACTTCCTCATGAAAAAGTCTTTAGTCCT
1321	CAAAGCCTCTGTAGCCGTTGCTACCCTCGTTCCGATGCTGTCTTTCGCTGCTGAGGGTGA
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1741	TGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAAACTCAGTGTTACGGTACAT
1801	GGGTTCCTATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTT
1861	CTGAGGGTGGCGGTTCTGAGGGTGGCGGTACTAAACCTCCTGAGTACGGTGATACACCTA
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2101	AAGGCACTGACCCCGTTAAAACTTATTACCAGTACACTCCTGTATCATCAAAAGCCATGT
2161	ATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTGGCTTTAATGAGG
2221	ATTTATTTGTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATG
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Table S2. Sequence of staple DNA strands for NT.

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NT-17	AGATAGGACGGTAAGTAAAGATTCAAAAGATGGTTACCAGGC
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NT-22	AACGCGCGCTTTCATAGTAGCATTAACAGAGGCATAAAAGAA
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NT-28	CAAGCTTGGAAGGGGATAAGAGGTCATTAAGCAAACGATAGT
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NT-36	CCACCAGGTCTGTCCACCAGTAGCACCATACCGAAAGGGCTT
NT-37	ACACCGCTGAGAAGCAATGAAACCATCGCAATAATTAATTTA
NT-38	GAAAAATCCGATTAAATCAAGTTTGCCTCGCTAATTAAAGTA
NT-39	CCCTCAAGTGCTTTCGGCATTTTCGGTCGAATTAAACAATAA
NT-40	AGGAATTTACAGGGTTTCATAATCAAAACAGAGAGATCAACA
NT-41	ACAACTACGCTGCGCGCCTCCCTCAGAGCGATTTTTCCTAAT
NT-42	GATTTAGCGAAAGGAGCCACCACCCTCAAAAATAATCTTTCC
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NT-44	GTAACATTAAATCGGGCCTTGATATTCATGCTATTGGAATCA
NT-45	GCGGAATCACCCAAAATGGAAAGCGCAGCCCGACTAGGCTTA

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NT-86	AGAGCTTTACCCTGCAACAACCATCGCCTGGGATTCCCCGGG
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NT-93	TAATTACAATAGTGTGAATGGCTATTAGGCCTGAGTCATTAA
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NT-102	TCGAGAACGTAAAACCGAACGTTATTAAGCCCCCGGTTGAGG
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NT-122	TTAAGAAGCAAAATCATCACGCAAATTAAAATACCCCCTTAG
NT-123	AGAAACAACGTCACTGTTTTTATAATCAGGCGGTCGAATAAC
NT-124	AGATAACGCGACAGAAGGGATTTTAGACAGCCAGCCCTTTTT
NT-125	CCCTGAATTTTCATCCTCGTTAGAATCACCTCAAAAGAAAAC
NT-126	TAAAAACGCCATCTCGCGTACTATGGTTAATCAACTTTCAAT
NT-127	ACGTCAACCGGAACCGTAACCACCACACCTTTAGGTTGAATA
NT-128	TATTATTCCCTCAGAGCGGGCGCTAGGGATAATACCTTTTAC
NT-129	TCTTTCCCCAGAGCGCCGGCGAACGTGGATTCGACGATTTTC
NT-130	CAGCTACGACGATTGAACCCTAAAGGGATTTTAAACAAAATT
NT-131	GGTTTTGAAGCCAGATCAAGTTTTTTGGAACCACCGATTATA
NT-132	ACCGGATGATGATAGACTCCAACGTCAAAGAGATCCCGTTCT
NT-133	GCATAGGGTGCCTTGTTGTTCCAGTTTGAGCAAACAAAGGCC
NT-134	CCAACTTTGCCTATATCCCTTATAAATCTGTCAATCAATGCC
NT-135	GGAACGAAGAGGCTCAGGCGAAAATCCTAAAACAGCGCAAGG
NT-136	AAATTGTTTTTGCTCTGAGAGAGTTGCATTAATATTATGACC
NT-137	GCGCGAAATATAAGCAGTGAGACGGGCAGCTCATTAAGCCTC
NT-138	TACACTAGGTTTAGGGCGGTTTGCGTATCGTCTGGAATCATA
NT-139	CCACTACCCACCCTTCGTGCCAGCTGCAGAGCGAGTGGCATC

NT-140	TTTCATGCCAATAGATTGCGTTGCGCTCCGGATTGCCTGTTT
NT-141	GAGGGTAGTACAAATGTAAAGCCTGGGGCGCATCGATTTAGT
NT-142	TGCGGGATAGTTAGCCGCTCACAATTCCAGTATCGCATTCCA
NT-143	ATATTCGTTAGTAATCGTAATCATGGTCCACCGCTCATGTTT
NT-144	TGCGCCGTCAACAGTGCAGGTCGACTCTATTCAGGATGGCTT
NT-145	TGCTTTCGGAATTGCACGACGTTGTAAACTCTTCGGTACCTT
NT-146	GGCTCCAAAAGGAGCTTCAAA
NT-147	GGAATAAGTTTACAATCGTCTGAAATGGATT
NT-148	TGGTTTATACATACTAAATTTAATGGTTGGTTATAGCCAACA
NT-149	TTGAGGGTTAAGACCGTTAAATAAGAATATAGGTCACGTGGC
NT-150	AGGTGAAGGAAACGAGCCTGTTTAGTATATTAAGATGCGCGA
NT-151	AGAGCCAAAGTAAGATAAAGCCAACGCTTAATTTTGAACGAA
NT-152	GCCGGAAATGAAATATATTTAACAACGCTGTGAGTAGTATTA
NT-153	ATCAGTACCACAAGCGAGCCAGTAATAATGAATTAAGCAAAT
NT-154	TAGCGCGCAAAGTCAGTAATTCTGTCCAAACATCATATCAAA
NT-155	AGCGTTTAGGGAAGTAATGCAGAACGCGTTATTCAAGTTGAA
NT-156	GCCACCAAAATGAAAACAAGAAAAATAAGATTGCTAGCACTA
NT-157	ACCGCCATATCCCAAAACCAATCAATAAACAGTACATTTGAG
NT-158	ACCACCAAGAGCCTACGGGTATTAAACCTTGCGTAAACTCGT
NT-159	CAGGTCAAATTTTAGCCGTTTTTATTTTACCATATAGTTTGA
NT-160	CTCATTAAAGCCTTAGCAAGCAAATCAGTTGTTTGAGAAGGA
NT-161	GTTCCAGAAGAGGCGTTTTAGCGAACCTTCTCTGAACTACGT
NT-162	GGCTTTTATTCATTGTGAATAAGGCTTGTATTCAATACAAAG
NT-163	GGGGTCACTGGCTGTAAATTGGGCTTGAGGGTGAGAAGAGAA
NT-164	TGCCCCCTGAAAGATGAATTACCTTATGTTAAATGCATATGT
NT-165	AGTATTAGGCGCAGGTCAGGACGTTGGGATTTCAAGAAGATT
NT-166	AGCGGGGGTCGAAATAACGGAACAACATAAAACATTTTGTTA
NT-167	AGGGTTGACAAAGTAGATTTAGGAATACAGCAATATTTTAAC
NT-168	CTCAGGAAAACACTCCAAAAGGAATTACTCCAATACCTTCCT
NT-169	AGAACCGGAAGGCAACCCTCGTTTACCAGAAAAGGTAACAAC
NT-170	AGCAAGCAGGAAGTGGCTTTTGCAAAAGTCAATAAACCGTAA
NT-171	GTCACCAGCAACGGATGTTTAGACTGGACGAGTAGTAACCGT
NT-172	GCCCTCATCGTCACAATATTCATTGAATGAAGTTTGCCTCAG
NT-173	CCAGACGGTCGCTGAAACGAGAATGACCAGCTCAATCTGGTG
NT-174	ACAACTTACAATGAACTATTATAGTCAGTTTGCGGCTGCGCA
NT-175	AACTAAAGAGGTGAAAGAGGAAGCCCGATTAGAGACTATTAC

Table S3. Sequence of staple DNA strands for DO.

Name	Sequence (5’ -> 3’)
DO-1	GCCAGTTATAATTTCAACTTTATTCATCAAGAG
DO-2	AGATAGGGTTGACACCAGAACGAGTCAAATCAACGTAA
DO-3	CCAGTTTGGTGATGGTGGTTCCGAAATCGGCACCTGGCCCT
DO-4	GGACTCCAAAGACGGGAGAATTAACTGAGCAGGCGAA
DO-5	CCAACGCTATTTTAAGAACTGGCAGATGAACGGTGT
DO-6	TATCCCAATTTTTCACCAGTGAGACAAAGCCTGGGGTGCCT
DO-7	AATCCTGTTAACAAGAGTCCACTATTAACAACATT
DO-8	GCGCATTCGTCAAAGGGCGAAAAAGGGAAGAAAAATCTAGATACATAAC
DO-9	ATAACATAAAAAATATCAGAGAGATAACCCACATTAATGAATCG
DO-10	ACGTCAAAAATGGGGAGAGGCGGTTTGCTCACTGCCCGC
DO-11	GGTGGTTTTTCCCAAATAAGAAACGGCCTAATTT
DO-12	TGCCCTTCACCGAAATCCCTTATAAATCAAACATATTATT
DO-13	GAGAGAGACCAGAAGGAAACCGAGGAACACAACATACGAGC
DO-14	ACGCTGGTTTGCCCCAACACCCTGAATCTTACCGAAGC
DO-15	GCCAACGCGCGAAAATAGCAGCCTTGAATCTTA
DO-16	ACATTAATTGCGTTGCGCGTATTGGGCGCCAG
DO-17	AATGAGTGAGCTCGAATTCGTAATCGTCACCGACTTGAGCCTTCGGTCA
DO-18	CGGAAGCATAAAGTGTGGGCAACAGCTGAT
DO-19	GCCGAACAAAGTTTTGCAGCAAGCGGTCC
DO-20	CCTTTTTAAGAACGCAGTATGTTAGCAAACGGAATAA
DO-21	ATAGCAATAGCTACAAAGTCAGAGGGTAATTGAGCGCTACAGGGAA
DO-22	ATAATAAGAGCGTGCTGCAAGGCGATTTTGGGAAG
DO-23	TGCCAGCTGCAAGAATTGAGTTAAGCCCA
DO-24	TTTCCAGTCGGGCGACGGCCAGTGCCAAGCCGGAAACG
DO-25	GGCATGATTATTCATATGGTTTACCACATTAAATGTGAGCGGAGTGTAC
DO-26	ATACATAAAGGTCAGCTGGCGAAAGGGGGATAAGAAACAATGAA
DO-27	CAGGGTTTTCCCAGTCGCAAAGCG
DO-28	GGTCGACTCTAGAGGGCAAAATCACCAGTAGCGCCTTTAG
DO-29	AATTATCACCATGGTCATAGCTGTTTCCTGTGTGAAATTTTGACGGA
DO-30	AATTATTCAATCAGCTCATTTTTTATATTTAAATTGTAACAAAGGCT
DO-31	AGGTAAATAGTTATCCGCTCACAATTCCAACGCAATAATCGACATTC
DO-32	AACCGATTGTAATTCGCGTCTGGCTAATCAG
DO-33	AATAGAAAAAGACTCCTTATTAAAGTAAGCAGATA
DO-34	GTTTATTTTGGGAACAAACGGCGACCGTTCCAGTAAGCTGCCCCCT
DO-35	CGCTATTACGCGGCAACATATAACGTTGGTG
DO-36	GGCGATCGGAGTTTGAGGGGACGAGCAGGTCAGACGATTATACTTTT
DO-37	CCATTCGCCCGCACTCCAGCCAGCACCACCACCAGAGCCAATTTTTA
DO-38	TCACCAATGAAATGCCGGAAACCAGACGACGTTGTAAAAAAACCTGTCG
DO-39	TCGGCATTATTTGGGAATTAGAGCCAATCCCCGGGTACCGAGCTAACTC
DO-40	TAGCCCCCTTATCGCATTAAATTTTTGTTAATTAAAGGTG
DO-41	CTTTCATCAAGCGCCAAAGACAAAAGGGAACGGAATACCCAAAAGAACT
DO-42	ATGGGATAGGTCAAAGAAACGCAAAGACACCACGTAGAAAATAC
DO-43	TAGATGGTCCTCATTAAAGCCAAGTATTAAGA
DO-44	CCTCAGGAAGATATTCAGGCTGCGCAACTGAAGTTGGGTAACGC

DO-45	CAGCACCGTACCGCCACCCTCAGAGAATGTGTAGGTAAAGAGTGGCATC
DO-46	AGAATCAAGTTTACCATTACCATTAGCAAGGCTTGCATGCCTGCA
DO-47	CGTCAGACACCACCGGAACCGCCAGTCAAATCACCATCCGCCTGTAGC
DO-48	TCACCGGAACCAGAGCCTGTAGCGCGTTTTCA
DO-49	TTGTTAAAATTTAGCGTTTGCCATCTTTTCATAAATTA
DO-50	AGATTGTATAAGCAAAACCAATAGGAACGCCATCAAAAAAGGGAGGGA
DO-51	AAAAGCCCGAGAATCGATGAACGGCCTCAGAACCGCCACCAGACCGG
DO-52	TGGTAATAAGTTAATCATATGTACCCCGGTTGACTTCCTGTAGCCAG
DO-53	CTTTTGATGATACAGAGTAACAACCCGTCGGATTCTCCGTGTCACAATC
DO-54	ACAAACAAATAAAGCGCATCGTAACCGTGCATCTGCCTGCGGGCCTCTT
DO-55	TTGACAGGAGGTTGAGCGACAGTATCGG
DO-56	CAGAGCCGCCACCAGATTTCCGGCACCGCTTCTGGCCATCGATAG
DO-57	ATGCCGGATGTACCGTAACACTGCCAGACGTTAGTAAAGAATAATA
DO-58	ATCAGGTCCCACCCTCATTTTCATAAACAACT
DO-59	AACTAGCATGTCTTAACGGGGTCAG
DO-60	TGCCTTGAAATAGGTGTATCACCTACCTTTAATTGCTCAGCAAAGCG
DO-61	GCCTATTTGGATAAGTGCCGTCGGGATGGCTTAGAGCTAAAATCAG
DO-62	CTGAAACATGAAGAATGGAAAGCGCAGTCTCTGAATTTGATTGACCGTA
DO-63	GGCTGAGACTCCAAAAACATTATGACCCTGTAGGCCTTGATATTC
DO-64	GCGGGAGAATAAAGCCTCAGAGCGGAAGTTT
DO-65	GAACCCTCTAAATCATACAGGCACGAACGAGTAGATTTGCTTGATAC
DO-66	AAGGCCGGAGACTCCCTCAGAGCCGCCACCCTCAGAAATCAGTAGCGAC
DO-67	GTACAAACTACAAAATATGATATTCAACCGTTCTAGCTGATAATCAAAA
DO-68	AATAGGAACCCAGAGGGTAGCTATTTTTGAGAGATCTAACGTTAATATT
DO-69	CCCTCAGAGCCAATTGCCTGAGAGTCTGGAGCAAACAACAAAAACAGGA
DO-70	GTATAGCCCGGGTAACAGTGCCCGTATAAACAGTTAAGTCATACATGG
DO-71	GATTAGGATCTCAACATGTTTTAATGAGGCTTGC
DO-72	CAAAATTAAGCAAGCCTTTATTTCAACGCAAGGATAAAGCCGCCAGCA
DO-73	CATTAACATCCAAATATATTTTAAATGCAATGCCTGAGTCCACCACCCT
DO-74	AATTCTACAAATGGTCAATAACTTATCAGCTTGCTTTCGCATGAGGAAG
DO-75	ATTCCACAGATTTGGGGCGCGAGCTGAAAAGTTCAAAAGGGTGAGA
DO-76	TTCAACAGTTTTTCGAGCTTCAAAGCGAACCCTCAGAACCGCCA
DO-77	AAGCAAAGCCCGAAAGACTTCAAAACTGGATAGCGTCCAA
DO-78	CAGGATTAGAGAGGTACTCAGGAGGTTTAGTACCGCCACTAATCGTAA
DO-79	ATGCTGTAGTAGCGGGGTTTTGCTCAGTACCAGGCCGGAACCTATTATT
DO-80	CTAAAGTACGGTGTCTATAAAGCTAAATCGGTTGTACCTCAAGAGAAG
DO-81	CATTCCAACCATCGCCCACGCATAAGACAGCATCGGAACG
DO-82	TTCCCAATTCTGAGGCAAAGAATTAG
DO-83	TATATTTTCACAGCCCTCATAGTTAGCGTAAAAAGGCTC
DO-84	TCTCCAAAAACGATCTAAAGTTTTGTCGTCTTTAGTTTCGTCACCA
DO-85	ATTTTTTCAAAAACGAAAGAGGCAAAAGAATACACTAAAAACAACTAA
DO-86	AGGAATTGCTGAATTTTCTGTATGGGATTTTGCGGGATAGCAAGCCC
DO-87	GAATAGAAAGGACACTCATCTTT
DO-88	GATTGCATCATAAATATTCATTGAGAGAGGCTTTTG
DO-89	ATAGTCAGACTTTTGATAAGAGGTCATTTTTGCAGAGGGTTGATATAA
DO-90	GTCTTTACCCTTTAAACAGTTCAGAAAACGAGAAGCCGCTTTTGC
DO-91	AGGGAGTTAAAGTGACCATAAATCATAATTGCTGAATATA

DO-92	CGATAGTTTACAGAGGCTTTGAGGCGCAGACGGTCAAT
DO-93	TCTTAAACAAGTTTGACCATTAGATACATTTCGCTAATAGTAGTAG
DO-94	CAAAAGGATACGTAATGCCACTACAATTGTGTCGAA
DO-95	GACCCCCAGAATGTTTAGTATCGCGTTTTAACAGCGGAGTGA
DO-96	TACTGCGGAATCGTCAAAAAGATTAAGAGGAACTCCAACAGGT
DO-97	GGGATCGTCAAACACTATCATAACCCTCGTTTACCACATTCA
DO-98	AGGGTAGCAACGGCGCGCCGACAATGACAACATATAACAGTTGA
DO-99	TTTCCATTAAACGGGTAAAAGCCTTTAATTGTATCGGTCTGTTTAGC
DO-100	ATCGCCTGATAGAAGGCACCAACCTCGTTGAAAA
DO-101	CGAAACAAAGTACACCGGATATTCATTACCAGTAAATTGGG
DO-102	CAAAAGAAGTTTTCAGTGAATAAGAAAGATTCATCAGT
DO-103	AAAACCAAAATAGCATCCCCCTCAAATGCTGACTATT
DO-104	GTAAGAGCCCCTCAGCAGCGAAACCGATATATTCGGTCGCATATGCAA
DO-105	CATAAGGGAACCGAAATTACGAGGCATA
DO-106	CCGGAACGAGGACTAAAGACTTTTTAGGTGAATT
DO-107	ATCCGCGACCTGCATAGGCTGGCTGACCATCATTGTGAA
DO-108	TAATCTTGACAAGAAACGGAGATTTGTATC
DO-109	CAAAGCTGCTCATTGCCAGAGGGGGTAATAGTAACGATTATACCAAGCG
DO-110	TGAGATTTAGGAATACCAGACGACGATA
DO-111	ACTAATGCACGTTAATAAAACGAACTAACGGAAAGAACGT
DO-112	GCCAAAAGGACTGACCAACTTTGAAAGAGGACTCATTATACC
DO-113	ACAGACCAGGCGCTCCATGTTACTTAG
DO-114	CTTGAGATGGTTCAAAATAAACAGCAGAATAGCCCG
DO-115	ATTACAGGTAGGCTTGCCCTGACGAGAAAGTGTTGTT
DO-116	AGTCAGGACGTTCCGTCTATCATTTTATCCTTACAGAGAGA
DO-117	TTACCTTATGCGAACGAGCGTCTTTCCAGAATTTTTTGTTTA

Supplemental Movie

Supplemental Movie S1. **K562 cell deformation process.** At *R*e = 189, a stream of cells formed by inertial effects enters and deforms with large strain in the extensional flow region, creating transient pores that facilitates effective exogenous materials transport into the cell cytoplasm.